

RID: 6SEPCXY6016

Job Title:17 seq of Rhipicephalus sanguineus Juarez. Mexico

Program: BLASTN

Database: nt Nucleotide collection (nt)

Query #1: TKCJJ084-19|TKCJ012018G12|Rhipicephalus sanguineus|COI-5P Query ID:

1c1|Query_26763 Length: 658

Sequences producing significant alignments:

							Scientific
Common		Max	Total Query	E	Per.	Acc.	
Description							Name
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00 688
MF425995.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00 703
MF425994.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00 702
MF425993.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00 693
MF425992.1							
Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 690
KT906183.1							
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 690
KT906182.1							
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 14711
OM368327.1							
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 14714
OM368323.1							
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 14713
OM368322.1							
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 707
JQ737084.1							
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 658
KF437543.1							
Rhipicephalus linnaei isolate LA032-2 clone JS5930...							
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00 14715
MW429383.1							
Rhipicephalus linnaei mitochondrion, complete sequence							
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00 14711
NC_060409.1							

Accession	Species	Length	Ident	Positives	Score	E-value	Gap
Ixodidae sp. sc_01082	cytochrome oxidase subunit 1 (COI) gene,...	Ixodidae					
sp.... NA	1901042	1210	1210	100%	0.0	99.85	658
KX053537.1							
Rhipicephalus sanguineus haplotype RsanColCorL	cytochrome c...						
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690
KT906185.1							
Rhipicephalus sanguineus haplotype RsanColTolC	cytochrome c...						
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690
KT906184.1							
Rhipicephalus sanguineus voucher CAS-T065	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	658
KF200113.1							
Rhipicephalus linnaei isolate SC931-1 clone JS5927...							
Rhipicephalu... NA	2138177	1210	1210	100%	0.0	99.85	14717
MW429382.1							
Rhipicephalus sanguineus voucher D0-311	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1205	1205	99%	0.0	99.85	658
KX360367.1							
Rhipicephalus sanguineus haplotype RsanColSamCM	cytochrome c...						
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	690
KT906186.1							
Rhipicephalus sanguineus voucher GRP5-154	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	658
KF200112.1							
Rhipicephalus sanguineus mitochondrion, complete genome							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	14714
JX416325.1							
Rhipicephalus sanguineus isolate T95D15	cytochrome c oxidase...						
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	100.00	661
MZ401443.1							
Rhipicephalus sanguineus isolate T81D7	cytochrome c oxidase...						
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	100.00	661
MZ401441.1							
Rhipicephalus sanguineus isolate T79D2	cytochrome c oxidase...						
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	99.85	664
MZ401440.1							
Rhipicephalus sanguineus isolate WZ004	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1190	1190	97%	0.0	100.00	664
MG969507.1							
Rhipicephalus sanguineus voucher GRP5-150	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1188	1188	98%	0.0	99.69	649
KF200084.1							
Rhipicephalus sanguineus isolate LIC6084B	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	768
KX383817.1							
Rhipicephalus sanguineus isolate T91D13	cytochrome c oxidase...						
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	657
MZ401442.1							
Rhipicephalus sanguineus isolate T63D1	cytochrome c oxidase...						
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	661
MZ401438.1							
Rhipicephalus sanguineus isolate WZ003	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969506.1							

Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632	1184	1184	97%	0.0	99.84	664		
MG969505.1								
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632	1184	1184	97%	0.0	99.84	664		
MG969504.1								
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632	1179	1179	97%	0.0	99.69	644		
KF200096.1								
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...								
Rhipicephalu... NA 2138177	1177	1177	100%	0.0	98.94	658		
OM984983.1								
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632	1177	1177	96%	0.0	100.00	802		
JX416302.1								
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632	1177	1177	96%	0.0	100.00	802		
JX416298.1								
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidas...								
Rhipicephalu... brown dog tick 34632	1177	1177	97%	0.0	99.69	670		
HM193873.1								
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632	1175	1175	97%	0.0	99.69	768		
KX383820.1								
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632	1171	1171	97%	0.0	99.53	724		
KX383816.1								
Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase...								
Rhipicephalu... NA 2138177	1171	1171	100%	0.0	98.78	658		
OM984984.1								
Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase...								
Rhipicephalu... NA 2138177	1171	1171	100%	0.0	98.78	658		
OM984974.1								
Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase...								
Rhipicephalu... NA 2138177	1171	1171	100%	0.0	98.78	658		
OM984973.1								
Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632	1171	1171	96%	0.0	99.84	802		
JX416308.1								
Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632	1171	1171	96%	0.0	99.84	802		
JX416304.1								
Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632	1171	1171	96%	0.0	99.84	802		
JX416300.1								
Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632	1171	1171	96%	0.0	99.84	802		
JX416299.1								
Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632	1171	1171	96%	0.0	99.84	802		
JX416297.1								
Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632	1171	1171	96%	0.0	99.84	802		
JX416296.1								

Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subun...									
Rhipicephalu... brown dog tick JX416293.1	34632	1171	1171	96%	0.0	99.84	802		
Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase...									
Rhipicephalu... brown dog tick MZ401439.1	34632	1171	1171	96%	0.0	100.00	650		
Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase...									
Rhipicephalu... brown dog tick KX383802.1	34632	1166	1166	96%	0.0	99.69	763		
Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984979.1	2138177	1166	1166	100%	0.0	98.63	658		
Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984968.1	2138177	1166	1166	100%	0.0	98.63	658		
Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subun...									
Rhipicephalu... brown dog tick JX416295.1	34632	1166	1166	96%	0.0	99.69	802		
Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subun...									
Rhipicephalu... brown dog tick JX416294.1	34632	1166	1166	96%	0.0	99.69	802		
Rhipicephalus sanguineus isolate sanguineus0926 cytochrome...									
Rhipicephalu... brown dog tick MH513252.1	34632	1162	1162	99%	0.0	98.77	658		
Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984985.1	2138177	1160	1160	100%	0.0	98.48	658		
Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984978.1	2138177	1160	1160	100%	0.0	98.48	658		
Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984977.1	2138177	1160	1160	100%	0.0	98.48	658		
Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984975.1	2138177	1160	1160	100%	0.0	98.48	658		
Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984971.1	2138177	1160	1160	100%	0.0	98.48	658		
Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984970.1	2138177	1160	1160	100%	0.0	98.48	658		
Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984969.1	2138177	1160	1160	100%	0.0	98.48	658		
Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subun...									
Rhipicephalu... brown dog tick JX416301.1	34632	1160	1160	96%	0.0	99.53	802		
Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrom...									
Rhipicephalu... brown dog tick MT010523.1	34632	1155	1155	95%	0.0	99.68	642		
Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase...									
Rhipicephalu... NA OM984988.1	2138177	1155	1155	100%	0.0	98.33	658		

Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658	
OM984976.1								
Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632		1155	1155	96%	0.0	99.37	802	
JX416303.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA	2138177	1153	1153	98%	0.0	98.77	826	
MF426003.1								
Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidas...								
Rhipicephalu... brown dog tick 34632		1146	1146	96%	0.0	99.21	665	
HM193874.1								
Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1140	1140	94%	0.0	99.84	630	
KX757914.1								
Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1136	1136	97%	0.0	98.60	768	
KX383800.1								
Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1131	1131	93%	0.0	99.68	744	
KX383796.1								
Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1127	1127	96%	0.0	98.59	698	
KX383798.1								
Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1125	1125	97%	0.0	98.29	768	
KX383814.1								
Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1122	1122	96%	0.0	98.43	763	
KX383801.1								
Rhipicephalus sanguineus isolate 400 cytochrome c oxidase...								
Rhipicephalu... brown dog tick 34632		1120	1120	97%	0.0	98.28	657	
MW558150.1								
Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604	
MZ726445.1								
Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604	
MZ726444.1								
Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604	
MZ726443.1								
Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604	
MZ726442.1								
Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604	
MZ726441.1								
Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604	
MZ726440.1								
Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604	
MZ726439.1								

Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726438.1							
Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726437.1							
Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726436.1							
Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726435.1							
Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726434.1							
Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726433.1							
Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726432.1							
Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726431.1							
Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726430.1							
Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726449.1							
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726429.1							
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726428.1							
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726427.1							
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726426.1							
Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1092	1092	91%	0.0	99.33	638
KX360338.1							

Alignments:

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
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Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACAACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 378 ATCACAACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
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Sbjct 498 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 558 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome
c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425994.1 Length: 703
>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome

c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425996.1 Length: 703
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 500 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 560 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
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>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccctTATCATCAAATTT 360
      |||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 500 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 560 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
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>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome
c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 500 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 560 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
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>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 498 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 558 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
|||||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 498 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 558 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome
Sequence ID: OM368327.1 Length: 14711
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccctTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome
Sequence ID: OM368323.1 Length: 14714
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccctTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome
Sequence ID: OM368322.1 Length: 14713
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 24 to 681

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 	60
Sbjct	24	GACAATATACTTAATTTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	83
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 	120
Sbjct	84	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	143
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 	180
Sbjct	144	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	203
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 	240
Sbjct	204	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	263
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 	300
Sbjct	264	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	323
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 	360
Sbjct	324	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	383
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 	420
Sbjct	384	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	443
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATATTGTAAATATACGATCCATTGGAAT 	480
Sbjct	444	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATATTGTAAATATACGATCCATTGGAAT	503
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 	540
Sbjct	504	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	563
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 	600
Sbjct	564	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	623
Query	601	TACATCATTTCTTTGACCCCTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 	658

Sbjct 624 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 681

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	600

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Sbjct  541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600
Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658

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>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome
Sequence ID: MW429383.1 Length: 14715
Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

```

Query   1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
        |||
Sbjct   45    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  104

Query   61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
        |||
Sbjct   105   AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  164

Query   121    AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG  180
        |||
Sbjct   165    AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG  224

Query   181    AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
        |||
Sbjct   225    AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  284

Query   241    AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
        |||
Sbjct   285    AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  344

Query   301    ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
        |||
Sbjct   345    ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  404

Query   361    ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
        |||
Sbjct   405    ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  464

Query   421    TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480
        |||
Sbjct   465    TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  524

Query   481    AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
        |||
Sbjct   525    AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  584

Query   541    ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600

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Sbjct	585	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus linnaei mitochondrion, complete sequence
Sequence ID: NC_060409.1 Length: 14711
>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome
Sequence ID: MW429381.1 Length: 14711
Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	405	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	 TTCAATTTTAGGTGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

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Sbjct  525  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  584
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  585  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  644
Query  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  645  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  702

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>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial
Sequence ID: KX053537.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccCTTATCATCAAATTT  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  361     ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420

Query  421     TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421     TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480

Query  481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

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Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78		AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198		AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT

Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	497

Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KF200113.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTTGTAAATATACGATCCATTGGAAT	480

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Sbjct  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
        |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
        |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||
Sbjct  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658

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>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome

Sequence ID: MW429382.1 Length: 14717

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
        |||
Sbjct  45    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  104
Query  61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT  120
        |||
Sbjct  105   AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT  164
Query  121   AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
        |||
Sbjct  165   AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  224
Query  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
        |||
Sbjct  225   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  284
Query  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
        |||
Sbjct  285   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  344
Query  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
        |||
Sbjct  345   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  404
Query  361   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
        |||
Sbjct  405   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC  464
Query  421   TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480

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Sbjct	465		TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	524
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	585		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	644
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KX360367.1 Length: 658
Range 1: 4 to 658

Score:1205 bits(652), Expect:0.0,
Identities:654/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

Query	4		AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Sbjct	4		AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Query	64		CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Sbjct	64		CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Query	124		TGTAACAGCACATGCATTTATTATAAAttttttTATAGTTATACCAATTATAATCGGAGG	183
Sbjct	124		TGTAACAGCACATGCATTTATTATAAAttttttTATAGTTATACCAATTATAATCGGAGG	183
Query	184		ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Sbjct	184		ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Query	244		AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Sbjct	244		AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Query	304		AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATC	363
Sbjct	304		AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTTATC	363
Query	364		ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTC	423
Sbjct	364		ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTC	423

Query	424	AATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAAC	483
Sbjct	424	AATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAAC	483
Query	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543	
Sbjct	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543	
Query	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATAC	603
Sbjct	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATAC	603
Query	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	

>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	77	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137	
Query	121	AATTGTAACAGCACATGCATTTATTATAA	atTTTTTTtATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAA	TTTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	257	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	437

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557	
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675	

>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200112.1 Length: 658
>Rhipicephalus sanguineus voucher DO-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360403.1 Length: 658
Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAAC	TTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAAC	TTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	TTTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	240	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus mitochondrion, complete genome

Sequence ID: JX416325.1 Length: 14714

Range 1: 1185 to 1842

Score:1205 bits(652), Expect:0.0,

Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCCTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATTATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT	1842

>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60
Query	74	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133
Sbjct	61	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120
Query	134	CATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300
Query	314	GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA	373

Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433
Sbjct	361	CCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434	GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540
Query	554	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	645

>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401441.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60
Query	74	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133
Sbjct	61	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120
Query	134	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300
Query	314	GGAGCAGGTACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGA	373

Sbjct	301		GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374		CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433
Sbjct	361		CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434		GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421		GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494		ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481		ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540
Query	554		GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	613
Sbjct	541		GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	600
Query	614		GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645	

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MZ401440.1 Length: 664
 Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,
 Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11		TTAATTTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	1		TTAATTTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	60
Query	71		GAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	61		GAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	120
Query	131		GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	121		GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	180
Query	191		AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181		AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251		ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	241		ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	300

Query	311	TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	301	TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	360
Query	371	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550
Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	540
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC	610
Sbjct	541	CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC	600
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	648

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1190 bits(644), Expect:0.0,
Identities:644/644(100%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300

Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTAGGTG	420
Query	435	CAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 1 to 649

Score:1188 bits(643), Expect:0.0,
Identities:647/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

Query	10	CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT	69
Sbjct	1	CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT	60
Query	70	AGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC	129
Sbjct	61	AGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC	120
Query	130	AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG	189
Sbjct	121	AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG	180
Query	190	AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA	249
Sbjct	181	AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA	240
Query	250	TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA	309

Sbjct	241	TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA	300
Query	310	ATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTA	369
Sbjct	301	ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA	360
Query	370	CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT	429
Sbjct	361	CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT	420
Query	430	AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA	489
Sbjct	421	AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA	480
Query	490	ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT	549
Sbjct	481	ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT	540
Query	550	ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT	609
Sbjct	541	ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT	600
Query	610	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	649

>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316

Sbjct	241		TTTTGGTTACTTCCTCCTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317		GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301		GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377		TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361		TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437		ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421		ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497		CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481		CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557		TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541		TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617		CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240

Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240

Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254

Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254

Sbjct	181	 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	 GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	 CAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	 TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	 TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	 ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180

Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGAGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGAGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	6	TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC	65
Sbjct	1	TATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCC	60
Query	66	GCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTG	125
Sbjct	61	GCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTG	120
Query	126	TAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGAT	185
Sbjct	121	TAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGAT	180

Query	186	TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAA	245
Sbjct	181	TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCACGAATAA	240
Query	246	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	305
Sbjct	241	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	300
Query	306	TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCAC	365
Sbjct	301	TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCAC	360
Query	366	ACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	425
Sbjct	361	ACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	420
Query	426	TTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAA	485
Sbjct	421	TTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAA	480
Query	486	TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	545
Sbjct	481	TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	540
Query	546	CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT	605
Sbjct	541	CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT	600
Query	606	CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA	649
Sbjct	601	CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA	644

>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 1 to 658

Score:1177 bits(637), Expect:0.0,
Identities:651/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGAATACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416302.1 Length: 802

>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416305.1 Length: 802

>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416306.1 Length: 802

>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416307.1 Length: 802

Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,

Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 1 to 642

Score:1177 bits(637), Expect:0.0,

Identities:642/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

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Query 15 TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 1 TTTTGGGA-CATGATCCGG-ATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 58

Query 75 TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 59 TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 118

Query 135 ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 119 ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 178

Query 195 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 179 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 238

Query 255 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 239 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 298

Query 315 GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 299 GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 358

Query 375 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG 434
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 359 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG 418

Query 435 CAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 419 CAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 478

Query 495 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 479 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 538

Query 555 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 539 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 598

Query 615 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 599 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
```

>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383820.1 Length: 768
Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,
Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
|||||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
|||||
Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
|||||
Sbjct 121 GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
|||||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
|||||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
|||||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 436
|||||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
|||||
Sbjct 421 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
|||||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 616
|||||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT 642
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>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383816.1 Length: 724
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
|||||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
|||||
Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
|||||
Sbjct 121 GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
|||||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
|||||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
|||||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 436
|||||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
|||||
Sbjct 421 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
|||||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 616
|||||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT 642
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>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658

Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,

Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGAGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| |||||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGAATACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||||||||||||||||||| |||||||||||| ||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCTGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAACATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416304.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      |||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT  120

Query  142  TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||
Sbjct  421  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct  601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637
```

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query 22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
          |||
Sbjct 1   AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
          |||
Sbjct 61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
          |||
Sbjct 121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT 180

Query 202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
          |||
Sbjct 181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
          |||
Sbjct 241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
          |||
Sbjct 301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
          |||
Sbjct 361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
          |||
Sbjct 421  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
          |||
Sbjct 481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
          |||
Sbjct 541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637
```

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416299.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416297.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAAttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAcCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      ||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTACTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||||||||||||||||||||||||||||||||||
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Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT  141
      |||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT  120

Query  142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||
Sbjct  121  TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||
Sbjct  421  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
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      ||||||||||||||||||||||||||||||||||
Sbjct  601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

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>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query   22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
      ||||||||||||||||||||||||||||||||||
Sbjct   1  AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query   82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
      ||||||||||||||||||||||||||||||||||
Sbjct   61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query   142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
      ||||||||||||||||||||||||||||||||||
Sbjct   121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query   202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
      ||||||||||||||||||||||||||||||||||
Sbjct   181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query   262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
      ||||||||||||||||||||||||||||||||||
Sbjct   241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query   322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
      ||||||||||||||||||||||||||||||||||
Sbjct   301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query   382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
      ||||||||||||||||||||||||||||||||||
Sbjct   361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query   442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
      ||||||||||||||||||||||||||||||||||
Sbjct   421  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query   502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
      ||||||||||||||||||||||||||||||||||
Sbjct   481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query   562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
      ||||||||||||||||||||||||||||||||||
Sbjct   541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

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Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401439.1 Length: 650
Range 1: 1 to 634

Score:1171 bits(634), Expect:0.0,
Identities:634/634(100%), Gaps:0/634(0%), Strand: Plus/Plus

Query	25	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	84
Sbjct	1	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	60
Query	85	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	144
Sbjct	61	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	120
Query	145	TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	204
Sbjct	121	TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	180
Query	205	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	264
Sbjct	181	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	240
Query	265	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	324
Sbjct	241	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	300
Query	325	AGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	384
Sbjct	301	AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	360
Query	385	TTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT	444
Sbjct	361	TTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT	420
Query	445	CATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	504
Sbjct	421	CATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	480
Query	505	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	564
Sbjct	481	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	540
Query	565	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	624
Sbjct	541	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	600

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Query   625  AGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||||||||||||||||||||||||||||||
Sbjct   601  AGGAGGTGACCCAATTCTATATCAACATTTATTT  634

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>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383802.1 Length: 763
>Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383803.1 Length: 763
>Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383804.1 Length: 763
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query   22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
        |||||||||||||||||||||||||||||||
Sbjct   1   AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query   82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
        |||||||||||||||||||||||||||||||
Sbjct   61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query   142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
        |||||||||||||||||||||||||||||||
Sbjct   121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query   202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
        |||||||||||||||||||||||||||||||
Sbjct   181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query   262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
        |||||||||||||||||||||||||||||||
Sbjct   241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query   322  TACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGT  381
        |||||||||||||||||||||||||||||||
Sbjct   301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query   382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
        ||||||||||||||||||| |||||||||||||||||||
Sbjct   361  AGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query   442  TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
        ||||||||||||||||||| |||||||||||||||||||
Sbjct   421  TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

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Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984979.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTTGTAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAACATTTGTAATATACGATCCATTGGGAT	480

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Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT  658

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>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121  AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG  180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT  360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC  420
        ||||||||||||| ||||||||||||||||||||||| ||||||||||||||| |||||||
Sbjct   361  ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTCTGCATCTTGCGGTGCTTC  420

Query   421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT  480
        |||||||||||||||| ||||||||||||||||||||||| |||||||||||||||

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Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416295.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501

Sbjct	421		TTTCATTACAAC	TATTGTAAATATA	CGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561		
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540		
Query	562		TGGCGCAATTACAATATTATTA	AACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621	
Sbjct	541		TGGCGCAATTACAATATTATTA	AACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600	
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658		
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT	637		

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420

Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658
Range 1: 6 to 658

Score:1162 bits(629), Expect:0.0,
Identities:645/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	6	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	65
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	66	AATTCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	125
Query	121	AATTGTAACAGCACATGCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	126	AATTGTAACAGCACATGCATTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGG	185
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	186	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	245
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	246	AATAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	305
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT AccccccTTATCATCAAATTT	360
Sbjct	306	ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTT ACCCCCCCTTATCATCAAATTT	365
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG CAGGTGCTTC	420
Sbjct	366	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG CAGGTGCTTC	425

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	426	TTCAATTTTAGGCGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	485
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Sbjct	486	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	545	
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAA	600
Sbjct	546	ATTATCTTTACCAGTCTTAGCTGGTGAATTACAATATTGT	TAACTGATCGAACTTTAA	605
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT	653	
Sbjct	606	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT	658	

>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984985.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420

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Sbjct  361  ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC  420
Query  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
      |||
Sbjct  421  TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
      |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
      |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT  658

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>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984978.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
      |||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60
Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
      |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
      |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
      |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
      |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
      |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT  360
Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420

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Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984977.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATGGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361		ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATTAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121		AATTGTAACAGCACATGCATTTATTATAAAttttttTATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416301.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300

Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCTATTACAATATTATTAAGTATCGAACTTTAATACATTATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT010523.1 Length: 642
Range 1: 1 to 631

Score:1155 bits(625), Expect:0.0,
Identities:629/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

Query	28	ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG	87
Sbjct	1	ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG	60
Query	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Sbjct	61	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	120
Query	148	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Sbjct	121	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	180
Query	208	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267
Sbjct	181	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	240
Query	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327

Sbjct	241	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	300
Query	328	GTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	387
Sbjct	301	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	360
Query	388	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	447
Sbjct	361	AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	420
Query	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Sbjct	421	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	480
Query	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	567
Sbjct	481	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	540
Query	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Sbjct	541	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	600
Query	628	AGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GGGTGACCCAATTCTATATCAACATTTATTT	631

>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416303.1 Length: 802

Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,

Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAATTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240

Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACCTATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1153 bits(624), Expect:0.0,
Identities:640/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	3	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATA	62
Query	71	GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	63	GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	122
Query	131	GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	123	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	182
Query	191	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250

Sbjct	183	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAAT	242
Query	251	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	243	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	302
Query	311	TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	303	TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	362
Query	371	GGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA	430
Sbjct	363	GGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA	422
Query	431	GGTGCAATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	423	GGCGCAATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAA	482
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550
Sbjct	483	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	542
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTC	610
Sbjct	543	CCAGTCTTAGCTGGTGAATTACAATATTGTAACTGATCGAAACTTTAATACATCATTC	602
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	603	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	650

>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1146 bits(620), Expect:0.0,
Identities:631/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	31	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	90
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	91	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	150
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	151	AATTGTAACAGCACATGCATTTATTATAATTTTTTTATAGTTATACCAATTATAATCGG	210
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	211		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	270
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	271		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	330
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	331		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	390
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	391		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	450
Query	421		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	451		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	510
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	511		AACAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	570
Query	541		ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	571		ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATAATATTAAGTATCGAAACTTTAA	630
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCC	636
Sbjct	631		TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC	665

>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG	98
Sbjct	1		TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG	60
Query	99		GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61		GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159		TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG	218
Sbjct	121		TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG	180

Query	219	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC	278
Sbjct	181	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC	240
Query	279	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	338
Sbjct	241	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	300
Query	339	AccccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTG	458
Sbjct	361	CTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTG	420
Query	459	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	518
Sbjct	421	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	480
Query	519	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	578
Sbjct	481	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	540
Query	579	TATTAACGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA	638
Sbjct	541	TATTAACGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA	600
Query	639	TTCTATATCAACATTTATTT	658
Sbjct	601	TTCTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383800.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383815.1 Length: 768
Range 1: 1 to 642

Score:1136 bits(615), Expect:0.0,
Identities:633/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120

Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383796.1 Length: 744
 Range 1: 1 to 618

Score:1131 bits(612), Expect:0.0,
 Identities:616/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

Query	41	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA	100
Sbjct	1	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA	60
Query	101	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttATA	160
Sbjct	61	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAATTTTTTTTATA	120

Query	161	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	220
Sbjct	121	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	180
Query	221	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	280
Sbjct	181	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	240
Query	281	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAc	340
Sbjct	241	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAC	300
Query	341	ccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	400
Sbjct	301	CCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	360
Query	401	CTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTA	460
Sbjct	361	CTACATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTA	420
Query	461	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	520
Sbjct	421	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	480
Query	521	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	580
Sbjct	481	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	540
Query	581	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT	640
Sbjct	541	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATT	600
Query	641	CTATATCAACATTTATTT	658
Sbjct	601	CTATATCAACATTTATTT	618

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383798.1 Length: 698
 Range 1: 1 to 637

Score:1127 bits(610), Expect:0.0,
 Identities:628/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141

Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383814.1 Length: 768
 Range 1: 1 to 642

Score:1125 bits(609), Expect:0.0,
 Identities:631/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136

Sbjct	61	 GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	 GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	 TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	 ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	 TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60

Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MW558150.1 Length: 657
 Range 1: 1 to 639

Score:1120 bits(606), Expect:0.0,
 Identities:628/639(98%), Gaps:0/639(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCAGGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60

Query	80	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199
Sbjct	121	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATGGATTA	180
Query	200	G TTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259
Sbjct	181	G TTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	240
Query	260	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	319
Sbjct	241	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	300
Query	320	GGTACAGGGTGAACAGTTTA cccccccTTATCATCAAATTTATCACACTACGGACCATCA	379
Sbjct	301	GGTACAGGGGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCA	360
Query	380	G TAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	439
Sbjct	361	G TAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC	420
Query	440	AATTTCAATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	499
Sbjct	421	AATTTCAATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	480
Query	500	TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	559
Sbjct	481	TTATTTGTAGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	540
Query	560	GCTGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCT	619
Sbjct	541	GCTGGTGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCT	600
Query	620	TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	639

>Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726445.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726444.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
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Sbjct	1	 GACAATATACTTAATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726441.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726440.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726438.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726437.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene,

partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726434.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726433.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726432.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      ||||
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Sbjct 601 TACA 604

>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726430.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACAACACGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACAACACGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAACATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAACATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
```

||||
Sbjct 601 TACA 604

>Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726449.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACGGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600

Query 601 TACA 604
||||
Sbjct 601 TACA 604

>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726429.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
```


Sbjct 601 TACA 604

Range 1: 1 to 604

Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

[illegible]

```

Sbjct  541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600
Query  601  TACA  604
          ||||
Sbjct  601  TACA  604

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>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```

Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121     AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC  420

Query  421     TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421     TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT  480

Query  481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query  541     ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600

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Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	600
Query	601	TACA	604	
Sbjct	601	TACA	604	

>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726426.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638
Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199
Sbjct	121	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	180
Query	200	GTTCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259
Sbjct	181	GTTCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	240
Query	260	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	319
Sbjct	241	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	300
Query	320	GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA	379
Sbjct	301	GGNACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCA	360
Query	380	GTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	439
Sbjct	361	GTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	420
Query	440	AATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	499
Sbjct	421	AATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	480
Query	500	TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCACTCTTA	559
Sbjct	481	TTATTTGTATGATCTGTTTTAATTACNGCAATTTTATTATTATTATCTTTACCACTCTTA	540

Query 560 GCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCT 619
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct 541 GCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCT 600

Query 620 T 620
 |
 Sbjct 601 T 601

Query #2: TKCJJ091-19|TKCJ012018H07|Rhipicephalus sanguineus|COI-5P Query ID:
 1c1|Query_26764 Length: 658

Sequences producing significant alignments:

							Scientific
Common		Max	Total Query	E	Per.	Acc.	
Description							Name
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 697
MF426019.1							
Rhipicephalus sanguineus haplotype III cytochrome oxidase...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 713
KU556745.1							
Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidas...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 710
MN593344.1							
Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidas...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 710
MN593343.1							
Rhipicephalus sanguineus isolate 11N cytochrome oxidase subuni...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 703
MN585197.1							
Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene,...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 793
AF132839.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 675
MF426018.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 680
MF426016.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 693
MF426013.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 679
MF426009.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							

Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690
MF426008.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	686
MF426007.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	684
MF426001.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	695
MF425997.1							
Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	658
MZ305546.1							
Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	658
MZ305545.1							
Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	676
MW152145.1							
Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	675
MW152144.1							
Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	676
MW152143.1							
Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	669
MW152142.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	692
MF426015.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	705
MF426006.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1199	1199	100%	0.0	99.54	680
MF426017.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1199	1199	100%	0.0	99.54	689
MF425998.1							
Rhipicephalus sanguineus haplotype IV cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1199	1257	100%	0.0	99.54	771
KU556746.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1194	1194	100%	0.0	99.39	684
MF426012.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	99.85	824
MF426010.1							
Rhipicephalus sanguineus haplotype II cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1190	1190	100%	0.0	99.24	787
KU556744.1							
Rhipicephalus sanguineus haplotype I cytochrome oxidase subuni...							

Rhipicephalu... brown dog tick	34632	1186	1186	98%	0.0	99.69	659
KU556743.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1182	1182	97%	0.0	99.84	812
MF426020.1							
Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1175	1175	97%	0.0	99.69	768
KX383818.1							
Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1168	1168	96%	0.0	99.69	764
KX383811.1							
Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	763
KX383807.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1164	1164	97%	0.0	99.38	809
MF426011.1							
Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1164	1164	96%	0.0	99.69	762
KX383809.1							
Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1164	1164	96%	0.0	99.69	714
KX383806.1							
Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1162	1162	96%	0.0	99.69	761
KX383805.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1160	1160	97%	0.0	99.38	654
MF425988.1							
Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	1157	1157	95%	0.0	100.00	654
KX519712.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1155	1155	95%	0.0	99.84	639
MF426002.1							
Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
MG855658.1							
Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
MG855657.1							
Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
MG855656.1							
Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
KX757910.1							
Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
KX757904.1							
Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
KX757902.1							
Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase...							

Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
KX757896.1							
Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
KX757889.1							
Rhipicephalus sanguineus isolate Rovind cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
KX757887.1							
Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
KX757879.1							
Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	636
KX519711.1							
Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1146	1146	94%	0.0	100.00	630
MW135448.1							
Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1144	1144	94%	0.0	99.84	644
MH630347.1							
Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1144	1144	94%	0.0	99.84	644
MH630346.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1144	1144	94%	0.0	99.84	635
MF426000.1							
Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
KX757905.1							
Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
KX757895.1							
Rhipicephalus sanguineus isolate Zadar cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
KX757892.1							
Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
KX757890.1							
Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
KX757888.1							
Rhipicephalus sanguineus isolate Petnica cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
KX757883.1							
Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	1140	1140	93%	0.0	100.00	629
KX519708.1							
Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
MW135447.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1138	1138	94%	0.0	99.68	649
MF426014.1							
Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I...							

Rhipicephalu... brown dog tick	34632	1138	1138	93%	0.0	100.00	626
KX519707.1							
Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1134	1134	94%	0.0	99.68	630
KX757901.1							
Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subuni...							
Rhipicephalu... brown dog tick	34632	1131	1131	95%	0.0	99.05	656
KU568516.1							
Rhipicephalus sanguineus clone #4 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	1129	1129	94%	0.0	99.52	635
KX519709.1							
Rhipicephalus sanguineus isolate LIC4723B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1092	1092	90%	0.0	99.66	723
KX714599.1							
Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	1072	1072	88%	0.0	100.00	580
KX519713.1							
Rhipicephalus sanguineus mitochondrial DNA, complete genome							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	14710
AF081829.1							
Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	1053	1053	86%	0.0	100.00	595
KX519706.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1014	1014	85%	0.0	99.29	574
MF425987.1							
Rhipicephalus sanguineus clone #5 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	989	989	83%	0.0	99.27	553
KX519710.1							
Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630
KX757903.1							
Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	629
KX757893.1							
Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidas...							
Rhipicephalu... brown dog tick	34632	979	979	94%	0.0	95.16	630
KX757909.1							
Rhipicephalus sanguineus isolate FT157 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	963	963	79%	0.0	99.81	535
MN223690.1							
Rhipicephalus sanguineus isolate FT154 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	957	957	79%	0.0	99.62	535
MN223688.1							
Rhipicephalus sanguineus isolate CE67 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	957	957	79%	0.0	99.62	535
MN223686.1							
Rhipicephalus sanguineus isolate CE61 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	952	952	79%	0.0	99.43	535
MN223689.1							
Rhipicephalus sanguineus isolate RI46 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	952	952	79%	0.0	99.43	535
MN223687.1							
Rhipicephalus sanguineus isolate RI08 cytochrome c oxidase...							

Rhipicephalu... brown dog tick	34632	948	948	79%	0.0	99.43	535
MN223684.1							
Rhipicephalus sanguineus isolate RI54 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	946	946	79%	0.0	99.24	535
MN223685.1							
Rhipicephalus sanguineus isolate FT044 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	946	946	79%	0.0	99.24	535
MN223683.1							
Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	900	900	100%	0.0	91.34	790
KY678135.1							
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (C01)...							
Rhipicephalu... brown dog tick	34632	898	898	98%	0.0	91.67	829
KU214592.1							
Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome...							
Rhipicephalu... brown dog tick	34632	889	889	100%	0.0	91.03	1539
KM494916.1							
Rhipicephalus sanguineus isolate Tehran cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	889	889	100%	0.0	91.03	1539
KM494915.1							
Rhipicephalus camicasi isolate SC0126 mitochondrion, complete...							
Rhipicephalu... NA	669981	889	889	100%	0.0	91.03	14725
NC_061616.1							
Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c...							
Rhipicephalu... NA	34633	883	883	100%	0.0	90.88	673
MT800313.1							
Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c...							
Rhipicephalu... NA	34633	881	881	99%	0.0	90.87	673
MT800314.1							
Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873
KY606303.1							
Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873
KY606302.1							
Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873
KY606301.1							
Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873
KY606300.1							
Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873
KY606299.1							
Rhipicephalus turanicus isolate COX1-7-Sheep cytochrome c...							
Rhipicephalu... NA	34633	865	865	99%	0.0	90.41	673
MT800312.1							
Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase...							
Rhipicephalu... NA	34633	861	861	99%	0.0	90.49	678
MT079206.1							
Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase...							
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	658
MZ305547.1							

Alignments:

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S827 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF426019.1 Length: 697

Range 1: 19 to 676

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	318
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	558
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	618
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	619	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

>Rhipicephalus sanguineus haplotype III cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556745.1 Length: 713
Range 1: 27 to 684

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 27  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 86

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 87  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 146

Query 121  AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 147  AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 206

Query 181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 207  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 266

Query 241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 300
      |||
Sbjct 267  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 326

Query 301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||
Sbjct 327  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 386

Query 361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||
Sbjct 387  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 446

Query 421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
      |||
Sbjct 447  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 506

Query 481  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||
Sbjct 507  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 566

Query 541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
      |||
Sbjct 567  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 626

Query 601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      |||
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Sbjct 627 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 684

>Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593344.1 Length: 710
Range 1: 27 to 684

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Minus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 684 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 625

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 624 AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT 565

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 564 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 505

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
|||||
Sbjct 504 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 445

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 300
|||||
Sbjct 444 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 385

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
|||||
Sbjct 384 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 325

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
|||||
Sbjct 324 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 265

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
|||||
Sbjct 264 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 205

Query 481 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
|||||
Sbjct 204 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 145

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
|||||
Sbjct 144 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 85

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
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      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  84  TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 27

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>Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593343.1 Length: 710
Range 1: 27 to 684

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Minus

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Query   1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  684  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 625

Query   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  624  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 565

Query   121  AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  564  AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 505

Query   181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  504  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 445

Query   241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  444  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 385

Query   301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  384  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 325

Query   361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 265

Query   421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 205

Query   481  AACAA TAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  204  AACAA TAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 145

Query   541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  144  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 85

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Query   601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
        |||
Sbjct   84   TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 27

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>Rhipicephalus sanguineus isolate 11N cytochrome oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MN585197.1 Length: 703
Range 1: 22 to 679

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Minus

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Query   1    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
        |||
Sbjct   679  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 620

Query   61    AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
        |||
Sbjct   619  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 560

Query   121   AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
        |||
Sbjct   559  AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 500

Query   181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
        |||
Sbjct   499  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 440

Query   241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
        |||
Sbjct   439  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 380

Query   301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
        |||
Sbjct   379  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 320

Query   361   ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
        |||
Sbjct   319  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 260

Query   421   TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
        |||
Sbjct   259  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 200

Query   481   AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
        |||
Sbjct   199  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 140

Query   541   TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
        |||
Sbjct   139  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 80

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Query 601 TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
 |||
 Sbjct 79 TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 22

>Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene, partial cds;
 mitochondrial gene for mitochondrial product
 Sequence ID: AF132839.1 Length: 793
 Range 1: 42 to 699

Score:1216 bits(658), Expect:0.0,
 Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
 |||
 Sbjct 42 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 101

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
 |||
 Sbjct 102 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 161

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
 |||
 Sbjct 162 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 221

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
 |||
 Sbjct 222 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 281

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 300
 |||
 Sbjct 282 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 341

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
 |||
 Sbjct 342 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 401

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
 |||
 Sbjct 402 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 461

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
 |||
 Sbjct 462 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 521

Query 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
 |||
 Sbjct 522 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 581

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
 |||


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Sbjct  582  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA  641
Query   601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658
          |||
Sbjct  642  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  699

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S58 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426018.1 Length: 675
Range 1: 11 to 668

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query   1    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
          |||
Sbjct  11    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  70

Query   61    AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT  120
          |||
Sbjct  71    AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT  130

Query   121   AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG  180
          |||
Sbjct  131   AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG  190

Query   181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
          |||
Sbjct  191   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  250

Query   241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  300
          |||
Sbjct  251   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  310

Query   301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
          |||
Sbjct  311   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  370

Query   361   ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  420
          |||
Sbjct  371   ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  430

Query   421   TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  480
          |||
Sbjct  431   TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  490

Query   481   AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
          |||
Sbjct  491   AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  550

Query   541   TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA  600

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Sbjct	551		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	610
Query	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	611		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S52 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426016.1 Length: 680
Range 1: 12 to 669

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	311
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	372	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACTTTATTACAACATTGTAAACATACGATCAATTGGAAT	480
Sbjct	432	TTCAATTTTAGGTGCAATTAACTTTATTACAACATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551

Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	611
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	612	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	669

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S37 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426013.1 Length: 693
Range 1: 20 to 677

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559

[illegible]

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S33 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426009.1 Length: 679
Range 1: 11 to 668

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACTTTATTACAACATTGTAAACATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACTTTATTACAACATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540

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Sbjct  491  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  550
Query   541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   551  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA  610
Query   601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   611  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  668

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S32 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426008.1 Length: 690
Range 1: 14 to 671

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   14  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  73
Query   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   74  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  133
Query  121  AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134  AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG  193
Query  181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  253
Query  241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  313
Query  301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  373
Query  361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  374  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC  433
Query  421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  434  TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT  493
Query  481  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540

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Sbjct	494		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	554		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	613
Query	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	614		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S29 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426007.1 Length: 686
Range 1: 14 to 671

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61		AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74		AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121		AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	134		AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	254		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	314		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361		ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	374		ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421		TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	434		TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	493

Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	613
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1570
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426001.1 Length: 684
Range 1: 14 to 671

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT	313
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	493

Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	613
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	614	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus


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Sbjct  442  TTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTGTAAACATACGATCAATTGGAAT  501
Query  481  AACAA TAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
        |||
Sbjct  502  AACAA TAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  561
Query  541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA  600
        |||
Sbjct  562  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA  621
Query  601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658
        |||
Sbjct  622  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  679

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>Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305546.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    AACAA TATATTTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        |||
Sbjct  1    AACAA TATATTTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
Query  61    AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT  120
        |||
Sbjct  61    AATTCGTATAGAGTTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT  120
Query  121   AATCGTAACAGCACATGCATTTATTATAA ttttttttATAGTTATACCAATCATAATCGG  180
        |||
Sbjct  121   AATCGTAACAGCACATGCATTTATTATAA TTTTTTTTATAGTTATACCAATCATAATCGG  180
Query  181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
        |||
Sbjct  181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
Query  241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA ACTCTTC  300
        |||
Sbjct  241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA ACTCTTC  300
Query  301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
        |||
Sbjct  301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
Query  361   ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  420
        |||
Sbjct  361   ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  420
Query  421   TTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTGTAAACATACGATCAATTGGAAT  480

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Sbjct	421		TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	480
Query	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT				540
Sbjct	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT				540
Query	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA				600
Sbjct	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA				600
Query	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT				658
Sbjct	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT				658

>Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: MZ305545.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61		AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61		AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121		AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	121		AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	301		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361		ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	361		ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420

Query	421	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGTATACCATTAT	TTTGT	TGATCTGTTT	AATTACAGCTATTTTATTACT	540
Sbjct	481	AACAATAGAACGTATACCATTAT	TTTGT	TGATCTGTTT	AATTACAGCTATTTTATTACT	540
Query	541	TTTATCTTTACCTGTATTAGCAGG	TGCCATTACA	ATATTGT	TAACTGATCGAAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGG	TGCCATTACA	ATATTGT	TAACTGATCGAAACTTTAA	600
Query	601	TACATCATTTTTT	GATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658		
Sbjct	601	TACATCATTTTTT	GATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658		

>Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MW152145.1 Length: 676
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAA	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAA	180
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	300
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420

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Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||
Sbjct 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
      |||
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658

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>Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152144.1 Length: 675
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||

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Sbjct  361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC  420
Query  421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  480
      |||
Sbjct  421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  480
Query  481  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
      |||
Sbjct  481  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
Query  541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA  600
      |||
Sbjct  541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA  600
Query  601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658
      |||
Sbjct  601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658

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>Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152143.1 Length: 676
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
      |||
Sbjct  1    AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
Query  61    AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT  120
      |||
Sbjct  61    AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT  120
Query  121   AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG  180
      |||
Sbjct  121   AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG  180
Query  181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
      |||
Sbjct  181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
Query  241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC  300
      |||
Sbjct  241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC  300
Query  301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
      |||
Sbjct  301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
Query  361   ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC  420

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Sbjct	361		ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Query	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Query	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152142.1 Length: 669
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61		AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61		AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121		AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	121		AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	301		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360

Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S48 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426015.1 Length: 692
Range 1: 19 to 676

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378

Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	558
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	618
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	619	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S1060
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426006.1 Length: 705
Range 1: 28 to 685

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	28	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	87
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	88	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	147
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	148	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	207
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	208	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	267
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	268	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	327
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360

Sbjct	328	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	387
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	388	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	447
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	448	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATTAATTGGAAT	507
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	508	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	567
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	568	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	627
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	628	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	685

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S56 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426017.1 Length: 680
Range 1: 11 to 668

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360

Sbjct	311		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT	370
Query	361		ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	371		ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421		TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	431		TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	491		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	551		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	610
Query	601		TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	611		TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1553
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425998.1 Length: 689
Range 1: 20 to 677

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60	
Sbjct	20		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120	
Sbjct	80		AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180	
Sbjct	140		AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240	
Sbjct	200		AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300	
Sbjct	260		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319

Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	560	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	619
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	620	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	677

>Rhipicephalus sanguineus haplotype IV cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556746.1 Length: 771
Range 1: 90 to 747

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	90	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	149
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	150	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	209
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	210	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	269
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	270	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	329
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	330	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	389

Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	390	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT	449
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	450	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	509
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	510	TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	569
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	570	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	629
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	630	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	689
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	690	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	747

Range 2: 30 to 64

Score:58.4 bits(31), Expect:0.001,
Identities:34/35(97%), Gaps:1/35(2%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCA-GGT	34
Sbjct	30	AACAATATATTTAATTTTTGGAGCATGATCATGGT	64

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S358 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426012.1 Length: 684
Range 1: 14 to 671

Score:1194 bits(646), Expect:0.0,
Identities:654/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	313
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTATAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	600
Sbjct	554	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	613
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S337 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426010.1 Length: 824
Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,
Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130

Sbjct	61		GAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	120
Query	131		GCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGA	190
Sbjct	121		GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGA	180
Query	191		AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181		AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251		ATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTCATTAATTGAA	310
Sbjct	241		ATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTCATTAATTGAA	300
Query	311		TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301		TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT	360
Query	371		GGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	430
Sbjct	361		GGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431		GGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421		GGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAA	480
Query	491		CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTA	550
Sbjct	481		CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTA	540
Query	551		CCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTT	610
Sbjct	541		CCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTT	600
Query	611		TTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	601		TTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 648	

>Rhipicephalus sanguineus haplotype II cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556744.1 Length: 787
Range 1: 29 to 688

Score:1190 bits(644), Expect:0.0,
Identities:655/660(99%), Gaps:2/660(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	29	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	88

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	89	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	148
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	149	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	208
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	209	AGGATTTGGAAACTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	268
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	269	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	328
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	329	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	388
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	389	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	448
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	449	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	508
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	509	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	568
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	569	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	628
Query	601	TACATCATTTTTTGATCCTTCAGGGGG-AGGAGATCC-AATTTTATATCAACATTTATTT	658
Sbjct	629	TACATCATTTTTTGATCCTTCAGGGGGGAGGAGATCCAAATTTTATATCAACTTTTATTT	688

>Rhipicephalus sanguineus haplotype I cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial

Sequence ID: KU556743.1 Length: 659

Range 1: 12 to 659

Score:1186 bits(642), Expect:0.0,

Identities:646/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATCATAATCGG	180
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	AGGATTTGGAAATTGATTAATCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	311
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	372	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	432	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	611
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCA	648
Sbjct	612	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCA	659

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S943 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426020.1 Length: 812
Range 1: 2 to 644

Score:1182 bits(640), Expect:0.0,
Identities:642/643(99%), Gaps:0/643(0%), Strand: Plus/Plus

Query	16	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	75

Sbjct	2	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	61
Query	76	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	135
Sbjct	62	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	121
Query	136	TGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	195
Sbjct	122	TGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	181
Query	196	ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	255
Sbjct	182	ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	241
Query	256	ATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGG	315
Sbjct	242	ATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGG	301
Query	316	AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCC	375
Sbjct	302	AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTCC	361
Query	376	TTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	435
Sbjct	362	TTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	421
Query	436	AATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	495
Sbjct	422	AATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	481
Query	496	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT	555
Sbjct	482	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT	541
Query	556	ATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGA	615
Sbjct	542	ATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGA	601
Query	616	TCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	602	TCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383818.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5554A cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383819.1 Length: 768
Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,

Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

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Query 17 TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA 76
|||||
Sbjct 1 TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA 60

Query 77 GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT 136
|||||
Sbjct 61 GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA 196
|||||
Sbjct 121 GCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
|||||
Sbjct 181 TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTCATTAATTGAATCTGGA 316
|||||
Sbjct 241 TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTCATTAATTGAATCTGGA 300

Query 317 GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT 376
|||||
Sbjct 301 GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA 436
|||||
Sbjct 361 TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA 496
|||||
Sbjct 421 ATTAACCTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATA 480

Query 497 CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA 556
|||||
Sbjct 481 CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA 540

Query 557 TTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGAT 616
|||||
Sbjct 541 TTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGAT 600

Query 617 CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
|||||
Sbjct 601 CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 642
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>Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383811.1 Length: 764
>Rhipicephalus sanguineus isolate LIC5533C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383812.1 Length: 764
Range 1: 1 to 638

Score:1168 bits(632), Expect:0.0,
Identities:636/638(99%), Gaps:0/638(0%), Strand: Plus/Plus

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Query 21  GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1    GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC 60

Query 81  AACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  AACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT 120

Query 141 TTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAG 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAG 180

Query 201  TCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  TCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT 240

Query 261  GACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTG 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  GACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTG 300

Query 321  GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG 360

Query 381  TAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA 440
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 361  TAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA 420

Query 441  ACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCAT 500
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct 421  ACTTTATTACAACACTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCAT 480

Query 501  TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG 540

Query 561  CAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTT 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  CAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTT 600

Query 621  CAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
          ||||||||||||||||||||||||||||||||
Sbjct 601  CAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 638
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>Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase subunit 1 (COI)

gene, partial cds; mitochondrial

Sequence ID: KX383807.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383808.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736F cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383810.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5535C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383813.1 Length: 763

Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,

Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA	81
Sbjct	1	AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA	60
Query	82	ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT	141
Sbjct	61	ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	CCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	CCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	ACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGG	321
Sbjct	241	ACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGG	300
Query	322	TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT	381
Sbjct	301	TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA	420
Query	442	CTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATT	501
Sbjct	421	CTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATT	480
Query	502	ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC	561
Sbjct	481	ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC	540
Query	562	AGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTC	621

Sbjct 541 AGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTC 600

Query 622 AGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
 |||

Sbjct 601 AGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 637

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S344 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
 Sequence ID: MF426011.1 Length: 809
 Range 1: 3 to 644

Score:1164 bits(630), Expect:0.0,
 Identities:638/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query 17 TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA 76
 |||

Sbjct 3 TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA 62

Query 77 GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT 136
 |||

Sbjct 63 GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAC 122

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA 196
 |||

Sbjct 123 GCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA 182

Query 197 TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
 |||

Sbjct 183 TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA 242

Query 257 TTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA 316
 |||

Sbjct 243 TTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA 302

Query 317 GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT 376
 |||

Sbjct 303 GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT 362

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA 436
 |||

Sbjct 363 TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA 422

Query 437 ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA 496
 |||

Sbjct 423 ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA 482

Query 497 CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA 556
 |||

Sbjct 483 CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA 542

Query 557 TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGAT 616

Sbjct	543		TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGTAT	602
Query	617		CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	603		CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383809.1 Length: 762
Range 1: 1 to 636

Score:1164 bits(630), Expect:0.0,
Identities:634/636(99%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23		GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
Sbjct	1		GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83		CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142
Sbjct	61		CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143		ATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	202
Sbjct	121		ATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203		CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181		CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263		CTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	322
Sbjct	241		CTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323		ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	382
Sbjct	301		ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383		GATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361		GATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443		TTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTA	502
Sbjct	421		TTTATTACAACATTTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503		TTTGTTTGATCTGTTTTAATTACAGCTATTTTTATTACTTTTATCTTTACCTGTATTAGCA	562
Sbjct	481		TTTGTTTGATCTGTTTTAATTACAGCTATTTTTATTACTTTTATCTTTACCTGTATTAGCA	540

Query	563	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	622
Sbjct	541	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT	636

>Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383806.1 Length: 714
Range 1: 1 to 636

Score:1164 bits(630), Expect:0.0,
Identities:634/636(99%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
Sbjct	1	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142
Sbjct	61	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143	ATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	202
Sbjct	121	ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	322
Sbjct	241	CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	382
Sbjct	301	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	GATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTTATTACAACATATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTA	502
Sbjct	421	TTTATTACAACATATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	562
Sbjct	481	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540

Query	563	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	622
Sbjct	541	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT	636

>Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383805.1 Length: 761
Range 1: 1 to 635

Score:1162 bits(629), Expect:0.0,
Identities:633/635(99%), Gaps:0/635(0%), Strand: Plus/Plus

Query	24	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	83
Sbjct	1	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	60
Query	84	CTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	143
Sbjct	61	CTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	120
Query	144	TTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	203
Sbjct	121	TTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	180
Query	204	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	263
Sbjct	181	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	240
Query	264	TTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTA	323
Sbjct	241	TTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTA	300
Query	324	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	383
Sbjct	301	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	360
Query	384	ATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	443
Sbjct	361	ATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	444	TTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTAT	503
Sbjct	421	TTATTACAACATTTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTAT	480
Query	504	TTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	563

Sbjct	481	TTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	540
Query	564	GTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAG	623
Sbjct	541	GTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAG	600
Query	624	GGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	GGGGAGGAGATCCAATTTTATATCAACATTTATTT	635

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SF3003
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425988.1 Length: 654
Range 1: 1 to 640

Score:1160 bits(628), Expect:0.0,
Identities:636/640(99%), Gaps:0/640(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	496
Sbjct	421	ATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	556

Sbjct	481		CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557		TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	616
Sbjct	541		TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	600
Query	617		CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTAT	656
Sbjct	601		CCTTCAGGGGGAGGACATCCAATTTTATATCACCATTTAT	640

>Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519712.1 Length: 654
Range 1: 3 to 628

Score:1157 bits(626), Expect:0.0,
Identities:626/626(100%), Gaps:0/626(0%), Strand: Plus/Plus

Query	33		GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT	92
Sbjct	3		GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT	62
Query	93		TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAtt	152
Sbjct	63		TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT	122
Query	153		tttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT	212
Sbjct	123		TTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT	182
Query	213		TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC	272
Sbjct	183		TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC	242
Query	273		CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA	332
Sbjct	243		CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA	302
Query	333		CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA	392
Sbjct	303		CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA	362
Query	393		TTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAA	452
Sbjct	363		TTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAA	422
Query	453		CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT	512
Sbjct	423		CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT	482

Query	513	CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA	572
Sbjct	483	CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA	542
Query	573	CAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG	632
Sbjct	543	CAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG	602
Query	633	ATCCAATTTTATATCAACATTTATTT	658
Sbjct	603	ATCCAATTTTATATCAACATTTATTT	628

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1575
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426002.1 Length: 639
Range 1: 1 to 628

Score:1155 bits(625), Expect:0.0,
Identities:627/628(99%), Gaps:0/628(0%), Strand: Plus/Plus

Query	31	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	90
Sbjct	1	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	60
Query	91	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAt	150
Sbjct	61	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	120
Query	151	tttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	210
Sbjct	121	TTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	180
Query	211	ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	270
Sbjct	181	ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	240
Query	271	TCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATG	330
Sbjct	241	TCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATG	300
Query	331	AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC	390
Sbjct	301	AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC	360
Query	391	TATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTAC	450
Sbjct	361	TATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTAC	420
Query	451	AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG	510
Sbjct	421	AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG	480

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Query   511  ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT  570
        |||
Sbjct   481  ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT  540

Query   571  TACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGG  630
        |||
Sbjct   541  TACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGG  600

Query   631  AGATCCAATTTTATATCAACATTTATTT  658
        |||
Sbjct   601  AGATCCAATTTTATATCAACATTTATTT  628

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>Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: MG855658.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  98
        |||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA  158
        |||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  218
        |||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  278
        |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  338
        |||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTT  398
        |||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTT  360

Query   399  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACATTTG  458
        |||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACATTTG  420

Query   459  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  518
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Sbjct  421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480
Query  519  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
          |||
Sbjct  481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540
Query  579  TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  638
          |||
Sbjct  541  TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600
Query  639  TTTTATATCAACATTTATTT  658
          |||
Sbjct  601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: MG855657.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

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Query  39  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  98
          |||
Sbjct  1  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  60
Query  99  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAatttttttA  158
          |||
Sbjct  61  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA  120
Query  159  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  218
          |||
Sbjct  121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180
Query  219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  278
          |||
Sbjct  181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240
Query  279  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  338
          |||
Sbjct  241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300
Query  339  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  398
          |||
Sbjct  301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360
Query  399  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACATTTG  458
          |||
Sbjct  361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACATTTG  420
Query  459  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  518

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Sbjct	421		TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579		TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541		TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639		TTTTATATCAACATTTATTT 658	
Sbjct	601		TTTTATATCAACATTTATTT 620	

>Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: MG855656.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420

Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757910.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420

Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757904.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458

Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757902.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458

Sbjct	361		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459		TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421		TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579		TGTTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541		TGTTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639		TTTTATATCAACATTTATTT	658
Sbjct	601		TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757896.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360

Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757889.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360

Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Rovind cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757887.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398

Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757879.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398

Sbjct	301		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459		TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421		TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579		TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541		TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639		TTTTATATCAACATTTATTT 658	
Sbjct	601		TTTTATATCAACATTTATTT 620	

>Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519711.1 Length: 636
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300

Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT 658	
Sbjct	601	TTTTATATCAACATTTATTT 620	

>Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135448.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300

Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630347.1 Length: 644
Range 1: 20 to 641

Score:1144 bits(619), Expect:0.0,
Identities:621/622(99%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTGGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTC	300

Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	619
Query	601	TACATCATTTTTTTGATCCTTCA	622
Sbjct	620	TACATCATTTTTTTGATCCTTCA	641

>Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630346.1 Length: 644
Range 1: 20 to 641

Score:1144 bits(619), Expect:0.0,
Identities:621/622(99%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTGGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300

Sbjct	260	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	320	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	380	 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	440	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	500	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	560	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	619
Query	601	TACATCATTTTTTTGATCCTTCA 622	
Sbjct	620	 TACATCATTTTTTTGATCCTTCA 641	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1568
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426000.1 Length: 635
Range 1: 14 to 635

Score:1144 bits(619), Expect:0.0,
Identities:621/622(99%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	134	 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253

Query	241	AATAAATAATATAAGATTTT	GACTTTTACCTCCTTCACTATTTTTATTAATTA	AACTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTT	GACTTTTACCTCCTTCACTATTTTTATTAATTA	AACTCTTC	313
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT			360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT			373
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC			420
Sbjct	374	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC			433
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT			480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT			493
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT			540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT			553
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA			600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA			613
Query	601	TACATCATTTTTTTGATCCTTCA		622	
Sbjct	614	TACATCATTTTTTTGATCCTTCA		635	

>Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757905.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	240

Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757895.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278

Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Zadar cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757892.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278

Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459		TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421		TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579		TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541		TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639		TTTTATATCAACATTTATTT 658	
Sbjct	601		TTTTATATCAACATTTATTT 620	

>Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757890.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180

Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757888.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180

Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Petnica cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757883.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218

Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519708.1 Length: 629
Range 1: 4 to 620

Score:1140 bits(617), Expect:0.0,
Identities:617/617(100%), Gaps:0/617(0%), Strand: Plus/Plus

Query	42	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	101
Sbjct	4	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	63
Query	102	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttATAG	161
Sbjct	64	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttATAG	123
Query	162	TTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCC	221

Sbjct	124		TTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCC	183
Query	222		CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT	281
Sbjct	184		CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT	243
Query	282		TTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC	341
Sbjct	244		TTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC	303
Query	342		CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTC	401
Sbjct	304		CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTC	363
Query	402		TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAA	461
Sbjct	364		TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAA	423
Query	462		ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA	521
Sbjct	424		ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA	483
Query	522		TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	581
Sbjct	484		TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	543
Query	582		TAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTT	641
Sbjct	544		TAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTT	603
Query	642		TATATCAACATTTATTT 658	
Sbjct	604		TATATCAACATTTATTT 620	

>Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135447.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120

Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGACCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S475 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426014.1 Length: 649
Range 1: 28 to 649

Score:1138 bits(616), Expect:0.0,
Identities:620/622(99%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	28	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	87
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	88	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	147

Query	121	AATCGTAACAGCACATGCATTTATTATAA	180
Sbjct	148	AATCGTAACAGCACATGCATTTATTATAA	207
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	208	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	267
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	300
Sbjct	268	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	327
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	328	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	387
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	388	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	447
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	448	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	507
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACT	540
Sbjct	508	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACT	567
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	600
Sbjct	568	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	627
Query	601	TACATCATTTTTTTGATCCTTCA	622
Sbjct	628	TACATCATTTTTTTGATCCTTCA	649

>Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519707.1 Length: 626
Range 1: 1 to 616

Score:1138 bits(616), Expect:0.0,
Identities:616/616(100%), Gaps:0/616(0%), Strand: Plus/Plus

Query	43	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	102
Sbjct	1	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	60
Query	103	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	162

Sbjct	61	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT	120
Query	163	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	222
Sbjct	121	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	180
Query	223	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	282
Sbjct	181	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	240
Query	283	TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	342
Sbjct	241	TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	300
Query	343	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT	402
Sbjct	301	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT	360
Query	403	TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA	462
Sbjct	361	TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA	420
Query	463	CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	522
Sbjct	421	CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	582
Sbjct	481	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	642
Sbjct	541	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	600
Query	643	ATATCAACATTTATTT	658
Sbjct	601	ATATCAACATTTATTT	616

>Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757901.1 Length: 630
Range 1: 1 to 620

Score:1134 bits(614), Expect:0.0,
Identities:618/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158

Sbjct	61	 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	 TAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT 658	
Sbjct	601	 TTTTATATCAACATTTATTT 620	

>Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU568516.1 Length: 656
Range 1: 27 to 656

Score:1131 bits(612), Expect:0.0,
Identities:624/630(99%), Gaps:0/630(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	27	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	86

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	87	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	146
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	147	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	206
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	207	AGGATTTGGAAATTGATTAATCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	266
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	267	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	326
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	327	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	386
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	387	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	446
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	447	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	506
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	507	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	566
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	567	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	626
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGG	630
Sbjct	627	TACATCATTTTTTTGACCCTTCAGGAGGAGG	656

>Rhipicephalus sanguineus clone #4 cytochrome oxidase subunit I (COI) gene,
 partial cds; mitochondrial
 Sequence ID: KX519709.1 Length: 635
 Range 1: 2 to 621

Score:1129 bits(611), Expect:0.0,
 Identities:617/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	2	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	61

Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	62	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCTTTTATTATAATTTTTTTTA	121
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	122	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	181
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	182	CCCCGGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	241
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	242	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	301
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	302	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGGAGATTTAGCTATTTTTT	361
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	362	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	421
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	422	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	481
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	482	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	541
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	542	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	601
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	602	TTTTATATCAACATTTATTT	621

>Rhipicephalus sanguineus isolate LIC4723B cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX714599.1 Length: 723
 >Rhipicephalus sanguineus isolate LIC4750B cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX714600.1 Length: 723
 Range 1: 1 to 597

Score:1092 bits(591), Expect:0.0,
 Identities:595/597(99%), Gaps:0/597(0%), Strand: Plus/Plus

Query	62	ATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTA	121
Sbjct	1	ATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTA	60
Query	122	ATCGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATCATAATCGGA	181
Sbjct	61	ATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATTGGA	120
Query	182	GGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGA	241
Sbjct	121	GGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGA	180
Query	242	ATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCA	301
Sbjct	181	ATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCA	240
Query	302	TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA	361
Sbjct	241	TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA	300
Query	362	TCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCT	421
Sbjct	301	TCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCT	360
Query	422	TCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATA	481
Sbjct	361	TCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATA	420
Query	482	ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT	541
Sbjct	421	ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT	480
Query	542	TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAAT	601
Sbjct	481	TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAAT	540
Query	602	ACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	541	ACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	597

>Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519713.1 Length: 580
Range 1: 1 to 580

Score:1072 bits(580), Expect:0.0,
Identities:580/580(100%), Gaps:0/580(0%), Strand: Plus/Plus

Query	43	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	102

Sbjct	1	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAA	60
Query	103	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttATAGT	162
Sbjct	61	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGT	120
Query	163	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	222
Sbjct	121	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	180
Query	223	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	282
Sbjct	181	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	240
Query	283	TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	342
Sbjct	241	TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	300
Query	343	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT	402
Sbjct	301	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT	360
Query	403	TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA	462
Sbjct	361	TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA	420
Query	463	CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	522
Sbjct	421	CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	582
Sbjct	481	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA	622
Sbjct	541	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA	580

>Rhipicephalus sanguineus mitochondrial DNA, complete genome
Sequence ID: AF081829.1 Length: 14710
Range 1: 1191 to 1848

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1191	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	1250
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	1251	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	1310
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	1311	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	1370
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	1371	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	1430
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	1431	AATAAATAATATAAGATTTTGACTTTTACCCCTCATTATTTTTATTGATTAACCTCTTC	1490
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	1491	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCTCTATCTTCAAATTT	1550
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	1551	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	1610
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	1611	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	1670
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	1671	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	1730
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Sbjct	1731	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	1790
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	1791	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	1848

>Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519706.1 Length: 595
Range 1: 1 to 570

Score:1053 bits(570), Expect:0.0,
Identities:570/570(100%), Gaps:0/570(0%), Strand: Plus/Plus

Query	89	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	148
Sbjct	1	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	60
Query	149	AttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATC	208

Sbjct	61		120
Query	209	ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	268
Sbjct	121	ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	180
Query	269	CCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGA	328
Sbjct	181	CCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGA	240
Query	329	TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA	388
Sbjct	241	TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA	300
Query	389	GCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATT	448
Sbjct	301	GCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATT	360
Query	449	ACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT	508
Sbjct	361	ACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT	420
Query	509	TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	568
Sbjct	421	TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	480
Query	569	ATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGA	628
Sbjct	481	ATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGA	540
Query	629	GGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	541	GGAGATCCAATTTTATATCAACATTTATTT 570	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SC3005
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425987.1 Length: 574
Range 1: 1 to 561

Score:1014 bits(549), Expect:0.0,
Identities:557/561(99%), Gaps:0/561(0%), Strand: Plus/Plus

Query	98	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAtttttttt	157
Sbjct	1	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACACGCATTTATTATAATTTTTTTT	60
Query	158	ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGT	217
Sbjct	61	ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATTATATTAGGT	120

Query	218	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA	277
Sbjct	121	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA	180
Query	278	CTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT	337
Sbjct	181	CTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT	240
Query	338	TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTT	397
Sbjct	241	TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTT	300
Query	398	TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATT	457
Sbjct	301	TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATT	360
Query	458	GTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTT	517
Sbjct	361	GTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTT	420
Query	518	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	577
Sbjct	421	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	480
Query	578	TTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCA	637
Sbjct	481	TTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCA	540
Query	638	ATTTTATATCAACATTTATTT	658
Sbjct	541	ATTTTATATCAACATTTATTT	561

>Rhipicephalus sanguineus clone #5 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519710.1 Length: 553
Range 1: 1 to 547

Score:989 bits(535), Expect:0.0,
Identities:543/547(99%), Gaps:0/547(0%), Strand: Plus/Plus

Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	1	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGGAATCGTAACAGCACAT	60
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	196
Sbjct	61	GCTTTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	120
Query	197	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	121	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	180

Query	257	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGA	316
Sbjct	181	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGA	240
Query	317	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTT	CAAATTTATCACATTATGGCCCT	376
Sbjct	241	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTT	CAAATTTATCACATTATGGCCCT	300
Query	377	TCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGG	TGCTTCTTCAATTTAGGTGCA	436
Sbjct	301	TCAGGAGATTTAGCTATTTTTCTCTTCATCTTGCTGG	TGCTTCTTCAATTTAGGTGCA	360
Query	437	ATTAACTTTATTACAAC	TATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	496
Sbjct	361	ATTAACTTTATTACAAC	TATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	420
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTT	ATTACTTTTATCTTTACCTGTA	556
Sbjct	421	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTT	ATTACTTTTATCTTTACCTGTA	480
Query	557	TTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAACTTTAATACATCATTTTTTTGAT	616
Sbjct	481	TTAGCAGGTGCCATTACAATATTGT	TAACTGATCGATACTTTAATACATCATTTTTTTGAT	540
Query	617	CCTTCAG	623	
Sbjct	541	CCTTCAG	547	

>Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757903.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	tttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	TTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	ATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTAT	ATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTAC	CTCCTTCAC	278

Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAATTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TATTAACGATCGAAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757893.1 Length: 629
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278

Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTTATTGATTA	ACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAA	ATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAA	ATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGT	GCTTCTTCAATTTTAGGTGCAATTA	458
Sbjct	361	CTCTTCACCTTGCTGGT	GCTTCTTCAATTTTAGGTGCAATTA	420
Query	459	TAAACATACGATCAATTGGA	ATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGA	ATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTTATT	ACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTTACT	ACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTA	ATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TATTAAGTATCGAAACTTTA	ACACATCATTTTTTTGACCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACATTTATTT		658
Sbjct	601	TTTTATATCAACACTTATTT		620

>Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757909.1 Length: 630
Range 1: 1 to 620

Score:979 bits(530), Expect:0.0,
Identities:590/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	120
Query	159	TAGTTATACCAATCATAAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATAATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180

Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCTGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGCCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TATTGACTGATCGAAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGGGATCCCA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate FT157 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223690.1 Length: 535
Range 1: 1 to 524

Score:963 bits(521), Expect:0.0,
Identities:523/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	194
Sbjct	1	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120
Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	180

Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTTTATCTTCAAATTTATCACATTATGGCC	240
Query	375	CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	241	CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300
Query	435	CAATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494
Sbjct	301	CAATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	360
Query	495	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554
Sbjct	361	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	420
Query	555	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG	614
Sbjct	421	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG	480
Query	615	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	481	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524	

>Rhipicephalus sanguineus isolate FT154 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223688.1 Length: 535
Range 1: 1 to 524

Score:957 bits(518), Expect:0.0,
Identities:522/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	194
Sbjct	1	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120
Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCACTAATTGAATCTG	180
Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	240
Query	375	CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434

Sbjct	241	CTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300
Query	435	CAATTAACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494
Sbjct	301	CAATTAACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	360
Query	495	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554
Sbjct	361	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	420
Query	555	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG	614
Sbjct	421	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG	480
Query	615	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	481	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	524

>Rhipicephalus sanguineus isolate CE67 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223686.1 Length: 535
Range 1: 1 to 524

Score:957 bits(518), Expect:0.0,
Identities:522/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	194
Sbjct	1	ATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120
Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	180
Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	240
Query	375	CTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	241	CTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300
Query	435	CAATTAACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494
Sbjct	301	CAATTAACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	360
Query	495	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554

Sbjct	361	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	420
Query	555	TATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAATACATCATTTTTTTG	614
Sbjct	421	TATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAATACATCATTTTTTTG	480
Query	615	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	481	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	524

>Rhipicephalus sanguineus isolate CE61 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223689.1 Length: 535
Range 1: 1 to 524

Score:952 bits(515), Expect:0.0,
Identities:521/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAAATT	194
Sbjct	1	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120
Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTG	180
Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTC	240
Query	375	CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	241	CTTCAGTAGATTTAACTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300
Query	435	CAATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494
Sbjct	301	CAATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	360
Query	495	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554
Sbjct	361	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTTTATCTTTACCTG	420
Query	555	TATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAATACATCATTTTTTTG	614
Sbjct	421	TATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAATACATCATTTTTTTG	480

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Query   615  ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524

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>Rhipicephalus sanguineus isolate RI46 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223687.1 Length: 535
Range 1: 1 to 524

Score:952 bits(515), Expect:0.0,
Identities:521/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

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Query   135  ATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT 194
        ||||||||||||||||||||||||||||||||||||||||
Sbjct    1  ATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT 60

Query   195  GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA 254
        ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct   61  GATTAGTCCCTATTATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA 120

Query   255  GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG 314
        ||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG 180

Query   315  GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC 374
        ||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACACTATGGCC 240

Query   375  CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG 434
        ||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG 300

Query   435  CAATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA 494
        ||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CAATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA 360

Query   495  TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG 554
        ||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TACCACTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG 420

Query   555  TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG 614
        ||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG 480

Query   615  ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
        ||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524

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>Rhipicephalus sanguineus isolate RI08 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223684.1 Length: 535
Range 1: 3 to 524

Score:948 bits(513), Expect:0.0,
Identities:519/522(99%), Gaps:0/522(0%), Strand: Plus/Plus

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Query 137 GCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA 196
          |||
Sbjct 3 GCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA 62

Query 197 TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
          |||
Sbjct 63 TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA 122

Query 257 TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA 316
          |||
Sbjct 123 TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA 182

Query 317 GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT 376
          |||
Sbjct 183 GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT 242

Query 377 TCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA 436
          |||
Sbjct 243 TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA 302

Query 437 ATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA 496
          |||
Sbjct 303 ATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA 362

Query 497 CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA 556
          |||
Sbjct 363 CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA 422

Query 557 TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT 616
          |||
Sbjct 423 TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT 482

Query 617 CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
          |||
Sbjct 483 CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524
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>Rhipicephalus sanguineus isolate RI54 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223685.1 Length: 535
Range 1: 1 to 524

Score:946 bits(512), Expect:0.0,
Identities:520/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	194
Sbjct	1	ATGCATTTATTATAATTTTTTTTATAGTTATACCGATCATAATCGGAGGATTTGGAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	GATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120
Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	180
Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	240
Query	375	CTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	241	CTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300
Query	435	CAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494
Sbjct	301	CAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	360
Query	495	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554
Sbjct	361	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTCTTATCTTTACCTG	420
Query	555	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG	614
Sbjct	421	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG	480
Query	615	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	481	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	524

>Rhipicephalus sanguineus isolate FT044 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MN223683.1 Length: 535
Range 1: 1 to 524

Score:946 bits(512), Expect:0.0,
Identities:520/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	194
Sbjct	1	ATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254

Sbjct	61	GATTAGTTCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120
Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	180
Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	240
Query	375	CTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	241	CTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300
Query	435	CAATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494
Sbjct	301	CAATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	360
Query	495	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554
Sbjct	361	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTGTTATCTTTACCTG	420
Query	555	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG	614
Sbjct	421	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG	480
Query	615	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	481	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	524

>Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase subunit 1 gene,
partial cds; mitochondrial
Sequence ID: KY678135.1 Length: 790
Range 1: 18 to 675

Score:900 bits(487), Expect:0.0,
Identities:601/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	18	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	77
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	78	AATTCGTATAGAATTAGGCCAACCTGGAACCCTAATTGGTAATGATCAAATTTATAATGT	137
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	138	AATTGTTACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGG	197
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240

Query	11	TTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGCCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGTAATTGTTACA	120
Query	131	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGA	190
Sbjct	121	GCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGGTGGATTTGGA	180

Query	191	AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTCTTCCTCCCTCATTATTTATATTAATTAATTCTTCATTAATTGAG	300
Query	311	TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCAGGAGCAGGTACAGGATGGACAGTTTATCCTCCCCTATCCTCAAATTTATCACATTAT	360
Query	371	GGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAATAACAATAGAA	480
Query	491	CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTA	550
Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACTATTATCTTTA	540
Query	551	CCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAATACATCATTT	610
Sbjct	541	CCTGTTTTTAGCAGGTGCCATTACAATATTATTAACCGATCGAAATTTTAACACTTCATTT	600
Query	611	TTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	TTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	648

Score:889 bits(481), Expect:0.0,
Identities:599/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCCTCCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCTTCAAATTT	404
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTATTACAACCTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	645	CACTTCATTTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus sanguineus isolate Tehran cytochrome oxidase subunit 1 gene,
complete cds; mitochondrial
Sequence ID: KM494915.1 Length: 1539
Range 1: 45 to 702

Score:889 bits(481), Expect:0.0,
Identities:599/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180

Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTCCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCTCAAATTT	404
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTATTACAACATATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	645	CACTTCATTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus camicasi isolate SC0126 mitochondrion, complete genome

Sequence ID: NC_061616.1 Length: 14725

>Rhipicephalus camicasi isolate SC0126 mitochondrion, complete genome

Sequence ID: MZ323229.1 Length: 14725

Range 1: 45 to 702

Score:889 bits(481), Expect:0.0,

Identities:599/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATACTTAATTTTTGGAGCATGATCTGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGACCAAATTTATAATGT	164

Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTAATACCAATTATGATTGG	224
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTCGGAATTGATTAGTCCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT	300
Sbjct	285	AATAAATAATATAAGATTTTGATTACTTCCTCCTTCATTATTTTTATTAATTAATTCTT	344
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAATCAGGAGCAGGGACAGGATGAACAGTTTACCCTCCTTATCATCAAATTT	404
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	405	ATCACACTATGGTCCATCAGTAGATCTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGCGCAATTAATTTTCATTACAACCATTGTAAACATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	525	AACAATAGAACGAATACCTTTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTTTATAGCTGGTGCAATTACAATATTATTAAGTATCGAAATTTTAA	644
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	645	TACCTCGTTCTTTGATCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800313.1 Length: 673
Range 1: 8 to 665

Score:883 bits(478), Expect:0.0,
Identities:598/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAACGT	127

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCCATTATAATTGG	187
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTTCACTATTTCTATTAATTAACCTCTC	307
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCGGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAACCTGATCGAAATTTCAA	607
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATT	657
Sbjct	608	TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATT	664

>Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606303.1 Length: 873
Range 1: 66 to 723

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	126		185
		AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTCAATACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	665
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	666	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606302.1 Length: 873
Range 1: 66 to 723

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 	240
Sbjct	246	AGGATTTGGAACTGATTAGTGCCCATTTATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT 	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTCAATACAACATATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCCTATTTTATTGCT	605
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	665
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query 1 AACAAATAATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Sbjct	66	 AACAATATATTTAATTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	 AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	186	 AATTGTAACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	 AGGATTTGGAAACTGATTAGTGCCCATTTAGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	306	 AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	366	 ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	426	 ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	486	 TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGTATAACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	546	 AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	606	 TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	666	 CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate COX1-7-Sheep cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800312.1 Length: 673
Range 1: 8 to 664

Score:865 bits(468), Expect:0.0,
Identities:594/657(90%), Gaps:0/657(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGACCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAAATTTTTTTTATGGTAATACCTATTATAATTGG	187
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATCATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTCATTATTTCTATTAATTAACCTCTC	307
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCGGGAGCAGGAACGGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACATATTCTAAACATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTCTGATCTGTTTTAATTACCACCATCTTACTTCT	547
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAACCTGATCGAAATTTCAA	607
Query	601	TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATT	657
Sbjct	608	TACCTCATTTTTTATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATT	664

>Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MT079206.1 Length: 678
Range 1: 1 to 652

Score:861 bits(466), Expect:0.0,
Identities:590/652(90%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCTG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCTG	60
Query	67	TATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATT	186
Sbjct	121	AACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	TGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181	TGGAAACTGGTTAGTTCCAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACA	366
Sbjct	301	TGAATCTGGGGCAGGGACAGGTGAACTGTTTATCCTCCTTTATCCTCAAATTTATCCCA	360
Query	367	TTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTTCATTACAACCTATTGTAAACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCTGATCGAAATTTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	ATTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTTATTT	652

>Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305547.1 Length: 658
Range 1: 1 to 658

Score:861 bits(466), Expect:0.0,

Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 1 AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 61 AATTCGAATAGAGTTAGGACAACCTGGGACTTTAATTGGAAATGATCAAATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG 180
|||
Sbjct 121 AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG 180

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGATTACTTCTCCTCATTATTCTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
|
Sbjct 301 ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT 360

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 420
|||
Sbjct 361 ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATTACAACCTATTGTAAATATACGATCTATTGGAAT 480

Query 481 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
|||||
Sbjct 481 AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT 540

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
|
Sbjct 541 TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA 600

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
||
Sbjct 601 CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT 658
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Query #3: TKCJJ092-19|TKCJ012018H08|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26765 Length: 658

Sequences producing significant alignments:

Common		Max	Total Query	E	Per.	Acc.	Scientific	
Description								Name
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession	
Rhipicephalus sanguineus mitochondrial DNA, complete genome								
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14710	
AF081829.1								
Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	629	
KX757893.1								
Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1129	1129	94%	0.0	99.52	630	
KX757903.1								
Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidas...								
Rhipicephalu... brown dog tick	34632	1112	1112	94%	0.0	99.03	630	
KX757909.1								
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	34632	1072	1072	100%	0.0	96.05	692	
MF426015.1								
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	675	
MF426018.1								
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	680	
MF426016.1								
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	693	
MF426013.1								
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	679	
MF426009.1								
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	686	
MF426007.1								
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	697	
MF426019.1								
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	705	
MF426006.1								
Rhipicephalus sanguineus haplotype III cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	713	
KU556745.1								
Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidas...								
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	710	
MN593344.1								
Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidas...								
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	710	
MN593343.1								
Rhipicephalus sanguineus isolate 11N cytochrome oxidase subuni...								
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	703	
MN585197.1								

Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene,...									
Rhipicephalu... brown dog tick	AF132839.1	34632	1061	1061	100%	0.0	95.74	793	
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...									
Rhipicephalu... brown dog tick	MF426017.1	34632	1055	1055	100%	0.0	95.59	680	
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...									
Rhipicephalu... brown dog tick	MF426008.1	34632	1055	1055	100%	0.0	95.59	690	
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...									
Rhipicephalu... brown dog tick	MF426001.1	34632	1055	1055	100%	0.0	95.59	684	
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...									
Rhipicephalu... brown dog tick	MF425998.1	34632	1055	1055	100%	0.0	95.59	689	
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...									
Rhipicephalu... brown dog tick	MF425997.1	34632	1055	1055	100%	0.0	95.59	695	
Rhipicephalus sanguineus haplotype IV cytochrome oxidase subun...									
Rhipicephalu... brown dog tick	KU556746.1	34632	1055	1113	100%	0.0	95.59	771	
Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase...									
Rhipicephalu... brown dog tick	MZ305546.1	34632	1055	1055	100%	0.0	95.59	658	
Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase...									
Rhipicephalu... brown dog tick	MZ305545.1	34632	1055	1055	100%	0.0	95.59	658	
Rhipicephalus sanguineus isolate SMSK cytochrome c oxidase...									
Rhipicephalu... brown dog tick	MW152145.1	34632	1055	1055	100%	0.0	95.59	676	
Rhipicephalus sanguineus isolate SMSK cytochrome c oxidase...									
Rhipicephalu... brown dog tick	MW152144.1	34632	1055	1055	100%	0.0	95.59	675	
Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase...									
Rhipicephalu... brown dog tick	MW152143.1	34632	1055	1055	100%	0.0	95.59	676	
Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase...									
Rhipicephalu... brown dog tick	MW152142.1	34632	1055	1055	100%	0.0	95.59	669	
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...									
Rhipicephalu... brown dog tick	MF426012.1	34632	1050	1050	100%	0.0	95.44	684	
Rhipicephalus sanguineus haplotype I cytochrome oxidase subuni...									
Rhipicephalu... brown dog tick	KU556743.1	34632	1048	1048	98%	0.0	95.83	659	
Rhipicephalus sanguineus haplotype II cytochrome oxidase subun...									
Rhipicephalu... brown dog tick	KU556744.1	34632	1046	1046	100%	0.0	95.30	787	
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...									
Rhipicephalu... brown dog tick	MF426020.1	34632	1038	1038	97%	0.0	95.80	812	
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...									
Rhipicephalu... brown dog tick	MF426010.1	34632	1037	1037	98%	0.0	95.52	824	

Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426011.1	34632	1031	1031	97%	0.0	95.64	809
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426014.1	34632	1022	1022	94%	0.0	96.30	649
Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX383818.1	34632	1020	1020	97%	0.0	95.33	768
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426000.1	34632	1016	1016	94%	0.0	96.14	635
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF425988.1	34632	1016	1016	97%	0.0	95.31	654
Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX383811.1	34632	1013	1013	96%	0.0	95.30	764
Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX383807.1	34632	1011	1011	96%	0.0	95.29	763
Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subuni...								
Rhipicephalu... brown dog tick	KU568516.1	34632	1009	1009	95%	0.0	95.56	656
Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX383809.1	34632	1009	1009	96%	0.0	95.28	762
Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX383806.1	34632	1009	1009	96%	0.0	95.28	714
Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX383805.1	34632	1007	1007	96%	0.0	95.28	761
Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MH630347.1	34632	1005	1005	94%	0.0	95.82	644
Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MH630346.1	34632	1005	1005	94%	0.0	95.82	644
Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I...								
Rhipicephalu... brown dog tick	KX519712.1	34632	1002	1002	95%	0.0	95.53	654
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426002.1	34632	1000	1000	95%	0.0	95.38	639
Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MG855658.1	34632	990	990	94%	0.0	95.48	630
Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MG855657.1	34632	990	990	94%	0.0	95.48	630
Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MG855656.1	34632	990	990	94%	0.0	95.48	630

Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630	
KX757910.1								
Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630	
KX757904.1								
Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630	
KX757902.1								
Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630	
KX757896.1								
Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630	
KX757889.1								
Rhipicephalus sanguineus isolate Rovind cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630	
KX757887.1								
Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630	
KX757879.1								
Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	636	
KX519711.1								
Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630	
MW135448.1								
Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630	
KX757905.1								
Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630	
KX757895.1								
Rhipicephalus sanguineus isolate Zadar cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630	
KX757892.1								
Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630	
KX757890.1								
Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630	
KX757888.1								
Rhipicephalus sanguineus isolate Petnica cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630	
KX757883.1								
Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I...								
Rhipicephalu... brown dog tick	34632	985	985	93%	0.0	95.46	629	
KX519708.1								
Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630	
MW135447.1								
Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I...								
Rhipicephalu... brown dog tick	34632	983	983	93%	0.0	95.45	626	
KX519707.1								

Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX757901.1	34632	979	979	94%	0.0	95.16	630
Rhipicephalus sanguineus clone #4 cytochrome oxidase subunit I...								
Rhipicephalu... brown dog tick	KX519709.1	34632	974	974	94%	0.0	95.00	635
Rhipicephalus sanguineus isolate LIC4723B cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX714599.1	34632	937	937	90%	0.0	94.97	723
Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I...								
Rhipicephalu... brown dog tick	KX519713.1	34632	933	933	88%	0.0	95.69	580
Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I...								
Rhipicephalu... brown dog tick	KX519706.1	34632	898	898	86%	0.0	95.09	595
Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase...								
Rhipicephalu... brown dog tick	KY678135.1	34632	883	883	100%	0.0	90.90	790
Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c...								
Rhipicephalu... NA	MT800313.1	34633	883	883	100%	0.0	90.88	673
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF425987.1	34632	881	881	85%	0.0	95.01	574
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (C01)...								
Rhipicephalu... brown dog tick	KU214592.1	34632	876	876	98%	0.0	91.05	829
Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase...								
Rhipicephalu... NA	MT079206.1	34633	872	872	99%	0.0	90.80	678
Rhipicephalus sanguineus isolate GY34 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MN862754.1	34632	872	872	99%	0.0	90.80	678
Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome...								
Rhipicephalu... brown dog tick	KM494916.1	34632	872	872	100%	0.0	90.58	1539
Rhipicephalus sanguineus isolate Tehran cytochrome oxidase...								
Rhipicephalu... brown dog tick	KM494915.1	34632	872	872	100%	0.0	90.58	1539
Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c...								
Rhipicephalu... NA	MT800314.1	34633	870	870	99%	0.0	90.56	673
Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606303.1	34633	861	861	100%	0.0	90.27	873
Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606302.1	34633	861	861	100%	0.0	90.27	873
Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606301.1	34633	861	861	100%	0.0	90.27	873
Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606300.1	34633	861	861	100%	0.0	90.27	873

Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit...								
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	873	
KY606299.1								
Rhipicephalus camicasi isolate SC0126 mitochondrion, complete...								
Rhipicephalu... NA	669981	861	861	100%	0.0	90.29	14725	
NC_061616.1								
Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase...								
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	658	
MZ305547.1								
Rhipicephalus turanicus isolate Xinjiang-WQIA cytochrome oxida...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002581.1								
Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002580.1								
Rhipicephalus turanicus isolate Xinjiang-BC cytochrome oxidase...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002579.1								
Rhipicephalus turanicus isolate Xinjiang-YC cytochrome oxidase...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002578.1								
Rhipicephalus turanicus isolate Xinjiang-PS cytochrome oxidase...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002577.1								
Rhipicephalus turanicus isolate SHZ cytochrome oxidase subunit...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY069271.1								
Rhipicephalus turanicus isolate FK-1 cytochrome oxidase subuni...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606291.1								
Rhipicephalus turanicus isolate YN3 cytochrome oxidase subunit...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606290.1								
Rhipicephalus turanicus isolate YN2 cytochrome oxidase subunit...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606289.1								

Alignments:

>Rhipicephalus sanguineus mitochondrial DNA, complete genome
Sequence ID: AF081829.1 Length: 14710
Range 1: 1191 to 1848

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1191	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	1250
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	1251	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	1310

Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	1311	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	1370
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	1371	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	1430
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	1431	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	1490
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	1491	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	1550
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	1551	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	1610
Query	421	TTCAATTTTAGGTGCAATTAACCTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	1611	TTCAATTTTAGGTGCAATTAACCTCATCACAACTATTGTAAATATACGATCAATTGGAAT	1670
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	1671	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	1730
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1731	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	1790
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	1791	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	1848

>Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757893.1 Length: 629
 Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
 Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158

Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757903.1 Length: 630
 Range 1: 1 to 620

Score:1129 bits(611), Expect:0.0,
 Identities:617/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158

Sbjct	61	 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120
Query	159	 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	 TATTTTTATTGATTAATTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATTACAACCTATTG	420
Query	459	 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	 TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	 TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	600
Query	639	 TTTTATATCAACACTTATTT	658
Sbjct	601	 TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757909.1 Length: 630
Range 1: 1 to 620

Score:1112 bits(602), Expect:0.0,
Identities:614/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60

Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATAATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCTGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGCCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTGACTGATCGAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGGGATCCCA	600
Query	639	TTTTATATCAACACTTATTT 658	
Sbjct	601	TTTTATATCAACACTTATTT 620	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S48 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426015.1 Length: 692
Range 1: 19 to 676

Score:1072 bits(580), Expect:0.0,
Identities:632/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	618
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	619	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S58 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426018.1 Length: 675
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60

Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S52 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426016.1 Length: 680
Range 1: 12 to 669

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
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Sbjct	12	 AACAATATATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	72	 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	132	 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	252	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	311
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	312	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	372	 ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	432	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	492	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	552	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	611
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	612	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	669

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S37 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426013.1 Length: 693
Range 1: 20 to 677

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	619
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	620	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S33 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426009.1 Length: 679
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S29 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426007.1 Length: 686
Range 1: 14 to 671

Score:1066 bits(577), Expect:0.0,

Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 14 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 74 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 134 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 193

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| || |||||
Sbjct 194 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 253

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
|||||
Sbjct 254 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 313

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 314 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 374 ATCACATTATGGTCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 434 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 493

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 494 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 553

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
| |||||
Sbjct 554 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAAGTATCGAAACTTTAA 613

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
|||||
Sbjct 614 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 671
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S827 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426019.1 Length: 697
Range 1: 19 to 676

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 19 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 78

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 79 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 138

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 139 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 198

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||||||
Sbjct 199 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 258

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||||||| || || |||||||||| |||||||||||
Sbjct 259 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 318

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||| |||||| |||||||||||||| || |||||||||||||||||||
Sbjct 319 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 378

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||| || |||||||||||||||||||||||||||||| |||||||||||
Sbjct 379 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 438

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||||||||||||| || |||||||||||||| |||||||||||||||
Sbjct 439 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 498

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||| |||||||||||||||||||||||||||||| |||||||||||
Sbjct 499 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 558

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      | |||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct 559 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA 618

Query 601 CACATCATTTTTTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||||||||||||||||| |||||| |||||| |||||| |||||||
Sbjct 619 TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 676
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S1060
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426006.1 Length: 705
Range 1: 28 to 685

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 28 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 87

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 88 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 147

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 148 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 207

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 208 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 267

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||||||| || || |||||||||| |||||||
Sbjct 268 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 327

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||| |||||| |||||||||||||| || |||||||||||||||
Sbjct 328 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 387

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||| |||||||||||||||||||||||||| |||||||||||
Sbjct 388 ATCACATTATGGTCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 447

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||| || |||||||||| |||||| |||||||
Sbjct 448 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATTAATTGGAAT 507

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||| |||||||||||||||||||||| |||||||
Sbjct 508 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 567

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      | |||||||||||||||||||||||||| |||||||||||
Sbjct 568 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 627

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||||||||| |||||| |||||||||| |||||
Sbjct 628 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 685
```

>Rhipicephalus sanguineus haplotype III cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556745.1 Length: 713

Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 27  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 86

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 87  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 146

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 147  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 206

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 207  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 266

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 267  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 326

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 327  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 386

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 387  ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 446

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 447  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 506

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 507  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 566

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |
Sbjct 567  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 626

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 627  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 684
```

>Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: MN593344.1 Length: 710
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

```
Query 1   AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||
Sbjct 684 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 625

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||
Sbjct 624 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 565

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
          |||
Sbjct 564 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 505

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          ||| || |||
Sbjct 504 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 445

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
          |||
Sbjct 444 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 385

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||
Sbjct 384 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 325

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||
Sbjct 324 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 265

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||
Sbjct 264 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 205

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          |||
Sbjct 204 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 145

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
          | |||
Sbjct 144 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 85

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||
Sbjct 84  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT 27
```

>Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidase subunit 1 (COI)

gene, partial cds; mitochondrial
Sequence ID: MN593343.1 Length: 710
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

```
Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 684 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 625

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 624 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 565

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 564 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 505

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| || |||||
Sbjct 504 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 445

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTT 300
|||||
Sbjct 444 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTT 385

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 384 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 325

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 324 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 265

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 264 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 205

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 204 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 145

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
| |||||
Sbjct 144 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 85

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
|||||
Sbjct 84 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 27
```

>Rhipicephalus sanguineus isolate 11N cytochrome oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MN585197.1 Length: 703
Range 1: 22 to 679

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

```
Query 1   AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||
Sbjct 679 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 620

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||
Sbjct 619 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 560

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
          |||
Sbjct 559 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 500

Query 181 AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          |||
Sbjct 499 AGGATTTGGAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 440

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTC 300
          |||
Sbjct 439 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTC 380

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||
Sbjct 379 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 320

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||
Sbjct 319 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 260

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||
Sbjct 259 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 200

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          |||
Sbjct 199 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 140

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
          |
Sbjct 139 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA 80

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||
Sbjct 79  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 22
```

>Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene, partial cds;
mitochondrial gene for mitochondrial product
Sequence ID: AF132839.1 Length: 793
Range 1: 42 to 699

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 42  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 101

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 102 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 161

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 162 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 221

Query 181  AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 222 AGGATTTGGAAATTGATTAGTTCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 281

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTT 300
      |||
Sbjct 282 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTT 341

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 342 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 401

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 402 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 461

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 462 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 521

Query 481  AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 522 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 581

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 582 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 641

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 642 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 699
```

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S56 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426017.1 Length: 680
Range 1: 11 to 668

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 11 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 70

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 71 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 130

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 131 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 190

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 191 AGGATTTGGAAATTGATTAGTTCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 250

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 251 AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTATTAATTAACCTCTTC 310

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 311 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 370

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 371 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 430

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 431 TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 490

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 491 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 550

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
      |||
Sbjct 551 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 610

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 611 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 668
```

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S32 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426008.1 Length: 690
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 14  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 74  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 134  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 193

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| || |||||
Sbjct 194  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 253

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
|||||
Sbjct 254  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 313

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 314  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 374  ATCACATTATGGCCCTTCACTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 434  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 493

Query 481  AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 494  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 553

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 600
| |||||
Sbjct 554  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 613

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
|||||
Sbjct 614  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 671
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1570
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426001.1 Length: 684
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 14  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 74  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 134  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 193

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 194  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 253

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
          |||||||||||||||||||||||||| || ||| ||||||||| |||||||||
Sbjct 254  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 313

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          ||||||||| ||||||| |||||||||||||| || |||||||||||||||
Sbjct 314  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
          ||||||||| || |||||||||||||| ||||||||| |||||||||
Sbjct 374  ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||||||||||||||||| || |||||||||||||| |||||||||||||||
Sbjct 434  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 493

Query 481  AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          ||||||||| |||||||||||||||||||||||||||||||||||||| ||||
Sbjct 494  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 553

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
          | |||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct 554  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 613

Query 601  CACATCATTTTTTATGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||||||||||||||||| ||||||||| ||||||||||||| |||||
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Sbjct 614 TACATCATTTTTTATGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1553
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425998.1 Length: 689
Range 1: 20 to 677

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 20 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 80 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 140 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 199

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| || |||||
Sbjct 200 AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
|||||
Sbjct 260 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 319

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 320 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 380 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 440 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 500 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 559

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
|||||
Sbjct 560 CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 619

Query 601 CACATCATTTTTTATGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
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|||||
Sbjct 620 TACATCATTTTTTGTCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 677

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1551
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425997.1 Length: 695
Range 1: 22 to 679

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	22	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	81
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	82	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	141
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	142	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	201
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	202	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	261
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	262	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	321
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	322	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	381
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	382	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	441
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	442	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	501
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	502	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	561
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	562	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	621

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Query   601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
        |||
Sbjct   622  TACATCATTTTTTTGATCCTTCAGGGGAGGAGATCCAATTTTATATCAACATTTATTT 679

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>Rhipicephalus sanguineus haplotype IV cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556746.1 Length: 771
Range 1: 90 to 747

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query   1    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
        |||
Sbjct   90    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 149

Query   61    AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
        |||
Sbjct   150  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 209

Query   121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
        |||
Sbjct   210  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 269

Query   181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
        |||
Sbjct   270  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 329

Query   241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
        |||
Sbjct   330  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 389

Query   301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
        |||
Sbjct   390  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 449

Query   361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
        |||
Sbjct   450  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 509

Query   421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
        |||
Sbjct   510  TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 569

Query   481  AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
        |||
Sbjct   570  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 629

Query   541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
        |||
Sbjct   630  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 689

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Query   601  CACATCATTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
        |||
Sbjct   690  TACATCATTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 747

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Range 2: 30 to 64

Score:58.4 bits(31), Expect:0.001,
Identities:34/35(97%), Gaps:1/35(2%), Strand: Plus/Plus

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Query   1    AACAAATATATTTAATTTTTGGAGCATGATCA-GGT 34
        |||
Sbjct   30  AACAAATATATTTAATTTTTGGAGCATGATCATGGT 64

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>Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305546.1 Length: 658
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query   1    AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
        |||
Sbjct   1    AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query   61    AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
        |||
Sbjct   61    AATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120

Query   121    AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
        |||
Sbjct   121    AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180

Query   181    AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
        |||
Sbjct   181    AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query   241    AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
        |||
Sbjct   241    AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 300

Query   301    ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
        |||
Sbjct   301    ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query   361    ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
        |||

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Sbjct  361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC  420
Query  421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT  480
          |||||
Sbjct  421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  480
Query  481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT  540
          |||||
Sbjct  481  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
Query  541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA  600
          |
Sbjct  541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA  600
Query  601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
          |||||
Sbjct  601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658

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>Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305545.1 Length: 658
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
          |||||
Sbjct  1    AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
Query  61    AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  120
          |||||
Sbjct  61    AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  120
Query  121   AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG  180
          |||||
Sbjct  121   AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG  180
Query  181   AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG  240
          ||| ||
Sbjct  181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
Query  241   AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC  300
          |||||
Sbjct  241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC  300
Query  301   ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT  360
          |||||
Sbjct  301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
Query  361   ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC  420

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Sbjct	361	 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAAC TATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAC TGATCGAAACTTTAA	600
Sbjct	541	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	 TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	658

>Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152144.1 Length: 675
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	658

>Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MW152143.1 Length: 676
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152142.1 Length: 669
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	301	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAAC TATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAC TGATCGAAACTTTAA	600
Sbjct	541	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	 TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

Score:1050 bits(568), Expect:0.0,
Identities:628/658(95%), Gaps:0/658(0%), Strand: Plus/Plus

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTATAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	554	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	671

>Rhipicephalus sanguineus haplotype I cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556743.1 Length: 659
Range 1: 12 to 659

Score:1048 bits(567), Expect:0.0,
Identities:621/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	AGGATTTGGAAATTGATTAATCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	311

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	372	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	432	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	611
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCA	648
Sbjct	612	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCA	659

>Rhipicephalus sanguineus haplotype II cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556744.1 Length: 787
Range 1: 29 to 688

Score:1046 bits(566), Expect:0.0,
Identities:629/660(95%), Gaps:2/660(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	29	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	88
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	89	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	148
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	149	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	208
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	209	AGGATTTGGAAACTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	268
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	269	AATAAATAATATAAGATTTT	GACTTTTACCTCCTTCACTATTTTTATTAATTA	AACTCTTC	328
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT			360
Sbjct	329	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT			388
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC			420
Sbjct	389	ATCACATTATGGTCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC			448
Query	421	TTCAATTTTAGGTGCAATTA	AACTTCATCACA	ACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	449	TTCAATTTTAGGTGCAATTA	AACTTTATTACA	ACTATTGTAAACATACGATCAATTGGAAT	508
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT			540
Sbjct	509	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT			568
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	AACTGATCGAACTTTAA		600
Sbjct	569	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAACTTTAA		628
Query	601	CACATCATTTTTTTGATCCTTCAGGAGG-AGGAGATCCC-ATTTTATATCAACACTTATTT			658
Sbjct	629	TACATCATTTTTTTGATCCTTCAGGGGGGAGGAGATCCAAATTTTATATCAACTTTTATTT			688

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S943 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426020.1 Length: 812
Range 1: 2 to 644

Score:1038 bits(562), Expect:0.0,
Identities:616/643(96%), Gaps:0/643(0%), Strand: Plus/Plus

Query	16	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	75
Sbjct	2	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	61
Query	76	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	135
Sbjct	62	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	121
Query	136	TGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTTCGGAAATTG	195
Sbjct	122	TGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	181
Query	196	ATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	255
Sbjct	182	ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	241
Query	256	ATTTTGA	315

Sbjct	242	 ATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGG	301
Query	316	AGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCC	375
Sbjct	302	 AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTCC	361
Query	376	ATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGC	435
Sbjct	362	 TTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	421
Query	436	AATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAAT	495
Sbjct	422	 AATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	481
Query	496	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGT	555
Sbjct	482	 ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT	541
Query	556	ATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGA	615
Sbjct	542	 ATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGA	601
Query	616	TCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658	
Sbjct	602	 TCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S337 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF426010.1 Length: 824

Range 1: 1 to 648

Score:1037 bits(561), Expect:0.0,

Identities:619/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	120
Query	131	GCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCCGGA	190
Sbjct	121	GCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTCGA	180
Query	191	AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	240

Query	251	ATAAGATTTTGGACTTTTACCCCCCTCATTATTTTATTGATTA	310
Sbjct	241	ATAAGATTTTGGACTTTTACCTCCTTCACTATTTTATTAATTA	300
Query	311	TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTT	370
Sbjct	301	TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTT	360
Query	371	GGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGT	430
Sbjct	361	GGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGT	420
Query	431	GGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCA	490
Sbjct	421	GGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCA	480
Query	491	CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTT	550
Sbjct	481	CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTT	540
Query	551	CCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAA	610
Sbjct	541	CCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACT	600
Query	611	TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTT	658
Sbjct	601	TTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATT	648

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S344 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426011.1 Length: 809
Range 1: 3 to 644

Score:1031 bits(558), Expect:0.0,
Identities:614/642(96%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	3	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	62
Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	63	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAC	122
Query	137	GCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	123	GCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	182
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	183	TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	242

Query	257	TTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGA	316
Sbjct	243	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGA	302
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	303	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	362
Query	377	TCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTAGGTGCA	436
Sbjct	363	TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTAGGTGCA	422
Query	437	ATTAAGTTCATCACAAGTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	423	ATTAAGTTTATTACAAGTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	482
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	483	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	542
Query	557	TTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTGGAT	616
Sbjct	543	TTAGCAGGTGCCATTACAATATTGTAAAGTATCGAACTTTAATACATCATTTTTTGGAT	602
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	603	CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	644

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S475 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426014.1 Length: 649
Range 1: 28 to 649

Score:1022 bits(553), Expect:0.0,
Identities:599/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	28	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	87
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	88	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	147
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	148	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	207
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240

Sbjct	208	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	267
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	268	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	327
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	328	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	387
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	388	ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	447
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	448	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	507
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	508	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	567
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	568	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	627
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	628	TACATCATTTTTTTGATCCTTCA	649

>Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383818.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5554A cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383819.1 Length: 768
Range 1: 1 to 642

Score:1020 bits(552), Expect:0.0,
Identities:612/642(95%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196

[illegible]

Score:1016 bits(550), Expect:0.0,
Identities:598/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Sbjct	134	 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	 ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	554	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	614	 TACATCATTTTTTTGATCCTTCA	635

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SF3003
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425988.1 Length: 654
Range 1: 1 to 640

Score:1016 bits(550), Expect:0.0,
Identities:610/640(95%), Gaps:0/640(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	 TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	 GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120

Query	137	GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	481	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557	TTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGAT	616
Sbjct	541	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	600
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTAT	656
Sbjct	601	CCTTCAGGGGGAGGACATCCAATTTTATATCACCATTAT	640

>Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383811.1 Length: 764
>Rhipicephalus sanguineus isolate LIC5533C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383812.1 Length: 764
Range 1: 1 to 638

Score:1013 bits(548), Expect:0.0,
Identities:608/638(95%), Gaps:0/638(0%), Strand: Plus/Plus

Query	21	GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC	80
Sbjct	1	GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC	60

Query	81	AACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT	140
Sbjct	61	AACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT	120
Query	141	TTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAG	200
Sbjct	121	TTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAG	180
Query	201	TTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	260
Sbjct	181	TCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	240
Query	261	GACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTG	320
Sbjct	241	GACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTG	300
Query	321	GAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAG	380
Sbjct	301	GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG	360
Query	381	TAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	440
Sbjct	361	TAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	420
Query	441	ACTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCAT	500
Sbjct	421	ACTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCAT	480
Query	501	TATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAG	560
Sbjct	481	TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG	540
Query	561	CAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTT	620
Sbjct	541	CAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTT	600
Query	621	CAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	CAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	638

>Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383807.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383808.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736F cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383810.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5535C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383813.1 Length: 763
Range 1: 1 to 637

Score:1011 bits(547), Expect:0.0,
Identities:607/637(95%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACA 81
      |||
Sbjct 1 AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACA 60

Query 82 ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT 141
      |||
Sbjct 61 ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT 120

Query 142 TATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGT 201
      |||
Sbjct 121 TATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
      |||
Sbjct 181 CCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 ACTTTTACCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGG 321
      |||
Sbjct 241 ACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGG 300

Query 322 AACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGT 381
      |||
Sbjct 301 TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT 360

Query 382 AGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA 441
      |||
Sbjct 361 AGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA 420

Query 442 CTTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATT 501
      |||
Sbjct 421 CTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATT 480

Query 502 ATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGC 561
      |||
Sbjct 481 ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC 540

Query 562 AGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTATCCTTC 621
      |||
Sbjct 541 AGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTATCCTTC 600

Query 622 AGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 601 AGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 637
```

>Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subunit I (COI) gene,

partial cds; mitochondrial
Sequence ID: KU568516.1 Length: 656
Range 1: 27 to 656

Score:1009 bits(546), Expect:0.0,
Identities:602/630(96%), Gaps:0/630(0%), Strand: Plus/Plus

```
Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 27  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 86

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 87  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 146

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 147  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 206

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||
Sbjct 207  AGGATTTGGAAATTGATTAATCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 266

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTT 300
      |||
Sbjct 267  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTT 326

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 327  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 386

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 387  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 446

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 447  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 506

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 507  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 566

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |||
Sbjct 567  CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 626

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGG 630
      |||
Sbjct 627  TACATCATTTTTTTGACCCTTCAGGAGGAGG 656
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>Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383809.1 Length: 762
Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
Sbjct	1	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83	CCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142
Sbjct	61	CCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143	ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT	202
Sbjct	121	ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA	322
Sbjct	241	CTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA	382
Sbjct	301	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	GATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA	502
Sbjct	421	TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA	562
Sbjct	481	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540
Query	563	GGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTGTATCCTTCA	622
Sbjct	541	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGTATCCTTCA	600
Query	623	GGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT	636

>Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383806.1 Length: 714
Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

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Query 23 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA 82
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA 60

Query 83 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT 142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT 120

Query 143 ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT 202
          ||||||||| ||||||||||||||||||||||||| || |||||||||||||
Sbjct 121 ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC 180

Query 203 CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA 262
          ||||| ||||| ||||||||||||||||||||||||| |||||||||||||
Sbjct 181 CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA 240

Query 263 CTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA 322
          ||||||||| || ||| ||||||||| ||||||||||||||||||||| |||||||||
Sbjct 241 CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT 300

Query 323 ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA 382
          ||||||||||||||||| || ||||||||||||||||||||||||| || |||||||
Sbjct 301 ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA 360

Query 383 GATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC 442
          ||||||||| ||||||||| ||||||||||||||||||||||||| |||||||||
Sbjct 361 GATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC 420

Query 443 TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA 502
          || || ||||||||||||| ||||| ||||||||||||||||||||| |||||||||
Sbjct 421 TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA 480

Query 503 TTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA 562
          ||||||||||||||||||||||||||||||||| ||||| |||||||||||||||||
Sbjct 481 TTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA 540

Query 563 GGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCA 622
          ||||||||||||||||| ||||||||||||||||| |||||||||||||||||
Sbjct 541 GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA 600

Query 623 GGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          || ||||||||| ||||||||| |||||
Sbjct 601 GGGGGAGGAGATCCAATTTTATATCAACATTTATTT 636
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>Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383805.1 Length: 761
Range 1: 1 to 635

Score:1007 bits(545), Expect:0.0,
Identities:605/635(95%), Gaps:0/635(0%), Strand: Plus/Plus

Query	24	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	83
Sbjct	1	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	60
Query	84	CTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	143
Sbjct	61	CTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	120
Query	144	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTC	203
Sbjct	121	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	180
Query	204	CTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	263
Sbjct	181	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	240
Query	264	TTTTACCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAA	323
Sbjct	241	TTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTA	300
Query	324	CAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAG	383
Sbjct	301	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	360
Query	384	ATTTAGCTATTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	443
Sbjct	361	ATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	444	TCATCACAACATTTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTAT	503
Sbjct	421	TTATTACAACATTTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTAT	480
Query	504	TTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAG	563
Sbjct	481	TTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	540
Query	564	GTGCCATTACAATATTATTAACGATCGAAACTTTAACACATCATTTTTTGATCCTTCAG	623
Sbjct	541	GTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAG	600
Query	624	GAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	GGGGAGGAGATCCAATTTTATATCAACATTTATTT	635

>Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630347.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 20  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 80  AATTGGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct 140  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 199

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||||
Sbjct 200  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 259

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||||||| || || |||||||||| |||||||||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTTATTAATTAACCTCTTC 319

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||| |||||| |||||||||||||| || |||||||||||||||||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||| || |||||||||||||||||||||||||||||||||||||
Sbjct 380  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||||||||| || |||||||||| |||||||||||||
Sbjct 440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct 500  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 559

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
      | |||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct 560  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 619

Query 601  CACATCATTTTTTTGATCCTTCA 622
      |||||||||
Sbjct 620  TACATCATTTTTTTGATCCTTCA 641
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>Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630346.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 20  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 80  AATTGGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct 140  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 199

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||||| |||| |||| ||||||||||||||||||||
Sbjct 200  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 259

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||||| || ||| ||||||||| |||||||||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 319

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      ||||||||| ||||||| |||||||||||||| || ||||||||||||||||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      ||||||||| || |||||||||||||| |||||||||||||| |||||||||
Sbjct 380  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||||||||||| || |||||||||||||| ||||||||||||||||
Sbjct 440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      ||||||||| |||||||||||||||||||||||||||||||||| ||||
Sbjct 500  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 559

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
      | |||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct 560  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 619

Query 601  CACATCATTTTTTTGATCCTTCA 622
      ||||||||||||||||
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Sbjct 620 TACATCATTTTTTGATCCTTCA 641

>Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519712.1 Length: 654
Range 1: 3 to 628

Score:1002 bits(542), Expect:0.0,
Identities:598/626(96%), Gaps:0/626(0%), Strand: Plus/Plus

```
Query 33 GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT 92
          |||
Sbjct 3 GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT 62

Query 93 TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT 152
          |||
Sbjct 63 TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT 122

Query 153 TCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATAT 212
          | |||
Sbjct 123 TTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT 182

Query 213 TAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCC 272
          | |||
Sbjct 183 TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC 242

Query 273 CCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAA 332
          | |||
Sbjct 243 CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA 302

Query 333 CAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTA 392
          |||
Sbjct 303 CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA 362

Query 393 TTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAA 452
          |||
Sbjct 363 TTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAA 422

Query 453 CTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGAT 512
          |||
Sbjct 423 CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT 482

Query 513 CTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTA 572
          |||
Sbjct 483 CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA 542

Query 573 CAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAG 632
          |||
Sbjct 543 CAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG 602

Query 633 ATCCCATTTTATATCAACACTTATTT 658
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Sbjct 603 |||| |||||||||||||| |||||
ATCCAATTTTATATCAACATTTATTT 628

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1575
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426002.1 Length: 639
Range 1: 1 to 628

Score:1000 bits(541), Expect:0.0,
Identities:599/628(95%), Gaps:0/628(0%), Strand: Plus/Plus

Query	31	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	90
Sbjct	1	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	60
Query	91	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	150
Sbjct	61	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	120
Query	151	TTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTAT	210
Sbjct	121	TTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	180
Query	211	ATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	270
Sbjct	181	ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	240
Query	271	CCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATG	330
Sbjct	241	TCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATG	300
Query	331	AACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGC	390
Sbjct	301	AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC	360
Query	391	TATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCAC	450
Sbjct	361	TATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTAC	420
Query	451	AACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTG	510
Sbjct	421	AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG	480
Query	511	ATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCAT	570
Sbjct	481	ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT	540
Query	571	TACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGG	630
Sbjct	541	TACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGG	600

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Query   631  AGATCCCATTTTATATCAACACTTATTT  658
        ||||| ||||||||||||| |||||
Sbjct   601  AGATCCAATTTTATATCAACATTTATTT  628

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>Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855658.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  98
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
        ||||||||||||||||||||| || ||||||||||||| ||||| ||||| |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
        ||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
        ||||||||| ||||||||||||||||||||| ||||||| |||||||||||||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
        | || ||||||||||||||||||||||||||||| || |||||||||||||||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG  458
        ||||||| ||||||||||||||||||||||||||||||||| || |||||||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
        ||||| ||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        ||||||||||||||||| ||||| |||||||||||||||||||||||||||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        | ||||||||||||||||| ||||||||||||| ||||||||| |||||
Sbjct   541  TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600

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Query   639   TTTTATATCAACACTTATTT   658
          |||||
Sbjct   601   TTTTATATCAACATTTATTT   620

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>Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855657.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
          |||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
          |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
          |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
          |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
          |||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
          |||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
          |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
          |||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
          |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAACGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
          |||||

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Sbjct 541 TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
 |||||

Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase subunit I (cox1)
 gene, partial cds; mitochondrial
 Sequence ID: MG855656.1 Length: 630
 Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
 Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
 |||||

Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
 |||||

Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
 |||||

Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
 |||||

Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
 |||||

Sbjct 241 TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
 |||||

Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAACCTATTG 458
 |||||

Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
 |||||

Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
 |||||

Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638

[illegible]

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	579	TATTA	ACTGATCGAA	ACTTTA	ACATCAT	TTTTTT	GATCCTTC	CAGGAGG	GAGAGAT	CCCA	638	
Sbjct	541	TGT	TA	ACTGATCGAA	ACTTTA	ATACATCAT	TTTTTT	GATCCTTC	CAGGGG	GAGAGAT	C	600
Query	639	TTTTATATCA	AACTTATTT	658								
Sbjct	601	TTTTATATCA	AATTTATTT	620								

>Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757904.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	TTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	TTTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTAT	ATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	ATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTAC	CCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTAC	CTCCTTAC	240
Query	279	TATTTTTATTGATTA	AACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTA	AACTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAG	CTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAG	CTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	AACTTCATCACA	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	AACTTTATTACA	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTG	TTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTG	TTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCC	ATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	ATTACAATAT	540

Query	579	TATTA	ACTGATCGAA	ACTTTA	ACATCAT	TTTTTT	GATCCTTC	CAGGAGG	GAGATCCCA	638
Sbjct	541	TGTTA	ACTGATCGAA	ACTTTA	ATACATCAT	TTTTTT	GATCCTTC	CAGGGGG	GAGATCCAA	600
Query	639	TTTTATATCA	AACTTATTT	658						
Sbjct	601	TTTTATATCA	AATTTATTT	620						

>Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757902.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158	
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120	
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218	
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180	
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278	
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240	
Query	279	TATTTTTATTGATTA	ACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398	
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360	
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	AACTTCATCACAACTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	AACTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518	
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480	
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578	

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757896.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757889.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTCGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480

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Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        |||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATGATCGAAACTTTAACACATCATTCTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        | |||
Sbjct   541  TGTTAAGTATGATCGAAACTTTAATACATCATTCTTTGATCCTTCAGGGGGAGGAGATCCAA  600

Query   639  TTTTATATCAACACTTATTT  658
        |||
Sbjct   601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate Rovind cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757887.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```

Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  98
        |||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA  158
        |||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
        |||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
        |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
        |||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
        | |||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG  458
        |||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
        |||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480

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Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
          |||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
          | |||
Sbjct   541  TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600

Query   639  TTTTATATCAACACTTATTT  658
          |||
Sbjct   601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757879.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```

Query   39  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  98
          |||
Sbjct   1  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  60

Query   99  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
          |||
Sbjct   61  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
          |||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
          |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
          |||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTT  398
          | ||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTT  360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG  458
          |||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
          |||

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Sbjct  421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480
Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        ||||||||||||||||| ||||| |||||||||||||||||||||||||||||||||||
Sbjct  481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540
Query   579  TATTAAGTATCGAAACTTTAACAACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        ||||||||||||||||||| ||||||||||||||||||| |||||||||||||
Sbjct  541  TGTTAAGTATCGAAACTTTAACAACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600
Query   639  TTTTATATCAACACTTATTT  658
        ||||||||||||| |||||
Sbjct  601  TTTTATATCAACATTATTT  620

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>Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519711.1 Length: 636
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  98
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  60
Query   99  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA  120
Query  159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
        ||||||||||||||||||||| || ||||||||||||| ||||| ||||| |||||
Sbjct 121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180
Query  219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
        ||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct 181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240
Query  279  TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
        ||||||||| ||||||||||||||||||||| ||||||| |||||||||||||||
Sbjct 241  TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300
Query  339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
        | || ||||||||||||||||||||||||||||| || |||||||||||||||||
Sbjct 301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360
Query  399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAACATTTG  458
        ||||||| ||||||||||||||||||||||||||||||||||||| || |||||||||
Sbjct 361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATTACAACATTTG  420
Query  459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518

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Sbjct	421		480
		TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135448.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420

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Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
      ||||| ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGACGTATACCATTATTTGTTTGATCTGTTT  480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
      |||||||||||||||| ||||| |||||||||||||||||||||||||||||||||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
      | |||||||||||||||| ||||||||||||||||||| |||||||||||||
Sbjct   541  TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600

Query   639  TTTTATATCAACACTTATTT  658
      |||||||||||| |||||
Sbjct   601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757905.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  98
      ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct   1  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  60

Query   99  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
      ||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct   61  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
      |||||||||||||||||| || ||||||||||||| ||||| ||||| |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
      ||||||||||||||||||||||||||||||||||| || |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
      ||||||||| ||||| |||||||||||||||| ||||||| |||||||||||||
Sbjct   241  TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
      | || |||||||||||||||||||||||||||| || |||||||||||||||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTT  360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG  458
      ||||||| ||||||||||||||||||||||||| || |||||||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

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Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```

Sbjct  361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTG  420
Query  459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
      ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480
Query  519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
      ||||||||||||||||||| ||||| |||||||||||||||||||
Sbjct  481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540
Query  579  TATTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
      | ||||||||||||||||| ||||||||||||||||||| |||||||||
Sbjct  541  TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600
Query  639  TTTTATATCAACACTTATTT  658
      ||||||||| |||||
Sbjct  601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate Zadar cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX757892.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```

Query  39  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  98
      |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1  TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACTTTAATTG  60
Query  99  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
      ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  61  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA  120
Query  159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
      ||||||||||||||||||| || ||||||||||||||| ||||| ||||| ||||
Sbjct  121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180
Query  219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
      ||||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct  181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240
Query  279  TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
      ||||||||| ||||||||||||||||||||| ||||||| |||||||||||||||
Sbjct  241  TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300
Query  339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
      | || ||||||||||||||||||||||||||||| || |||||||||||||||
Sbjct  301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360
Query  399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACATTG  458

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Sbjct	361		420
		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757890.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAATGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTT	360

Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACCTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757888.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360

Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACCTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Petnica cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757883.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398

Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519708.1 Length: 629
Range 1: 4 to 620

Score:985 bits(533), Expect:0.0,
Identities:589/617(95%), Gaps:0/617(0%), Strand: Plus/Plus

Query	42	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	101
Sbjct	4	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	63
Query	102	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAG	161
Sbjct	64	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAG	123
Query	162	TTATACCAATCATAATCGGAGGGTTCGGAATGATTAGTTCCTATTATATTAGGTGCCC	221
Sbjct	124	TTATACCAATCATAATCGGAGGATTTGGAATGATTAGTCCCTATCATATTGGGTGCCC	183
Query	222	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCTCATTAT	281
Sbjct	184	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT	243
Query	282	TTTTATTGATTAACCTTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATC	341
Sbjct	244	TTTTATTAATTAACCTTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC	303
Query	342	CCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTC	401

Sbjct	304		CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTC	363
Query	402		TTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACATTGTAA	461
Sbjct	364		TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACATTGTAA	423
Query	462		ATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAA	521
Sbjct	424		ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA	483
Query	522		TTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTAT	581
Sbjct	484		TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	543
Query	582		TAACTGATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATT	641
Sbjct	544		TAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGAGGAGATCCAATT	603
Query	642		TATATCAACACTTATTT 658	
Sbjct	604		TATATCAACATTTATTT 620	

>Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135447.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTA	120
Query	159		TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTAC	240
Query	279		TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300

[illegible]

Score:983 bits(532), Expect:0.0,
Identities:588/616(95%), Gaps:0/616(0%), Strand: Plus/Plus

Query	343	CCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT	402
Sbjct	301	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT	360
Query	403	TCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAA	462
Sbjct	361	TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA	420
Query	463	TATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT	522
Sbjct	421	CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523	TACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT	582
Sbjct	481	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583	AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	642
Sbjct	541	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	600
Query	643	ATATCAACACTTATTT 658	
Sbjct	601	ATATCAACATTTATTT 616	

>Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757901.1 Length: 630
Range 1: 1 to 620

Score:979 bits(530), Expect:0.0,
Identities:590/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338

Sbjct	241	TATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:974 bits(527), Expect:0.0,
Identities:589/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	62	ATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTA	121
Sbjct	1	ATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTA	60
Query	122	ATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGA	181
Sbjct	61	ATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATTGGA	120
Query	182	GGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGA	241
Sbjct	121	GGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGA	180
Query	242	ATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCA	301

Sbjct	181		ATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCA	240
Query	302		TTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTA	361
Sbjct	241		TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA	300
Query	362		TCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCT	421
Sbjct	301		TCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCT	360
Query	422		TCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATA	481
Sbjct	361		TCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATA	420
Query	482		ACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTT	541
Sbjct	421		ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT	480
Query	542		CTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAAC	601
Sbjct	481		TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAAT	540
Query	602		ACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	541		ACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	597

>Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519713.1 Length: 580
Range 1: 1 to 580

Score:933 bits(505), Expect:0.0,
Identities:555/580(96%), Gaps:0/580(0%), Strand: Plus/Plus

Query	43		ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	102
Sbjct	1		ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	60
Query	103		TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGT	162
Sbjct	61		TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT	120
Query	163		TATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCC	222
Sbjct	121		TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	180
Query	223		AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATT	282
Sbjct	181		AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	240

Query	283	TTTATTGATTA	ACTCTTCATTA	AATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC	342
Sbjct	241	TTTATTAATTA	ACTCTTCATTA	AATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	300
Query	343	CCCTCTATCTT	CAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT	402	
Sbjct	301	TCCTCTATCTT	CAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT	360	
Query	403	TCACCTTGCTGGT	GCTTCTTCAATTTTAGGTGCAATTA	AACTTCATCACA	ACTATTGTAAA
Sbjct	361	TCATCTTGCTGGT	GCTTCTTCAATTTTAGGTGCAATTA	AACTTTATTACA	ACTATTGTAAA
Query	463	TATACGATCAATT	GGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT	522	
Sbjct	421	CATACGATCAATT	GGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480	
Query	523	TACAGCTATTTT	ACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT	582	
Sbjct	481	TACAGCTATTTT	ATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540	
Query	583	AACTGATCGAA	ACTTTTAACACATCATTTTTTTGATCCTTCA	622	
Sbjct	541	AACTGATCGAA	ACTTTTAATACATCATTTTTTTGATCCTTCA	580	

>Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519706.1 Length: 595
Range 1: 1 to 570

Score:898 bits(486), Expect:0.0,
Identities:542/570(95%), Gaps:0/570(0%), Strand: Plus/Plus

Query	89	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	148		
Sbjct	1	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	60		
Query	149	ATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATT	208		
Sbjct	61	ATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATC	120		
Query	209	ATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	268		
Sbjct	121	ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	180		
Query	269	CCCCCTCATTATTTTTATTGATTA	ACTCTTCATTA	AATTGAATCCGGAGCTGGAACAGGA	328
Sbjct	181	CCTCCTTCACTATTTTTATTAATTA	AACTCTTCATTA	AATTGAATCTGGAGCTGGTACAGGA	240
Query	329	TGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTA	388		
Sbjct	241	TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA	300		

Query	389	GCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTCATC	448
Sbjct	301	GCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTTATT	360
Query	449	ACAAC TATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTT	508
Sbjct	361	ACAAC TATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT	420
Query	509	TGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCC	568
Sbjct	421	TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	480
Query	569	ATTACAATATTATTAAC TATGATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGA	628
Sbjct	481	ATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGA	540
Query	629	GGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	541	GGAGATCCAATTTTATATCAACATT TATTT	570

>Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase subunit 1 gene,
partial cds; mitochondrial
Sequence ID: KY678135.1 Length: 790
Range 1: 18 to 675

Score:883 bits(478), Expect:0.0,
Identities:599/659(91%), Gaps:2/659(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	18	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	77
Query	61	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	78	AATTCGTATAGAATTAGGCCAACCTGGAAC CCTAATTGGTAATGATCAAATTTATAATGT	137
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	138	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	197
Query	181	AGGGTTCGGA AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	198	TGGATTTGGAACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAAC TCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	317
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC-CCCTCTATCTTCAAATT	359

Sbjct	318	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCT-TATCCTCAAATT	376
Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTT	419
Sbjct	377	TATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTT	436
Query	420	CTTCAATTTTAGGTGCAATTAACCTTCATCACAACATTGTAAATATACGATCAATTGGAA	479
Sbjct	437	CTTCAATTTTAGGTGCAATTAATTTTATTACAACATTGTAAATATACGATCTATTGGAA	496
Query	480	TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	497	TAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAC	556
Query	540	TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACGATCGAAACTTTA	599
Sbjct	557	TATTATCTTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCGATCGAAATTTA	616
Query	600	ACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	617	ACACTTCATTTTTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	675

>Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800313.1 Length: 673
Range 1: 8 to 665

Score:883 bits(478), Expect:0.0,
Identities:598/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCTATTATAATTGG	187
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTTCATTATTTCTATTAATTAACCTCTTC	307
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	308	 ATTAATTGAATCAGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	 ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	 TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	488	 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	548	 CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAACCTGATCGAAATTTCAA	607
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	608	 TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATTT	665

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SC3005
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425987.1 Length: 574
Range 1: 1 to 561

Score:881 bits(477), Expect:0.0,
Identities:533/561(95%), Gaps:0/561(0%), Strand: Plus/Plus

Query	98	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTT	157
Sbjct	1	 GGAAATGATCAGATTTATAATGTAATCGTAACAGCACACGCATTTATTATAATTTTTTTT	60
Query	158	ATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGT	217
Sbjct	61	 ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATTATATTAGGT	120
Query	218	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCA	277
Sbjct	121	 GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA	180
Query	278	TTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTT	337
Sbjct	181	 CTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT	240
Query	338	TATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTT	397
Sbjct	241	 TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTT	300

Query	398	TCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATT	457
Sbjct	301	TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATT	360
Query	458	GTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTT	517
Sbjct	361	GTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTT	420
Query	518	TTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	577
Sbjct	421	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	480
Query	578	TTATTAACCTGATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCC	637
Sbjct	481	TTGTTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCA	540
Query	638	ATTTTATATCAACACTTATTT	658
Sbjct	541	ATTTTATATCAACATTTATTT	561

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (C01) gene, partial cds;
mitochondrial

Sequence ID: KU214592.1 Length: 829

Range 1: 1 to 648

Score:876 bits(474), Expect:0.0,

Identities:590/648(91%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGCCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGTAATTGTTACA	120
Query	131	GCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGA	190
Sbjct	121	GCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGTGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTCATTAATTGAG	300
Query	311	TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCAGGAGCAGGTACAGGATGGACAGTTTATCCTCCCCTATCCTCAAATTTATCACATTAT	360

Query	371	GGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA	550
Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACTATTATCTTTA	540
Query	551	CCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTT	610
Sbjct	541	CCTGTTTTAGCAGGTGCCATTACAATATTATTAACCGATCGAAATTTTAACACTTCATTT	600
Query	611	TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	648

>Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MT079206.1 Length: 678
Range 1: 1 to 652

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCTG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCTG	60
Query	67	TATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTT	186
Sbjct	121	AACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	CGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAAA	246
Sbjct	181	TGGAAACTGGTTAGTTCCTAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACA	366

Sbjct	301	TGAATCTGGGGCAGGGACAGGGTGAAGTGTATCTCTCTTTATCTCAAATTTATCCCA	360
Query	367	TTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTTCATTACAACCTATTGTAAACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCTGATCGAAATTTAACACTTC	600
Query	607	ATTTTTTGATCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	ATTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTATTT	652

>Rhipicephalus sanguineus isolate GY34 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MN862754.1 Length: 678
Range 1: 1 to 652

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCTG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCTG	60
Query	67	TATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTT	186
Sbjct	121	AACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	CGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181	TGGAAACTGGTTAGTTCCAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACA	366

Sbjct	301	TGAATCTGGGGCAGGGACAGGGTGAAGTGTATCTCTTATCTCTCAAAATTTATCCCA	360
Query	367	TTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTTCATTACAACCTATTGTAAACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCCTATTATTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAAGTATCGAAATTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	ATTTTTTGACCTTCAGGAGGAGGTGACCAATTTTATATCAACATTTATTT	652

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCTCAAATTT	404
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	645	CACTTCATTTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTATTT	702

>Rhipicephalus sanguineus isolate Tehran cytochrome oxidase subunit 1 gene,
complete cds; mitochondrial
Sequence ID: KM494915.1 Length: 1539
Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	344

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCCTCAAATTT	404
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTATTACAACCTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	645	CACCTCATTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACACTTATTT	702

>Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800314.1 Length: 673
Range 1: 8 to 664

Score:870 bits(471), Expect:0.0,
Identities:595/657(91%), Gaps:0/657(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCCATTATAATTGG	187
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTTCATTATTTCTATTAATTAACCTCTC	307
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCGGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTATCCTCAAATTT	367
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAACCTGATCGAAATTTCAA	607
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATT	657
Sbjct	608	TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATT	664

>Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606303.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300

Sbjct	306	 AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTCAATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial

Sequence ID: KY606302.1 Length: 873

Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,

Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATTTATGTTAGGAGCTCCAGACATAGCATTTCCACG	305

Query	241	AATAAATAATATAAGATTTTGA	CTTTTACCCCCCTCATTATTTT	TATTGATTA	AACTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGA	TACTTCTCCCTCATTATTCTT	ATTAATTA	ATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGA	ACAGGATGAACAGTTTATCCC	CCTCTATCTT	CAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGG	ACAGGATGAACTGTCTACC	CTCCTTTATCTT	CAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTA	GATTTAGCTATTTTTTCTCTT	CACCTTGCTGGT	GCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTA	GATTTAGCTATCTTCTCTCTT	CATCTCGCTGGT	GCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAAC	TTCATCACA	ACTATTGTAA	TATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAAT	TCATTACA	ACTATTGTAA	ACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTAT	TTGTTTGATCTGTTTTAATTAC	AGCTATTTTACTACT		540
Sbjct	546	AACAATAGAACGAATACCATTAT	TCGTTTGATCTGTTTTAATCAC	CGCTATTTTATTGCT		605
Query	541	TCTATCTTTACCTGTATTAGCAG	GTGCCATTACAATATTATTAAC	TGATCGAAACTTTAA		600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAG	GTGCCATTACAATATTATTAAC	TGATCGAAATTTCAA		665
Query	601	CACATCATTTTTTTGATCCTTC	AGGAGGAGGAGATCCCATTTT	TATCAACACTTATTT		658
Sbjct	666	CACTTCATTTTTTTGACCCTTC	AGGAGGAGGTGACCCTATTTT	TATCAACATTTATTT		723

>Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial

Sequence ID: KY606301.1 Length: 873

Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,

Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTTGG	AGCATGATCAGGTATATTAGG	ACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTTGG	AGCATGATCCGGGATATTAGG	ATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAAC	CTGGAACTTTAATTGGAAATG	ATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAAC	CTGGAACTTTAATTGGAAATG	ATCAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTT	ATTATAATTTCTTTATAGTT	TATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTT	ATTATAATTTTTTTTATAGT	AATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTT	CTATTATATTAGGTGCCCCAG	ATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGT	GCCCATTATGTTAGGAGCTC	CAGACATAGCATTTCCACG	305

Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTCAATACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606300.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240

Sbjct	246	AGGATTTGGAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTCAATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KY606299.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240

Query	181	AGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTCGGAAATTGATTAGTCCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGATTACTTCCTCCTTCATTATTTTTATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC-CCCTCTATCTTCAAATT	359
Sbjct	345	ATTAATTGAATCAGGAGCAGGGACAGGATGAACAGTTTACCCTCCCT-TATCATCAAATT	403
Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTT	419
Sbjct	404	TATCACACTATGGTCCATCAGTAGATCTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTT	463
Query	420	CTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAA	479
Sbjct	464	CTTCAATTTTAGGCGCAATTAATTTTCATTACAACCATTGTAAACATACGATCTATTGGAA	523
Query	480	TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	524	TAACAATAGAACGAATACCTTTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAT	583
Query	540	TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTA	599
Sbjct	584	TATTATCTTTACCAGTTTTAGCTGGTGCAATTACAATATTATTAACCTGATCGAAATTTTA	643
Query	600	ACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	644	ATACCTCGTTCTTTGATCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Sbjct	121	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTTATAGTAATACCAATCATAATTGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCTCCTTTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAACCTATTGTAAATATACGATCTATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	600
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	658

>Rhipicephalus turanicus isolate Xinjiang-WQIA cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: MF002581.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATAACCAATCATAATCGG	180

Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCTCGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACAG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCACAG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAC TGGATGAAC TGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTAC GACTATTATAA ATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA AACTGATCGAAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTA AACTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002580.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	134		193
		AATTCGAATAGAATTAGGCCAACCTGGAACTTAATTGGAAATGATCAAATTTATAATGT	
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate SHZ cytochrome oxidase subunit I (C01) gene,
partial cds; mitochondrial
Sequence ID: KY069271.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate FK-1 cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial

Sequence ID: KY606291.1 Length: 889

Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,

Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate YN3 cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606290.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60

Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate YN2 cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606289.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
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Sbjct	74	 AACAATATATTTAATTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	 AATTCGAATAGAATTAGGCCAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	 AATTGTAACAGCCCATGCATTTATTATAATTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	 TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTC	300
Sbjct	314	 AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	 ATTAATTGAATCAGGAGCAGGAACCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	 ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	 TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	 AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	614	 TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	 CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Query #4: TKCJJ093-19|TKCJ012018H09|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26766 Length: 658

Sequences producing significant alignments:

Common	Max	Total Query	E	Per.	Acc.	Scientific
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Description Name	Taxid	Score	Score cover	Value	Ident	Len	Name Accession
Rhipicephalus sanguineus mitochondrial DNA, complete genome							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14710
AF081829.1							
Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	629
KX757893.1							
Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1129	1129	94%	0.0	99.52	630
KX757903.1							
Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidas...							
Rhipicephalu... brown dog tick	34632	1112	1112	94%	0.0	99.03	630
KX757909.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1072	1072	100%	0.0	96.05	692
MF426015.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	675
MF426018.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	680
MF426016.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	693
MF426013.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	679
MF426009.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	686
MF426007.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	697
MF426019.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	705
MF426006.1							
Rhipicephalus sanguineus haplotype III cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	713
KU556745.1							
Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	710
MN593344.1							
Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	710
MN593343.1							
Rhipicephalus sanguineus isolate 11N cytochrome oxidase subuni...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	703
MN585197.1							
Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene,...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	793
AF132839.1							

Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426017.1	34632	1055	1055	100%	0.0	95.59	680
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426008.1	34632	1055	1055	100%	0.0	95.59	690
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426001.1	34632	1055	1055	100%	0.0	95.59	684
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF425998.1	34632	1055	1055	100%	0.0	95.59	689
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF425997.1	34632	1055	1055	100%	0.0	95.59	695
Rhipicephalus sanguineus haplotype IV cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	KU556746.1	34632	1055	1113	100%	0.0	95.59	771
Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MZ305546.1	34632	1055	1055	100%	0.0	95.59	658
Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MZ305545.1	34632	1055	1055	100%	0.0	95.59	658
Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MW152145.1	34632	1055	1055	100%	0.0	95.59	676
Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MW152144.1	34632	1055	1055	100%	0.0	95.59	675
Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MW152143.1	34632	1055	1055	100%	0.0	95.59	676
Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MW152142.1	34632	1055	1055	100%	0.0	95.59	669
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426012.1	34632	1050	1050	100%	0.0	95.44	684
Rhipicephalus sanguineus haplotype I cytochrome oxidase subuni...								
Rhipicephalu... brown dog tick	KU556743.1	34632	1048	1048	98%	0.0	95.83	659
Rhipicephalus sanguineus haplotype II cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	KU556744.1	34632	1046	1046	100%	0.0	95.30	787
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426020.1	34632	1038	1038	97%	0.0	95.80	812
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426010.1	34632	1037	1037	98%	0.0	95.52	824
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426011.1	34632	1031	1031	97%	0.0	95.64	809

Rhipicephalus camicasi isolate SC0126 mitochondrion, complete...								
Rhipicephalu... NA	669981	861	861	100%	0.0	90.29	14725	
NC_061616.1								
Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase...								
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	658	
MZ305547.1								
Rhipicephalus turanicus isolate Xinjiang-WQIA cytochrome oxida...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002581.1								
Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002580.1								
Rhipicephalus turanicus isolate Xinjiang-BC cytochrome oxidase...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002579.1								
Rhipicephalus turanicus isolate Xinjiang-YC cytochrome oxidase...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002578.1								
Rhipicephalus turanicus isolate Xinjiang-PS cytochrome oxidase...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002577.1								
Rhipicephalus turanicus isolate SHZ cytochrome oxidase subunit...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY069271.1								
Rhipicephalus turanicus isolate FK-1 cytochrome oxidase subuni...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606291.1								
Rhipicephalus turanicus isolate YN3 cytochrome oxidase subunit...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606290.1								
Rhipicephalus turanicus isolate YN2 cytochrome oxidase subunit...								
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606289.1								

Alignments:

>Rhipicephalus sanguineus mitochondrial DNA, complete genome
Sequence ID: AF081829.1 Length: 14710
Range 1: 1191 to 1848

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1191	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	1250
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	1251	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	1310
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180

Sbjct	1311	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	1370
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	1371	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	1430
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	1431	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	1490
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	1491	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	1550
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	1551	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	1610
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	1611	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	1670
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	1671	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	1730
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1731	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	1790
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	1791	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	1848

>Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757893.1 Length: 629
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218

Sbjct	121		180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTAACCTGATCGAAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757903.1 Length: 630
 Range 1: 1 to 620

Score:1129 bits(611), Expect:0.0,
 Identities:617/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120

Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTCATTAAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAATTCTTCATTAAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTAACCTGATCGAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757909.1 Length: 630
Range 1: 1 to 620

Score:1112 bits(602), Expect:0.0,
Identities:614/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120

Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATAATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTCATTAATTGAATCTGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGCCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTGACTGATCGAAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGGGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S48 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426015.1 Length: 692
Range 1: 19 to 676

Score:1072 bits(580), Expect:0.0,
Identities:632/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGGTTCGGAATTTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGTCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	618
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	619	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S58 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426018.1 Length: 675
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	71	 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	251	 AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTTATTAATTAACCTCTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	 ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	551	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S52 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426016.1 Length: 680
Range 1: 12 to 669

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	12	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	311
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	372	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	432	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	611
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	612	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	669

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S37 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426013.1 Length: 693
Range 1: 20 to 677

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	619
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	620	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	677

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S33 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426009.1 Length: 679
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60

Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S29 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426007.1 Length: 686
Range 1: 14 to 671

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
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Sbjct	14	 AACAATATATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	 ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	554	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S827 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426019.1 Length: 697
Range 1: 19 to 676

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	618
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	619	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S1060
 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
 Sequence ID: MF426006.1 Length: 705
 Range 1: 28 to 685

Score:1061 bits(574), Expect:0.0,
 Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	28	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	87
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	88	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	147
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	148	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	207
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	208	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	267
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	268	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	327
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	328	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	387
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	388	ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	447
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	448	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATTAATTGGAAT	507
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	508	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	567
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	568	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	627
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	628	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	685

>Rhipicephalus sanguineus haplotype III cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556745.1 Length: 713
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,

Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 27 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 86

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 87 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 146

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 147 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 206

Query 181 AGGGTTCGGAATTTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 207 AGGATTTGGAAATTTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 266

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 267 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 326

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
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Sbjct 327 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 386

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 387 ATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 446

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 447 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 506

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 507 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 566

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 567 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAAGTATCGAAACTTTAA 626

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 627 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 684
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>Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593344.1 Length: 710
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 684 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 625

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 624 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 565

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 564 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 505

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 504 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 445

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||| || || |||||||||| |||||||||||
Sbjct 444 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 385

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||| |||||| |||||||||||||| || |||||||||||||||
Sbjct 384 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 325

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||| || |||||||||||||||||||||||||| |||||||||||
Sbjct 324 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 265

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||||||||| || |||||||||||||| |||||||||||
Sbjct 264 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 205

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||| |||||||||||||||||||||||||| |||||||||||
Sbjct 204 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 145

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      | |||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct 144 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA 85

Query 601 CACATCATTTTTTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||||||||||||||||| |||||| |||||| |||||| |||||
Sbjct 84 TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 27
```

>Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593343.1 Length: 710
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 684 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 625

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 624 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 565

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 564 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 505

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 504 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 445

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||||||| || || |||||||||| |||||||
Sbjct 444 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 385

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||| |||||| |||||||||||||| || |||||||||||||||
Sbjct 384 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 325

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||| || |||||||||||||||||||||||||| |||||||||||
Sbjct 324 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 265

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||||||||| || |||||||||| |||||||||||||||
Sbjct 264 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 205

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||| |||||||||||||||||| |||||||||||||||
Sbjct 204 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 145

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
      | |||||||||||||||||||||||||| |||||||||||||||
Sbjct 144 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 85

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||||||||||||||||| |||||| |||||||||| |||||
Sbjct 84 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 27
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>Rhipicephalus sanguineus isolate 11N cytochrome oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MN585197.1 Length: 703

Range 1: 22 to 679

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 679 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 620

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 619 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 560

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 559 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 500

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 499 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 440

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 439 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 380

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 379 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 320

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 319 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 260

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 259 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 200

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 199 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 140

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |
Sbjct 139 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 80

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 79 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 22
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>Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene, partial cds;
mitochondrial gene for mitochondrial product

Sequence ID: AF132839.1 Length: 793
Range 1: 42 to 699

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 42  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 101

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 102 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 161

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 162 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 221

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||
Sbjct 222 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 281

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||
Sbjct 282 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 341

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 342 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 401

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 402 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 461

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 462 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 521

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 522 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 581

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      | |||
Sbjct 582 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA 641

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 642 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 699
```

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S56 cytochrome

c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426017.1 Length: 680
Range 1: 11 to 668

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 11 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 70

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 71 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 130

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 131 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 190

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| ||
Sbjct 191 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 250

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 251 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 310

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 311 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 370

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 371 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 430

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 431 TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 490

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 491 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 550

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |
Sbjct 551 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 610

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 611 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 668
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S32 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426008.1 Length: 690
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 14  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 74  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 134  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 193

Query 181  AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| ||
Sbjct 194  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 253

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC 300
      |||
Sbjct 254  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC 313

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 314  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 374  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 434  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 493

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 494  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 553

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |
Sbjct 554  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 613

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 614  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 671
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1570
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426001.1 Length: 684
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 14  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 74  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 134 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 193

Query 181 AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 194 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 253

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTT 300
      |||
Sbjct 254 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTT 313

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 314 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 374 ATCACATTATGGCCCTTCACTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 434 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 493

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 494 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 553

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 600
      |
Sbjct 554 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 613

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 614 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 671
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1553
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425998.1 Length: 689
Range 1: 20 to 677

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 20  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 80  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 140 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 199

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| ||
Sbjct 200  AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
|||||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 319

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 380  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 500  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 559

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
|||||
Sbjct 560  CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 619

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
|||||
Sbjct 620  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 677
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1551
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425997.1 Length: 695
Range 1: 22 to 679

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 22  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 81

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 82  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 141

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 142  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 201

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 202  AGGATTTGGAAATTGATTAGTTCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 261

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 262  AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTATTAATTAACCTCTTC 321

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 322  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 381

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 382  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 441

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 442  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 501

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 502  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 561

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 600
      |
Sbjct 562  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 621

Query 601  CACATCATTTTTTATGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 622  TACATCATTTTTTATGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 679
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>Rhipicephalus sanguineus haplotype IV cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556746.1 Length: 771
Range 1: 90 to 747

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 90  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 149

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 150 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 209

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 210  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 269

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 270  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 329

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
          |||||||||||||||||||||||||| || || |||||||||| |||||||||||
Sbjct 330  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 389

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||||||||| |||||| |||||||||||||||||| |||||||||||||||
Sbjct 390  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 449

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||||||||| || |||||||||||||||||| |||||||||||||||
Sbjct 450  ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 509

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||||||||| |||||| || |||||||||||||| |||||||||||||||
Sbjct 510  TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 569

Query 481  AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          |||||||||| |||||||||||||||||||||||||||||||||| ||||
Sbjct 570  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 629

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
          | |||||||||||||||||||||||||||||| |||||||||||||||
Sbjct 630  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 689

Query 601  CACATCATTTTTTATGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||||||||||||||||| |||||| |||||||||| |||||
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Sbjct 690 TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 747

Range 2: 30 to 64

Score:58.4 bits(31), Expect:0.001,
Identities:34/35(97%), Gaps:1/35(2%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCA-GGT 34
      |||
Sbjct 30 AACAAATATATTTAATTTTTGGAGCATGATCATGGT 64
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>Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305546.1 Length: 658
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 61 AATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTATTAATTAACCTCTTC 300

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
```

Sbjct	421		TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540				
Sbjct	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540			
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAAACTTTAA	600			
Sbjct	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAAACTTTAA	600		
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658				
Sbjct	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658			

>Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: MZ305545.1 Length: 658
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60	
Sbjct	1		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120	
Sbjct	61		AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180	
Sbjct	121		AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240	
Sbjct	181		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA	ACTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360	
Sbjct	301		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420	
Sbjct	361		ATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420

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Query   421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT  480
        |||
Sbjct   421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  480

Query   481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT  540
        |||
Sbjct   481  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540

Query   541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA  600
        |||
Sbjct   541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA  600

Query   601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        |||
Sbjct   601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658

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>Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152145.1 Length: 676
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        |||
Sbjct    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60

Query   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  120
        |||
Sbjct   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  120

Query   121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG  180
        |||
Sbjct   121  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG  180

Query   181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG  240
        |||
Sbjct   181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240

Query   241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC  300
        |||
Sbjct   241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC  300

Query   301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT  360
        |||
Sbjct   301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360

Query   361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC  420
        |||
Sbjct   361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC  420

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Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152144.1 Length: 675
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420

Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152143.1 Length: 676
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420

Sbjct	361	 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	541	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152142.1 Length: 669
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	658

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S358 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426012.1 Length: 684
Range 1: 14 to 671

Score:1050 bits(568), Expect:0.0,
Identities:628/658(95%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAATGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTATAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	554	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	671

>Rhipicephalus sanguineus haplotype I cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial

Sequence ID: KU556743.1 Length: 659

Range 1: 12 to 659

Score:1048 bits(567), Expect:0.0,

Identities:621/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	AGGATTTGGAAATTGATTAATCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	311
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	372	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	432	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	611
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTTATATCA	648
Sbjct	612	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTTATATCA	659

>Rhipicephalus sanguineus haplotype II cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556744.1 Length: 787
Range 1: 29 to 688

Score:1046 bits(566), Expect:0.0,
Identities:629/660(95%), Gaps:2/660(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	29	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	88
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	89	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	148
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	149	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	208
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	209	AGGATTTGGAACTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	268
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	269	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	328
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	329	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	388
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	389	 ATCACATTATGGTCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	448
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	449	 TTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTGTAAACATACGATCAATTGGAAT	508
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	509	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	568
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAC TGATCGAAACTTTAA	600
Sbjct	569	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA	628
Query	601	CACATCATTTTTTGGATCCTTCAGGAGG-AGGAGATCCC-ATTTTATATCAACACTTATTT	658
Sbjct	629	 TACATCATTTTTTGGATCCTTCAGGGGGGAGGAGATCCAAATTTTATATCAAC TTTTATTT	688

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S943 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426020.1 Length: 812
Range 1: 2 to 644

Score:1038 bits(562), Expect:0.0,
Identities:616/643(96%), Gaps:0/643(0%), Strand: Plus/Plus

Query	16	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	75
Sbjct	2	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	61
Query	76	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	135
Sbjct	62	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	121
Query	136	TGCATTTATTATAAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTG	195
Sbjct	122	TGCATTTATTATAAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	181
Query	196	ATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	255
Sbjct	182	ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	241
Query	256	ATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGG	315
Sbjct	242	ATTTTGACTTTTACCTCCTTCACTATTTTTATTAAATTAACCTCTTCATTAATTGAATCTGG	301

Query	316	AGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCC	375
Sbjct	302	AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTCC	361
Query	376	ATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGC	435
Sbjct	362	TTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	421
Query	436	AATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAAT	495
Sbjct	422	AATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	481
Query	496	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGT	555
Sbjct	482	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT	541
Query	556	ATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGA	615
Sbjct	542	ATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGA	601
Query	616	TCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	602	TCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	644

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S337 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426010.1 Length: 824
Range 1: 1 to 648

Score:1037 bits(561), Expect:0.0,
Identities:619/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	120
Query	131	GCACATGCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTTCGGA	190
Sbjct	121	GCACATGCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTAC CCCCCTCATTATTTTTATTGATTA ACTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTTTAC CTCTTCACTATTTTTATTAATTA ACTCTTCATTAATTGAA	300

Query	311	TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT	360
Query	371	GGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA	550
Sbjct	481	CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTA	540
Query	551	CCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAAACTTTA ACATCATTTT	610
Sbjct	541	CCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTA ATACATCATTTT	600
Query	611	TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	648

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S344 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426011.1 Length: 809
Range 1: 3 to 644

Score:1031 bits(558), Expect:0.0,
Identities:614/642(96%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	3	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	62
Query	77	GGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	63	GGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAC	122
Query	137	GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	123	GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTCGGAAATTGA	182
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	183	TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	242
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGA	316

Sbjct	243	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTCATTAATTGAATCTGGA	302
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	303	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	362
Query	377	TCAGTAGATTTAGCTATTTTTCTCTTACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	363	TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	422
Query	437	ATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	423	ATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	482
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	483	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	542
Query	557	TTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGAT	616
Sbjct	543	TTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGAT	602
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658	
Sbjct	603	CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT 644	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S475 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426014.1 Length: 649
Range 1: 28 to 649

Score:1022 bits(553), Expect:0.0,
Identities:599/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	28	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	87
Query	61	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	88	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	147
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	148	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	207
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	208	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	267
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA ACTCTTC	300

Sbjct	268		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	327
Query	301		ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	328		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	387
Query	361		ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	388		ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	447
Query	421		TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	448		TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	507
Query	481		AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	508		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	567
Query	541		TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	568		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	627
Query	601		CACATCATTTTTTTGATCCTTCA	622
Sbjct	628		TACATCATTTTTTTGATCCTTCA	649

>Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial

Sequence ID: KX383818.1 Length: 768

>Rhipicephalus sanguineus isolate LIC5554A cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial

Sequence ID: KX383819.1 Length: 768

Range 1: 1 to 642

Score:1020 bits(552), Expect:0.0,

Identities:612/642(95%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1		60
Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61		120
Query	137	GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	121		180
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256

[illegible]

Score:1016 bits(550), Expect:0.0,
Identities:598/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	614	TACATCATTTTTTTGATCCTTCA	635

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SF3003
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425988.1 Length: 654
Range 1: 1 to 640

Score:1016 bits(550), Expect:0.0,
Identities:610/640(95%), Gaps:0/640(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180

Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	481	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557	TTAGCAGGTGCCATTACAATATTATTAAC TATCGAAACTTTAACACATCATTTTTTGAT	616
Sbjct	541	TTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAATACATCATTTTTTGAT	600
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTAT	656
Sbjct	601	CCTTCAGGGGGAGGACATCCAATTTTATATCACCATTAT	640

>Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383811.1 Length: 764
>Rhipicephalus sanguineus isolate LIC5533C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383812.1 Length: 764
Range 1: 1 to 638

Score:1013 bits(548), Expect:0.0,
Identities:608/638(95%), Gaps:0/638(0%), Strand: Plus/Plus

Query	21	GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC	80
Sbjct	1	GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC	60
Query	81	AACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT	140
Sbjct	61	AACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT	120

Query	141	TTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTTCGGAAATTGATTAG	200
Sbjct	121	TTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAG	180
Query	201	TTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	260
Sbjct	181	TCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	240
Query	261	GACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTG	320
Sbjct	241	GACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTG	300
Query	321	GAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAG	380
Sbjct	301	GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG	360
Query	381	TAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	440
Sbjct	361	TAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	420
Query	441	ACTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCAT	500
Sbjct	421	ACTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCAT	480
Query	501	TATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAG	560
Sbjct	481	TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG	540
Query	561	CAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTT	620
Sbjct	541	CAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTT	600
Query	621	CAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	CAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	638

>Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383807.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383808.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736F cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383810.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5535C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383813.1 Length: 763

Range 1: 1 to 637

Score:1011 bits(547), Expect:0.0,
Identities:607/637(95%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query 22 AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA 81
|||||
Sbjct 1 AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA 60

Query 82 ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT 120

Query 142 TATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 CCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 ACTTTTACCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGG 321
|||||
Sbjct 241 ACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGG 300

Query 322 AACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGT 381
|||||
Sbjct 301 TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT 360

Query 382 AGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA 441
|||||
Sbjct 361 AGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA 420

Query 442 CTTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATT 501
|||
Sbjct 421 CTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATT 480

Query 502 ATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGC 561
|||||
Sbjct 481 ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC 540

Query 562 AGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTC 621
|||||
Sbjct 541 AGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTC 600

Query 622 AGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
|||
Sbjct 601 AGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 637
```

>Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU568516.1 Length: 656
Range 1: 27 to 656

Score:1009 bits(546), Expect:0.0,
Identities:602/630(96%), Gaps:0/630(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 27 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 86

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 87 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 146

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 147 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 206

Query 181 AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||| | |||| | |||||||||||||||||||||||||||||
Sbjct 207 AGGATTTGGAAATTGATTAATCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 266

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||||||||||| || || |||||||||| |||||||
Sbjct 267 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 326

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||| |||||| | |||||||||||||| || |||||||||||||||
Sbjct 327 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 386

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||| || |||||||||||||| ||||||| |||||||||||
Sbjct 387 ATCACATTATGGCCCTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 446

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||||||||| || |||||||||| |||||||
Sbjct 447 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 506

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||| ||||||| ||||||| |||||||
Sbjct 507 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 566

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||||||||||||||||| ||||||| |||||||
Sbjct 567 CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 626

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGG 630
      |||||||||| |||||||
Sbjct 627 TACATCATTTTTTGACCCTTCAGGAGGAGG 656
```

>Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383809.1 Length: 762

Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

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Query 23 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA 82
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA 60

Query 83 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT 142
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT 120

Query 143 ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT 202
      ||||||||| |||||||||||||||||||||||||||| || |||||||||||||
Sbjct 121 ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC 180

Query 203 CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA 262
      ||||| ||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA 240

Query 263 CTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA 322
      ||||||| || ||| ||||||||||| ||||||||||| ||||||| |||||||
Sbjct 241 CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT 300

Query 323 ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA 382
      |||||||||||||||| || |||||||||||||||||||||||||||| || |||||
Sbjct 301 ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA 360

Query 383 GATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC 442
      ||||||||| ||||||||| |||||||||||||||||||||||||||||||||||
Sbjct 361 GATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC 420

Query 443 TTCATCACAACACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA 502
      || || ||||||||||||| ||||| ||||||||||||||||||||||| |||||||
Sbjct 421 TTTATTACAACACTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA 480

Query 503 TTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA 562
      |||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||
Sbjct 481 TTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA 540

Query 563 GGTGCCATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTGATCCTTCA 622
      |||||||||||||||| |||||||||||||||||||| |||||||||||||||||
Sbjct 541 GGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCA 600

Query 623 GGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      || ||||||||| ||||||||| |||||
Sbjct 601 GGGGGAGGAGATCCAATTTTATATCAACATTTATTT 636
```

>Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383806.1 Length: 714
Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

```
Query 23 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA 82
      |||
Sbjct 1 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA 60

Query 83 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT 142
      |||
Sbjct 61 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT 120

Query 143 ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT 202
      |||
Sbjct 121 ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC 180

Query 203 CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA 262
      |||
Sbjct 181 CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA 240

Query 263 CTTTTACCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA 322
      |||
Sbjct 241 CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT 300

Query 323 ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA 382
      |||
Sbjct 301 ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA 360

Query 383 GATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC 442
      |||
Sbjct 361 GATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC 420

Query 443 TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA 502
      |||
Sbjct 421 TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA 480

Query 503 TTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA 562
      |||
Sbjct 481 TTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA 540

Query 563 GGTGCCATTACAATATTATTAAGTATCGAAACTTTAATACATCATTTTTTATCCTTCA 622
      |||
Sbjct 541 GGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTATCCTTCA 600

Query 623 GGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 601 GGGGGAGGAGATCCAATTTTATATCAACACTTATTT 636
```

>Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase subunit 1 (COI)

gene, partial cds; mitochondrial
Sequence ID: KX383805.1 Length: 761
Range 1: 1 to 635

Score:1007 bits(545), Expect:0.0,
Identities:605/635(95%), Gaps:0/635(0%), Strand: Plus/Plus

Query	24	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	83
Sbjct	1	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	60
Query	84	CTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	143
Sbjct	61	CTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	120
Query	144	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTC	203
Sbjct	121	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	180
Query	204	CTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	263
Sbjct	181	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	240
Query	264	TTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAA	323
Sbjct	241	TTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTA	300
Query	324	CAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAG	383
Sbjct	301	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	360
Query	384	ATTTAGCTATTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	443
Sbjct	361	ATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	444	TCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTAT	503
Sbjct	421	TTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTAT	480
Query	504	TTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAG	563
Sbjct	481	TTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	540
Query	564	GTGCCATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTGATCCTTCAG	623
Sbjct	541	GTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAG	600
Query	624	GAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	GGGGAGGAGATCCAATTTTATATCAACACTTATTT	635

>Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630347.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 20  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 80  AATTGGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct 140  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 199

Query 181  AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || ||||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 200  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 259

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC 300
      |||||||||||||||||||||||||||| || ||| |||||||||| ||||||||||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC 319

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||||| ||||||| ||||||||||||||||| || |||||||||||||||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||||| || ||||||||||||||||||||||||||| |||||||||||
Sbjct 380  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||| ||||||||||| ||||||||||| |||||||||||
Sbjct 440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||||| ||||||||||| ||||||||||| ||||||||||| ||||
Sbjct 500  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 559

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
      | ||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct 560  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA 619

Query 601  CACATCATTTTTTTGATCCTTCA 622
      ||||||||||||||||
Sbjct 620  TACATCATTTTTTTGATCCTTCA 641
```


>Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630346.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

```
Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||
Sbjct 20  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||
Sbjct 80  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
          |||
Sbjct 140  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 199

Query 181  AGGGTTCGGAATTTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          |||
Sbjct 200  AGGATTTGGAAATTTGATTAGTTCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 259

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
          |||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTGATTAACCTCTTC 319

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCTCCTCTATCTTCAAATTT 379

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||
Sbjct 380  ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||
Sbjct 440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481  AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          |||
Sbjct 500  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 559

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 600
          |
Sbjct 560  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 619

Query 601  CACATCATTTTTTTGATCCTTCA 622
          |||
Sbjct 620  TACATCATTTTTTTGATCCTTCA 641
```

>Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519712.1 Length: 654
Range 1: 3 to 628

Score:1002 bits(542), Expect:0.0,
Identities:598/626(96%), Gaps:0/626(0%), Strand: Plus/Plus

```
Query 33 GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCT 92
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 3 GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCT 62

Query 93 TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT 152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 63 TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT 122

Query 153 TCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATAT 212
          | |||||||||||||||||||||||| || |||||||||||||| |||| ||||
Sbjct 123 TTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT 182

Query 213 TAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCC 272
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 183 TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC 242

Query 273 CCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAA 332
          | || |||||||||| |||||||||||||||||||||| |||||| ||||||||
Sbjct 243 CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA 302

Query 333 CAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTA 392
          |||||| || |||||||||||||||||||||||||||| || ||||||||||||||
Sbjct 303 CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA 362

Query 393 TTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAA 452
          |||||||||||| |||||||||||||||||||||||||||||||||||| || ||||
Sbjct 363 TTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAA 422

Query 453 CTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGAT 512
          |||||||| |||||||||||||||||||||||||||| ||||||||||||||||
Sbjct 423 CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT 482

Query 513 CTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTA 572
          |||||||||||||||||||| |||| ||||||||||||||||||||||||||||
Sbjct 483 CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA 542

Query 573 CAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAG 632
          |||||| |||||||||||||||||| |||||||||||||||||| ||||||
Sbjct 543 CAATATTGTTAACCTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG 602

Query 633 ATCCCATTTTATATCAACACTTATTT 658
          ||| |||||||||||| ||||
Sbjct 603 ATCCAATTTTATATCAACATTTATTT 628
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1575
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426002.1 Length: 639
Range 1: 1 to 628

Score:1000 bits(541), Expect:0.0,
Identities:599/628(95%), Gaps:0/628(0%), Strand: Plus/Plus

Query	31	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	90
Sbjct	1	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	60
Query	91	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	150
Sbjct	61	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	120
Query	151	TTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTAT	210
Sbjct	121	TTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	180
Query	211	ATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	270
Sbjct	181	ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	240
Query	271	CCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATG	330
Sbjct	241	TCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATG	300
Query	331	AACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGC	390
Sbjct	301	AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC	360
Query	391	TATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCAC	450
Sbjct	361	TATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTAC	420
Query	451	AACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTG	510
Sbjct	421	AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG	480
Query	511	ATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCAT	570
Sbjct	481	ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT	540
Query	571	TACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGG	630
Sbjct	541	TACAATATTGTTAACCTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGG	600
Query	631	AGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	AGATCCAATTTTATATCAACATTTATTT	628

>Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855658.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTG 218
          |||||||||||||||||||||||| || |||||||||||||| |||| |||| ||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
          |||||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
          ||||||||| |||||||||||||||||||||| ||||||| |||||||||||||||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
          | || |||||||||||||||||||||||||| || |||||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
          ||||||| ||||||||||||||||||||||||||||||||| || |||||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
          |||| |||||||||||||||||||||||||| |||||||||||||||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
          ||||||||||||||| |||| |||||||||||||||||||||||||||||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
          | |||||||||||||||| |||||||||||||||||| ||||||||| |
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
          |||||||||||| |||||
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Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855657.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      | ||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      | ||
Sbjct 541 TGTTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
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Sbjct 601 ||||| |||||
TTTTATATCAACATTTATT 620

>Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855656.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAAACCTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTAACTGATCGAAACCTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600

Query 639 TTTTATATCAACACTTATTT 658
 |||||
 Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
 Sequence ID: KX757910.1 Length: 630
 Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
 Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
 |||||
 Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
 |||||
 Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
 |||||
 Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
 |||||
 Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
 |||||
 Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
 |||||
 Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
 |||||
 Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
 |||||
 Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
 |||||
 Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAC TGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
 |||||
 Sbjct 541 TGTTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

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Query   639   TTTTATATCAACACTTATTT   658
          |||||
Sbjct   601   TTTTATATCAACATTTATTT   620

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>Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757904.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG   98
          |||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
          |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
          |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
          |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
          |||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
          |||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
          |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
          |||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
          |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAACGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
          |||||

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Sbjct 541 TGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
 |||||

Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757902.1 Length: 630
 Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
 Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
 |||||

Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
 |||||

Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
 |||||

Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
 |||||

Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
 |||||

Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
 |||||

Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
 |||||

Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
 |||||

Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
 |||||

Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638

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Sbjct  541  TGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600
Query  639  TTTTATATCAACTTATTT  658
Sbjct  601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757896.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTGGAATGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540

Query	579	TATTA	ACTGATCGAA	ACTTTA	ACATCAT	TTTTTT	GATCCTTC	CAGGAGG	GAGATCCCA	638
Sbjct	541	TGTTA	ACTGATCGAA	ACTTTA	ATACATCAT	TTTTTT	GATCCTTC	CAGGGGG	GAGATCCAA	600
Query	639	TTTTATATCA	AACTTATTT	658						
Sbjct	601	TTTTATATCA	AATTTATTT	620						

>Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757889.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98	
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	60	
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158		
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120		
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218		
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180		
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278		
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240		
Query	279	TATTTTTATTGATTA	AACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338	
Sbjct	241	TATTTTTATTAATTA	AACTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300	
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398		
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360		
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	AACTTCATCACA	ACTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	AACTTTATTACA	ACTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518		
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480		
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578		
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540		

Query	579	TATTA	ACTGATCGAA	ACTTTA	ACATCAT	TTTTTT	GATCCTT	CAGGAGG	AGGAGAT	CCCA	638
Sbjct	541	TGTTA	ACTGATCGAA	ACTTTA	ATACATCAT	TTTTTT	GATCCTT	CAGGGGG	AGGAGAT	CCAA	600
Query	639	TTTTATATCA	AACTTATTT	658							
Sbjct	601	TTTTATATCA	AATTTATTT	620							

>Rhipicephalus sanguineus isolate Rovind cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757887.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158	
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120	
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218	
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180	
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278	
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240	
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338	
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300	
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398	
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360	
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTG	458	
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420	
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518	
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480	
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578	

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757879.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCACAACTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519711.1 Length: 636
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCACAACTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480

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Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATGATCGAACTTTAACAACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        | |||||
Sbjct   541  TGTTAAGTATGATCGAACTTTAATAACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600

Query   639  TTTTATATCAACACTTATTT  658
        |||||
Sbjct   601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135448.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  98
        |||||
Sbjct   1     TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
        |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
        |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
        |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
        |||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
        | ||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG  458
        |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
        ||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480

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Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        |||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATCGAACTTTAATACATCATTCTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        | |||
Sbjct   541  TGTTAAGTATCGAACTTTAATACATCATTCTTTGATCCTTCAGGGGGAGGAGATCCAA  600

Query   639  TTTTATATCAACACTTATTT  658
        |||
Sbjct   601  TTTTATATCAACACTTATTT  620

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>Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757905.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  98
        |||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA  158
        |||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
        |||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
        |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTGATTAACCTCTCATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
        |||
Sbjct   241  TATTTTTATTGAATTAATCTTCATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
        | ||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTAGGTGCAATTAACCTTCATCACAACCTATTG  458
        |||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
        |||

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Sbjct  421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480
Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
          |||||
Sbjct  481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540
Query   579  TATTAAGTATCGAAACTTTAACAACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
          |||||
Sbjct  541  TGTTAAGTATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600
Query   639  TTTTATATCAACACTTATTT  658
          |||||
Sbjct  601  TTTTATATCAACATTATTT  620

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>Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757895.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  98
          |||||
Sbjct   1  TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG  60
Query   99  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
          |||||
Sbjct  61  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  120
Query  159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
          |||||
Sbjct 121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180
Query  219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
          |||||
Sbjct 181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240
Query  279  TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
          |||||
Sbjct 241  TATTTTTATTAAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300
Query  339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
          |||||
Sbjct 301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360
Query  399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTG  458
          |||||
Sbjct 361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATTACAAGTATTG  420
Query  459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518

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Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTATTTTATGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTATTTTATGATCCTTCAGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus isolate Petnica cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757883.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTATTGAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACATTG	458

Sbjct	361		420
		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519708.1 Length: 629
Range 1: 4 to 620

Score:985 bits(533), Expect:0.0,
Identities:589/617(95%), Gaps:0/617(0%), Strand: Plus/Plus

Query	42	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	101
Sbjct	4	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	63
Query	102	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAG	161
Sbjct	64	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAG	123
Query	162	TTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCC	221
Sbjct	124	TTATACCAATCATAATCGGAGGATTTGGAATGATTAGTCCCTATCATATTGGGTGCCC	183
Query	222	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTAT	281
Sbjct	184	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT	243
Query	282	TTTTATTGATTAACCTTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATC	341
Sbjct	244	TTTTATTAATTAACCTTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC	303
Query	342	CCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTC	401
Sbjct	304	CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTC	363

Query	402	TTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAA	461
Sbjct	364	TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAA	423
Query	462	ATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAA	521
Sbjct	424	ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA	483
Query	522	TTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTAT	581
Sbjct	484	TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	543
Query	582	TAACTGATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATT	641
Sbjct	544	TAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATT	603
Query	642	TATATCAACACTTATTT	658
Sbjct	604	TATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135447.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360

Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACCTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGACCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519707.1 Length: 626
Range 1: 1 to 616

Score:983 bits(532), Expect:0.0,
Identities:588/616(95%), Gaps:0/616(0%), Strand: Plus/Plus

Query	43	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	102
Sbjct	1	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	60
Query	103	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGT	162
Sbjct	61	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT	120
Query	163	TATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCC	222
Sbjct	121	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	180
Query	223	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATT	282
Sbjct	181	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	240
Query	283	TTTATTGATTAACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC	342
Sbjct	241	TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	300
Query	343	CCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT	402

Sbjct	301	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT	360
Query	403	TCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAA	462
Sbjct	361	TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA	420
Query	463	TATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT	522
Sbjct	421	CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523	TACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT	582
Sbjct	481	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583	AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	642
Sbjct	541	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	600
Query	643	ATATCAACACTTATTT 658	
Sbjct	601	ATATCAACATTATTT 616	

>Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757901.1 Length: 630
Range 1: 1 to 620

Score:979 bits(530), Expect:0.0,
Identities:590/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398

Sbjct	301		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTT	360
Query	399		CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459		TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421		TAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519		TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579		TATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541		TGTTAACCTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639		TTTTATATCAACACTTATTT 658	
Sbjct	601		TTTTATATCAACATTTATTT 620	

>Rhipicephalus sanguineus clone #4 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519709.1 Length: 635
Range 1: 2 to 621

Score:974 bits(527), Expect:0.0,
Identities:589/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	2		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	61
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	62		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCTTTTATTATAATTTTCTTTA	121
Query	159		TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	122		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	181
Query	219		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	182		CCCCGGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	241
Query	279		TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	242		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	301

Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	302	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGGAGATTTAGCTATTTTTT	361
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTG	458
Sbjct	362	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTG	421
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	422	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	481
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	482	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	541
Query	579	TATTAAC TGATCGAAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	542	TGTTAAC TGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	601
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	602	TTTTATATCAACATTTATTT	621

Score:937 bits(507), Expect:0.0,
Identities:567/597(95%), Gaps:0/597(0%), Strand: Plus/Plus

Query	302	TTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTA	361
Sbjct	241	TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA	300
Query	362	TCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCT	421
Sbjct	301	TCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCT	360
Query	422	TCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATA	481
Sbjct	361	TCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATA	420
Query	482	ACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTT	541
Sbjct	421	ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT	480
Query	542	CTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAAC	601
Sbjct	481	TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAAT	540
Query	602	ACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	541	ACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	597

>Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519713.1 Length: 580
Range 1: 1 to 580

Score:933 bits(505), Expect:0.0,
Identities:555/580(96%), Gaps:0/580(0%), Strand: Plus/Plus

Query	43	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	102
Sbjct	1	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	60
Query	103	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGT	162
Sbjct	61	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT	120
Query	163	TATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCC	222
Sbjct	121	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	180
Query	223	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATT	282
Sbjct	181	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	240
Query	283	TTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC	342
Sbjct	241	TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	300

Query	343	CCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT	402
Sbjct	301	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT	360
Query	403	TCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAA	462
Sbjct	361	TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA	420
Query	463	TATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT	522
Sbjct	421	CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523	TACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT	582
Sbjct	481	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583	AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCA	622
Sbjct	541	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA	580

>Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519706.1 Length: 595
Range 1: 1 to 570

Score:898 bits(486), Expect:0.0,
Identities:542/570(95%), Gaps:0/570(0%), Strand: Plus/Plus

Query	89	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	148
Sbjct	1	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	60
Query	149	ATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATT	208
Sbjct	61	ATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATC	120
Query	209	ATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	268
Sbjct	121	ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	180
Query	269	CCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGA	328
Sbjct	181	CCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGA	240
Query	329	TGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTA	388
Sbjct	241	TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA	300
Query	389	GCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATC	448

Sbjct	301	GCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATT	360
Query	449	ACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTT	508
Sbjct	361	ACAACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT	420
Query	509	TGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCC	568
Sbjct	421	TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	480
Query	569	ATTACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGA	628
Sbjct	481	ATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGA	540
Query	629	GGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	541	GGAGATCCAATTTTATATCAACATTTATTT	570

>Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase subunit 1 gene,
partial cds; mitochondrial
Sequence ID: KY678135.1 Length: 790
Range 1: 18 to 675

Score:883 bits(478), Expect:0.0,
Identities:599/659(91%), Gaps:2/659(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	18	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	77
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	78	AATTCGTATAGAATTAGGCCAACCTGGAACCCTAATTGGTAATGATCAAATTTATAATGT	137
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	138	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	197
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	198	TGGATTTGGAAACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	317
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC-CCCTCTATCTTCAAATT	359
Sbjct	318	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCT-TATCCTCAAATT	376
Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTT	419

Sbjct	377		TATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTT	436
Query	420		CTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAA	479
Sbjct	437		CTTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAA	496
Query	480		TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	497		TAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAC	556
Query	540		TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTA	599
Sbjct	557		TATTATCTTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCGATCGAAATTTTA	616
Query	600		ACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	617		AACTTCATTTTTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	675

>Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800313.1 Length: 673
Range 1: 8 to 665

Score:883 bits(478), Expect:0.0,
Identities:598/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8		AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61		AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68		AATTCGCATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121		AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128		AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCTATTATAATTGG	187
Query	181		AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188		TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241		AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	248		TATAAATAACATAAGATTTTGATTACTTCCTCCTCATTATTTCTATTAATTAACCTCTTC	307
Query	301		ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	308		ATTAATTGAATCAGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAACCTGATCGAAATTTCAA	607
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	608	TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATTT	665

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SC3005
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425987.1 Length: 574
Range 1: 1 to 561

Score:881 bits(477), Expect:0.0,
Identities:533/561(95%), Gaps:0/561(0%), Strand: Plus/Plus

Query	98	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTT	157
Sbjct	1	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACACGCATTTATTATAATTTTTTTT	60
Query	158	ATAGTTATACCAATCATAATCGGAGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGT	217
Sbjct	61	ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATTATATTAGGT	120
Query	218	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCA	277
Sbjct	121	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA	180
Query	278	TTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTT	337
Sbjct	181	CTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT	240
Query	338	TATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTT	397
Sbjct	241	TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTT	300
Query	398	TCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATT	457
Sbjct	301	TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATT	360

Query	458	GTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTT	517
Sbjct	361	GTAAACATACGATCAATTGGAATAACAATAGACGTATACCATTATTTGTTTGATCTGTT	420
Query	518	TTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	577
Sbjct	421	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	480
Query	578	TTATTAACCTGATCGAAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCC	637
Sbjct	481	TTGTTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCA	540
Query	638	ATTTTATATCAACACTTATTT	658
Sbjct	541	ATTTTATATCAACATTTATTT	561

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (CO1) gene, partial cds;
mitochondrial
Sequence ID: KU214592.1 Length: 829
Range 1: 1 to 648

Score:876 bits(474), Expect:0.0,
Identities:590/648(91%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGCCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGTAATTGTTACA	120
Query	131	GCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGA	190
Sbjct	121	GCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGTGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTCTTCCTCCCTCATTATTTATATTAATTAATTCTTCATTAATTGAG	300
Query	311	TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCAGGAGCAGGTACAGGATGGACAGTTTATCCTCCCCTATCTCAAATTTATCACATTAT	360
Query	371	GGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA	430

Sbjct	361	GGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATTAATTTTATTACA ACTATTGTAAATATACGATCTATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA	550
Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACTATTATCTTTA	540
Query	551	CCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAAACTTTAACACATCATTT	610
Sbjct	541	CCTGTTTTAGCAGGTGCCATTACAATATTATTAACCGATCGAAATTTTAACACTTCATTT	600
Query	611	TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TTTGACCCTTCAGGGGAGGGGATCCAATTTTATATCAACATTTATTT	648

>Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MT079206.1 Length: 678
Range 1: 1 to 652

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCG	60
Query	67	TATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTT	186
Sbjct	121	AACAGCTCATGCATTTATTATAATTTTCTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	CGGAAATTGATTAGTTCTTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181	TGGAAACTGGTTAGTTCCAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA ACTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACA	366
Sbjct	301	TGAATCTGGGGCAGGGACAGGGTGA ACTGTTTATCCTCCTTTATCCTCAAATTTATCCCA	360
Query	367	TTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAAT	426

Sbjct	361		420
		TTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTTGCTGGTGCTTCTTCAAT	
Query	427	TTTAGGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTT CATTACA ACTATTGTAAACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCCTATTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTA ACTGATCGAAATTTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	ATTTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTTATTT	652

>Rhipicephalus sanguineus isolate GY34 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MN862754.1 Length: 678
Range 1: 1 to 652

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCG	60
Query	67	TATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTT	186
Sbjct	121	AACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	CGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181	TGGAAACTGGTTAGTTC CAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA ACTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACA	366
Sbjct	301	TGAATCTGGGGCAGGGACAGGGTGAAC TTTATCCTCCTTTATCCTCAAATTTATCCCA	360

Query	367	TTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTCACTACAACCTATTGTAAACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCCTATTTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCTGATCGAAATTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	ATTTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTATTT	652

>Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome oxidase subunit 1 gene, complete cds; mitochondrial
Sequence ID: KM494916.1 Length: 1539
Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCCTCAAATTT	404

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	645	CACTTCATTTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTATTT	702

>Rhipicephalus sanguineus isolate Tehran cytochrome oxidase subunit 1 gene,
complete cds; mitochondrial

Sequence ID: KM494915.1 Length: 1539

Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,

Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGGTTCGGAATTTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCCTCAAATTT	404
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	645	CACTTCATTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800314.1 Length: 673
Range 1: 8 to 664

Score:870 bits(471), Expect:0.0,
Identities:595/657(91%), Gaps:0/657(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCCATTATAATTGG	187
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTTCATTATTTCTATTAATTAACCTCTC	307
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	308	 ATTAATTGAATCGGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	 ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	 TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	488	 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	548	 CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAACCTGATCGAAATTTCAA	607
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATT	657
Sbjct	608	 TACTTCATTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATT	664

>Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606303.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	 AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	 AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	 AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	 AGGATTTGGAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	306	 AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTCATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTATTT	723

>Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606302.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTCATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606301.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTTCATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606300.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAACTGATTAGTGCCCATTTATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	306		AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301		ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366		ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361		ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426		ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421		TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486		TTCAATTTTAGGTGCAATTAATTTCAATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481		AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546		AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541		TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606		TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601		CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666		CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial

Sequence ID: KY606299.1 Length: 873

Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,

Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATTTATGTTAGGAGCTCCAGACATAGCATTTCCACG	305

Query	241	AATAAATAATATAAGATTTTGA	CTTTTACCCCCCTCATTATTTT	TATTGATTA	AACTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGA	TACTTCTCCCTCATTATTCTT	ATTAATTA	ATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGA	ACAGGATGAACAGTTTATCCC	CCTCTATCTT	CAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGG	ACAGGATGAACTGTCTACCCT	CCTTTATCTT	CAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTA	GATTTAGCTATTTTTTCTCTT	CACCTTGCTGGT	GCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTA	GATTTAGCTATCTTCTCTCTT	CATCTCGCTGGT	GCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAAC	TTTCATCACA	ACTATTGTAA	TATACGATCA	ATTGGAAT
Sbjct	486	TTCAATTTTAGGTGCAATTAAT	TTTCATTACA	ACTATTGTAA	ACATACGATCT	ATTGGAAT
Query	481	AACAATAGAACGAATACCATTAT	TTGTTTGATCTGTTTTAATTAC	AGCTATTTTACT	ACT	540
Sbjct	546	AACAATAGAACGAATACCATTAT	TCGTTTGATCTGTTTTAATCAC	CGCTATTTTATT	GCT	605
Query	541	TCTATCTTTACCTGTATTAGCAG	GTGCCATTACAATATTATTAAC	TGATCGAA	ACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAG	GTGCCATTACAATATTATTAAC	TGATCGAA	ATTTCAA	665
Query	601	CACATCATTTTTTGATCCTTCAG	GAGGAGGAGATCCCATTTTAT	ATCAAC	ACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAG	GAGGAGGTGACCCTATTTTAT	ATCAAC	ATTTATTT	723

>Rhipicephalus camicasi isolate SC0126 mitochondrion, complete genome

Sequence ID: NC_061616.1 Length: 14725

>Rhipicephalus camicasi isolate SC0126 mitochondrion, complete genome

Sequence ID: MZ323229.1 Length: 14725

Range 1: 45 to 702

Score:861 bits(466), Expect:0.0,

Identities:595/659(90%), Gaps:2/659(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAG	CATGATCAGGTATATTAGGACTT	AGTATAAGA	AATATT	60
Sbjct	45	AACAATATACTTAATTTTTGGAG	CATGATCTGGAATATTAGGATTA	AGAATAAGA	ATACT	104
Query	61	AATTCGTATAGAATTAGGACAAC	CTGGAACTTTAATTGGAAATGA	TCAGATTTATA	AATGT	120
Sbjct	105	AATTCGTATAGAATTAGGCCAAC	CTGGAACTTTAATTGGAAATGA	CCAAATTTATA	AATGT	164
Query	121	AATCGTAACAGCACATGCATTTA	TATAATTTTCTTTATAGTTATA	ACCAATCATA	ATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTA	TATAATTTTTTTATAGTAATA	CCAATTATGA	TGG	224
Query	181	AGGGTTCGGAAATTGATTAGTTC	CTATTATATTAGGTGCCCCAGA	TATAGCATTTCC	CACG	240

Sbjct	225	AGGATTCGGAAATTGATTAGTCCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	285	AATAAATAATATAAGATTTTGATTACTTCCTCCTTCATTATTTTTATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC-CCCTCTATCTTCAAATT	359
Sbjct	345	ATTAATTGAATCAGGAGCAGGGACAGGATGAACAGTTTACCCTCCCT-TATCATCAAATT	403
Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTT	419
Sbjct	404	TATCACACTATGGTCCATCAGTAGATCTAGCTATTTTTCTCTTCATCTTGCTGGTGCTT	463
Query	420	CTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAA	479
Sbjct	464	CTTCAATTTTAGGCGCAATTAATTTTCATTACAACCATTGTAAACATACGATCTATTGGAA	523
Query	480	TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	524	TAACAATAGAACGAATACCTTTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAT	583
Query	540	TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTA	599
Sbjct	584	TATTATCTTTACCAGTTTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAATTTA	643
Query	600	ACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	644	ATACCTCGTTCTTTGATCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305547.1 Length: 658
Range 1: 1 to 658

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGAATAGAGTTAGGACAACCTGGGACTTTAATTGGAAATGATCAAAATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACCTATTGTAAATATACGATCTATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	541	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	658

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	181	AGGGTTCGGA AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCTCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAAGTGTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAACTTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002580.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253

Query	181	AGGGTTTCGGAAATTGATTAGTTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAACCTGGATGAAGTGTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGA AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAAGTGTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-YC cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002578.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193

Query	121	AATCGTAAACAGCACATGCATTTATTATAAATTTCTTTATAGTTATACCAATCATAATCGG 	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAAATTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC 	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACATTGTAAATATACGATCAATTGGAAT 	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120

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Query    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
      |||
Sbjct   74  AACAAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT  133

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Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACACTTATTT	731

Query #5: TKCJJ095-19|TKCJ012018H11|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26767 Length: 658

Sequences producing significant alignments:

Common		Max	Total Query	E	Per.	Acc.	Scientific
Description							
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession

Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	697
MF426019.1							
Rhipicephalus sanguineus haplotype III cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	713
KU556745.1							
Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	710
MN593344.1							
Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	710
MN593343.1							
Rhipicephalus sanguineus isolate 11N cytochrome oxidase subuni...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	703
MN585197.1							
Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene,...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	793
AF132839.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	675
MF426018.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	680
MF426016.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	693
MF426013.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	679
MF426009.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690
MF426008.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	686
MF426007.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	684
MF426001.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	695
MF425997.1							
Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	658
MZ305546.1							
Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	658
MZ305545.1							
Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	676
MW152145.1							
Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	675
MW152144.1							

Rhipicephalus turanicus isolate	COX1-225-Goat cytochrome c...							
Rhipicephalu... NA	34633	883	883	100%	0.0	90.88	673	
MT800313.1								
Rhipicephalus turanicus isolate	COX1-18-Sheep cytochrome c...							
Rhipicephalu... NA	34633	881	881	99%	0.0	90.87	673	
MT800314.1								
Rhipicephalus turanicus isolate	31X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873	
KY606303.1								
Rhipicephalus turanicus isolate	19X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873	
KY606302.1								
Rhipicephalus turanicus isolate	19C cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873	
KY606301.1								
Rhipicephalus turanicus isolate	12X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873	
KY606300.1								
Rhipicephalus turanicus isolate	12C cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	872	872	100%	0.0	90.58	873	
KY606299.1								
Rhipicephalus turanicus isolate	COX1-7-Sheep cytochrome c...							
Rhipicephalu... NA	34633	865	865	99%	0.0	90.41	673	
MT800312.1								
Rhipicephalus turanicus isolate	GY34-1 cytochrome c oxidase...							
Rhipicephalu... NA	34633	861	861	99%	0.0	90.49	678	
MT079206.1								
Rhipicephalus turanicus voucher	CROBB808 cytochrome oxidase...							
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	658	
MZ305547.1								

Alignments:

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S827 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426019.1 Length: 697
Range 1: 19 to 676

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	198

Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	558
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	618
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	619	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

>Rhipicephalus sanguineus haplotype III cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556745.1 Length: 713
Range 1: 27 to 684

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	27	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	86
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	87	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	146
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	147	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	206

Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	207	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	266
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	267	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	326
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	327	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	386
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	387	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	446
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	447	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	506
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	507	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	566
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	567	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	626
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	627	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	684

>Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593344.1 Length: 710
Range 1: 27 to 684

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	684	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	625
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	624	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	565
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180

Sbjct	564	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCAATCATAATCGG	505
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	504	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	445
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	444	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	385
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	384	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	325
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	324	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	265
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	264	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	205
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	204	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	145
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	144	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	85
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	84	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	27

>Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593343.1 Length: 710
Range 1: 27 to 684

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	684	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	625
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	624	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	565
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180

Sbjct	564		AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	505
Query	181		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	504		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	445
Query	241		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	444		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	385
Query	301		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	384		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	325
Query	361		ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	324		ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	265
Query	421		TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	264		TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	205
Query	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	204		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	145
Query	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	144		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	85
Query	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	84		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	27

>Rhipicephalus sanguineus isolate 11N cytochrome oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MN585197.1 Length: 703
Range 1: 22 to 679

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	679		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	620
Query	61		AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	619		AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	560

Query	121	AATCGTAACAGCACATGCATTTATTATAA	180
Sbjct	559	AATCGTAACAGCACATGCATTTATTATAA	500
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	499	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	440
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	300
Sbjct	439	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	380
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	379	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	320
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	319	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	260
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	259	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	200
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	199	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	140
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	600
Sbjct	139	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	80
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	79	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	22

>Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene, partial cds;
mitochondrial gene for mitochondrial product
Sequence ID: AF132839.1 Length: 793
Range 1: 42 to 699

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	42	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	101
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	102	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	161

Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	162	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	221
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	222	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	281
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT	300
Sbjct	282	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT	341
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	342	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	401
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	402	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	461
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	462	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	521
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	522	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	581
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	600
Sbjct	582	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	641
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	642	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	699

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S58 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426018.1 Length: 675
Range 1: 11 to 668

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	610
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	611	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S52 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426016.1 Length: 680
Range 1: 12 to 669

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	72	 AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	132	 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	252	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	311
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	312	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	372	 ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	432	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	492	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	552	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	611
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	612	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	669

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S37 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426013.1 Length: 693
Range 1: 20 to 677

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	619
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	620	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S33 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426009.1 Length: 679
Range 1: 11 to 668

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	610
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	611	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S32 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426008.1 Length: 690
Range 1: 14 to 671

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60

Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	613
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S29 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426007.1 Length: 686
Range 1: 14 to 671

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
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Sbjct	14	 AACAATATATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	134	 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	254	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	314	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	374	 ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	434	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	494	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Sbjct	554	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	613
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	614	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1570
 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
 Sequence ID: MF426001.1 Length: 684
 Range 1: 14 to 671

Score:1210 bits(655), Expect:0.0,
 Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	313
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	613
Query	601	TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	614	TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1551
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425997.1 Length: 695
Range 1: 22 to 679

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	22	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	81
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	82	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	141
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	142	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	201
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	202	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	261
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	262	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	321
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	322	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	381
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	382	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	441
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	442	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	501
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	502	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	561
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	562	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	621
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	622	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	679

>Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305546.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 61 AATTCGTATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
|||||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
|||||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
|||||
Sbjct 481 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
|||||
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305545.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACTTTATTACAACATATTGTAAACATACGATCAATTGGAAT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAACTTTATTACAACATATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152145.1 Length: 676
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAAT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152144.1 Length: 675

Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||
Sbjct 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
      |||
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: MW152143.1 Length: 676
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||
Sbjct 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA 600
      |||
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA 600

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
```

>Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: MW152142.1 Length: 669
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATCTT 300

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||
Sbjct 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
      |||
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
```

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S48 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426015.1 Length: 692
Range 1: 19 to 676

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	318
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	558
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	618
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	619	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S1060
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426006.1 Length: 705
Range 1: 28 to 685

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 28  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 87

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 88  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 147

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 148 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 207

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 208  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 267

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
      |||
Sbjct 268  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 327

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||
Sbjct 328  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 387

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||
Sbjct 388  ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 447

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
      |||
Sbjct 448  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATTAATTGGAAT 507

Query 481 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      |||
Sbjct 508  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 567

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA 600
      |||
Sbjct 568  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA 627

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      |||
Sbjct 628  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 685
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S56 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426017.1 Length: 680
Range 1: 11 to 668

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 11  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 70

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 71  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 130

Query 121  AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 131  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 190

Query 181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 191  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 250

Query 241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 251  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 310

Query 301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 311  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 370

Query 361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 371  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 430

Query 421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
      |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 431  TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 490

Query 481  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 491  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 550

Query 541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 551  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 610

Query 601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 611  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 668
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1553
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425998.1 Length: 689
Range 1: 20 to 677

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	319
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	560	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	619
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	620	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	677

>Rhipicephalus sanguineus haplotype IV cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556746.1 Length: 771
Range 1: 90 to 747

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||
Sbjct 90  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 149

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||
Sbjct 150 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 209

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
          |||
Sbjct 210 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 269

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
          |||
Sbjct 270 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 329

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 300
          |||
Sbjct 330 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 389

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
          |||
Sbjct 390 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 449

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 420
          |||
Sbjct 450 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 509

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
          |||
Sbjct 510 TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 569

Query 481 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
          |||
Sbjct 570 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 629

Query 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 600
          |||
Sbjct 630 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 689

Query 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
          |||
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Sbjct 690 TACATCATTTTTTGGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 747

Range 2: 30 to 64

Score:58.4 bits(31), Expect:0.001,
Identities:34/35(97%), Gaps:1/35(2%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCA-GGT 34
      |||||||||||||||||||||||||||||||||
Sbjct 30 AACAAATATATTTAATTTTTGGAGCATGATCATGGT 64
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S358 cytochrome
c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426012.1 Length: 684
Range 1: 14 to 671

Score:1194 bits(646), Expect:0.0,
Identities:654/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 14 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 74 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121 AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 134 AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 193

Query 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 194 AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 253

Query 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 254 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 313

Query 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 314 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 374 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
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Sbjct	434		TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTATA	AAACATACGATCAATTGGAAT	493
Query	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT				540
Sbjct	494		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT				553
Query	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA				600
Sbjct	554		CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA				613
Query	601		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT				658
Sbjct	614		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT				671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S337 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426010.1 Length: 824
Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,
Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	120
Query	131	GCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGA	190
Sbjct	121	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGA	180
Query	191	AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAA	300
Query	311	TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT	360
Query	371	GGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420

Query	431	GGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCA	AATTGGAATA	ACAATAGAA	490
Sbjct	421	GGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCA	AATTGGAATA	ACAATAGAA	480
Query	491	CGTATACCATT	ATTTGTTTG	ATCTGTTTT	AATTACAGCT	ATTTTATTAC	TTTTATCTTTA	550
Sbjct	481	CGTATACCATT	ATTTGTTTG	ATCTGTTTT	AATTACAGCT	ATTTTATTAC	TTTTATCTTTA	540
Query	551	CCTGTATTAGC	AGGTGCCATT	ACAATATTGT	TAACTGATCG	AAACTTTAAT	ACATCATTT	610
Sbjct	541	CCTGTATTAGC	AGGTGCCATT	ACAATATTGT	TAACTGATCG	AAACTTTAAT	ACATCATTT	600
Query	611	TTTGATCCTTC	AGGGGGAGG	AGATCCAAT	TTTTATATCA	ACATTTATTT	658	
Sbjct	601	TTTGATCCTTC	AGGGGGAGG	AGATCCAAT	TTTTATATCA	ACATTTATTT	648	

>Rhipicephalus sanguineus haplotype II cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KU556744.1 Length: 787
Range 1: 29 to 688

Score:1190 bits(644), Expect:0.0,
Identities:655/660(99%), Gaps:2/660(0%), Strand: Plus/Plus

Query	1	AACAATATATTT	AATTTTTGG	AGCATGATC	AGGTATATT	AGGACTTAGT	ATAAGAATATT	60
Sbjct	29	AACAATATATTT	AATTTTTGG	AGCATGATC	AGGTATATT	AGGACTTAGT	ATAAGAATATT	88
Query	61	AATTCGTATAG	AATTAGGACA	ACCTGGAAC	TTTAATTGG	AAATGATCAG	ATTTATAATGT	120
Sbjct	89	AATTCGTATAG	AATTAGGACA	ACCTGGAAC	TTTAATTGG	AAATGATCAG	ATTTATAATGT	148
Query	121	AATCGTAACAG	CACATGCAT	TTTATTATA	Aatttttttt	ATAGTTATAC	CAATCATAATCGG	180
Sbjct	149	AATCGTAACAG	CACATGCAT	TTTATTATA	AATTTTTTTT	ATAGTTATAC	CAATCATAATCGG	208
Query	181	AGGATTTGGAA	ATTGATTAG	TCCCTATCA	TATTGGGTG	CCCCAGATA	TAGCATTTCCACG	240
Sbjct	209	AGGATTTGGAA	ACTGATTAG	TCCCTATCA	TATTGGGTG	CCCCAGATA	TAGCATTTCCACG	268
Query	241	AATAAATAAT	AATAAGAT	TTTTGACT	TTTACCTC	CTTCACTAT	TTTTTATTA	300
Sbjct	269	AATAAATAAT	AATAAGAT	TTTTGACT	TTTACCTC	CTTCACTAT	TTTTTATTA	328
Query	301	ATTAATTGAAT	CTGGAGCT	GGTACAGG	ATGAACAG	TTTACCCTC	CTCTATCTT	360
Sbjct	329	ATTAATTGAAT	CTGGAGCT	GGTACAGG	ATGAACAG	TTTACCCTC	CTCTATCTT	388
Query	361	ATCACATTAT	GGCCCTTC	AGTAGATT	TTAGCTAT	TTTTTCTC	TTTCATCTT	420
Sbjct	389	ATCACATTAT	GGTCCTTC	AGTAGATT	TTAGCTAT	TTTTTCTC	TTTCATCTT	448

Query	421	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	480
Sbjct	449	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	508
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540			
Sbjct	509	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	568			
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAACTTTAA	600		
Sbjct	569	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAACTTTAA	628		
Query	601	TACATCATTTTTTTGATCCTTCAGGGGG-AGGAGATCC-AATTTTATATCAACATTTATTT	658			
Sbjct	629	TACATCATTTTTTTGATCCTTCAGGGGGGAGGAGATCCAAATTTTATATCAACTTTTATTT	688			

>Rhipicephalus sanguineus haplotype I cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KU556743.1 Length: 659
Range 1: 12 to 659

Score:1186 bits(642), Expect:0.0,
Identities:646/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60	
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71	
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120	
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	131	
Query	121	AATCGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAA	tttttttttTATAGTTATACCAATCATAATCGG	191
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240	
Sbjct	192	AGGATTTGGAAATTGATTAATCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251	
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTC	311
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360	
Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371	
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420	

Sbjct	372	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	432	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	611
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCA	648
Sbjct	612	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCA	659

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S943 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426020.1 Length: 812
Range 1: 2 to 644

Score:1182 bits(640), Expect:0.0,
Identities:642/643(99%), Gaps:0/643(0%), Strand: Plus/Plus

Query	16	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	75
Sbjct	2	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	61
Query	76	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	135
Sbjct	62	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	121
Query	136	TGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	195
Sbjct	122	TGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	181
Query	196	ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	255
Sbjct	182	ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	241
Query	256	ATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGG	315
Sbjct	242	ATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGG	301
Query	316	AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCC	375
Sbjct	302	AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTCC	361
Query	376	TTCAAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	435

Sbjct	362		TTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	421
Query	436		AATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	495
Sbjct	422		AATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	481
Query	496		ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT	555
Sbjct	482		ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT	541
Query	556		ATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGA	615
Sbjct	542		ATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGA	601
Query	616		TCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	602		TCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383818.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5554A cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383819.1 Length: 768
Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,
Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	376

Sbjct	301		GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377		TCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTAGGTGCA	436
Sbjct	361		TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTAGGTGCA	420
Query	437		ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	496
Sbjct	421		ATTAACCTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATA	480
Query	497		CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	556
Sbjct	481		CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557		TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	616
Sbjct	541		TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	600
Query	617		CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	601		CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383811.1 Length: 764
>Rhipicephalus sanguineus isolate LIC5533C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383812.1 Length: 764
Range 1: 1 to 638

Score:1168 bits(632), Expect:0.0,
Identities:636/638(99%), Gaps:0/638(0%), Strand: Plus/Plus

Query	21	GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC	80
Sbjct	1		60
Query	81	AACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT	140
Sbjct	61		120
Query	141	TTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAG	200
Sbjct	121		180
Query	201	TCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	260
Sbjct	181		240
Query	261	GACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTG	320

Sbjct	241		GACTTTTACCTCCTTCACTATTTTATTAATTA	300
Query	321		GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG	380
Sbjct	301		GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG	360
Query	381		TAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	440
Sbjct	361		TAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	420
Query	441		ACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCAT	500
Sbjct	421		ACTTTATTACAACACTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCAT	480
Query	501		TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG	560
Sbjct	481		TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG	540
Query	561		CAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTT	620
Sbjct	541		CAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTT	600
Query	621		CAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	601		CAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 638	

>Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383807.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383808.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736F cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383810.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5535C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383813.1 Length: 763

Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,

Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA	81
Sbjct	1	AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA	60
Query	82	ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT	141
Sbjct	61	ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT	120

Query	142	TATTATAA		201
Sbjct	121	TATTATAA		180
Query	202	CCCTATCATATTGGGTGCCCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		261
Sbjct	181	CCCTATCATATTGGGTGCCCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		240
Query	262	ACTTTTACCTCCTTCACTATTTTATTAATTA		321
Sbjct	241	ACTTTTACCTCCTTCACTATTTTATTAATTA		300
Query	322	TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT		381
Sbjct	301	TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT		360
Query	382	AGATTTAGCTATTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA		441
Sbjct	361	AGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA		420
Query	442	CTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATT		501
Sbjct	421	CTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATT		480
Query	502	ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC		561
Sbjct	481	ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC		540
Query	562	AGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTC		621
Sbjct	541	AGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTC		600
Query	622	AGGGGGAGGAGATCCAATTTTATATCAACATTTATTT		658
Sbjct	601	AGGGGGAGGAGATCCAATTTTATATCAACATTTATTT		637

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S344 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426011.1 Length: 809
Range 1: 3 to 644

Score:1164 bits(630), Expect:0.0,
Identities:638/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA		76
Sbjct	3	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA		62
Query	77	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT		136

Sbjct	63	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAC	122
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	196
Sbjct	123	GCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	182
Query	197	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	183	TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	242
Query	257	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	316
Sbjct	243	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	302
Query	317	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	376
Sbjct	303	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	362
Query	377	TCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	363	TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	422
Query	437	ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	496
Sbjct	423	ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	482
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	556
Sbjct	483	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	542
Query	557	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	616
Sbjct	543	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	602
Query	617	CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	603	CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383809.1 Length: 762
 Range 1: 1 to 636

Score:1164 bits(630), Expect:0.0,
 Identities:634/636(99%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
Sbjct	1	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83	CCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142

Sbjct	61	 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143	ATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	202
Sbjct	121	 ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	 CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	322
Sbjct	241	 CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	382
Sbjct	301	 ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	 GATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTA	502
Sbjct	421	 TTTATTACAACATTTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	562
Sbjct	481	 TTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540
Query	563	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	622
Sbjct	541	 GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	601	 GGGGGAGGAGATCCAATTTTATATCAACATTTATTT 636	

>Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383806.1 Length: 714
 Range 1: 1 to 636

Score:1164 bits(630), Expect:0.0,
 Identities:634/636(99%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
Sbjct	1	 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60

Query	83	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142
Sbjct	61	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143	ATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	202
Sbjct	121	ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	322
Sbjct	241	CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	382
Sbjct	301	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	GATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTA	502
Sbjct	421	TTTATTACAACATTTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	562
Sbjct	481	TTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540
Query	563	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	622
Sbjct	541	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	601	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT 636	

>Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383805.1 Length: 761
Range 1: 1 to 635

Score:1162 bits(629), Expect:0.0,
Identities:633/635(99%), Gaps:0/635(0%), Strand: Plus/Plus

Query	24	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	83
Sbjct	1	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	60

Query	84	CTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	143
Sbjct	61	CTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	120
Query	144	TTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	203
Sbjct	121	TTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	180
Query	204	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	263
Sbjct	181	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	240
Query	264	TTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTA	323
Sbjct	241	TTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTA	300
Query	324	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	383
Sbjct	301	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	360
Query	384	ATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	443
Sbjct	361	ATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	444	TTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTAT	503
Sbjct	421	TTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTAT	480
Query	504	TTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	563
Sbjct	481	TTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	540
Query	564	GTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAG	623
Sbjct	541	GTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAG	600
Query	624	GGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	GGGGAGGAGATCCAATTTTATATCAACATTTATTT	635

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SF3003
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425988.1 Length: 654
Range 1: 1 to 640

Score:1160 bits(628), Expect:0.0,
Identities:636/640(99%), Gaps:0/640(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76

Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	496
Sbjct	421	ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	556
Sbjct	481	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	616
Sbjct	541	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	600
Query	617	CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTAT	656
Sbjct	601	CCTTCAGGGGGAGGACATCCAATTTTATATCACCATTTAT	640

>Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519712.1 Length: 654
Range 1: 3 to 628

Score:1157 bits(626), Expect:0.0,
Identities:626/626(100%), Gaps:0/626(0%), Strand: Plus/Plus

Query	33	GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCT	92
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Sbjct	3	 GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCT	62
Query	93	TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttt	152
Sbjct	63	 TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT	122
Query	153	tttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT	212
Sbjct	123	 TTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT	182
Query	213	TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC	272
Sbjct	183	 TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC	242
Query	273	CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA	332
Sbjct	243	 CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA	302
Query	333	CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA	392
Sbjct	303	 CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA	362
Query	393	TTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAA	452
Sbjct	363	 TTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAA	422
Query	453	CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT	512
Sbjct	423	 CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT	482
Query	513	CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA	572
Sbjct	483	 CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA	542
Query	573	CAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG	632
Sbjct	543	 CAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG	602
Query	633	ATCCAATTTTATATCAACATTTATTT 658	
Sbjct	603	 ATCCAATTTTATATCAACATTTATTT 628	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1575
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426002.1 Length: 639
Range 1: 1 to 628

Score:1155 bits(625), Expect:0.0,
Identities:627/628(99%), Gaps:0/628(0%), Strand: Plus/Plus

Query	31	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	90
Sbjct	1	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	60
Query	91	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	150
Sbjct	61	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	120
Query	151	tttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	210
Sbjct	121	TTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	180
Query	211	ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	270
Sbjct	181	ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	240
Query	271	TCCTTCACTATTTTTATTAATTAACCTCTCATTAATTGAATCTGGAGCTGGTACAGGATG	330
Sbjct	241	TCCTTCACTATTTTTATTAATTAACCTCTCATTAATTGAATCTGGAGCTGGTACAGGATG	300
Query	331	AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC	390
Sbjct	301	AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC	360
Query	391	TATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTAC	450
Sbjct	361	TATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTAC	420
Query	451	AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG	510
Sbjct	421	AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG	480
Query	511	ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT	570
Sbjct	481	ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT	540
Query	571	TACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGG	630
Sbjct	541	TACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGG	600
Query	631	AGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	AGATCCAATTTTATATCAACATTTATTT	628

>Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: MG855658.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: MG855657.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,

Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
      |||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
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>Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855656.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
      |||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome oxidase subunit I
(COI) gene, partial cds; mitochondrial
Sequence ID: KX757910.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
      |||||||||||||||
Sbjct 601 TTTTATATCAACATTTATTT 620
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>Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757904.1 Length: 630

Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,

Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
      |||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
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>Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial

Sequence ID: KX757902.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTT 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
      |||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
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>Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase subunit I (COI)

gene, partial cds; mitochondrial
Sequence ID: KX757896.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
|||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA 158
|||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTtA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
|||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
|||||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
|||||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
|||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
|||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
|||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
|||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
|||||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
|||||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757889.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
|||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
|||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
|||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
|||||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
|||||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
|||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
|||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
|||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
|||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
|||||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
|||||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Rovind cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757887.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA   158
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   218
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   278
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   338
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTT   398
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTT   360

Query   399  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACATTG   458
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACATTG   420

Query   459  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   518
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA   638
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA   600

Query   639  TTTTATATCAACATTTATTT   658
        ||||||||||||||||
Sbjct   601  TTTTATATCAACATTTATTT   620
```

>Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757879.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
      |||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```


>Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519711.1 Length: 636
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
          ||||||||||||||||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135448.1 Length: 630
Range 1: 1 to 620

Score:1146 bits(620), Expect:0.0,
Identities:620/620(100%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 TAATTACAGCTATTTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
      |||||||||||||||||||
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Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630347.1 Length: 644
Range 1: 20 to 641

Score:1144 bits(619), Expect:0.0,
Identities:621/622(99%), Gaps:0/622(0%), Strand: Plus/Plus

```
Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 20  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT 120
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 80  AATTGGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121  AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 140  AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG 199

Query 181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 200  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 259

Query 241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 319

Query 301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 380  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 500  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 559

Query 541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 560  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 619

Query 601  TACATCATTTTTTTGATCCTTCA 622
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|||||
Sbjct  620  TACATCATTTTTTGATCCTTCA  641
```

>Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630346.1 Length: 644
Range 1: 20 to 641

Score:1144 bits(619), Expect:0.0,
Identities:621/622(99%), Gaps:0/622(0%), Strand: Plus/Plus

```
Query   1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
      |||
Sbjct  20  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  79

Query   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT  120
      ||| |||
Sbjct   80  AATTGGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT  139

Query   121  AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG  180
      |||
Sbjct   140  AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG  199

Query   181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
      |||
Sbjct   200  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  259

Query   241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC  300
      |||
Sbjct   260  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC  319

Query   301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
      |||
Sbjct   320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  379

Query   361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  420
      |||
Sbjct   380  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  439

Query   421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  480
      |||
Sbjct   440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  499

Query   481  AACAAAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
      |||
Sbjct   500  AACAAAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  559

Query   541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA  600
      |||
Sbjct   560  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA  619
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Query   601  TACATCATTTTTTTGATCCTTCA  622
        |||||
Sbjct   620  TACATCATTTTTTTGATCCTTCA  641

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1568
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426000.1 Length: 635
Range 1: 14 to 635

Score:1144 bits(619), Expect:0.0,
Identities:621/622(99%), Gaps:0/622(0%), Strand: Plus/Plus

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Query   1    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        |||||
Sbjct   14    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  73

Query   61    AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT  120
        |||||
Sbjct   74    AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT  133

Query   121   AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG  180
        |||||
Sbjct   134   AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG  193

Query   181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
        |||||
Sbjct   194   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  253

Query   241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  300
        |||||
Sbjct   254   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  313

Query   301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
        |||||
Sbjct   314   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  373

Query   361   ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  420
        |||||
Sbjct   374   ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  433

Query   421   TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  480
        |||||
Sbjct   434   TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT  493

Query   481   AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
        |||||
Sbjct   494   AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  553

Query   541   TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA  600
        |||||
Sbjct   554   TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA  613

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Query   601  TACATCATTTTTTTGATCCTTCA  622
        ||||||||||||||||||
Sbjct   614  TACATCATTTTTTTGATCCTTCA  635

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>Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757905.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  98
        ||||||||||||||||||
Sbjct   1     TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA  158
        ||||||||||||||||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  218
        ||||||||||||||||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  278
        ||||||||||||||||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTAATTAACTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  338
        ||||||||||||||||
Sbjct   241  TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  398
        ||||||||||||||||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360

Query   399  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  458
        ||||||||||||||||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

Query   459  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  518
        ||||||||||||||||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480

Query   519  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        ||||||||||||||||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TGTAACTGATCGAAACCTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  638
        ||||||||||||||||||

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Sbjct 541 TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACATTTATTT 658
 |||||

Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757895.1 Length: 630
 Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
 Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
 |||||

Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
 |||||

Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
 |||||

Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
 |||||

Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
 |||||

Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
 |||||

Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
 |||||

Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
 |||||

Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
 |||||

Sbjct 481 TAATTACAGCTATTTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638

Sbjct	541		TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639		TTTTATATCAACATTTATTT	658
Sbjct	601		TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Zadar cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX757892.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540

Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757890.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540

Query	579	TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757888.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAATCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Petnica cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757883.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578

Sbjct	481		TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579		TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541		TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639		TTTTATATCAACATTTATTT 658	
Sbjct	601		TTTTATATCAACATTTATTT 620	

>Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519708.1 Length: 629
Range 1: 4 to 620

Score:1140 bits(617), Expect:0.0,
Identities:617/617(100%), Gaps:0/617(0%), Strand: Plus/Plus

Query	42	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	101
Sbjct	4		GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA 63
Query	102	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttATAG	161
Sbjct	64		ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAG 123
Query	162	TTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCC	221
Sbjct	124		TTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCC 183
Query	222	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT	281
Sbjct	184		CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT 243
Query	282	TTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC	341
Sbjct	244		TTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC 303
Query	342	CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTC	401
Sbjct	304		CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTC 363
Query	402	TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAA	461
Sbjct	364		TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAA 423
Query	462	ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA	521
Sbjct	424		ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA 483

Query	522	TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	581
Sbjct	484	TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	543
Query	582	TAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTT	641
Sbjct	544	TAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTT	603
Query	642	TATATCAACATTTATTT	658
Sbjct	604	TATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135447.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480

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Query   519  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        |||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  638
        |||
Sbjct   541  TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGACCCAA  600

Query   639  TTTTATATCAACATTTATTT  658
        |||
Sbjct   601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S475 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426014.1 Length: 649
Range 1: 28 to 649

Score:1138 bits(616), Expect:0.0,
Identities:620/622(99%), Gaps:0/622(0%), Strand: Plus/Plus

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Query    1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        |||
Sbjct   28  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  87

Query   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  120
        |||
Sbjct   88  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  147

Query   121  AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG  180
        |||
Sbjct   148  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG  207

Query   181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
        |||
Sbjct   208  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  267

Query   241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  300
        |||
Sbjct   268  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  327

Query   301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
        |||
Sbjct   328  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  387

Query   361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  420
        |||
Sbjct   388  ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  447

Query   421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT  480
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Sbjct  448  TTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTGTAAACATACGATCAATTGGAAT  507
Query  481  AACAA TAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  508  AACAA TAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT  567
Query  541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA  600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  568  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA  627
Query  601  TACATCATTTTTTTGATCCTTCA  622
        |||||||||||||||||||
Sbjct  628  TACATCATTTTTTTGATCCTTCA  649

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>Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519707.1 Length: 626
Range 1: 1 to 616

Score:1138 bits(616), Expect:0.0,
Identities:616/616(100%), Gaps:0/616(0%), Strand: Plus/Plus

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Query  43  ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAA  102
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAA  60
Query  103  TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA ttttttttATAGT  162
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA TTTTTTTTATAGT  120
Query  163  TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC  222
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC  180
Query  223  AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT  282
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT  240
Query  283  TTTATTAATTAAC TCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC  342
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TTTATTAATTAAC TCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC  300
Query  343  TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT  402
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT  360
Query  403  TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTGTAAA  462
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTGTAAA  420
Query  463  CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT  522

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Sbjct	421		CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523		TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	582
Sbjct	481		TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583		AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	642
Sbjct	541		AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	600
Query	643		ATATCAACATTTATTT 658	
Sbjct	601		ATATCAACATTTATTT 616	

>Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757901.1 Length: 630
Range 1: 1 to 620

Score:1134 bits(614), Expect:0.0,
Identities:618/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTT	360
Query	399		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420

Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	541	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KU568516.1 Length: 656
Range 1: 27 to 656

Score:1131 bits(612), Expect:0.0,
Identities:624/630(99%), Gaps:0/630(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	27	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	86
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	87	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	146
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	147	AATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGG	206
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	207	AGGATTTGGAAATTGATTAATCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	266
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	267	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	326
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	327	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	386
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	387	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	446

Query	421	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	480
Sbjct	447	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	506
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540			
Sbjct	507	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	566			
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAACTTTAA	600		
Sbjct	567	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAACTTTAA	626		
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGG	630			
Sbjct	627	TACATCATTTTTTTGACCCTTCAGGAGGAGG	656			

>Rhipicephalus sanguineus clone #4 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX519709.1 Length: 635
Range 1: 2 to 621

Score:1129 bits(611), Expect:0.0,
Identities:617/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	2	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	61
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	ttttttttA	158
Sbjct	62	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCTTTTATTATAA	TTTTTTTTTA	121
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218	
Sbjct	122	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	181	
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278	
Sbjct	182	CCCCGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	241	
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338	
Sbjct	242	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	301	
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398	
Sbjct	302	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGGAGATTTAGCTATTTTTT	361	
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	TTTATTACA	458

Sbjct	362	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTG	421
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	422	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	481
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	482	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	541
Query	579	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	638
Sbjct	542	TGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	601
Query	639	TTTTATATCAACATTTATTT	658
Sbjct	602	TTTTATATCAACATTTATTT	621

>Rhipicephalus sanguineus isolate LIC4723B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX714599.1 Length: 723

>Rhipicephalus sanguineus isolate LIC4750B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX714600.1 Length: 723

Range 1: 1 to 597

Score:1092 bits(591), Expect:0.0,

Identities:595/597(99%), Gaps:0/597(0%), Strand: Plus/Plus

Query	62	ATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTA	121
Sbjct	1	ATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTA	60
Query	122	ATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGA	181
Sbjct	61	ATCGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATTGGA	120
Query	182	GGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGA	241
Sbjct	121	GGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGA	180
Query	242	ATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCA	301
Sbjct	181	ATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCA	240
Query	302	TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA	361
Sbjct	241	TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA	300
Query	362	TCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCT	421

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Sbjct  301  TCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCT  360
Query  422  TCAATTTTAGGTGCAATTAACCTTTATTACAACATTGTAAACATACGATCAATTGGAATA  481
        |||
Sbjct  361  TCAATTTTAGGTGCAATTAACCTTTATTACAACATTGTAAACATACGATCAATTGGAATA  420
Query  482  ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT  541
        |||
Sbjct  421  ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT  480
Query  542  TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAAT  601
        |||
Sbjct  481  TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAAT  540
Query  602  ACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658
        |||
Sbjct  541  ACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  597

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>Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519713.1 Length: 580
Range 1: 1 to 580

Score:1072 bits(580), Expect:0.0,
Identities:580/580(100%), Gaps:0/580(0%), Strand: Plus/Plus

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Query  43  ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA  102
        |||
Sbjct  1  ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA  60
Query  103  TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAttttttttATAGT  162
        |||
Sbjct  61  TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT  120
Query  163  TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC  222
        |||
Sbjct  121  TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC  180
Query  223  AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT  282
        |||
Sbjct  181  AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT  240
Query  283  TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC  342
        |||
Sbjct  241  TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC  300
Query  343  TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT  402
        |||
Sbjct  301  TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT  360
Query  403  TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACATTGTAAA  462

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Sbjct	361		TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA	420
Query	463		CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	522
Sbjct	421		CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523		TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	582
Sbjct	481		TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583		AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA	622
Sbjct	541		AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA	580

>Rhipicephalus sanguineus mitochondrial DNA, complete genome
Sequence ID: AF081829.1 Length: 14710
Range 1: 1191 to 1848

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60	
Sbjct	1191		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	1250
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120	
Sbjct	1251		AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	1310
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATCATAATCGG	180	
Sbjct	1311		AATCGTAACAGCACATGCATTTATTATAAATTTCTTTATAGTTATACCAATCATAATCGG	1370
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240	
Sbjct	1371		AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	1430
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC	300	
Sbjct	1431		AATAAATAATATAAGATTTTGACTTTTACCCCCTCATTATTTTATTGATTAACCTCTTC	1490
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360	
Sbjct	1491		ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	1550
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420	
Sbjct	1551		ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	1610
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480	

Sbjct	1611		TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	1670
Query	481		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	1671		AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	1730
Query	541		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	1731		TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	1790
Query	601		TACATCATTTTTTGTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	1791		CACATCATTTTTTGTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	1848

>Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519706.1 Length: 595
Range 1: 1 to 570

Score:1053 bits(570), Expect:0.0,
Identities:570/570(100%), Gaps:0/570(0%), Strand: Plus/Plus

Query	89	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	148
Sbjct	1	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	60
Query	149	AttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATC	208
Sbjct	61	ATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATC	120
Query	209	ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	268
Sbjct	121	ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	180
Query	269	CCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGA	328
Sbjct	181	CCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGA	240
Query	329	TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA	388
Sbjct	241	TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA	300
Query	389	GCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATT	448
Sbjct	301	GCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATT	360
Query	449	ACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT	508
Sbjct	361	ACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT	420

Query	509	TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	568
Sbjct	421	TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	480
Query	569	ATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGA	628
Sbjct	481	ATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGA	540
Query	629	GGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	541	GGAGATCCAATTTTATATCAACATTTATTT	570

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SC3005
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425987.1 Length: 574
Range 1: 1 to 561

Score:1014 bits(549), Expect:0.0,
Identities:557/561(99%), Gaps:0/561(0%), Strand: Plus/Plus

Query	98	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAA	157
Sbjct	1	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACACGCATTTATTATAA	60
Query	158	ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGT	217
Sbjct	61	ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATTATATTAGGT	120
Query	218	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA	277
Sbjct	121	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA	180
Query	278	CTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT	337
Sbjct	181	CTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT	240
Query	338	TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTT	397
Sbjct	241	TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTT	300
Query	398	TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAAC	457
Sbjct	301	TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAAC	360
Query	458	GTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTT	517
Sbjct	361	GTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTT	420
Query	518	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	577
Sbjct	421	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	480

Query	578	TTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCA	637
Sbjct	481	TTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCA	540
Query	638	ATTTTATATCAACATTTATTT	658
Sbjct	541	ATTTTATATCAACATTTATTT	561

>Rhipicephalus sanguineus clone #5 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519710.1 Length: 553
Range 1: 1 to 547

Score:989 bits(535), Expect:0.0,
Identities:543/547(99%), Gaps:0/547(0%), Strand: Plus/Plus

Query	77	GGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	1	GGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGGAATCGTAACAGCACAT	60
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	196
Sbjct	61	GCTTTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	120
Query	197	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	121	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	180
Query	257	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	316
Sbjct	181	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	240
Query	317	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	376
Sbjct	241	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	300
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	301	TCAGGAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	360
Query	437	ATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	496
Sbjct	361	ATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	420
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	556
Sbjct	421	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	480
Query	557	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	616

Sbjct 481 TTAGCAGGTGCCATTACAATATTGTAACTGATCGATACTTTAATACATCATTTTTTTGAT 540

Query 617 CCTTCAG 623
 |||||

Sbjct 541 CCTTCAG 547

>Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757903.1 Length: 630
 Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
 Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
 |||||

Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA 158
 |||||

Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 218
 |||||

Sbjct 121 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 278
 |||||

Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 240

Query 279 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 338
 |||||

Sbjct 241 TATTTTTATTGATTAATTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 300

Query 339 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 398
 |||||

Sbjct 301 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 458
 |||||

Sbjct 361 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATTACAACCTATTG 420

Query 459 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 518
 |||||

Sbjct 421 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
 |||||

Sbjct 481 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 638

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Sbjct   541 TATTAAGTGCACGAACTTTAACACATCATTTTTTGACCCTTCAGGAGGAGGAGATCCCA    600
Query    639 TTTTATATCAACATTTATTT      658
          |||||
Sbjct   601 TTTTATATCAACTTATTT      620

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>Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757893.1 Length: 629
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540

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Query    579   TGTTAACTGATCGAAACTTTAATACATCATTTTTTGGATCCTTCAGGGGGAGGAGATCCAA   638
        | ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    541   TATTAACTGATCGAAACTTTAACACATCATTTTTTGACCCTTCAGGAGGAGGAGATCCCA   600

Query    639   TTTTATATCAACATTTATTT   658
        ||||||| |||||
Sbjct    601   TTTTATATCAACACTTATTT   620
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>Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757909.1 Length: 630
Range 1: 1 to 620

Score:979 bits(530), Expect:0.0,
Identities:590/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAatttttttta	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	218
Sbjct	121	TAGTTATACCAATAATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCTGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGCCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540

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Query    579  TGTTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGGAGGAGATCCAA  638
      ||| ||||||||||||||||||| ||||||||||||||| ||||||| ||||| ||||| |
Sbjct    541  TATTGACTGATCGAAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGGGATCCCA  600

Query    639  TTTTATATCAACATTTATTT  658
      ||||||||||||| |||||
Sbjct    601  TTTTATATCAACACTTATTT  620

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Query    639  TTTTATATCAACATTTATTT  658
        |||||
Sbjct    601  TTTTATATCAACACTTATTT  620

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>Rhipicephalus sanguineus isolate FT157 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223690.1 Length: 535
Range 1: 1 to 524

Score:963 bits(521), Expect:0.0,
Identities:523/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAA		ATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	194
Sbjct	1	ATGCATTTATTATAA		ATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	60

Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120

Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTG	180

Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTTTATCTTCAAATTTATCACATTATGGCC	240

Query	375	CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	241	CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300

Query	435	CAATTAACTTTATTACAAC	TATTGTA	AACATACGATCAATTGGAATAACAATAGAACGTA	494
Sbjct	301	CAATTAACTTTATTACAAC	TATTGTA	AACATACGATCAATTGGAATAACAATAGAACGTA	360

Query	495	TACCATTATTTGTTTGATCTGTTTAAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554
Sbjct	361	TACCATTATTTGTTTGATCTGTTTAAATTACAGCTATTTTATTACTTTTATCTTTACCTG	420

Query	555	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTG	614
Sbjct	421	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTG	480

Query 615 ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATT 658
|||||

Sbjct 481 ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524

>Rhipicephalus sanguineus isolate FT154 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223688.1 Length: 535
Range 1: 1 to 524

Score:957 bits(518), Expect:0.0,
Identities:522/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

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Query 135 ATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT 194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT 60

Query 195 GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA 254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA 120

Query 255 GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG 314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCACTAATTGAATCTG 180

Query 315 GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC 374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAACCTTATCACATTATGGCC 240

Query 375 CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG 434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG 300

Query 435 CAATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA 494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 CAATTAACTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA 360

Query 495 TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG 554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG 420

Query 555 TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG 614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG 480

Query 615 ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524
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>Rhipicephalus sanguineus isolate CE67 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial

Sequence ID: MN223686.1 Length: 535
Range 1: 1 to 524

Score:957 bits(518), Expect:0.0,
Identities:522/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

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Query 135 ATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT 194
          |||
Sbjct 1 ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT 60

Query 195 GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA 254
          |||
Sbjct 61 GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA 120

Query 255 GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG 314
          |||
Sbjct 121 GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG 180

Query 315 GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC 374
          |||
Sbjct 181 GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC 240

Query 375 CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG 434
          |||
Sbjct 241 CTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG 300

Query 435 CAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA 494
          |||
Sbjct 301 CAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA 360

Query 495 TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG 554
          |||
Sbjct 361 TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG 420

Query 555 TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG 614
          |||
Sbjct 421 TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG 480

Query 615 ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658
          |||
Sbjct 481 ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524
```

>Rhipicephalus sanguineus isolate CE61 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223689.1 Length: 535
Range 1: 1 to 524

Score:952 bits(515), Expect:0.0,
Identities:521/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

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Query 135 ATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT 194
```

Sbjct	1	 ATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	 GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120
Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	 GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	180
Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	 GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTC	240
Query	375	CTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	241	 CTTCAGTAGATTTAACTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300
Query	435	CAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494
Sbjct	301	 CAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	360
Query	495	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554
Sbjct	361	 TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTTTATCTTTACCTG	420
Query	555	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG	614
Sbjct	421	 TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTG	480
Query	615	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	481	 ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524	

>Rhipicephalus sanguineus isolate RI46 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223687.1 Length: 535
Range 1: 1 to 524

Score:952 bits(515), Expect:0.0,
Identities:521/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	194
Sbjct	1	 ATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	 GATTAGTCCCTATTATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120

Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTCATTAATTGAATCTG	180
Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374	
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACACTATGGCC	240	
Query	375	CTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434	
Sbjct	241	CTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300	
Query	435	CAATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494	
Sbjct	301	CAATTAACTTTATTACAACATTTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	360	
Query	495	TACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	554	
Sbjct	361	TACCACTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTG	420	
Query	555	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG	614	
Sbjct	421	TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG	480	
Query	615	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658	
Sbjct	481	ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	524	

>Rhipicephalus sanguineus isolate RI08 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MN223684.1 Length: 535
Range 1: 3 to 524

Score:948 bits(513), Expect:0.0,
Identities:519/522(99%), Gaps:0/522(0%), Strand: Plus/Plus

Query	137	GCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	196	
Sbjct	3	GCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	62	
Query	197	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256	
Sbjct	63	TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	122	
Query	257	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGA	316
Sbjct	123	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGA	182
Query	317	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	376	
Sbjct	183	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	242	

Query	377	TCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	243	TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	302
Query	437	ATTAACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	496
Sbjct	303	ATTAACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	362
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	556
Sbjct	363	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	422
Query	557	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	616
Sbjct	423	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGAT	482
Query	617	CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658	
Sbjct	483	CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 524	

>Rhipicephalus sanguineus isolate RI54 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223685.1 Length: 535
Range 1: 1 to 524

Score:946 bits(512), Expect:0.0,
Identities:520/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGAAATT	194
Sbjct	1	ATGCATTTATTATAATTTTTTTTATAGTTATACCGATCATAATCGGAGGATTTGGAAATT	60
Query	195	GATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	61	GATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAA	120
Query	255	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	314
Sbjct	121	GATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTG	180
Query	315	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	374
Sbjct	181	GAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCC	240
Query	375	CTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	241	CTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTG	300
Query	435	CAATTAACTTTATTACAACACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTA	494

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Sbjct  301  CAATTAAC TTTATTACA ACTATTGTAA ACATACGATCA ATTGGAATA ACAATAGAACGTA 360
Query  495  TACCATTAT TTTGTTTGATCTG TTTTAATTACAGCTAT TTTTATTACTTTTATCT TTTACCTG 554
      |||
Sbjct  361  TACCATTAT TTTGTTTGATCTG TTTTAATTACAGCTAT TTTTATTACTCTTATCT TTTACCTG 420
Query  555  TATTAGCAG GTGCCATTACA ATATTGT TAACTGATCGAA ACTTTAATACATCAT TTTTTTG 614
      |||
Sbjct  421  TATTAGCAG GTGCCATTACA ATATTGT TAACTGATCGAA ACTTTAATACATCAT TTTTTTG 480
Query  615  ATCCTTCAG GGGGAGGAGATCCA ATTTTATATCAACAT TTTATTT 658
      |||
Sbjct  481  ATCCTTCAG GGGGAGGAGATCCA ATTTTATATCAACAT TTTATTT 524

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>Rhipicephalus sanguineus isolate FT044 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MN223683.1 Length: 535
Range 1: 1 to 524

Score:946 bits(512), Expect:0.0,
Identities:520/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

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Query  135  ATGCATTTAT TATAA tttttttt ATAGTTATACCAATC ATAATCGGAGGAT TTGGAAATT 194
      |||
Sbjct   1   ATGCATTTAT TATAA TTTTTTTT ATAGTTATACCAATC ATAATCGGAGGAT TTGGAAATT 60
Query  195  GATTAGTCC CTATCATATTG GGTGCCCCAGATAT AGCATTTCCACGAATA AATAATATAA 254
      |||
Sbjct  61   GATTAGTCC CTATCATATTG GGTGCCCCAGATAT AGCATTTCCACGAATA AATAATATAA 120
Query  255  GATTTTGAC TTTTACCTCCTT CACTATTTTTTATTA ATTA ACTCTTCATTA ATTGAATCTG 314
      |||
Sbjct  121  GATTTTGAC TTTTACCTCCTT CACTATTTTTTATTA ATTA ACTCTTCATTA ATTGAATCTG 180
Query  315  GAGCTGGTAC AGGATGAACAGTTT ACCCTCCTCTATCTTCAA ATTTATCACATTATGG CC 374
      |||
Sbjct  181  GAGCTGGTAC AGGATGAACAGTTT ACCCTCCTCTATCTTCAA ATTTATCACATTATGG CC 240
Query  375  CTTCAGTAGA TTTAGCTATTTT TCTCTTCATCTTGCT GGTGCTTCTTCAAT TTTAGGTG 434
      |||
Sbjct  241  CTTCAGTAGA TTTAGCTATCTT TCTCTTCATCTTGCT GGTGCTTCTTCAAT TTTAGGTG 300
Query  435  CAATTAAC TTTATTACA ACTATTGTAA ACATACGATCA ATTGGAATA ACAATAGAACGTA 494
      |||
Sbjct  301  CAATTAAC TTTATTACA ACTATTGTAA ACATACGATCA ATTGGAATA ACAATAGAACGTA 360
Query  495  TACCATTAT TTTGTTTGATCTG TTTTAATTACAGCTAT TTTTATTACTTTTATCT TTTACCTG 554
      |||
Sbjct  361  TACCATTAT TTTGTTTGATCTG TTTTAATTACAGCTAT TTTTATTACTGTTATCT TTTACCTG 420
Query  555  TATTAGCAG GTGCCATTACA ATATTGT TAACTGATCGAA ACTTTAATACATCAT TTTTTTG 614

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Sbjct	421		TATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTG	480
Query	615		ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	481		ATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	524

>Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase subunit 1 gene,
partial cds; mitochondrial
Sequence ID: KY678135.1 Length: 790
Range 1: 18 to 675

Score:900 bits(487), Expect:0.0,
Identities:601/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	18	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	77
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	78	AATTCGTATAGAATTAGGCCAACCTGGAACCCTAATTGGTAATGATCAAATTTATAATGT	137
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	138	AATTGTTACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGG	197
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	198	TGGATTTGGAACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGACTTCTCCTCCCTCATTATTTATATTAATTAATTCTTC	317
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	318	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCTTATCCTCAAATTT	377
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	378	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAAT	497
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	557

Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCGATCGAAATTTTAA	617
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	618	CACTTCATTTTTTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	675

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (C01) gene, partial cds;
mitochondrial

Sequence ID: KU214592.1 Length: 829

Range 1: 1 to 648

Score:898 bits(486), Expect:0.0,

Identities:594/648(92%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGCCAACCTGGAACCTAATTGGTAATGATCAAATTTATAATGTAATTGTTACA	120
Query	131	GCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATTTGGA	190
Sbjct	121	GCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGGTGGATTTGGA	180
Query	191	AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTACCTCCTTCACTATTTTTTATTAATTAACCTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTCTCCTCCCTCATTATTTATATTAATTAATTCTTCATTAATTGAG	300
Query	311	TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCAGGAGCAGGTACAGGATGGACAGTTTATCCTCCCCTATCCTCAAATTTATCACATTAT	360
Query	371	GGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAATAACAATAGAA	480
Query	491	CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTA	550
Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACTATTATCTTTA	540

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Query   551  CCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTT  610
        ||||| |||||||||||||||||||||||| ||||| |||||||| ||||| || |||||
Sbjct   541  CCTGTTTTAGCAGGTGCCATTACAATATTATTAACCGATCGAAATTTTAACACTTCATTT  600

Query   611  TTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658
        ||||| |||||||||||||||| ||||||||||||||||||||||||
Sbjct   601  TTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT  648

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>Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome oxidase subunit 1 gene, complete cds; mitochondrial
Sequence ID: KM494916.1 Length: 1539
Range 1: 45 to 702

Score:889 bits(481), Expect:0.0,
Identities:599/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        |||||||||||||||||||||||||||| || |||||||| | || |||||||| |
Sbjct   45  AACAAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT  104

Query   61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT  120
        |||||||||||||||| |||||||||| |||||| |||||| ||||||||
Sbjct  105  AATTCGTATAGAATTAGGTCAACCTGGAACCTAATTGGTAATGATCAAATTTATAATGT  164

Query   121  AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG  180
        ||| || ||||| |||||||||||||||||||||||| |||||| ||||| ||
Sbjct  165  AATTGTTACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATTATAATTGG  224

Query   181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  240
        ||||||||| ||||||| ||||| ||| | || || |||||||||||| |||||
Sbjct  225  TGGATTTGGAAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTCCCACG  284

Query   241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC  300
        |||||||||||||||||||| ||||| || ||||| |||||||| |||||
Sbjct  285  AATAAATAATATAAGATTTTGACTTCTTCTCCTCCTCATTATTTATATTAATTAATTCTTC  344

Query   301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  360
        |||||||| || ||||| |||||||||||||||||| |||| ||||| |||||||
Sbjct  345  ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCCTCAAATTT  404

Query   361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  420
        ||||||||| || |||||||||||||||||||||||||||||||||||||||
Sbjct  405  ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  464

Query   421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT  480
        |||||||||||||||||| |||||||||||||||| || ||||||| |||||||
Sbjct  465  TTCAATTTTAGGTGCAATTAATTTTATTACAACATATTGTGAATATACGATCTATTGGAAT  524

Query   481  AACAAAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540
        ||||||||| |||||||||||| |||||||||||||||| || |||||||||

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Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	645	CACTTCATTTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus sanguineus isolate Tehran cytochrome oxidase subunit 1 gene,
complete cds; mitochondrial
Sequence ID: KM494915.1 Length: 1539
Range 1: 45 to 702

Score:889 bits(481), Expect:0.0,
Identities:599/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCTCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCTCAAATTT	404
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTTATTACAACATATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540

Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	645	CAC TTCATTTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

Score:889 bits(481), Expect:0.0,
Identities:599/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	525	AACAATAGAACGAATACCTTTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTTTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAATTTTAA	644
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	645	TACCTCGTTCTTTGATCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800313.1 Length: 673
Range 1: 8 to 665

Score:883 bits(478), Expect:0.0,
Identities:598/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAAATTTTTTTTATGGTAATACCTATTATAATTGG	187
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTTCATTATTTCTATTAATTAACCTCTTC	307
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCAGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480

Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAAGTATCGAAATTTCAA	607
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	608	TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATTT	665

>Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800314.1 Length: 673
Range 1: 8 to 664

Score:881 bits(477), Expect:0.0,
Identities:597/657(91%), Gaps:0/657(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAAATTTTTTTTATGGTAATACCCATTATAATTGG	187
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAAGTCTTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTTCACTATTTCTATTAATTAAGTCTTC	307
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCGGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCTTCAAATTT	367
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480

[illegible]

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	421	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAAT	TTTCATTACA	ACTATTGTAA	CATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGTATACCATT	ATTTGTTTGATCTGTTTTA	AATTACAGCTATTTTATTACT	540	
Sbjct	546	AACAATAGAACGAATACCATT	ATTCGTTTGATCTGTTTTA	AATCACC	GCTATTTTATTGCT 605	
Query	541	TTTATCTTTACCTGTATTAG	CAGGTGCCATTACA	ATATTGT	TAAGTATCGAAACTTTAA 600	
Sbjct	606	TCTATCTTTACCTGTTTTAG	CAGGTGCCATTACA	ATATTATTA	AGTATCGAAATTTCAA 665	
Query	601	TACATCATTTTTTTGATCCT	TCAGGGGAGGAGATCCA	ATTTTATATCAACATTTATTT 658		
Sbjct	666	CACTTCATTTTTTGACCCT	TCAGGAGGAGGTGACC	CTATTTTATATCAACATTTATTT 723		

>Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KY606302.1 Length: 873
Range 1: 66 to 723

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATCATAATCGG 180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAA	TTTTTTTTTATAGTAATACCAATCATAATTGG 245
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	AACTCTTC 300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTA	ATTCTTC 365
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485

Query	421	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAAT	TTTCATTACA	ACTATTGTAA	CATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGTATACCATT	ATTTGTTTGATCTGTTTTA	AATTACAGCTATTTTATTACT	540	
Sbjct	546	AACAATAGAACGAATACCATT	ATTCGTTTGATCTGTTTTA	AATCACC	GCTATTTTATTGCT	605
Query	541	TTTATCTTTACCTGTATTAGC	AGGTGCCATTACA	ATATTGT	TAACTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGC	AGGTGCCATTACA	ATATTAT	TAACTGATCGAAATTTCAA	665
Query	601	TACATCATTTTTTTGATCCT	TCAGGGGGAGGAGATCCA	ATTTTATATCAACATTTATTT	658	
Sbjct	666	CACTTCATTTTTTTGACCCT	TCAGGAGGAGGTGACCCT	ATTTTATATCAACATTTATTT	723	

>Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KY606301.1 Length: 873
Range 1: 66 to 723

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAA	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAA	245
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTA	365
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420

Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTCAATACAACATATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	665
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606300.1 Length: 873
Range 1: 66 to 723

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCTCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420

Sbjct	426	 ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	486	 TTCAATTTTAGGTGCAATTAATTTTATTACAACATATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	546	 AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	606	 TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACGATCGAAATTTCAA	665
Query	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	666	 CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACATATTGTAAACATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTCATTACAACATATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	665
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate COX1-7-Sheep cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800312.1 Length: 673
Range 1: 8 to 664

Score:865 bits(468), Expect:0.0,
Identities:594/657(90%), Gaps:0/657(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGACCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCTATTATAATTGG	187
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATCATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTTCACTATTTCTATTAATTAACCTCTC	307
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCGGGAGCAGGAACGGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367

Query	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTCTAAACATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTCTGATCTGTTTTAATTACCACCATCTTACTTCT	547
Query	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAAGTATCGAAATTTCAA	607
Query	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATT	657
Sbjct	608	TACCTCATTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATT	664

>Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MT079206.1 Length: 678
Range 1: 1 to 652

Score:861 bits(466), Expect:0.0,
Identities:590/652(90%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCTG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCTG	60
Query	67	TATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATCATAATCGGAGGATT	186
Sbjct	121	AACAGCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	TGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181	TGGAAACTGGTTAGTTCCAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACA	366

Sbjct	301	TGAATCTGGGGCAGGGACAGGGTGAAGTGTATCTCTCTTTATCTCAAATTTATCCCA	360
Query	367	TTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAACCTTTATTACAACCTATTGTA AACATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTTCATTACAACCTATTGTA AACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGTATACCATTATTTGTTTGATCTGTTTAAATTACAGCTATTTTATTACTTTTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTAAATCACCCTATTTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAATACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTA ACTGATCGAAATTTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658
Sbjct	601	ATTTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTTATTT	652

>Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305547.1 Length: 658
Range 1: 1 to 658

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	61	AATTCGAATAGAGTTAGGACAACCTGGGACTTTAATTGGAAATGATCAAATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAA t t t t t t t t t t ATAGTTATACCAATCATAATCGG 	180
Sbjct	121	AATTGTAACAGCTCATGCATTTATTATAA T T T T T T T T T T ATAGTAATACCAATCATAATTGG	180
Query	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 	240
Sbjct	181	AGGATTTGGAAACTGATTAGTGCCCATTTATGTTAGGAGCTCCAGACATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 	300
Sbjct	241	AATAAATAATATAAGATTTTGATTACTTCTCCCTCATTATTCTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360

KT906182.1
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...
Rhipicephalu... brown dog tick 34632 1216 1216 100% 0.0 100.00 14711
OM368327.1
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...
Rhipicephalu... brown dog tick 34632 1216 1216 100% 0.0 100.00 14714
OM368323.1
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...
Rhipicephalu... brown dog tick 34632 1216 1216 100% 0.0 100.00 14713
OM368322.1
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1216 1216 100% 0.0 100.00 707
JQ737084.1
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...
Rhipicephalu... brown dog tick 34632 1216 1216 100% 0.0 100.00 658
KF437543.1
Rhipicephalus linnaei isolate LA032-2 clone JS5930...
Rhipicephalu... NA 2138177 1216 1216 100% 0.0 100.00 14715
MW429383.1
Rhipicephalus linnaei mitochondrion, complete sequence
Rhipicephalu... NA 2138177 1216 1216 100% 0.0 100.00 14711
NC_060409.1
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,... Ixodidae
sp.... NA 1901042 1210 1210 100% 0.0 99.85 658
KX053537.1
Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...
Rhipicephalu... brown dog tick 34632 1210 1210 100% 0.0 99.85 690
KT906185.1
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...
Rhipicephalu... brown dog tick 34632 1210 1210 100% 0.0 99.85 690
KT906184.1
Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1210 1210 100% 0.0 99.85 658
KF200113.1
Rhipicephalus linnaei isolate SC931-1 clone JS5927...
Rhipicephalu... NA 2138177 1210 1210 100% 0.0 99.85 14717
MW429382.1
Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1205 1205 99% 0.0 99.85 658
KX360367.1
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...
Rhipicephalu... brown dog tick 34632 1205 1205 100% 0.0 99.70 690
KT906186.1
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1205 1205 100% 0.0 99.70 658
KF200112.1
Rhipicephalus sanguineus mitochondrion, complete genome
Rhipicephalu... brown dog tick 34632 1205 1205 100% 0.0 99.70 14714
JX416325.1
Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1192 1192 98% 0.0 100.00 661
MZ401443.1
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1192 1192 98% 0.0 100.00 661

MZ401441.1							
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...							
Rhipicephalu...	brown dog tick	34632	1192	1192	98%	0.0	99.85 664
MZ401440.1							
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1190	1190	97%	0.0	100.00 664
MG969507.1							
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1188	1188	98%	0.0	99.69 649
KF200084.1							
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1186	1186	97%	0.0	100.00 768
KX383817.1							
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...							
Rhipicephalu...	brown dog tick	34632	1186	1186	97%	0.0	100.00 657
MZ401442.1							
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...							
Rhipicephalu...	brown dog tick	34632	1186	1186	97%	0.0	100.00 661
MZ401438.1							
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1184	1184	97%	0.0	99.84 664
MG969506.1							
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1184	1184	97%	0.0	99.84 664
MG969505.1							
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1184	1184	97%	0.0	99.84 664
MG969504.1							
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1179	1179	97%	0.0	99.69 644
KF200096.1							
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...							
Rhipicephalu...	NA	2138177	1177	1177	100%	0.0	98.94 658
OM984983.1							
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...							
Rhipicephalu...	brown dog tick	34632	1177	1177	96%	0.0	100.00 802
JX416302.1							
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...							
Rhipicephalu...	brown dog tick	34632	1177	1177	96%	0.0	100.00 802
JX416298.1							
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidas...							
Rhipicephalu...	brown dog tick	34632	1177	1177	97%	0.0	99.69 670
HM193873.1							
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1175	1175	97%	0.0	99.69 768
KX383820.1							
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1171	1171	97%	0.0	99.53 724
KX383816.1							
Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase...							
Rhipicephalu...	NA	2138177	1171	1171	100%	0.0	98.78 658
OM984984.1							
Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase...							
Rhipicephalu...	NA	2138177	1171	1171	100%	0.0	98.78 658

OM984974.1								
Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1171	1171	100%	0.0	98.78	658
OM984973.1								
Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416308.1								
Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416304.1								
Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416300.1								
Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416299.1								
Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416297.1								
Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416296.1								
Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416293.1								
Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase...								
Rhipicephalu...	brown dog tick	34632	1171	1171	96%	0.0	100.00	650
MZ401439.1								
Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase...								
Rhipicephalu...	brown dog tick	34632	1166	1166	96%	0.0	99.69	763
KX383802.1								
Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1166	1166	100%	0.0	98.63	658
OM984979.1								
Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1166	1166	100%	0.0	98.63	658
OM984968.1								
Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416295.1								
Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416294.1								
Rhipicephalus sanguineus isolate sanguineus0926 cytochrome...								
Rhipicephalu...	brown dog tick	34632	1162	1162	99%	0.0	98.77	658
MH513252.1								
Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1160	1160	100%	0.0	98.48	658
OM984985.1								
Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1160	1160	100%	0.0	98.48	658
OM984978.1								
Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1160	1160	100%	0.0	98.48	658

OM984977.1								
Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658	
OM984975.1								
Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658	
OM984971.1								
Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658	
OM984970.1								
Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658	
OM984969.1								
Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632		1160	1160	96%	0.0	99.53	802	
JX416301.1								
Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrom...								
Rhipicephalu... brown dog tick 34632		1155	1155	95%	0.0	99.68	642	
MT010523.1								
Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658	
OM984988.1								
Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658	
OM984976.1								
Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subun...								
Rhipicephalu... brown dog tick 34632		1155	1155	96%	0.0	99.37	802	
JX416303.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA	2138177	1153	1153	98%	0.0	98.77	826	
MF426003.1								
Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidas...								
Rhipicephalu... brown dog tick 34632		1146	1146	96%	0.0	99.21	665	
HM193874.1								
Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1140	1140	94%	0.0	99.84	630	
KX757914.1								
Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1136	1136	97%	0.0	98.60	768	
KX383800.1								
Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1131	1131	93%	0.0	99.68	744	
KX383796.1								
Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1127	1127	96%	0.0	98.59	698	
KX383798.1								
Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1125	1125	97%	0.0	98.29	768	
KX383814.1								
Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase...								
Rhipicephalu... brown dog tick 34632		1122	1122	96%	0.0	98.43	763	
KX383801.1								
Rhipicephalus sanguineus isolate 400 cytochrome c oxidase...								
Rhipicephalu... brown dog tick 34632		1120	1120	97%	0.0	98.28	657	

MW558150.1							
Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726445.1							
Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726444.1							
Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726443.1							
Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726442.1							
Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726441.1							
Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726440.1							
Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726439.1							
Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726438.1							
Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726437.1							
Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726436.1							
Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726435.1							
Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726434.1							
Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726433.1							
Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726432.1							
Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726431.1							
Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726430.1							
Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726449.1							
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604

MZ726429.1
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1110 1110 91% 0.0 99.83 604
MZ726428.1
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1110 1110 91% 0.0 99.83 604
MZ726427.1
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1110 1110 91% 0.0 99.83 604
MZ726426.1
Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1092 1092 91% 0.0 99.33 638
KX360338.1

Alignments:

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480

Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATTACAACCTATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Sbjct	380		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	560		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	619
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121		AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	318		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome
Sequence ID: OM368327.1 Length: 14711
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1185		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	1245		AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180	
Sbjct	1305		AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	1365		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	1425		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360	

Sbjct	1485	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	 TTCAATTTTAGGTGCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTATTATT	540
Sbjct	1665	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome
Sequence ID: OM368323.1 Length: 14714
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	 AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	1485	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	 TTCAATTTTAGGTGCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTATTATT	540
Sbjct	1665	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome
Sequence ID: OM368322.1 Length: 14713
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	 AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	1485	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	 TTCAATTTTAGGTGCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 24 to 681

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	24	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	83
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	84	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	143
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	144	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	203
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	204	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	263
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	264	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	323

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	324	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	383
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	384	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	443
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	444	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	503
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	504	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	563
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	564	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	623
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	624	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	681

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome

Sequence ID: MW429383.1 Length: 14715

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	585	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus linnaei mitochondrion, complete sequence

Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome

Sequence ID: MW429381.1 Length: 14711

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial
Sequence ID: KX053537.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	138	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	138	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	378	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200113.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome

Sequence ID: MW429382.1 Length: 14717

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164

Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX360367.1 Length: 658
 Range 1: 4 to 658

Score:1205 bits(652), Expect:0.0,
 Identities:654/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

Query	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Sbjct	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Query	64	CCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAAT	123

Sbjct	64	CCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Query	124	TGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGG	183
Sbjct	124	TGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGG	183
Query	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Sbjct	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Query	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Sbjct	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Query	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATC	363
Sbjct	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATC	363
Query	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTC	423
Sbjct	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTC	423
Query	424	AATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAAC	483
Sbjct	424	AATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAAC	483
Query	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Sbjct	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Query	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC	603
Sbjct	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC	603
Query	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	78	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	 TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KF200112.1 Length: 658

>Rhipicephalus sanguineus voucher D0-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX360403.1 Length: 658

Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,

Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
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Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus mitochondrion, complete genome

Sequence ID: JX416325.1 Length: 14714

Range 1: 1185 to 1842

Score:1205 bits(652), Expect:0.0,

Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
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Sbjct	1185	 GACAATATACTTAATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT	1842

>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60
Query	74	TTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133
Sbjct	61	TTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120
Query	134	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300
Query	314	GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA	373
Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433
Sbjct	361	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434	GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540
Query	554	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	645

>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MZ401441.1 Length: 661
 Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
 Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60
Query	74	TTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133
Sbjct	61	TTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120
Query	134	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300
Query	314	GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA	373
Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433
Sbjct	361	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434	GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540
Query	554	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	645

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,

Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

```
Query 11 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 70
|||||
Sbjct 1 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 60

Query 71 GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 130
|||||
Sbjct 61 GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 120

Query 131 GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA 190
|||||
Sbjct 121 GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA 180

Query 191 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 250
|||||
Sbjct 181 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 240

Query 251 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 310
|||||
Sbjct 241 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 300

Query 311 TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC 370
|||||
Sbjct 301 TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC 360

Query 371 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA 430
|||||
Sbjct 361 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA 420

Query 431 GGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA 490
|||||
Sbjct 421 GGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA 480

Query 491 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 550
|||||
Sbjct 481 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 540

Query 551 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC 610
|||||
Sbjct 541 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC 600

Query 611 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 648
```

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1190 bits(644), Expect:0.0,
Identities:644/644(100%), Gaps:0/644(0%), Strand: Plus/Plus

```
Query 15 TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
|||||
Sbjct 1 TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query 75 TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
|||||
Sbjct 61 TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query 135 ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
|||||
Sbjct 121 ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query 195 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
|||||
Sbjct 181 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query 255 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
|||||
Sbjct 241 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query 315 GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
|||||
Sbjct 301 GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query 375 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
|||||
Sbjct 361 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query 435 CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
|||||
Sbjct 421 CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query 495 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
|||||
Sbjct 481 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query 555 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
|||||
Sbjct 541 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

Query 615 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644
```

>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 1 to 649

Score:1188 bits(643), Expect:0.0,
Identities:647/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

```
Query 10  CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT 69
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1    CTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCAT 60

Query 70  AGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 129
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  AGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 120

Query 130 AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG 189
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGG 180

Query 190 AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA 249
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA 240

Query 250 TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 309
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 300

Query 310 ATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTA 369
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA 360

Query 370 CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 429
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 420

Query 430 AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA 489
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA 480

Query 490 ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 549
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 540

Query 550 ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 609
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 600

Query 610 CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 649
```

>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768

Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,

Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
|||||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
|||||
Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
|||||
Sbjct 121 GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
|||||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
|||||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
|||||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 436
|||||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
|||||
Sbjct 421 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
|||||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 616
|||||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
```

>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17   TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
          |||
Sbjct 1    TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77   GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
          |||
Sbjct 61   GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137  GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
          |||
Sbjct 121  GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
          |||
Sbjct 181  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
          |||
Sbjct 241  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317  GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
          |||
Sbjct 301  GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 436
          |||
Sbjct 361  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437  ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
          |||
Sbjct 421  ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
          |||
Sbjct 481  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 616
          |||
Sbjct 541  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 600

Query 617  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 601  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
```

>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17   TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
          |||
Sbjct 1    TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77   GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
          |||
Sbjct 61   GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137  GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
          |||
Sbjct 121  GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
          |||
Sbjct 181  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
          |||
Sbjct 241  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317  GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
          |||
Sbjct 301  GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 436
          |||
Sbjct 361  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437  ATCAATTTCAATACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
          |||
Sbjct 421  ATCAATTTCAATACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
          |||
Sbjct 481  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 616
          |||
Sbjct 541  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 600

Query 617  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 601  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
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>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query 15 TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
      || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query 75 TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query 135 ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query 195 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query 255 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query 315 GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query 375 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG 434
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG 420

Query 435 CAATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 CAATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query 495 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query 555 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG 614
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG 600

Query 615 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644
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>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query 15  TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query 75  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query 135  ATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  ATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query 195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query 255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query 315  GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query 375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG 434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG 420

Query 435  CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query 495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query 555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

Query 615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          ||||||||||||||||||
Sbjct 601  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644
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>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query 6 TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC 65
      |||
Sbjct 1 TATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCC 60

Query 66 GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG 125
      |||
Sbjct 61 GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG 120

Query 126 TAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGGAGGAT 185
      |||
Sbjct 121 TAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGAT 180

Query 186 TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAA 245
      |||
Sbjct 181 TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAA 240

Query 246 ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA 305
      |||
Sbjct 241 ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA 300

Query 306 TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCAC 365
      |||
Sbjct 301 TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTTATCAC 360

Query 366 ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA 425
      |||
Sbjct 361 ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA 420

Query 426 TTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAA 485
      |||
Sbjct 421 TTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAA 480

Query 486 TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT 545
      |||
Sbjct 481 TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT 540

Query 546 CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT 605
      |||
Sbjct 541 CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT 600

Query 606 CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA 649
      |||
Sbjct 601 CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA 644
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>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 1 to 658

Score:1177 bits(637), Expect:0.0,
Identities:651/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
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Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416302.1 Length: 802

>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416305.1 Length: 802

>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416306.1 Length: 802

>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416307.1 Length: 802

Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,

Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480

Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGACGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGACGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480

Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

Score:1177 bits(637), Expect:0.0,
Identities:642/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

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Sbjct  419  CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA  478
Query   495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG  554
        |||
Sbjct  479  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG  538
Query   555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG  614
        |||
Sbjct  539  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG  598
Query   615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||
Sbjct  599  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  642

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>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383820.1 Length: 768
Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,
Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

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Query   17  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA  76
        |||
Sbjct   1  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA  60
Query   77  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT  136
        |||
Sbjct   61  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT  120
Query   137  GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA  196
        |||
Sbjct   121  GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA  180
Query   197  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA  256
        |||
Sbjct   181  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA  240
Query   257  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA  316
        |||
Sbjct   241  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA  300
Query   317  GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA  376
        |||
Sbjct   301  GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA  360
Query   377  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA  436
        |||
Sbjct   361  TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTCTTCAATTTTAGGTGCA  420
Query   437  ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA  496

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Sbjct	421		ATCAATTTCACTACAATAATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497		CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481		CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557		TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541		TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617		CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KX383816.1 Length: 724
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17		TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1		TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77		GGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61		GGTCAACCAGGAACCTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137		GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121		GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197		TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181		TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257		TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241		TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317		GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301		GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377		TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361		TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	420


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Query  437  ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA  496
          |||
Sbjct  421  ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA  480

Query  497  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC  556
          |||
Sbjct  481  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC  540

Query  557  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC  616
          |||
Sbjct  541  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC  600

Query  617  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
          |||
Sbjct  601  CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT  642

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>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||
Sbjct  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query  61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct  61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121   AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct  121   AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||
Sbjct  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query  361   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC  420
          |||
Sbjct  361   ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC  420

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Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658	

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420

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Sbjct  361  ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC  420
Query  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
      |||
Sbjct  421  TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
      |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
      |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct  601  TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT  658

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>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
      |||
Sbjct  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60
Query  61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
      |||
Sbjct  61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121   AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
      |||
Sbjct  121   AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
      |||
Sbjct  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
      |||
Sbjct  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
      |||
Sbjct  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360
Query  361   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC  420

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Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360

Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAACATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416304.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT	120
Query	142	TATTATAAATTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAAATTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360

Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416300.1 Length: 802

Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,

Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381

Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416299.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGT	381

Sbjct	301		TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442		TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421		TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416297.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142		TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121		TATTATAATTTTTTTT ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262		GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241		GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300

Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTATTATTACTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300

Query	322	TACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321

Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401439.1 Length: 650
Range 1: 1 to 634

Score:1171 bits(634), Expect:0.0,
Identities:634/634(100%), Gaps:0/634(0%), Strand: Plus/Plus

Query	25	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	84
Sbjct	1	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	60
Query	85	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	144
Sbjct	61	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	120
Query	145	TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	204
Sbjct	121	TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	180
Query	205	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	264
Sbjct	181	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	240
Query	265	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	324

Sbjct	241		ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	300
Query	325		AGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	384
Sbjct	301		AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	360
Query	385		TTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT	444
Sbjct	361		TTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT	420
Query	445		CATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	504
Sbjct	421		CATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	480
Query	505		TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	564
Sbjct	481		TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	540
Query	565		CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	624
Sbjct	541		CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	600
Query	625		AGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		AGGAGGTGACCCAATTCTATATCAACATTTATTT 634	

>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KX383802.1 Length: 763
>Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KX383803.1 Length: 763
>Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KX383804.1 Length: 763
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142		TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201

Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984979.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416295.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120

Query	142	TATTATAA		201
Sbjct	121	TATTATAA		180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG		321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG		300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT		381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT		360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA		441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA		420
Query	442	TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT		501
Sbjct	421	TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT		480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC		561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC		540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC		621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC		600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT		637

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA		81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA		60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT		141

Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658
Range 1: 6 to 658

Score:1162 bits(629), Expect:0.0,
Identities:645/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	6	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	65
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	66	 AATTCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	125
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	126	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	185
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACG	240
Sbjct	186	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACG	245
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	246	 AATAAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	305
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	306	 ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	365
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	366	 ATCACACTACGGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTC	425
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	426	 TTCAATTTTAGGCGCAATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAAT	485
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	486	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	545
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	546	 ATTATCTTTACCAGTCTTAGCTGGTGAATTACAATATTGTAACTGATCGAACTTTAA	605
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT	653
Sbjct	606	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT	658

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984978.1 Length: 658
 Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
 Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984977.1 Length: 658
 Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
 Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAAATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
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Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATGGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,

Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGAATACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416301.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
|||||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
|||||
Sbjct 241 GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
|||||
Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
|||||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
|||||
Sbjct 421 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
|||||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
|||||
Sbjct 541 TGGCGCTATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637
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>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase
subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT010523.1 Length: 642
Range 1: 1 to 631

Score:1155 bits(625), Expect:0.0,
Identities:629/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

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Query  28  ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG  87
      |||
Sbjct  1    ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG  60

Query  88  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  147
      |||
Sbjct  61  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  120

Query  148  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  207
      |||
Sbjct  121  AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  180

Query  208  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  267
      |||
Sbjct  181  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  240

Query  268  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG  327
      |||
Sbjct  241  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG  300

Query  328  GTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  387
      |||
Sbjct  301  GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  360

Query  388  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  447
      |||
Sbjct  361  AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  420

Query  448  TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  507
      |||
Sbjct  421  TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  480

Query  508  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  567
      |||
Sbjct  481  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  540

Query  568  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  627
      |||
Sbjct  541  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  600

Query  628  AGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct  601  GGGTGACCCAATTCTATATCAACATTTATTT  631

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>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658

Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGAATACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,

partial cds; mitochondrial
Sequence ID: JX416303.1 Length: 802
Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,
Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1153 bits(624), Expect:0.0,
Identities:640/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

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Query 11  TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 70
          |||
Sbjct 3    TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATA 62

Query 71  GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 130
          |||
Sbjct 63  GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 122

Query 131  GCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA 190
          |||
Sbjct 123  GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA 182

Query 191  AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 250
          |||
Sbjct 183  AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAAT 242

Query 251  ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 310
          |||
Sbjct 243  ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 302

Query 311  TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC 370
          |||
Sbjct 303  TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC 362

Query 371  GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA 430
          |||
Sbjct 363  GGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA 422

Query 431  GGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA 490
          ||
Sbjct 423  GGC GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA 482

Query 491  CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 550
          |||
Sbjct 483  CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 542

Query 551  CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC 610
          |||
Sbjct 543  CCAGTCTTAGCTGGTGAATACAATATTGTAACTGATCGAACTTTAATACATCATTC 602

Query 611  TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 603  TTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 650
```

>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1146 bits(620), Expect:0.0,
Identities:631/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 31 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 90

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 91 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 150

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 151 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 210

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 211 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 270

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 271 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 330

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 331 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 390

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 391 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 450

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 451 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 510

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 511 AACAAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 570

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct 571 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAATATTAAGTATCGAAACTTTAA 630

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCC 636
      |||||||||||||||| ||||||||| |||||
Sbjct 631 TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC 665
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>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG 98
      |||
Sbjct 1 TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG 60

Query 99 GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttA 158
      |||
Sbjct 61 GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query 159 TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG 218
      |||
Sbjct 121 TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG 180

Query 219 CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC 278
      |||
Sbjct 181 CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC 240

Query 279 TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT 338
      |||
Sbjct 241 TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT 300

Query 339 AccccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTG 458
      |||
Sbjct 361 CTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTG 420

Query 459 TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT 518
      |||
Sbjct 421 TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT 480

Query 519 TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT 578
      |||
Sbjct 481 TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA 638
      |||
Sbjct 541 TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA 600

Query 639 TTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TTCTATATCAACATTTATTT 620
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>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383800.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383815.1 Length: 768
Range 1: 1 to 642

Score:1136 bits(615), Expect:0.0,
Identities:633/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

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Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
      |||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
      |||
Sbjct 61 GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
      |||
Sbjct 121 GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
      |||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
      |||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
      |||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 436
      |||
Sbjct 361 TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCA 420

Query 437 ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
      |||
Sbjct 421 ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
      |||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 616
      |||
Sbjct 541 TTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 600
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Query   617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||||
Sbjct   601 CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 642

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>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383796.1 Length: 744
Range 1: 1 to 618

Score:1131 bits(612), Expect:0.0,
Identities:616/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

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Query   41  GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA 100
        |||||
Sbjct   1  GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA 60

Query   101 AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAttttttttATA 160
        |||||
Sbjct   61 AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAATTTTTTTTATA 120

Query   161 GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT 220
        |||||
Sbjct   121 GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT 180

Query   221 CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA 280
        |||||
Sbjct   181 CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA 240

Query   281 TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAc 340
        |||||
Sbjct   241 TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAC 300

Query   341 ccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT 400
        |||||
Sbjct   301 CCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT 360

Query   401 CTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTA 460
        || |||||
Sbjct   361 CTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTA 420

Query   461 AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA 520
        |||||
Sbjct   421 AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA 480

Query   521 ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA 580
        |||||
Sbjct   481 ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA 540

Query   581 TTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT 640
        |||||
Sbjct   541 TTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATT 600

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Query 641 CTATATCAACATTTATTT 658
 |||||
 Sbjct 601 CTATATCAACATTTATTT 618

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383798.1 Length: 698
 Range 1: 1 to 637

Score:1127 bits(610), Expect:0.0,
 Identities:628/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
 |||||
 Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
 |||||
 Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
 |||||
 Sbjct 121 TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
 |||||
 Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
 |||||
 Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
 |||||
 Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
 |||||
 Sbjct 361 AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA 420

Query 442 TTTCAATACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
 |||||
 Sbjct 421 TTTCAATACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
 |||||
 Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
 |||

Sbjct 541 TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
 |||

Sbjct 601 AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 637

>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383814.1 Length: 768
 Range 1: 1 to 642

Score:1125 bits(609), Expect:0.0,
 Identities:631/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
 |||

Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
 |||

Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
 |||

Sbjct 121 GCATTTATTATAAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
 |||

Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
 |||

Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGTGAACAGTTTAcCCCCcTTATCATCAAATTTATCACACTACGGACCA 376
 |||

Sbjct 301 GCAGGTACAGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 436
 |||

Sbjct 361 TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGCGCA 420

Query 437 ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
 |||

Sbjct 421 ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
 |||

Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 616

Sbjct	541		600
		TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540


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Query   560  GCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCT  619
        |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCT  600

Query   620  TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||||  |||||||||||||||||||||||||||||||
Sbjct   601  TCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT  639

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>Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726445.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420

Query   421  TTCAATTTTAGGTGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TTCAATTTTAGGTGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480

Query   481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||

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Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
        |||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query   601  TACA  604
        |||
Sbjct   601  TACA  604

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>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726444.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
        |||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
        |||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
        |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
        |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
        |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
        |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
        |||
Sbjct   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420

Query   421  TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480
        |||
Sbjct   421  TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480

Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

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Sbjct  481  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 540
          AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
Query  601  TACA 604
          ||||
Sbjct  601  TACA 604

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>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query  61  AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query  121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query  181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query  241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query  301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query  361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query  421 TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421 TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT 480

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Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

Query   601  TACA  604
        ||||
Sbjct   601  TACA  604

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>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420

Query   421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT  480

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Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```

Sbjct  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601  TACA  604
          |||
Sbjct  601  TACA  604

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>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726440.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT  360
          |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360
Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
          |||
Sbjct  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
Query  421     TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480

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Sbjct	421		TTCAATTTTAGGTGCAATCAATTCATTACAAC	ATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT		540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT		540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA	600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA	600
Query	601		TACA	604	
Sbjct	601		TACA	604	

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAc	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTG	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTG

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA	604	
Sbjct	601	TACA	604	

>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726438.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120	
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420

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Query  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
          |||
Sbjct  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480

Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

Query  601  TACA  604
          |||
Sbjct  601  TACA  604

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>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726437.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
          |||

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Sbjct  361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC  420
Query  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
      |||
Sbjct  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
      |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
      |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601  TACA  604
      |||
Sbjct  601  TACA  604

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>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
      |||
Sbjct  1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
Query  61  AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT  120
      |||
Sbjct  61  AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
      |||
Sbjct  121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
      |||
Sbjct  181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
      |||
Sbjct  241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
      |||
Sbjct  301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360
Query  361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC  420

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Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726434.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial

Sequence ID: MZ726433.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726432.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC

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Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC 420

Query   421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct   421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query   601  TACA 604
      |||
Sbjct   601  TACA 604

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>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726430.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

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Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726449.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACGGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726429.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726428.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAAATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAAATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726426.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638
Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199
Sbjct	121	TTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	180
Query	200	GTTCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259

Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX757909.1	34632	1112	1112	94%	0.0	99.03	630
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426015.1	34632	1072	1072	100%	0.0	96.05	692
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426018.1	34632	1066	1066	100%	0.0	95.90	675
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426016.1	34632	1066	1066	100%	0.0	95.90	680
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426013.1	34632	1066	1066	100%	0.0	95.90	693
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426009.1	34632	1066	1066	100%	0.0	95.90	679
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426007.1	34632	1066	1066	100%	0.0	95.90	686
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426019.1	34632	1061	1061	100%	0.0	95.74	697
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426006.1	34632	1061	1061	100%	0.0	95.74	705
Rhipicephalus sanguineus haplotype III cytochrome oxidase...								
Rhipicephalu... brown dog tick	KU556745.1	34632	1061	1061	100%	0.0	95.74	713
Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MN593344.1	34632	1061	1061	100%	0.0	95.74	710
Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MN593343.1	34632	1061	1061	100%	0.0	95.74	710
Rhipicephalus sanguineus isolate 11N cytochrome oxidase subuni...								
Rhipicephalu... brown dog tick	MN585197.1	34632	1061	1061	100%	0.0	95.74	703
Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene,...								
Rhipicephalu... brown dog tick	AF132839.1	34632	1061	1061	100%	0.0	95.74	793
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426017.1	34632	1055	1055	100%	0.0	95.59	680
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426008.1	34632	1055	1055	100%	0.0	95.59	690
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426001.1	34632	1055	1055	100%	0.0	95.59	684
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF425998.1	34632	1055	1055	100%	0.0	95.59	689

Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF425997.1	34632	1055	1055	100%	0.0	95.59	695
Rhipicephalus sanguineus haplotype IV cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	KU556746.1	34632	1055	1113	100%	0.0	95.59	771
Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MZ305546.1	34632	1055	1055	100%	0.0	95.59	658
Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase...								
Rhipicephalu... brown dog tick	MZ305545.1	34632	1055	1055	100%	0.0	95.59	658
Rhipicephalus sanguineus isolate SMSK cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MW152145.1	34632	1055	1055	100%	0.0	95.59	676
Rhipicephalus sanguineus isolate SMSK cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MW152144.1	34632	1055	1055	100%	0.0	95.59	675
Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MW152143.1	34632	1055	1055	100%	0.0	95.59	676
Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MW152142.1	34632	1055	1055	100%	0.0	95.59	669
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426012.1	34632	1050	1050	100%	0.0	95.44	684
Rhipicephalus sanguineus haplotype I cytochrome oxidase subuni...								
Rhipicephalu... brown dog tick	KU556743.1	34632	1048	1048	98%	0.0	95.83	659
Rhipicephalus sanguineus haplotype II cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	KU556744.1	34632	1046	1046	100%	0.0	95.30	787
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426020.1	34632	1038	1038	97%	0.0	95.80	812
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426010.1	34632	1037	1037	98%	0.0	95.52	824
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426011.1	34632	1031	1031	97%	0.0	95.64	809
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426014.1	34632	1022	1022	94%	0.0	96.30	649
Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase...								
Rhipicephalu... brown dog tick	KX383818.1	34632	1020	1020	97%	0.0	95.33	768
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF426000.1	34632	1016	1016	94%	0.0	96.14	635
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF425988.1	34632	1016	1016	97%	0.0	95.31	654

Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase...								
Rhipicephalu... brown dog tick	KY678135.1	34632	883	883	100%	0.0	90.90	790
Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c...								
Rhipicephalu... NA	MT800313.1	34633	883	883	100%	0.0	90.88	673
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...								
Rhipicephalu... brown dog tick	MF425987.1	34632	881	881	85%	0.0	95.01	574
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (C01)...								
Rhipicephalu... brown dog tick	KU214592.1	34632	876	876	98%	0.0	91.05	829
Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase...								
Rhipicephalu... NA	MT079206.1	34633	872	872	99%	0.0	90.80	678
Rhipicephalus sanguineus isolate GY34 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	MN862754.1	34632	872	872	99%	0.0	90.80	678
Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome...								
Rhipicephalu... brown dog tick	KM494916.1	34632	872	872	100%	0.0	90.58	1539
Rhipicephalus sanguineus isolate Tehran cytochrome oxidase...								
Rhipicephalu... brown dog tick	KM494915.1	34632	872	872	100%	0.0	90.58	1539
Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c...								
Rhipicephalu... NA	MT800314.1	34633	870	870	99%	0.0	90.56	673
Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606303.1	34633	861	861	100%	0.0	90.27	873
Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606302.1	34633	861	861	100%	0.0	90.27	873
Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606301.1	34633	861	861	100%	0.0	90.27	873
Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606300.1	34633	861	861	100%	0.0	90.27	873
Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit...								
Rhipicephalu... NA	KY606299.1	34633	861	861	100%	0.0	90.27	873
Rhipicephalus camicasi isolate SC0126 mitochondrion, complete...								
Rhipicephalu... NA	NC_061616.1	669981	861	861	100%	0.0	90.29	14725
Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase...								
Rhipicephalu... NA	MZ305547.1	34633	861	861	100%	0.0	90.27	658
Rhipicephalus turanicus isolate Xinjiang-WQIA cytochrome oxida...								
Rhipicephalu... NA	MF002581.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase...								
Rhipicephalu... NA	MF002580.1	34633	850	850	100%	0.0	89.97	889

Rhipicephalus turanicus isolate	Xinjiang-BC cytochrome oxidase...							
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002579.1								
Rhipicephalus turanicus isolate	Xinjiang-YC cytochrome oxidase...							
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002578.1								
Rhipicephalus turanicus isolate	Xinjiang-PS cytochrome oxidase...							
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
MF002577.1								
Rhipicephalus turanicus isolate	SHZ cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY069271.1								
Rhipicephalus turanicus isolate	FK-1 cytochrome oxidase subuni...							
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606291.1								
Rhipicephalus turanicus isolate	YN3 cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606290.1								
Rhipicephalus turanicus isolate	YN2 cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	850	850	100%	0.0	89.97	889	
KY606289.1								

Alignments:

>Rhipicephalus sanguineus mitochondrial DNA, complete genome

Sequence ID: AF081829.1 Length: 14710

Range 1: 1191 to 1848

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1191	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	1250
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	1251	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	1310
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	1311	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	1370
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	1371	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	1430
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	1431	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	1490
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	1491	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	1550
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	1551	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	1610
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	1611	TTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTGTAAATATACGATCAATTGGAAT	1670
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	1671	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	1730
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1731	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	1790
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	1791	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	1848

>Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757893.1 Length: 629
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398

Sbjct	301		ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399		CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361		CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459		TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421		TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519		TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481		TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579		TATTAAGTATCGAACTTTAACAACATCATTCTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541		TATTAAGTATCGAACTTTAACAACATCATTCTTTGATCCTTCAGGAGGAGGAGATCCCA	600
Query	639		TTTTATATCAACACTTATTT 658	
Sbjct	601		TTTTATATCAACACTTATTT 620	

>Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757903.1 Length: 630
Range 1: 1 to 620

Score:1129 bits(611), Expect:0.0,
Identities:617/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120
Query	159		TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121		TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279		TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241		TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300

Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTAGGTGCAATTAACCTTCATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757909.1 Length: 630
Range 1: 1 to 620

Score:1112 bits(602), Expect:0.0,
Identities:614/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATAATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCTGGAGCTGGAACAGGATGAACAGTTT	300

Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGCCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTGACTGATCGAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGGGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S48 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426015.1 Length: 692
Range 1: 19 to 676

Score:1072 bits(580), Expect:0.0,
Identities:632/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGTCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	618
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	619	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S58 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426018.1 Length: 675
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	251		AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301		ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361		ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371		ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421		TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431		TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481		AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541		TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	551		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	610
Query	601		CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S52 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426016.1 Length: 680
Range 1: 12 to 669

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60	
Sbjct	12		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120	
Sbjct	72		AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180	
Sbjct	132		AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240	
Sbjct	192		AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251

Query	241	AATAAATAATATAAGATTTTGGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTGGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	311
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	372	ATCACATTATGGTCTTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	432	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	611
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	612	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	669

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S37 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426013.1 Length: 693
Range 1: 20 to 677

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259

Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	619
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	620	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S33 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426009.1 Length: 679
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240

Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S29 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426007.1 Length: 686
Range 1: 14 to 671

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240

[illegible]

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	181	AGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACG 	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCTCATTATTTTTATTGATTAACCTCTTC 	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 	420
Sbjct	379	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAAT 	480
Sbjct	439	TTCAATTTTAGGTGCAATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAC TGATCGAAACTTTAA 	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA	618
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 	658
Sbjct	619	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Sbjct	147	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	206
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	207	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	266
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	267	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	326
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	327	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	386
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	387	ATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	446
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	447	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	506
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	507	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	566
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	567	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	626
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	627	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	684

>Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593344.1 Length: 710
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	684	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	625
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	624	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	565
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180

Sbjct	564	 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	505
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	504	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	445
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	444	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	385
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	384	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	325
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	324	 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	265
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	264	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	205
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	204	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	145
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	144	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	85
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	84	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	27

>Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: MN593343.1 Length: 710
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	684	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	625
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	624	 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	565

Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	564	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	505
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	504	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	445
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTT	300
Sbjct	444	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT	385
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	384	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	325
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	324	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	265
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	264	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	205
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	204	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	145
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	144	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	85
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	84	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	27

>Rhipicephalus sanguineus isolate 11N cytochrome oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MN585197.1 Length: 703
Range 1: 22 to 679

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	679	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	620
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	619	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	560

Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	559	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	500
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	499	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	440
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	439	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	380
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	379	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	320
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	319	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	260
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	259	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	200
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	199	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	140
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	139	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	80
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	79	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	22

>Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene, partial cds;
mitochondrial gene for mitochondrial product
Sequence ID: AF132839.1 Length: 793
Range 1: 42 to 699

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	42	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	101
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	102	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	161
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	162	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	221
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	222	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	281
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTT	300
Sbjct	282	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT	341
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	342	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	401
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	402	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	461
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	462	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	521
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	522	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	581
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	582	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	641
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	642	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	699

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S56 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426017.1 Length: 680
Range 1: 11 to 668

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	71	 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	251	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	 TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	551	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S32 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426008.1 Length: 690
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	613
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1570
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426001.1 Length: 684
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1553
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425998.1 Length: 689
Range 1: 20 to 677

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60

Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	560	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	619
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	620	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	677

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1551
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425997.1 Length: 695
Range 1: 22 to 679

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
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Sbjct	22	 AACAATATATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	81
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	82	 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	141
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	142	 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	201
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	202	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	261
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	262	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	321
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	322	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	381
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	382	 ATCACATTATGGCCCTTCACTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	441
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	442	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	501
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	502	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	561
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	562	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	621
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	622	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	679

>Rhipicephalus sanguineus haplotype IV cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556746.1 Length: 771
Range 1: 90 to 747

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	90	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	149
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	150	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	209
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	210	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	269
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	270	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	329
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	330	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	389
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	390	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT	449
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	450	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	509
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	510	TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	569
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	570	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	629
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	630	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	689
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	690	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	747

Range 2: 30 to 64

Score:58.4 bits(31), Expect:0.001,
Identities:34/35(97%), Gaps:1/35(2%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCA-GGT	34

Sbjct 30 AACAAATATATTTAATTTTTGGAGCATGATCATGGT 64

>Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305546.1 Length: 658
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 61 AATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| ||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 300

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
|
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA 600

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
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      ||||||||||||||||||| ||||||||||| ||||||||||| |||||
Sbjct 601 TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658

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>Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305545.1 Length: 658
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      ||||||||||||||||||| ||||||||||| ||||||||||| |||||
Sbjct 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      ||||||||||||||||||| ||||||||||| ||||||||||| |||||
Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      ||||||||||||||||||| ||||||||||| ||||||||||| |||||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || ||||||||||||| ||||| ||||| ||||||||||| |||||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      ||||||||||||||||||| ||||| ||| ||||||||| ||||| |||||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      ||||||||||||| ||||||||| ||||||||||| ||||| ||||||||||| |||||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      ||||||||||||| || ||||||||||| ||||||||||| ||||||||||| |||||
Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      ||||||||||| ||||||||| ||||||||||| ||||||||||| |||||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      ||||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||
Sbjct 481 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      | ||||||||||| ||||||||||| ||||||||||| |||||
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600

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Query   601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
        ||||||||||||||||||| ||||||||||| ||||||||||||||| |||||
Sbjct   601  TACATCATTTTTTTGATCCTTCAGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658

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>Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152145.1 Length: 676
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
        ||||||||||||||||||| ||||||||||| ||||||||||||||| |||||
Sbjct    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
        ||||||||||||||||||| ||||||||||| ||||||||||||||| |||||
Sbjct   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120

Query   121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
        ||||||||||||||||||| ||||||||||| ||||||||||||||| |||||
Sbjct   121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180

Query   181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
        ||| || ||||||||||||| ||||| ||||| ||||||||||||||| |||||
Sbjct   181  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query   241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
        ||||||||||||||||||| || ||| ||||||||| ||||| |||||
Sbjct   241  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query   301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
        ||||||||||||| ||||||| ||||||||||||| || |||||||||||||
Sbjct   301  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query   361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
        ||||||||||||| || ||||||||||||| ||||||||||||| |||||||||||||
Sbjct   361  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query   421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
        ||||||||||||| || ||||||||||||| ||||||||||||| |||||||||||||
Sbjct   421  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query   481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
        ||||||||||||| ||||||||||||| ||||||||||||| ||||||||||||| |||||
Sbjct   481  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query   541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
        | ||||||||||||| ||||||||||||| ||||||||||||| |||||||||||||
Sbjct   541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 600

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Query   601  CACATCATTTTTTGGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
        |||
Sbjct   601  TACATCATTTTTTGGATCCTTCAGGGGAGGAGATCCAATTTTATATCAACATTATTT 658

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>Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152144.1 Length: 675
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query   1    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
        |||
Sbjct   1    AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query   61    AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
        |||
Sbjct   61    AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120

Query   121   AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
        |||
Sbjct   121   AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180

Query   181   AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
        ||| ||
Sbjct   181   AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query   241   AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
        |||
Sbjct   241   AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query   301   ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
        |||
Sbjct   301   ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query   361   ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
        |||
Sbjct   361   ATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query   421   TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
        |||
Sbjct   421   TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query   481   AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
        |||
Sbjct   481   AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query   541   TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
        |

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Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA 600

Query 601 CACATCATTTTTTGGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
 |||||

Sbjct 601 TACATCATTTTTTGGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT 658

>Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MW152143.1 Length: 676
 Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
 Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
 |||||

Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
 |||||

Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
 |||||

Sbjct 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
 ||| || |||||

Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
 |||||

Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
 |||||

Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
 |||||

Sbjct 361 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
 |||||

Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
 |||||

Sbjct 481 AACAAAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 600

[illegible]

>Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152142.1 Length: 669
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACG 	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAAC TATTGTAAATATACGATCAATTGGAAT 	480
Sbjct	421	TTCAATTTTAGGTGCAATTAAC TTATTACAAC TATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540

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Query    541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA  600
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct    541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA  600

Query    601  CACATCATTTTTTGGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct    601  TACATCATTTTTTGGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  658

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S358 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426012.1 Length: 684
Range 1: 14 to 671

Score:1050 bits(568), Expect:0.0,
Identities:628/658(95%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 	193
Query	181	AGGGTTCGGA AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 	240
Sbjct	194	AGGATTTGGAA AATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA AACTCTTC 	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA AACTCTTC 	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCTCCTCTATCTTCAAATTT 	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 	433
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACA AACTATTGTAAATATACGATCAATTGGAAT 	480
Sbjct	434	TTCAATTTTAGGTGCAATTAAC TTTATTACA AACTATTATAA ACATACGATCAATTGGAAT 	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 	553

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Query   541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 600
          |||
Sbjct   554  CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 613

Query   601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||
Sbjct   614  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 671

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>Rhipicephalus sanguineus haplotype I cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial

Sequence ID: KU556743.1 Length: 659

Range 1: 12 to 659

Score:1048 bits(567), Expect:0.0,

Identities:621/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

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Query    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||
Sbjct   12  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 71

Query   61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||
Sbjct   72  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 131

Query  121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
          |||
Sbjct  132  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 191

Query  181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          ||| || |||
Sbjct  192  AGGATTTGGAAATTGATTAATCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 251

Query  241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
          |||
Sbjct  252  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 311

Query  301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||
Sbjct  312  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 371

Query  361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||
Sbjct  372  ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 431

Query  421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||
Sbjct  432  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 491

Query  481  AACAAAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          |||

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Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTAAATTACAGCTATTTTATTACT	551
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	611
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCA	648
Sbjct	612	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCA	659

Score:1046 bits(566), Expect:0.0,
Identities:629/660(95%), Gaps:2/660(0%), Strand: Plus/Plus

Sbjct	509	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	568
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	569	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	628
Query	601	CACATCATTTTTTTGATCCTTCAGGAGG-AGGAGATCCC-ATTTTATATCAAACTTATTT	658
Sbjct	629	 TACATCATTTTTTTGATCCTTCAGGGGGGAGGAGATCCAAATTTTATATCAACTTTTATTT	688

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S943 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426020.1 Length: 812
Range 1: 2 to 644

Score:1038 bits(562), Expect:0.0,
Identities:616/643(96%), Gaps:0/643(0%), Strand: Plus/Plus

Query	16	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	75
Sbjct	2	 TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	61
Query	76	AGGACAACCTGGAACCTTAATTGGAATGATCAGATTTATAATGTAATCGTAACAGCACA	135
Sbjct	62	 AGGACAACCTGGAACCTTAATTGGAATGATCAGATTTATAATGTAATCGTAACAGCACA	121
Query	136	TGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTG	195
Sbjct	122	 TGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	181
Query	196	ATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	255
Sbjct	182	 ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	241
Query	256	ATTTTGACTTTTACCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGG	315
Sbjct	242	 ATTTTGACTTTTACCTCCTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGG	301
Query	316	AGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCC	375
Sbjct	302	 AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTCC	361
Query	376	ATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGC	435
Sbjct	362	 TTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	421
Query	436	AATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAAT	495
Sbjct	422	 AATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	481

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Query   496  ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGT  555
        |||
Sbjct   482  ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT  541

Query   556  ATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTTGA  615
        |||
Sbjct   542  ATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGA  601

Query   616  TCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        |||
Sbjct   602  TCCTTCAGGGGAGGAGATCCAATTTTATATCAACACTTATTT  644

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S337 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426010.1 Length: 824
Range 1: 1 to 648

Score:1037 bits(561), Expect:0.0,
Identities:619/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

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Query   11   TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA  70
        |||
Sbjct    1   TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA  60

Query   71   GAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA  130
        |||
Sbjct   61   GAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA  120

Query   131  GCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGA  190
        |||
Sbjct   121  GCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGA  180

Query   191  AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT  250
        |||
Sbjct   181  AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT  240

Query   251  ATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAAGTCTTCATTAATTGAA  310
        |||
Sbjct   241  ATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAAGTCTTCATTAATTGAA  300

Query   311  TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT  370
        |||
Sbjct   301  TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT  360

Query   371  GGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA  430
        |||
Sbjct   361  GGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA  420

Query   431  GGTGCAATTAAGTTCATCACAAGTATTGTAAATATACGATCAATTGGAATAACAATAGAA  490
        |||
Sbjct   421  GGTGCAATTAAGTTTATTACAAGTATTGTAAACATACGATCAATTGGAATAACAATAGAA  480

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Query   491  CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA  550
      || ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||
Sbjct   481  CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTA  540

Query   551  CCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATCATTT  610
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct   541  CCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTT  600

Query   611  TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
      ||||||||||||| ||||||||| ||||||||| |||||
Sbjct   601  TTTGATCCTTCAGGGGAGGAGATCCAATTTTATATCAACACTTATTT  648

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S344 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426011.1 Length: 809
Range 1: 3 to 644

Score:1031 bits(558), Expect:0.0,
Identities:614/642(96%), Gaps:0/642(0%), Strand: Plus/Plus

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Query   17  TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA  76
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    3  TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA  62

Query   77  GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT  136
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   63  GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAC  122

Query   137  GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA  196
      ||||||||||||| ||||||||||| ||||||||| || |||||||
Sbjct   123  GCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA  182

Query   197  TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA  256
      ||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct   183  TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA  242

Query   257  TTTTGACTTTTACCCCCCTCATTATTTTATTGATTAAGTCTTCATTAATTGAATCCGGA  316
      ||||||||||||| || ||| ||||||||| ||||||||||||||||| |||
Sbjct   243  TTTTGACTTTTACCTCCTTCACTATTTTATTAATTAAGTCTTCATTAATTGAATCTGGA  302

Query   317  GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA  376
      ||||| ||||||||||||||||| || ||||||||||||||||||||| ||
Sbjct   303  GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT  362

Query   377  TCAGTAGATTTAGCTATTTTTTCTCTTCACTTGCTGGTGCTTCTTCAATTTTAGGTGCA  436
      ||||||||||||| ||||||||| ||||||||||| |||||||||
Sbjct   363  TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA  422

Query   437  ATTAAGTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA  496
      ||||||| || ||||||||||||| ||||||||||| ||||||||| |||

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Sbjct  423  ATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA  482
Query   497  CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA  556
          |||||
Sbjct   483  CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA  542
Query   557  TTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGAT  616
          |||||
Sbjct   543  TTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGAT  602
Query   617  CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
          |||||
Sbjct   603  CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  644

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S475 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426014.1 Length: 649
Range 1: 28 to 649

Score:1022 bits(553), Expect:0.0,
Identities:599/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

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Query    1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
          |||||
Sbjct   28  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  87
Query   61  AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT  120
          |||||
Sbjct   88  AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT  147
Query   121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG  180
          |||||
Sbjct   148  AATCGTAACAGCACATGCATTTATTATAATTTT TTTATAGTTATACCAATCATAATCGG  207
Query   181  AGGGTTCGGA AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG  240
          ||| ||
Sbjct   208  AGGATTTGGAA AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG  267
Query   241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA ACTCTTC  300
          |||||
Sbjct   268  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA ACTCTTC  327
Query   301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT  360
          |||||
Sbjct   328  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  387
Query   361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC  420
          |||||
Sbjct   388  ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  447
Query   421  TTCAATTTTAGGTGCAATTA ACTTCATCACAACTATTGTAAATATACGATCAATTGGAAT  480

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Sbjct	448		TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	507
Query	481		AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT				540
Sbjct	508		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT				567
Query	541		TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	AACTGATCGAA	ACTTTTAA		600
Sbjct	568		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAA	ACTTTTAA		627
Query	601		CACATCATTTTTTTGATCCTTCA				622
Sbjct	628		TACATCATTTTTTTGATCCTTCA				649

>Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383818.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5554A cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383819.1 Length: 768
Range 1: 1 to 642

Score:1020 bits(552), Expect:0.0,
Identities:612/642(95%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	300
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436

Sbjct	361		TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437		ATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	421		ATTAAC TTTATTACA ACTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATA	480
Query	497		CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	481		CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557		TTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGAT	616
Sbjct	541		TTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGAT	600
Query	617		CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658	
Sbjct	601		CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1568
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426000.1 Length: 635
Range 1: 14 to 635

Score:1016 bits(550), Expect:0.0,
Identities:598/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCTCATTATTTTTATTGATTA ACTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA ACTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	614	TACATCATTTTTTTGATCCTTCA	635

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SF3003
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425988.1 Length: 654
Range 1: 1 to 640

Score:1016 bits(550), Expect:0.0,
Identities:610/640(95%), Gaps:0/640(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360

Query	377	TCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	481	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557	TTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGAT	616
Sbjct	541	TTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGAT	600
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTAT	656
Sbjct	601	CCTTCAGGGGGAGGACATCCAATTTTATATCACCATTAT	640

>Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383811.1 Length: 764

>Rhipicephalus sanguineus isolate LIC5533C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383812.1 Length: 764

Range 1: 1 to 638

Score:1013 bits(548), Expect:0.0,

Identities:608/638(95%), Gaps:0/638(0%), Strand: Plus/Plus

Query	21	GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC	80
Sbjct	1	GAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGAC	60
Query	81	AACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT	140
Sbjct	61	AACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT	120
Query	141	TTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAG	200
Sbjct	121	TTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAG	180
Query	201	TTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	260
Sbjct	181	TCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	240
Query	261	GACTTTTACCCCCCTCATTATTTTATTGATTA ACTCTTCATTAATTGAATCCGGAGCTG	320
Sbjct	241	GACTTTTACCTCCTTCACTATTTTATTAATTA ACTCTTCATTAATTGAATCTGGAGCTG	300

Query	321	GAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAG	380
Sbjct	301	GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG	360
Query	381	TAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	440
Sbjct	361	TAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	420
Query	441	ACTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCAT	500
Sbjct	421	ACTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCAT	480
Query	501	TATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAG	560
Sbjct	481	TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG	540
Query	561	CAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTGATCCTT	620
Sbjct	541	CAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTT	600
Query	621	CAGGAGGAGGAGATCCCATTTTATATCAACACTTTATTT	658
Sbjct	601	CAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	638

Score:1011 bits(547), Expect:0.0,
Identities:607/637(95%), Gaps:0/637(0%), Strand: Plus/Plus

Sbjct	121	 TATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATATTAGGTGCCCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 CCCTATCATATTGGGTGCCCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	240
Query	262	ACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGG	321
Sbjct	241	 ACTTTTACCTCCTTCACATTTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGG	300
Query	322	AACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGT	381
Sbjct	301	 TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA	441
Sbjct	361	 AGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA	420
Query	442	CTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 CTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATT	480
Query	502	ATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGC	561
Sbjct	481	 ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC	540
Query	562	AGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTC	621
Sbjct	541	 AGGTGCCATTACAATATTGTAAAGTATCGAACTTTAATACATCATTTTTTGATCCTTC	600
Query	622	AGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658	
Sbjct	601	 AGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU568516.1 Length: 656
Range 1: 27 to 656

Score:1009 bits(546), Expect:0.0,
Identities:602/630(96%), Gaps:0/630(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	27	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	86
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	87	 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	146

Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	147	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	206
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	207	AGGATTTGGAAATTGATTAATCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	266
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	267	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	326
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	327	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	386
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	387	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	446
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	447	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	506
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	507	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	566
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	567	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	626
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGG	630
Sbjct	627	TACATCATTTTTTTGACCCTTCAGGAGGAGG	656

>Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383809.1 Length: 762
 Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
 Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
Sbjct	1	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142
Sbjct	61	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120

Query	143	ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT	202
Sbjct	121	ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCCCCCTCATTATTTTTATTGATTAACCTTTCATTAATTGAATCCGGAGCTGGA	322
Sbjct	241	CTTTTACCTCCTTCACTATTTTTATTAATTAACCTTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA	382
Sbjct	301	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	GATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA	502
Sbjct	421	TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA	562
Sbjct	481	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540
Query	563	GGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCA	622
Sbjct	541	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	GGGGGAGGAGATCCAATTTTATATCAACATTATTT	636

>Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383806.1 Length: 714
Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
Sbjct	1	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83	CCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142

Sbjct	61	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143	ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT	202
Sbjct	121	ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA	322
Sbjct	241	CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA	382
Sbjct	301	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	GATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA	502
Sbjct	421	TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA	562
Sbjct	481	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540
Query	563	GGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCA	622
Sbjct	541	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGAGGAGGAGATCCCATTTTTATATCAACACTTATTT	658
Sbjct	601	GGGGGAGGAGATCCAATTTTTATATCAACATTTATTT	636

>Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383805.1 Length: 761
Range 1: 1 to 635

Score:1007 bits(545), Expect:0.0,
Identities:605/635(95%), Gaps:0/635(0%), Strand: Plus/Plus

Query	24	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAAC	83
Sbjct	1	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAAC	60
Query	84	CTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	143

Sbjct	61	 CTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	120
Query	144	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTC	203
Sbjct	121	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	180
Query	204	CTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	263
Sbjct	181	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	240
Query	264	TTTTACCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAA	323
Sbjct	241	TTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTA	300
Query	324	CAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAG	383
Sbjct	301	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	360
Query	384	ATTTAGCTATTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	443
Sbjct	361	ATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	444	TCATCACAAC TATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTAT	503
Sbjct	421	TTATTACAAC TATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTAT	480
Query	504	TTGTTTGATCTGTTTAAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAG	563
Sbjct	481	TTGTTTGATCTGTTTAAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	540
Query	564	GTGCCATTACAATATTATTAAC TATCGAAACTTTAACACATCATTTTTTGATCCTTCAG	623
Sbjct	541	GTGCCATTACAATATTGTTAAC TATCGAAACTTTAATACATCATTTTTTGATCCTTCAG	600
Query	624	GAGGAGGAGATCCCATTTTATATCAACACTTATTT 658	
Sbjct	601	GGGGAGGAGATCCAATTTTATATCAACACTTATTT 635	

>Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase subunit I (cox1)
 gene, partial cds; mitochondrial
 Sequence ID: MH630347.1 Length: 644
 Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
 Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTGGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	619
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	620	TACATCATTTTTTTGATCCTTCA	641

>Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630346.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTGGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAAGTATCGAACTTTAA	619
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	620	TACATCATTTTTTTGATCCTTCA	641

>Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519712.1 Length: 654
Range 1: 3 to 628

Score:1002 bits(542), Expect:0.0,
Identities:598/626(96%), Gaps:0/626(0%), Strand: Plus/Plus

Query	33	GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT	92

Sbjct	3	GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC TT	62
Query	93	TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT	152
Sbjct	63	TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT	122
Query	153	TCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATAT	212
Sbjct	123	TTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT	182
Query	213	TAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCC	272
Sbjct	183	TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC	242
Query	273	CCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAA	332
Sbjct	243	CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA	302
Query	333	CAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTA	392
Sbjct	303	CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA	362
Query	393	TTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAA	452
Sbjct	363	TTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAA	422
Query	453	CTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGAT	512
Sbjct	423	CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT	482
Query	513	CTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTA	572
Sbjct	483	CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA	542
Query	573	CAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAG	632
Sbjct	543	CAATATTGTTAACCTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG	602
Query	633	ATCCCATTTTATATCAACACTTATTT	658
Sbjct	603	ATCCAATTTTATATCAACACTTATTT	628

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1575
 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
 Sequence ID: MF426002.1 Length: 639
 Range 1: 1 to 628

Score:1000 bits(541), Expect:0.0,
 Identities:599/628(95%), Gaps:0/628(0%), Strand: Plus/Plus

Query	31	AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	90
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Sbjct	1	 AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	60
Query	91	TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	150
Sbjct	61	 TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	120
Query	151	TTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTAT	210
Sbjct	121	 TTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	180
Query	211	ATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	270
Sbjct	181	 ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC	240
Query	271	CCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATG	330
Sbjct	241	 TCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATG	300
Query	331	AACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGC	390
Sbjct	301	 AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC	360
Query	391	TATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCAC	450
Sbjct	361	 TATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTAC	420
Query	451	AACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTG	510
Sbjct	421	 AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG	480
Query	511	ATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCAT	570
Sbjct	481	 ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT	540
Query	571	TACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGG	630
Sbjct	541	 TACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGG	600
Query	631	AGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	 AGATCCAATTTTATATCAACATTTATTT	628

>Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: MG855658.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTCTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTCTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: MG855657.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAC TGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAC TGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: MG855656.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,

Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
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>Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757910.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
        ||||||||||||||||||||| || |||||||||||||| ||||| ||||| |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
        ||||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
        ||||||||| ||||||||||||||||||||||| ||||||| |||||||||||||||
Sbjct   241  TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
        | || ||||||||||||||||||||||||||| || |||||||||||||||||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
        ||||||| ||||||||||||||||||||||||||||||||||||| || |||||||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
        ||||| ||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
        ||||||||||||||||| ||||| ||||||||||||||||||||||| |||||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
        | ||||||||||||||||| ||||||||||||||||||| ||||||| |||||
Sbjct   541  TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA   600

Query   639  TTTTATATCAACACTTATTT   658
        ||||||||| |||||
Sbjct   601  TTTTATATCAACATTTATTT   620

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>Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757904.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
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>Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757902.1 Length: 630

Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
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>Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial

Sequence ID: KX757896.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase subunit I (COI)

gene, partial cds; mitochondrial
Sequence ID: KX757889.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
|||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
|||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
|||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
|||||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
|||||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
| ||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
|||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
|||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
|||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
| ||
Sbjct 541 TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
|||||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Rovind cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757887.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
        |||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
        |||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
        |||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
        |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACCTCTCATTGAATCCGGAGCTGGAACAGGATGAACAGTTT     338
        |||
Sbjct   241  TATTTTTATTAATTAACCTCTCATTGAATCTGGAGCTGGTACAGGATGAACAGTTT     300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
        |||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
        |||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
        |||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
        |||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
        |||
Sbjct   541  TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA   600

Query   639  TTTTATATCAACACTTATTT      658
        |||
Sbjct   601  TTTTATATCAACATTTATTT      620
```

>Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757879.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```


>Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519711.1 Length: 636
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135448.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      ||||||||||||||||||||||||| || ||||||||||||||| ||||| ||||| |||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      ||||||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      ||||||||| ||||||||||||||||||||||| ||||||| |||||||||||||||
Sbjct 241 TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      | || ||||||||||||||||||||||||||| || |||||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTG 458
      ||||||| ||||||||||||||||||||||| ||||||||||||||| || |||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATTACAAGTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      ||||| ||||||||||||||||||||||| ||||||||||||||| || |||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      ||||||||||||||||| ||||| ||||||||||||||||||||||| |||||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      | ||||||||||||||||||| ||||||||||||||||||| ||||||||| |
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      ||||||||| |||||
Sbjct 601 TTTTATATCAACACTTATTT 620
```

>Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757905.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
          |||||||||||||||||||||||| || |||||||||||| |||| |||| ||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
          |||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
          ||||||||| |||| |||||||||||||||| ||||||| |||||||||||||||
Sbjct 241 TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
          | || |||||||||||||||||||||||| || |||||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
          ||||||| |||||||||||||||||||||||| || ||||||||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
          |||| |||||||||||||||||||||||| |||||||||||||||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
          |||||||||||||||| |||| |||||||||||||||||||||||||||||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAACAACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
          | |||||||||||||||| |||||||||||||||||| ||||||||| |
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
          |||||||||||| |||||
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Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757895.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
```

Sbjct 601 ||||| |||||
TTTTATATCAACATTTATT 620

>Rhipicephalus sanguineus isolate Zadar cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX757892.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAC TGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAC TGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600

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Query   639   TTTTATATCAACACTTATTT   658
          |||||
Sbjct   601   TTTTATATCAACATTTATTT   620

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>Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757890.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
          |||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
          |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
          |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
          |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
          |||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
          |||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
          |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
          |||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
          |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAAC TGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
          |||||
Sbjct   541  TGTTAAC TGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA   600

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Query   639   TTTTATATCAACACTTATTT   658
          |||||
Sbjct   601   TTTTATATCAACATTTATTT   620

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>Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757888.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
          |||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
          |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
          |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
          |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
          |||||
Sbjct   241  TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
          |||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
          |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
          |||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
          |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAACGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
          |||||

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Sbjct 541 TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
 |||||

Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Petnica cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757883.1 Length: 630
 Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
 Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
 |||||

Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
 |||||

Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
 |||||

Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
 |||||

Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
 |||||

Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
 |||||

Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
 |||||

Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
 |||||

Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
 |||||

Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAACGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638

Sbjct	541		TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639		TTTTATATCAACACTTATTT	658
Sbjct	601		TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519708.1 Length: 629
Range 1: 4 to 620

Score:985 bits(533), Expect:0.0,
Identities:589/617(95%), Gaps:0/617(0%), Strand: Plus/Plus

Query	42	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAA	101
Sbjct	4	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAA	63
Query	102	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAG	161
Sbjct	64	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAG	123
Query	162	TTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCC	221
Sbjct	124	TTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCC	183
Query	222	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTAT	281
Sbjct	184	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT	243
Query	282	TTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATC	341
Sbjct	244	TTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC	303
Query	342	CCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTC	401
Sbjct	304	CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTC	363
Query	402	TTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAA	461
Sbjct	364	TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAA	423
Query	462	ATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAA	521
Sbjct	424	ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA	483
Query	522	TTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTAT	581
Sbjct	484	TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	543

Query	582	TAACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTT	641
Sbjct	544	TAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGAGGAGATCCAATTT	603
Query	642	TATATCAACACTTATTT	658
Sbjct	604	TATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135447.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540

Query	579	TATTA	ACTGATCGAA	ACTTTA	ACATCAT	TTTTTT	GATCCTT	CAGGAGG	GAGATCC	CA	638
Sbjct	541	TGTTA	ACTGATCGAA	ACTTTA	ATACAT	TTTTTT	GATCCTT	CAGGGGG	GAGACCC	AA	600
Query	639	TTTTAT	ATCAAC	ACTTAT	TT	658					
Sbjct	601	TTTTAT	ATCAAC	ATTTAT	TT	620					

>Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519707.1 Length: 626
Range 1: 1 to 616

Score:983 bits(532), Expect:0.0,
Identities:588/616(95%), Gaps:0/616(0%), Strand: Plus/Plus

Query	43	ACTTAGTATAAGA	ATATTAATTCG	TATAGAATTAGG	ACAACCTGGA	ACTTTAATTGG	AAA	102
Sbjct	1	ACTTAGTATAAGA	ATATTAATTCG	TATAGAATTAGG	ACAACCTGGA	ACTTTAATTGG	AAA	60
Query	103	TGATCAGATTTA	TAAATGTAATCG	TAAACAGCACAT	GCATTTATTATA	ATTTTCTTTAT	AGT	162
Sbjct	61	TGATCAGATTTA	TAAATGTAATCG	TAAACAGCACAT	GCATTTATTATA	ATTTTCTTTAT	AGT	120
Query	163	TATACCAATCATA	AATCGGAGGGTTC	GGAATTGATTAG	TTCCTATTATAT	TAGGTGCC	CCCC	222
Sbjct	121	TATACCAATCATA	AATCGGAGGATTT	GGAATTGATTAG	TCCCTATCATAT	TGGGTGCC	CCCC	180
Query	223	AGATATAGCATTT	CCACGAATAAATA	AATATAAGATTTT	GACTTTTACCCC	CTCATTATT		282
Sbjct	181	AGATATAGCATTT	CCACGAATAAATA	AATATAAGATTTT	GACTTTTACCTC	CTTCACTATT		240
Query	283	TTTATTGATTAAC	TCTTCATTAATTG	AATCCGGAGCTG	GAACAGGATGA	ACAGTTTATCC		342
Sbjct	241	TTTATTAATTAAC	TCTTCATTAATTG	AATCTGGAGCTGG	TACAGGATGAAC	AGTTTATCCC		300
Query	343	CCCTCTATCTTCA	AATTTATCACATT	ATGGTCCATCAG	TAGATTTAGCTA	TTTTTTCTCT		402
Sbjct	301	TCCTCTATCTTCA	AATTTATCACATT	ATGGCCCTTCAG	TAGATTTAGCTA	TTTTTTCTCT		360
Query	403	TCACCTTGCTGGT	GCTTCTTCAATTT	TAGGTGCAATTA	ACTTCATCACA	ACTATTGTAAA		462
Sbjct	361	TCATCTTGCTGGT	GCTTCTTCAATTT	TAGGTGCAATTA	ACTTTATTACA	ACTATTGTAAA		420
Query	463	TATACGATCAATT	GGAATAACAATA	GAAACGAATACC	ATTATTTGTTTG	ATCTGTTTTAAT		522
Sbjct	421	CATACGATCAATT	GGAATAACAATA	GAAACGTATACC	ATTATTTGTTTG	ATCTGTTTTAAT		480
Query	523	TACAGCTATTTT	ACTACTTCTATCT	TTTACCTGTATT	AGCAGGTGCC	ATTACAATATTATT		582

Sbjct	481	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583	AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	642
Sbjct	541	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	600
Query	643	ATATCAACACTTATTT	658
Sbjct	601	ATATCAACATTTATTT	616

>Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757901.1 Length: 630
Range 1: 1 to 620

Score:979 bits(530), Expect:0.0,
Identities:590/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:974 bits(527), Expect:0.0,
Identities:589/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        |||
Sbjct   482  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  541

Query   579  TATTAAGTATGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        | |||
Sbjct   542  TGTTAAGTATGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  601

Query   639  TTTTATATCAACACTTATTT  658
        |||
Sbjct   602  TTTTATATCAACATTTATTT  621

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>Rhipicephalus sanguineus isolate LIC4723B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX714599.1 Length: 723
>Rhipicephalus sanguineus isolate LIC4750B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX714600.1 Length: 723
Range 1: 1 to 597

Score:937 bits(507), Expect:0.0,
Identities:567/597(95%), Gaps:0/597(0%), Strand: Plus/Plus

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Query   62   ATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTA  121
        |||
Sbjct   1     ATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTA  60

Query   122  ATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGA  181
        |||
Sbjct   61   ATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATTGGA  120

Query   182  GGGTTTCGGAATTTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACGA  241
        || ||
Sbjct   121  GGATTTGGAAATTTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCACGA  180

Query   242  ATAAATAATATAAGATTTTGACTTTTACCCCCTCATTATTTTATTGATTAACCTCTTCA  301
        |||
Sbjct   181  ATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCA  240

Query   302  TTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTA  361
        |||
Sbjct   241  TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA  300

Query   362  TCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCT  421
        |||
Sbjct   301  TCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCT  360

Query   422  TCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATA  481
        |||
Sbjct   361  TCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATA  420

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Query   482  ACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTT  541
        |||
Sbjct   421  ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT  480

Query   542  CTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAAC  601
        |||
Sbjct   481  TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAAT  540

Query   602  ACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        |||
Sbjct   541  ACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  597

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>Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519713.1 Length: 580
Range 1: 1 to 580

Score:933 bits(505), Expect:0.0,
Identities:555/580(96%), Gaps:0/580(0%), Strand: Plus/Plus

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Query   43   ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAA  102
        |||
Sbjct   1     ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAA  60

Query   103  TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGT  162
        |||
Sbjct   61   TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGT  120

Query   163  TATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCC  222
        |||
Sbjct   121  TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC  180

Query   223  AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATT  282
        |||
Sbjct   181  AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT  240

Query   283  TTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC  342
        |||
Sbjct   241  TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC  300

Query   343  CCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT  402
        |||
Sbjct   301  TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT  360

Query   403  TCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAA  462
        |||
Sbjct   361  TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA  420

Query   463  TATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT  522
        |||
Sbjct   421  CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT  480

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Query	523	TACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT	582
Sbjct	481	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583	AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCA	622
Sbjct	541	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA	580

>Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519706.1 Length: 595
Range 1: 1 to 570

Score:898 bits(486), Expect:0.0,
Identities:542/570(95%), Gaps:0/570(0%), Strand: Plus/Plus

Query	89	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	148
Sbjct	1	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA	60
Query	149	ATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATT	208
Sbjct	61	ATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATC	120
Query	209	ATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	268
Sbjct	121	ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA	180
Query	269	CCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGA	328
Sbjct	181	CCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGA	240
Query	329	TGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTA	388
Sbjct	241	TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA	300
Query	389	GCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATC	448
Sbjct	301	GCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATT	360
Query	449	ACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTT	508
Sbjct	361	ACAACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT	420
Query	509	TGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCC	568
Sbjct	421	TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	480
Query	569	ATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGA	628


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Sbjct  481  ATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGA  540
Query   629  GGAGATCCCATTTTATATCAACACTTATTT  658
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Sbjct  541  GGAGATCCAATTTTATATCAACATTTATTT  570

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>Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase subunit 1 gene,
partial cds; mitochondrial
Sequence ID: KY678135.1 Length: 790
Range 1: 18 to 675

Score:883 bits(478), Expect:0.0,
Identities:599/659(91%), Gaps:2/659(0%), Strand: Plus/Plus

Query	1	AACAATATATTTTAATTTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	18	AACAATATATTTTAATTTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	77
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	78	AATTCGTATAGAATTAGGCCAACCTGGAACCTAATTGGTAATGATCAAATTTATAATGT	137
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	138	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	197
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	198	TGGATTTGGAACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGACTTCTTCCCTCCCTCATTATTTATATTAATTAATTCTTC	317
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC-CCCTCTATCTTCAAATT	359
Sbjct	318	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCT-TATCCTCAAATT	376
Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTT	419
Sbjct	377	TATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTT	436
Query	420	CTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAA	479
Sbjct	437	CTTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAA	496
Query	480	TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	497	TAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAC	556
Query	540	TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTA	599

Sbjct	557	TATTATCTTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCGATCGAAATTTTA	616
Query	600	ACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	617	ACACTTCATTTTTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	675

>Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800313.1 Length: 673
Range 1: 8 to 665

Score:883 bits(478), Expect:0.0,
Identities:598/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCTATTATAATTGG	187
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTCCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTTCATTATTTCTATTAATTAACCTCTTC	307
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCAGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAAC TATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAAC TATTGTAAATATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547

Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTA	607
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	658
Sbjct	608	TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTT	665

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SC3005
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425987.1 Length: 574
Range 1: 1 to 561

Score:881 bits(477), Expect:0.0,
Identities:533/561(95%), Gaps:0/561(0%), Strand: Plus/Plus

Query	98	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTT	157
Sbjct	1	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACACGCATTTATTATAATTTTTTTT	60
Query	158	ATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGT	217
Sbjct	61	ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATTATATTAGGT	120
Query	218	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCA	277
Sbjct	121	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA	180
Query	278	TTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTT	337
Sbjct	181	CTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT	240
Query	338	TATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTT	397
Sbjct	241	TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTT	300
Query	398	TCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATT	457
Sbjct	301	TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATT	360
Query	458	GTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTT	517
Sbjct	361	GTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTT	420
Query	518	TTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	577
Sbjct	421	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	480
Query	578	TTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCC	637
Sbjct	481	TTGTTAACCTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCA	540

Query 638 ATTTTATATCAACACTTATTT 658
 |||||
 Sbjct 541 ATTTTATATCAACATTTATTT 561

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (C01) gene, partial cds;
 mitochondrial
 Sequence ID: KU214592.1 Length: 829
 Range 1: 1 to 648

Score:876 bits(474), Expect:0.0,
 Identities:590/648(91%), Gaps:0/648(0%), Strand: Plus/Plus

Query 11 TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA 70
 |||||
 Sbjct 1 TTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACTAATTCGTATA 60

Query 71 GAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA 130
 |||||
 Sbjct 61 GAATTAGGCCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGTAATTGTTACA 120

Query 131 GCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGA 190
 || |||||
 Sbjct 121 GCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGTGGATTTGGA 180

Query 191 AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT 250
 || |||||
 Sbjct 181 AACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 240

Query 251 ATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAA 310
 |||||
 Sbjct 241 ATAAGATTTTGACTTCTCCTCCCTCATTATTTATATTAATTAATTCTTCATTAATTGAG 300

Query 311 TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT 370
 || |||||
 Sbjct 301 TCAGGAGCAGGTACAGGATGGACAGTTTATCCTCCCCTATCCTCAAATTTATCACATTAT 360

Query 371 GGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA 430
 || |||||
 Sbjct 361 GGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA 420

Query 431 GGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAA 490
 |||||
 Sbjct 421 GGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAATAACAATAGAA 480

Query 491 CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA 550
 |||||
 Sbjct 481 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACTATTATCTTTA 540

Query 551 CCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTT 610
 |||||

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Sbjct  541  CCTGTTTTAGCAGGTGCCATTACAATATTATTAACCGATCGAAATTTTAACACTTCATTT  600
Query  611  TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  601  TTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT  648

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>Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MT079206.1 Length: 678
Range 1: 1 to 652

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCG	60
Query	67	TATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTT	186
Sbjct	121	AACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	CGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181	TGGAAACTGGTTAGTTCCAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACA	366
Sbjct	301	TGAATCTGGGGCAGGGACAGGGTGAAC TGTTTATCCTCCTTTATCCTCAAATTTATCCCA	360
Query	367	TTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTTATTACA ACTATTGTAAACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACC GCTATTTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAAACTTTAACACATC	606

[illegible]

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAACTTTAACACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTA	ACTGATCGAAATTTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	TATATCAACACTTATTT	658
Sbjct	601	ATTTTTTGACCCTTCAGGAGGAGGTGACCCAATTTT	TATATCAACATTTATTT	652

>Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome oxidase subunit 1 gene, complete cds; mitochondrial
Sequence ID: KM494916.1 Length: 1539
Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTCCTCCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCCTCAAATTT	404
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584

Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTA	644
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	658
Sbjct	645	CACTTCATTTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTT	702

>Rhipicephalus sanguineus isolate Tehran cytochrome oxidase subunit 1 gene,
complete cds; mitochondrial
Sequence ID: KM494915.1 Length: 1539
Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCCTCAAATTT	404
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540

Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	645	CACTTCATTTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800314.1 Length: 673
Range 1: 8 to 664

Score:870 bits(471), Expect:0.0,
Identities:595/657(91%), Gaps:0/657(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCCATTATAATTGG	187
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTCATTATTTCTATTAATTAACCTCTC	307
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCGGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCTCAAATTT	367
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540

Sbjct	488		AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541		TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	548		CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAAGTATCGAAATTTCAA	607
Query	601		CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATT	657
Sbjct	608		TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATT	664

>Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606303.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	545

Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606302.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATTTATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTCATTACAACCTATTGTAAACATACGATCTATTGGAAT	545

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Query  481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT  540
        |||
Sbjct  546  AACAAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT  605

Query  541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA  600
        |||
Sbjct  606  TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA  665

Query  601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        |||
Sbjct  666  CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT  723

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>Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606301.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        |||
Sbjct  66    AACAAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT  125

Query  61    AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT  120
        |||
Sbjct  126   AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT  185

Query  121   AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG  180
        |||
Sbjct  186   AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG  245

Query  181   AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG  240
        |||
Sbjct  246   AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG  305

Query  241   AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC  300
        |||
Sbjct  306   AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC  365

Query  301   ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT  360
        |||
Sbjct  366   ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCTCCTTTATCTTCAAATTT  425

Query  361   ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC  420
        |||
Sbjct  426   ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC  485

Query  421   TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT  480
        |||

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Sbjct	486	TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	723

>Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KY606300.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAATGATTAGTTCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACACTATTGTAAATATACGATCAATTGGAAT	480

Sbjct	486	 TTCAATTTTAGGTGCAATTAATTTTCATTACAACATATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	 AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	606	 TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	 CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606299.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	 AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	 AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	 AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	 AGGATTTGGAAACTGATTAGTGCCCATTATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	306	 AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	 ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	 ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485

Query	421	TTCAATTTTAGGTGCAATTA	AACTTCATCACA	ACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTA	AATTTTCATTACA	ACTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540		
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605		
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAAACTTTAA	600	
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAAATTTCAA	665	
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658		
Sbjct	666	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723		

>Rhipicephalus camicasi isolate SC0126 mitochondrion, complete genome
Sequence ID: NC_061616.1 Length: 14725
>Rhipicephalus camicasi isolate SC0126 mitochondrion, complete genome
Sequence ID: MZ323229.1 Length: 14725
Range 1: 45 to 702

Score:861 bits(466), Expect:0.0,
Identities:595/659(90%), Gaps:2/659(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATACTTAATTTTTGGAGCATGATCTGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGCCAACCTGGAACTTTAATTGGAAATGACCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATGATTGG	224
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTCGGAAATTGATTAGTCCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA	ACTCTTC
Sbjct	285	AATAAATAATATAAGATTTTGATTACTTCCTCCTCATTATTTTTATTAATTA	ATTCTTC
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC-CCCTCTATCTTCAAATT	359
Sbjct	345	ATTAATTGAATCAGGAGCAGGGACAGGATGAACAGTTTACCCTCCCT-TATCATCAAATT	403
Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTT	419

Sbjct	404	TATCACACTATGGTCCATCAGTAGATCTAGCTATTTTTCTCTTCATCTTGCTGGTGCTT	463
Query	420	CTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAA	479
Sbjct	464	CTTCAATTTTAGGCGCAATTAATTTCAATACAACCATTGTAAACATACGATCTATTGGAA	523
Query	480	TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	524	TAACAATAGAACGAATACCTTTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAT	583
Query	540	TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTA	599
Sbjct	584	TATTATCTTTACCAGTTTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTA	643
Query	600	ACACATCATTTTTTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	644	ATACCTCGTTCTTTATCCTTCAGGAGGAGGGATCCAATTTTATATCAACACTTATTT	702

>Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305547.1 Length: 658
Range 1: 1 to 658

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGAATAGAGTTAGGACAACCTGGGACTTTAATTGGAAATGATCAAATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGATTACTTCTCCCTCATTATTCTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420

Sbjct	361	 ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTCATTACAAC TATTGTAAATATACGATCTATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACC GCTATTTTATTGCT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAC TGATCGAACTTTAA	600
Sbjct	541	 TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAC TGATCGAAATTTCAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	 CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	658

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002580.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTCATTATTTCTATTAATTAATTCTCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAACCTGGATGAACCTGTTTATCCGCCTTTATCATCAAATTT	433

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-BC cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002579.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTCATTATTTCTATTAATTAATTCTCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	374	ATTAATTGAATCAGGAGCAGGAACTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTA ACTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-YC cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002578.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT 	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT 	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG 	253
Query	181	AGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG 	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCTCATTATTTTATTGATTAACCTCTTC 	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC 	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 	360

Sbjct	374	 ATTAATTGAATCAGGAGCAGGAACTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	 ATCACACTATGGACCATCAGTAGATTTAGCTATTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACA ACTATTGTAAATATA CGATCAATTGGAAT	480
Sbjct	494	 TTCAATTTTAGGTGCAATCAATTTTATTAC GACTATTATAAAATATA CGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	 AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAAA CTTTAA	600
Sbjct	614	 TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTA ACTGATCGAAA TTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	 CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-PS cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002577.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 	300
Sbjct	314	AATAAATAACATAAGATTTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate SHZ cytochrome oxidase subunit I (C01) gene,
partial cds; mitochondrial
Sequence ID: KY069271.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate FK-1 cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606291.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	314	AATAAATAACATAAGATTTTGGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate YN3 cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606290.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300

Sbjct	314	 AATAAAATACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	 ATTAATTGAATCAGGAGCAGGAACGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	 ATCACACTATGGACCATCAGTAGATTTAGCTATTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	 TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	 AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGT TACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAA	600
Sbjct	614	 TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTA ACTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	 CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Common							Scientific
Description	Max	Total	Query	E	Per.	Acc.	Name
Name	Taxid	Score	Score	cover	Value	Ident	Len
							Accession
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	688
MF425995.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	703
MF425994.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	702
MF425993.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	693
MF425992.1							

Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	690
KT906183.1							
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	690
KT906182.1							
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14711
OM368327.1							
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14714
OM368323.1							
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14713
OM368322.1							
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	707
JQ737084.1							
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	658
KF437543.1							
Rhipicephalus linnaei isolate LA032-2 clone JS5930...							
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	14715
MW429383.1							
Rhipicephalus linnaei mitochondrion, complete sequence							
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	14711
NC_060409.1							
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,... Ixodidae							
sp.... NA	1901042	1210	1210	100%	0.0	99.85	658
KX053537.1							
Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690
KT906185.1							
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690
KT906184.1							
Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	658
KF200113.1							
Rhipicephalus linnaei isolate SC931-1 clone JS5927...							
Rhipicephalu... NA	2138177	1210	1210	100%	0.0	99.85	14717
MW429382.1							
Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1205	1205	99%	0.0	99.85	658
KX360367.1							
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	690
KT906186.1							
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	658
KF200112.1							
Rhipicephalus sanguineus mitochondrion, complete genome							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	14714
JX416325.1							

Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	100.00	661
MZ401443.1							
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	100.00	661
MZ401441.1							
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	99.85	664
MZ401440.1							
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1190	1190	97%	0.0	100.00	664
MG969507.1							
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1188	1188	98%	0.0	99.69	649
KF200084.1							
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	768
KX383817.1							
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	657
MZ401442.1							
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	661
MZ401438.1							
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969506.1							
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969505.1							
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969504.1							
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	644
KF200096.1							
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1177	1177	100%	0.0	98.94	658
OM984983.1							
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416302.1							
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416298.1							
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1177	1177	97%	0.0	99.69	670
HM193873.1							
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1175	1175	97%	0.0	99.69	768
KX383820.1							
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	97%	0.0	99.53	724
KX383816.1							

Rhipicephalus linnaei voucher P1/22_18-5	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658	
OM984984.1								
Rhipicephalus linnaei voucher P1/22_8-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658	
OM984974.1								
Rhipicephalus linnaei voucher P1/22_6-2	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658	
OM984973.1								
Rhipicephalus sanguineus isolate SZM2	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416308.1								
Rhipicephalus sanguineus isolate GTF3	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416304.1								
Rhipicephalus sanguineus isolate GBM1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416300.1								
Rhipicephalus sanguineus isolate GBF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416299.1								
Rhipicephalus sanguineus isolate CHF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416297.1								
Rhipicephalus sanguineus isolate DGM1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416296.1								
Rhipicephalus sanguineus isolate FSF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416293.1								
Rhipicephalus sanguineus isolate T78D2	cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	100.00	650	
MZ401439.1								
Rhipicephalus sanguineus isolate LIC5762	cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	763	
KX383802.1								
Rhipicephalus linnaei voucher P1/22_16-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658	
OM984979.1								
Rhipicephalus linnaei voucher P1/22_1-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658	
OM984968.1								
Rhipicephalus sanguineus isolate DGF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802	
JX416295.1								
Rhipicephalus sanguineus isolate FSM1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802	
JX416294.1								
Rhipicephalus sanguineus isolate sanguineus0926	cytochrome...							
Rhipicephalu... brown dog tick	34632	1162	1162	99%	0.0	98.77	658	
MH513252.1								
Rhipicephalus linnaei voucher P1/22_19-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658	
OM984985.1								

Rhipicephalus linnaei voucher	P1/22_14-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984978.1									
Rhipicephalus linnaei voucher	P1/22_13-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984977.1									
Rhipicephalus linnaei voucher	P1/22_10-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984975.1									
Rhipicephalus linnaei voucher	P1/22_5-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984971.1									
Rhipicephalus linnaei voucher	P1/22_4-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984970.1									
Rhipicephalus linnaei voucher	P1/22_3-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984969.1									
Rhipicephalus sanguineus isolate	GHF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	802		
JX416301.1									
Rhipicephalus sanguineus isolate	Tropical lineage RJ	cytochrom...							
Rhipicephalu... brown dog tick	34632	1155	1155	95%	0.0	99.68	642		
MT010523.1									
Rhipicephalus linnaei voucher	P1/22_21-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984988.1									
Rhipicephalus linnaei voucher	P1/22_12-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984976.1									
Rhipicephalus sanguineus isolate	GTF2	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1155	1155	96%	0.0	99.37	802		
JX416303.1									
Rhipicephalus sanguineus sensu lato	'tropical lineage' isolate...								
Rhipicephalu... NA	2138177	1153	1153	98%	0.0	98.77	826		
MF426003.1									
Rhipicephalus sanguineus voucher	AMMS-RS-4	cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1146	1146	96%	0.0	99.21	665		
HM193874.1									
Rhipicephalus sanguineus isolate	Abidjan	cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630		
KX757914.1									
Rhipicephalus sanguineus isolate	LIC5960	cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1136	1136	97%	0.0	98.60	768		
KX383800.1									
Rhipicephalus sanguineus isolate	LIC5682B	cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1131	1131	93%	0.0	99.68	744		
KX383796.1									
Rhipicephalus sanguineus isolate	LIC5958B	cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1127	1127	96%	0.0	98.59	698		
KX383798.1									
Rhipicephalus sanguineus isolate	LIC5584D	cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1125	1125	97%	0.0	98.29	768		
KX383814.1									

Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726449.1								
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726429.1								
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726428.1								
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726427.1								
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726426.1								
Rhipicephalus sanguineus voucher D0-306 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1092	1092	91%	0.0	99.33	638	
KX360338.1								

Alignments:

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425994.1 Length: 703

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425996.1 Length: 703

Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	258	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome

Sequence ID: OM368327.1 Length: 14711

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome

Sequence ID: OM368323.1 Length: 14714

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome

Sequence ID: OM368322.1 Length: 14713

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 24 to 681

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	24	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	83
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	84	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	143
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	144	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	203
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	204	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	263

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	264	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	323
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	324	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	383
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	384	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	443
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	444	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	503
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	504	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	563
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	564	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	623
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	624	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	681

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome

Sequence ID: MW429383.1 Length: 14715

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	165	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus linnaei mitochondrion, complete sequence

Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome

Sequence ID: MW429381.1 Length: 14711

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAA	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial
Sequence ID: KX053537.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	78	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	 AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	 TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	 GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT	77

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KF200113.1 Length: 658
 Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
 Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome

Sequence ID: MW429382.1 Length: 14717

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus sanguineus voucher D0-311 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX360367.1 Length: 658
 Range 1: 4 to 658

Score:1205 bits(652), Expect:0.0,
 Identities:654/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

Query	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
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Sbjct	4	 AATATACTTAATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Query	64	CCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Sbjct	64	 CCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Query	124	TGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGG	183
Sbjct	124	 TGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGG	183
Query	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Sbjct	184	 ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Query	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Sbjct	244	 AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Query	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATC	363
Sbjct	304	 AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATC	363
Query	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTC	423
Sbjct	364	 ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTC	423
Query	424	AATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAAC	483
Sbjct	424	 AATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAAC	483
Query	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Sbjct	484	 AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Query	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC	603
Sbjct	544	 ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC	603
Query	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	604	 ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200112.1 Length: 658
>Rhipicephalus sanguineus voucher D0-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360403.1 Length: 658
Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus mitochondrion, complete genome
Sequence ID: JX416325.1 Length: 14714
Range 1: 1185 to 1842

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1185 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 1244

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 1245 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 1304

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 1305 AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG 1364

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 1365 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG 1424

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 1425 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 1484

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 1485 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 1544

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 1545 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC 1604

Query 421 TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 1605 TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT 1664

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 1665 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 1724

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 1725 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 1784

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 1785 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT 1842
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>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661

Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,

Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

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Query 14  ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 73
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 60

Query 74  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 120

Query 134  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  CATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 180

Query 194  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 240

Query 254  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 300

Query 314  GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA 373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA 360

Query 374  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 420

Query 434  GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 480

Query 494  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 540

Query 554  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT 613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT 600

Query 614  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645
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>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: MZ401441.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

```
Query 14  ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 73
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1    ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 60

Query 74  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 120

Query 134  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 180

Query 194  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATA 253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATA 240

Query 254  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 300

Query 314  GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA 373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA 360

Query 374  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 420

Query 434  GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 480

Query 494  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 540

Query 554  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT 613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT 600

Query 614  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645
```

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,
Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

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Query 11 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 70
|||||
Sbjct 1 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 60

Query 71 GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 130
|||||
Sbjct 61 GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 120

Query 131 GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA 190
|||||
Sbjct 121 GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA 180

Query 191 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 250
|||||
Sbjct 181 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 240

Query 251 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 310
|||||
Sbjct 241 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 300

Query 311 TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC 370
|||||
Sbjct 301 TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC 360

Query 371 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA 430
|||||
Sbjct 361 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA 420

Query 431 GGTGCAATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAA 490
|||||
Sbjct 421 GGTGCAATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAA 480

Query 491 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 550
|||||
Sbjct 481 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 540

Query 551 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC 610
|||||
Sbjct 541 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC 600

Query 611 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 648
```

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1190 bits(644), Expect:0.0,
Identities:644/644(100%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 1 to 649

Score:1188 bits(643), Expect:0.0,
Identities:647/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

```
Query 10  CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT 69
          |||
Sbjct 1    CTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCAT 60

Query 70  AGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 129
          |||
Sbjct 61  AGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 120

Query 130 AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG 189
          |||
Sbjct 121 AGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGG 180

Query 190 AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA 249
          |||
Sbjct 181 AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA 240

Query 250 TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 309
          |||
Sbjct 241 TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 300

Query 310 ATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTA 369
          |||
Sbjct 301 ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA 360

Query 370 CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 429
          |||
Sbjct 361 CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 420

Query 430 AGGTGCAATCAATTTTCATTACAACATTGTAATATACGATCCATTGGAATAACAATAGA 489
          |||
Sbjct 421 AGGTGCAATCAATTTTCATTACAACATTGTAATATACGATCCATTGGAATAACAATAGA 480

Query 490 ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 549
          |||
Sbjct 481 ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 540

Query 550 ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 609
          |||
Sbjct 541 ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 600

Query 610 CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 601 CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 649
```

>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
      |||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
      |||
Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
      |||
Sbjct 121 GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
      |||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
      |||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
      |||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 436
      |||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
      |||
Sbjct 421 ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
      |||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 616
      |||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
```

>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 436
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          ||||||||||||||||||||||||||||||||||||||||
Sbjct 601 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
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>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

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Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
|||||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
|||||
Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
|||||
Sbjct 121 GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
|||||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
|||||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCA 376
|||||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 436
|||||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
|||||
Sbjct 421 ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
|||||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 616
|||||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
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Sbjct 601 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query 15  TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
          || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query 75  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query 135  ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query 195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query 255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query 315  GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query 375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query 435  CAATCAATTTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAA 494
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  CAATCAATTTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query 495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query 555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

Query 615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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      |||||||||||||||||||||||||||||||||||||||
Sbjct  601 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644

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>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query   15  TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
      || |||||||||||||||||||||||||||||||||||||||
Sbjct   1  TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query   75  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
      |||||||||||||||||||||||||||||||||||||||
Sbjct   61  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query   135  ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
      |||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query   195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
      |||||||||||||||||||||||||||||||||||||||
Sbjct   181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query   255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
      |||||||||||||||||||||||||||||||||||||||
Sbjct   241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query   315  GAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGAC 374
      |||||||||||||||||||||||||||||||||||||||
Sbjct   301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query   375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
      |||||||||||||||||||||||||||||||||||||||
Sbjct   361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query   435  CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
      |||||||||||||||||||||||||||||||||||||||
Sbjct   421  CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query   495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
      |||||||||||||||||||||||||||||||||||||||
Sbjct   481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query   555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
      |||||||||||||||||||||||||||||||||||||||
Sbjct   541  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

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Query   615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   601  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644

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>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query   15  TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
        || ||||||||||||||||||||||||||||||||||||||||
Sbjct    1  TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query   75  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   61  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query   135  ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query   195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query   255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query   315  GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query   375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query   435  CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query   495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query   555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

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Query   615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct   601  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644

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>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query    6   TATACTTAATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC 65
          |||
Sbjct    1   TATACTTAATTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCC 60

Query   66   GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG 125
          |||
Sbjct   61   GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG 120

Query   126   TAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGAT 185
          |||
Sbjct   121   TAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGAT 180

Query   186   TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAA 245
          |||
Sbjct   181   TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAA 240

Query   246   ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA 305
          |||
Sbjct   241   ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA 300

Query   306   TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCAC 365
          |||
Sbjct   301   TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCAC 360

Query   366   ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA 425
          |||
Sbjct   361   ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA 420

Query   426   TTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAA 485
          |||
Sbjct   421   TTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAA 480

Query   486   TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT 545
          |||
Sbjct   481   TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT 540

Query   546   CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT 605
          |||

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Sbjct  541  CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT  600
Query   606  CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA  649
          |||||
Sbjct   601  CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA  644

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>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 1 to 658

Score:1177 bits(637), Expect:0.0,
Identities:651/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||||
Sbjct   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query   61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||||
Sbjct   61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121     AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG  180
          |||||
Sbjct   121     AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||||
Sbjct   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||||
Sbjct   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||||
Sbjct   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query   361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC  420
          |||||
Sbjct   361     ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC  420

Query   421     TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480
          |||||
Sbjct   421     TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480

Query   481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||||
Sbjct   481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query   541     ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600

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Sbjct	541		ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416302.1 Length: 802
>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416305.1 Length: 802
>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416306.1 Length: 802
>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416307.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420

Query	442	TTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561	
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540	
Query	562	TGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637	

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81	
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60	
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141	
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120	
Query	142	TATTATAA	tttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAA	tttttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261	
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240	
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321	
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300	
Query	322	TACAGGGTGAACAGTTT	AccccccctTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441	

Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 1 to 642

Score:1177 bits(637), Expect:0.0,
Identities:642/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGG-CATGATCCGG-ATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	58
Query	75	TAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	59	TAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	118
Query	135	ATGCATTTATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	119	ATGCATTTATTATAA TTTTTTTT ATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	178
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	179	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	238
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	239	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	298
Query	315	GAGCAGGTACAGGGTGAACAGTTT Acccccc TTATCATCAAATTTATCACACTACGGAC	374
Sbjct	299	GAGCAGGTACAGGGTGAACAGTTT ACCCCCC TTATCATCAAATTTATCACACTACGGAC	358
Query	375	CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434

Sbjct	359	 CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	418
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	419	 CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	478
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	479	 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	538
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	539	 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	598
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	599	 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383820.1 Length: 768
Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,
Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	 GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360

Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383816.1 Length: 724
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360

Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCTGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccctTATCATCAAATTT	360

Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttTATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300

Query	322	TACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAACATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416304.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321

Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321

Sbjct	241		GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322		TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301		TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382		AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361		AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442		TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421		TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416299.1 Length: 802

Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,

Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1		AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142		TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121		TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240

Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416297.1 Length: 802

Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,

Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAATTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAAATTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240

Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTATTATTACTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401439.1 Length: 650
Range 1: 1 to 634

Score:1171 bits(634), Expect:0.0,
Identities:634/634(100%), Gaps:0/634(0%), Strand: Plus/Plus

Query	25	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	84
Sbjct	1	 ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	60
Query	85	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	144
Sbjct	61	 AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	120
Query	145	TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	204
Sbjct	121	 TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	180

Query	205	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	264
Sbjct	181	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	240
Query	265	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	324
Sbjct	241	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	300
Query	325	AGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	384
Sbjct	301	AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	360
Query	385	TTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTT	444
Sbjct	361	TTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTT	420
Query	445	CATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	504
Sbjct	421	CATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	480
Query	505	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	564
Sbjct	481	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	540
Query	565	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	624
Sbjct	541	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	600
Query	625	AGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGTGACCCAATTCTATATCAACATTTATTT	634

>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383802.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383803.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383804.1 Length: 763
 Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
 Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141

Sbjct	61	 ACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAA TTTTTTTT ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTT Acccccc TTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTT ACCCCCC TTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGGGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984979.1 Length: 658
 Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
 Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene,
 partial cds; mitochondrial
 Sequence ID: JX416295.1 Length: 802
 Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
 Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81

Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT	637

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
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Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658
Range 1: 6 to 658

Score:1162 bits(629), Expect:0.0,
Identities:645/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	6	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	65
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	66	AATTCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	125
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	126	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	185
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	186	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	245
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	246	AATAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	305
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	306	ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	365
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	366	ATCACACTACGGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTC	425
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	426	TTCAATTTTAGGCGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	485
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	486	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	545
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	546	ATTATCTTTACCACTCTTAGCTGGTGAATACAATATTGTAACTGATCGAAACTTTAA	605
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT	653
Sbjct	606	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT	658

>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984985.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984978.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,

Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984977.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658

Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATGGTAAATATACGATCCATTGGGAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGAATACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416301.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      |||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||
Sbjct  241  GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||
Sbjct  421  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||
Sbjct  541  TGGCGCTATTACAATATTATTAAGTATCGAACTTTAATACATTATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct  601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637
```

>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT010523.1 Length: 642
Range 1: 1 to 631

Score:1155 bits(625), Expect:0.0,
Identities:629/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

```
Query 28 ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG 87
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG 60

Query 88 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 120

Query 148 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 180

Query 208 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 240

Query 268 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 300

Query 328 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 387
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 360

Query 388 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 447
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 361 AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 420

Query 448 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 480

Query 508 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 567
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 540

Query 568 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 600

Query 628 AGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||
Sbjct 601 GGGTGACCCAATTCTATATCAACATTTATTT 631
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>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| |||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||| |||||||||||||||||||||| |||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416303.1 Length: 802
Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,
Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA  420

Query  442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCATTACAAC TATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC  621
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      ||||||||||||||||||||||||||||||||||||
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Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1153 bits(624), Expect:0.0,
Identities:640/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

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Query 11  TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 70
          |||
Sbjct 3   TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATA 62

Query 71  GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 130
          |||
Sbjct 63  GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 122

Query 131 GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA 190
          |||
Sbjct 123 GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA 182

Query 191 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 250
          |||
Sbjct 183 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAAT 242

Query 251 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 310
          |||
Sbjct 243 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 302

Query 311 TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC 370
          |||
Sbjct 303 TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC 362

Query 371 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA 430
          |||
Sbjct 363 GGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA 422

Query 431 GGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA 490
          ||
Sbjct 423 GGC GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA 482

Query 491 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 550
          |||
Sbjct 483 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 542

Query 551 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC 610
          |||
Sbjct 543 CCAGTCTTAGCTGGTGCAATTACAATATTGTAAAGTATCGAACTTTAATACATCATTC 602

Query 611 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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|||||
Sbjct  603  TTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 650
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>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1146 bits(620), Expect:0.0,
Identities:631/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

```
Query  1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct  31  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 90

Query  61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct  91  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 150

Query  121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct  151  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 210

Query  181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct  211  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 270

Query  241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct  271  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 330

Query  301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct  331  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 390

Query  361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      |||
Sbjct  391  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 450

Query  421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct  451  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 510

Query  481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct  511  AACAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 570

Query  541  ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct  571  ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATAATATTAAGTATCGAAACTTTAA 630
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Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCC   636
        ||||||||||||||||| ||||||||| |||||
Sbjct   631  TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC   665

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>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG   98
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1     TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG   60

Query   99   GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttA   158
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAATTTTTTTTA   120

Query   159  TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG   218
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG   180

Query   219  CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC   278
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC   240

Query   279  TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT   338
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT   300

Query   339  AccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT   398
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTG   458
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTG   420

Query   459  TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT   518
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT   480

Query   519  TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT   578
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT   540

Query   579  TATTAACGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA   638
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TATTAACGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA   600

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Query 639 TTCTATATCAACATTTATTT 658
 |||||
 Sbjct 601 TTCTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383800.1 Length: 768
 >Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383815.1 Length: 768
 Range 1: 1 to 642

Score:1136 bits(615), Expect:0.0,
 Identities:633/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
 |||||
 Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
 |||||
 Sbjct 61 GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
 |||||
 Sbjct 121 GCATTTATTATAAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
 |||||
 Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
 |||||
 Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
 |||||
 Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGACGGTGCTTCTTCAATTTTAGGTGCA 436
 |||||
 Sbjct 361 TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGACGGTGCTTCTTCAATTTTAGGCGCA 420

Query 437 ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
 |||||
 Sbjct 421 ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
 |||||
 Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTC 540

Query	557	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATT	658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATT	642	

>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383796.1 Length: 744
Range 1: 1 to 618

Score:1131 bits(612), Expect:0.0,
Identities:616/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

Query	41	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAAC	TTAATTGGA	100
Sbjct	1	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAAC	TTAATTGGA	60
Query	101	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAA	tttttttATA	160
Sbjct	61	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAA	TTTTTTTTTATA	120
Query	161	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATA	CTAGGAGCT	220
Sbjct	121	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATA	CTAGGAGCT	180
Query	221	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCT	CCTTCTCTA	280
Sbjct	181	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCT	CCTTCTCTA	240
Query	281	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGA	ACAGTTTAc	340
Sbjct	241	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGA	ACAGTTTAC	300
Query	341	ccccccTTATCATCAAATTTATCACA	CTACGGACCATCAGTAGATTTAGCTATTTTTTCT	400
Sbjct	301	CCCCCTTATCATCAAATTTATCACA	CTACGGACCATCAGTAGATTTAGCTATTTTTTCT	360
Query	401	CTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACA	AACTATTGTA	460
Sbjct	361	CTACATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACA	AACTATTGTA	420
Query	461	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGAT	CTGTTTTA	520
Sbjct	421	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGAT	CTGTTTTA	480
Query	521	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACA	ATATTA	580

Sbjct	481	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	540
Query	581	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT	640
Sbjct	541	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATT	600
Query	641	CTATATCAACATTTATTT	658
Sbjct	601	CTATATCAACATTTATTT	618

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383798.1 Length: 698
Range 1: 1 to 637

Score:1127 bits(610), Expect:0.0,
Identities:628/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561

Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383814.1 Length: 768
Range 1: 1 to 642

Score:1125 bits(609), Expect:0.0,
Identities:631/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480

Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480

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Query   502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||
Sbjct   481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC  540

Query   562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||
Sbjct   541  TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query   622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct   601  AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT  637

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>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW558150.1 Length: 657
Range 1: 1 to 639

Score:1120 bits(606), Expect:0.0,
Identities:628/639(98%), Gaps:0/639(0%), Strand: Plus/Plus

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Query   20   GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT  79
      |||
Sbjct    1   GGAGCAGGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT  60

Query   80   CAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA  139
      |||
Sbjct   61   CAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA  120

Query   140  TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  199
      |||
Sbjct   121  TTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATGGATTA  180

Query   200  GTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  259
      |||
Sbjct   181  GTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  240

Query   260  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  319
      |||
Sbjct   241  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  300

Query   320  GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA  379
      |||
Sbjct   301  GGTACAGGGGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCA  360

Query   380  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC  439
      |||
Sbjct   361  GTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC  420

Query   440  AATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  499
      |||

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Sbjct  421  AATTTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA 480
Query  500  TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA 559
        |||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTATTTGTAGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA 540
Query  560  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT 619
        |||||  |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT 600
Query  620  TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||||||  |||||||||||||||||||||||||||||||
Sbjct  601  TCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT 639

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>Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726445.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
Query  61    AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT 120
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT 120
Query  121   AATTGTAACAGCACATGCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGG 180
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AATTGTAACAGCACATGCATTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGG 180
Query  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
Query  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
Query  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360
Query  361   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
Query  421   TTCAATTTTAGGTGCAATCAATTTTATTACAAC TATTGTAAATATACGATCCATTGGAAT 480

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Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	ATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT		540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT		540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA	600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA	600
Query	601		TACA	604	
Sbjct	601		TACA	604	

>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726444.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAc	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTG	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTG

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA	604	
Sbjct	601	TACA	604	

>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120	
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420

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Query  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
          |||
Sbjct  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480

Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACATGATCGAAACTTTAA  600
          |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACATGATCGAAACTTTAA  600

Query  601  TACA  604
          |||
Sbjct  601  TACA  604

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>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
          |||

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Sbjct  361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC  420
Query  421  TTCAATTTTAGGTGCAATCAATTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
      |||
Sbjct  421  TTCAATTTTAGGTGCAATCAATTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
      |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
      |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601  TACA  604
      |||
Sbjct  601  TACA  604

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>Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726441.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
      |||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT  120
      |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
      |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
      |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
      |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
      |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360
Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC  420

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Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726440.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial

Sequence ID: MZ726438.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726437.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726434.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726433.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726432.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726430.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726449.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726429.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726428.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726426.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638
Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	 GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	 CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120

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Query  140  TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  180

Query  200  GTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  259
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   181  GTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  240

Query  260  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  319
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  300

Query  320  GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA  379
          || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GGNACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCA  360

Query  380  GTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  439
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  GTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  420

Query  440  AATTTCAATACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  499
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  AATTTCAATACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  480

Query  500  TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA  559
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct   481  TTATTTGTATGATCTGTTTTAATTACNGCAATTTTATTATTATTATCTTTACCAGTCTTA  540

Query  560  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  600

Query  620  T    620
          |
Sbjct   601  T    601

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Query #9: TKCJJ034-19|TKCJ012018C10|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26771 Length: 658

Sequences producing significant alignments:

							Scientific
Common		Max	Total Query	E	Per.	Acc.	
Description							Name
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession
Rhipicephalus sanguineus mitochondrial DNA, complete genome							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 14710
AF081829.1							
Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase...							

Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	629
KX757893.1							
Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1129	1129	94%	0.0	99.52	630
KX757903.1							
Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidas...							
Rhipicephalu... brown dog tick	34632	1112	1112	94%	0.0	99.03	630
KX757909.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1072	1072	100%	0.0	96.05	692
MF426015.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	675
MF426018.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	680
MF426016.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	693
MF426013.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	679
MF426009.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1066	1066	100%	0.0	95.90	686
MF426007.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	697
MF426019.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	705
MF426006.1							
Rhipicephalus sanguineus haplotype III cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	713
KU556745.1							
Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	710
MN593344.1							
Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	710
MN593343.1							
Rhipicephalus sanguineus isolate 11N cytochrome oxidase subuni...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	703
MN585197.1							
Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene,...							
Rhipicephalu... brown dog tick	34632	1061	1061	100%	0.0	95.74	793
AF132839.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	680
MF426017.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	690
MF426008.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							

Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	684
MF426001.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	689
MF425998.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	695
MF425997.1							
Rhipicephalus sanguineus haplotype IV cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1055	1113	100%	0.0	95.59	771
KU556746.1							
Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	658
MZ305546.1							
Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	658
MZ305545.1							
Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	676
MW152145.1							
Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	675
MW152144.1							
Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	676
MW152143.1							
Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1055	1055	100%	0.0	95.59	669
MW152142.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1050	1050	100%	0.0	95.44	684
MF426012.1							
Rhipicephalus sanguineus haplotype I cytochrome oxidase subuni...							
Rhipicephalu... brown dog tick	34632	1048	1048	98%	0.0	95.83	659
KU556743.1							
Rhipicephalus sanguineus haplotype II cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1046	1046	100%	0.0	95.30	787
KU556744.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1038	1038	97%	0.0	95.80	812
MF426020.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1037	1037	98%	0.0	95.52	824
MF426010.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1031	1031	97%	0.0	95.64	809
MF426011.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1022	1022	94%	0.0	96.30	649
MF426014.1							
Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1020	1020	97%	0.0	95.33	768
KX383818.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							

Rhipicephalu... brown dog tick	34632	1016	1016	94%	0.0	96.14	635
MF426000.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1016	1016	97%	0.0	95.31	654
MF425988.1							
Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1013	1013	96%	0.0	95.30	764
KX383811.1							
Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1011	1011	96%	0.0	95.29	763
KX383807.1							
Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subuni...							
Rhipicephalu... brown dog tick	34632	1009	1009	95%	0.0	95.56	656
KU568516.1							
Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1009	1009	96%	0.0	95.28	762
KX383809.1							
Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1009	1009	96%	0.0	95.28	714
KX383806.1							
Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1007	1007	96%	0.0	95.28	761
KX383805.1							
Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1005	1005	94%	0.0	95.82	644
MH630347.1							
Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1005	1005	94%	0.0	95.82	644
MH630346.1							
Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	1002	1002	95%	0.0	95.53	654
KX519712.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1000	1000	95%	0.0	95.38	639
MF426002.1							
Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
MG855658.1							
Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
MG855657.1							
Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
MG855656.1							
Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
KX757910.1							
Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
KX757904.1							
Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
KX757902.1							
Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase...							

Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
KX757896.1							
Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
KX757889.1							
Rhipicephalus sanguineus isolate Rovind cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
KX757887.1							
Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
KX757879.1							
Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	636
KX519711.1							
Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
MW135448.1							
Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630
KX757905.1							
Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630
KX757895.1							
Rhipicephalus sanguineus isolate Zadar cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630
KX757892.1							
Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630
KX757890.1							
Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630
KX757888.1							
Rhipicephalus sanguineus isolate Petnica cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630
KX757883.1							
Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	985	985	93%	0.0	95.46	629
KX519708.1							
Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	985	985	94%	0.0	95.32	630
MW135447.1							
Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	983	983	93%	0.0	95.45	626
KX519707.1							
Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	979	979	94%	0.0	95.16	630
KX757901.1							
Rhipicephalus sanguineus clone #4 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	974	974	94%	0.0	95.00	635
KX519709.1							
Rhipicephalus sanguineus isolate LIC4723B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	937	937	90%	0.0	94.97	723
KX714599.1							
Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I...							

Rhipicephalu... brown dog tick	34632	933	933	88%	0.0	95.69	580
KX519713.1							
Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	898	898	86%	0.0	95.09	595
KX519706.1							
Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	883	883	100%	0.0	90.90	790
KY678135.1							
Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c...							
Rhipicephalu... NA	34633	883	883	100%	0.0	90.88	673
MT800313.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	881	881	85%	0.0	95.01	574
MF425987.1							
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (CO1)...							
Rhipicephalu... brown dog tick	34632	876	876	98%	0.0	91.05	829
KU214592.1							
Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase...							
Rhipicephalu... NA	34633	872	872	99%	0.0	90.80	678
MT079206.1							
Rhipicephalus sanguineus isolate GY34 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	872	872	99%	0.0	90.80	678
MN862754.1							
Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome...							
Rhipicephalu... brown dog tick	34632	872	872	100%	0.0	90.58	1539
KM494916.1							
Rhipicephalus sanguineus isolate Tehran cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	872	872	100%	0.0	90.58	1539
KM494915.1							
Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c...							
Rhipicephalu... NA	34633	870	870	99%	0.0	90.56	673
MT800314.1							
Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	873
KY606303.1							
Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	873
KY606302.1							
Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	873
KY606301.1							
Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	873
KY606300.1							
Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit...							
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	873
KY606299.1							
Rhipicephalus camicasi isolate SC0126 mitochondrion, complete...							
Rhipicephalu... NA	669981	861	861	100%	0.0	90.29	14725
NC_061616.1							
Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase...							
Rhipicephalu... NA	34633	861	861	100%	0.0	90.27	658
MZ305547.1							
Rhipicephalus turanicus isolate Xinjiang-WQIA cytochrome oxida...							

Rhipicephalu... NA MF002581.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase...							
Rhipicephalu... NA MF002580.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate Xinjiang-BC cytochrome oxidase...							
Rhipicephalu... NA MF002579.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate Xinjiang-YC cytochrome oxidase...							
Rhipicephalu... NA MF002578.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate Xinjiang-PS cytochrome oxidase...							
Rhipicephalu... NA MF002577.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate SHZ cytochrome oxidase subunit...							
Rhipicephalu... NA KY069271.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate FK-1 cytochrome oxidase subuni...							
Rhipicephalu... NA KY606291.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate YN3 cytochrome oxidase subunit...							
Rhipicephalu... NA KY606290.1	34633	850	850	100%	0.0	89.97	889
Rhipicephalus turanicus isolate YN2 cytochrome oxidase subunit...							
Rhipicephalu... NA KY606289.1	34633	850	850	100%	0.0	89.97	889

Alignments:

>Rhipicephalus sanguineus mitochondrial DNA, complete genome
Sequence ID: AF081829.1 Length: 14710
Range 1: 1191 to 1848

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1191	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	1250
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	1251	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	1310
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	1311	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	1370
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	1371	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	1430
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCTCATTATTTTATTGATTAACCTCTTC	300

Sbjct	1431	 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	1490
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	1491	 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	1550
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	1551	 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	1610
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	1611	 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	1670
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	1671	 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	1730
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1731	 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	1790
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	1791	 CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	1848

>Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757893.1 Length: 629
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61	 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240

Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATGATCGAACTTTAACACATCATTGTTTATGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTAAGTATGATCGAACTTTAACACATCATTGTTTATGATCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757903.1 Length: 630
Range 1: 1 to 620

Score:1129 bits(611), Expect:0.0,
Identities:617/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240

Query	279	TATTTTTATTGATTA	ACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338	
Sbjct	241	TATTTTTATTGATTA	ATTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300	
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398		
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360		
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	ACTTCATCACA	ACTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	ACTTCATTACA	ACTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518		
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480		
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578		
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540		
Query	579	TATTA	ACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638	
Sbjct	541	TATTA	ACTGATCGAAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGAGATCCCA	600	
Query	639	TTTTATATCAACACTTATTT	658		
Sbjct	601	TTTTATATCAACACTTATTT	620		

>Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757909.1 Length: 630
Range 1: 1 to 620

Score:1112 bits(602), Expect:0.0,
Identities:614/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158	
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120	
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218	
Sbjct	121	TAGTTATACCAATAATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180	
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278	

Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTTCATTAATTGAATCTGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGCCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTGACTGATCGAAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGGGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S48 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426015.1 Length: 692
Range 1: 19 to 676

Score:1072 bits(580), Expect:0.0,
Identities:632/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240

Sbjct	199	AGGATTGTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCACG	258
Query	241	AATAAATAATATAAGATTTTACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	618
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	619	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	181	AGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	610
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	619
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	620	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S33 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426009.1 Length: 679
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180

Sbjct	131	 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	251	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	 ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	551	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S29 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426007.1 Length: 686
Range 1: 14 to 671

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	133

Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTT	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTT	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S827 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426019.1 Length: 697
Range 1: 19 to 676

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	138

Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	618
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	619	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S1060
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426006.1 Length: 705
Range 1: 28 to 685

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	28	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	87
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	88	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	147
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	148	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	207
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	208	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	267
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	268	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	327
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	328	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	387
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	388	ATCACATTATGGTCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	447
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	448	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATTAATTGGAAT	507
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	508	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	567
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	568	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	627
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	628	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	685

>Rhipicephalus sanguineus haplotype III cytochrome oxidase subunit I (COI) gene,
 partial cds; mitochondrial
 Sequence ID: KU556745.1 Length: 713
 Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
 Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	27	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	86
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	87	 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	146
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	147	 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	206
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	207	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	266
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	267	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	326
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	327	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	386
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	387	 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	446
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	447	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	506
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	507	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	566
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	567	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	626
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	627	 TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	684

>Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: MN593344.1 Length: 710
 Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
 Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	684	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	625

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	624	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	565
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	564	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	505
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	504	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	445
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	444	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	385
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	384	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	325
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	324	ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	265
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	264	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	205
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	204	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	145
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	144	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	85
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	84	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	27

>Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593343.1 Length: 710
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	684	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	625

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	624	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	565
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	564	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	505
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	504	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	445
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	444	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	385
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	384	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	325
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	324	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	265
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	264	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	205
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	204	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	145
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	144	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	85
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	84	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	27

>Rhipicephalus sanguineus isolate 11N cytochrome oxidase subunit I (COX1) gene,
 partial cds; mitochondrial
 Sequence ID: MN585197.1 Length: 703
 Range 1: 22 to 679

Score:1061 bits(574), Expect:0.0,
 Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60

Sbjct	679	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	620
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	619	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	560
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	559	AATCGTAACAGCACATGCATTTATTATAATTTTTTTATAGTTATACCAATCATAATCGG	500
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	499	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	440
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	439	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	380
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	379	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	320
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	319	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	260
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	259	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	200
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	199	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	140
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	139	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	80
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	79	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	22

>Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene, partial cds;
mitochondrial gene for mitochondrial product
Sequence ID: AF132839.1 Length: 793
Range 1: 42 to 699

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
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Sbjct	42	 AACAATATATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	101
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	102	 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	161
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	162	 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	221
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	222	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	281
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	282	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	341
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	342	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	401
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	402	 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	461
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	462	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	521
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	522	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	581
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	582	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	641
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	642	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	699

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S56 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426017.1 Length: 680
Range 1: 11 to 668

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S32 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426008.1 Length: 690
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1570
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426001.1 Length: 684
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,

Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 14 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 74 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 134 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 193

Query 181 AGGGTTCGGAATTTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| || |||||
Sbjct 194 AGGATTTGGAAATTTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 253

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
|||||
Sbjct 254 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 313

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 314 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 374 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 434 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 493

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 494 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 553

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
| |||||
Sbjct 554 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAAGTATCGAAACTTTAA 613

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
|||||
Sbjct 614 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 671
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1553
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425998.1 Length: 689
Range 1: 20 to 677

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 20 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 80 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 140 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 199

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200 AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||
Sbjct 260 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 319

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 320 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 380 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 440 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 500 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 559

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |||
Sbjct 560 CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA 619

Query 601 CACATCATTTTTTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 620 TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 677
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1551
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425997.1 Length: 695
Range 1: 22 to 679

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 22 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 81

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 82 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 141

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 142 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 201

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 202 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 261

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||||||| || || |||||||||| |||||||
Sbjct 262 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 321

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||| |||||| |||||||||||||| || |||||||||||||||
Sbjct 322 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 381

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||| || |||||||||||||| |||||||||| |||||||||||
Sbjct 382 ATCACATTATGGCCCTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 441

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||||||||||||| || |||||||||||||| |||||||||||
Sbjct 442 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 501

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||| |||||||||||||| |||||||||| |||||||||||
Sbjct 502 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 561

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
      | |||||||||||||||||||||||||||||| |||||||||||||||
Sbjct 562 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 621

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||||||||||||||||| |||||| |||||||||| |||||
Sbjct 622 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 679
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>Rhipicephalus sanguineus haplotype IV cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556746.1 Length: 771

Range 1: 90 to 747

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 90  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 149

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 150  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 209

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 210  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 269

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 270  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 329

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 330  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 389

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 390  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 449

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 450  ATCACATTATGGCCCTTCACTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 509

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 510  TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 569

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 570  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 629

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |
Sbjct 630  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 689

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 690  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 747
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Range 2: 30 to 64

Score:58.4 bits(31), Expect:0.001,
Identities:34/35(97%), Gaps:1/35(2%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCA-GGT 34
          |||||||||||||||||||||||||||||||||
Sbjct 30 AACAAATATATTTAATTTTTGGAGCATGATCATGGT 64
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>Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305546.1 Length: 658
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
          ||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
          ||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          ||| || ||||||||||||||| ||||| ||||| |||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
          ||||||||||||||||||||||||||||||| || ||| ||||||||||| |||||||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 300

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          ||||||||||| ||||||| ||||||||||||||||| || |||||||||||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
          ||||||||||| || ||||||||||||||||||||||||||||||| |||||||
Sbjct 361 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          ||||||||||||||||||||||| || ||||||||||| |||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          ||||||||||| ||||||||||||||||||||||||||||||| |||||
Sbjct 481 AACAAAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
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Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTGGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTGGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAC TGATCGAAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAAC TGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	658

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>Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152145.1 Length: 676
Range 1: 1 to 658
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Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 	420
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAAC TATTGTAAATATACGATCAATTGGAAT 	480
Sbjct	421	TTCAATTTTAGGTGCAATTAAC TTATTACAAC TATTGTAAACATACGATCAATTGGAAT 	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 	540

Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTAAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAACTTTAA	600
Query	601	CACATCATTTTTTGTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTGTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152144.1 Length: 675
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Sbjct	1	AACAATATATTTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGA AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 	240
Sbjct	181	AGGATTTGGAA AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA AACTCTTC 	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTA AACTTCATCACA AACTATTGTAAATATACGATCAATTGGAAT 	480
Sbjct	421	TTCAATTTTAGGTGCAATTA AACTTTATTACA AACTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540

Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTAAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTGGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTGGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	658

>Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MW152142.1 Length: 669
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480

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Query   481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT  540
        |||
Sbjct   481  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT  540

Query   541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA  600
        | |||
Sbjct   541  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA  600

Query   601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        |||
Sbjct   601  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT  658

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S358 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426012.1 Length: 684
Range 1: 14 to 671

Score:1050 bits(568), Expect:0.0,
Identities:628/658(95%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        |||
Sbjct   14  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  73

Query   61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  120
        |||
Sbjct   74  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  133

Query   121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG  180
        |||
Sbjct   134  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG  193

Query   181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG  240
        ||| || |||
Sbjct   194  AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG  253

Query   241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC  300
        |||
Sbjct   254  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC  313

Query   301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT  360
        |||
Sbjct   314  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT  373

Query   361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC  420
        |||
Sbjct   374  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC  433

Query   421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT  480
        |||

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Sbjct	434	TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTATA	AAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540			
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553			
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAAACTTTAA	600		
Sbjct	554	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACTGATCGAAACTTTAA	613			
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658			
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671			

>Rhipicephalus sanguineus haplotype I cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: KU556743.1 Length: 659

Range 1: 12 to 659

Score:1048 bits(567), Expect:0.0,
Identities:621/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60			
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71			
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120			
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	131			
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180			
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	191			
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240			
Sbjct	192	AGGATTTGGAAATTGATTAATCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251			
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA	ACTCTTC	300		
Sbjct	252	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA	ACTCTTC	311		
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360			
Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371			
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420			
Sbjct	372	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	431			
Query	421	TTCAATTTTAGGTGCAATTAAC	TTTCATCACA	ACTATTGTAA	TATACGATCAATTGGAAT	480

Sbjct	432		TTCAATTTTAGGTGCAATTAAC	TTTATTACA	ACTATTGTAA	CATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540				
Sbjct	492		AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551			
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAAACTTTAA	600			
Sbjct	552		TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAAACTTTAA	611		
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCA	648				
Sbjct	612		TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCA	659			

>Rhipicephalus sanguineus haplotype II cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KU556744.1 Length: 787
Range 1: 29 to 688

Score:1046 bits(566), Expect:0.0,
Identities:629/660(95%), Gaps:2/660(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60		
Sbjct	29		AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	88	
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120		
Sbjct	89		AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	148	
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180		
Sbjct	149		AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	208	
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240		
Sbjct	209		268		
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA	ACTCTTC	300	
Sbjct	269		AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTTATTAATTA	ACTCTTC	328
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360		
Sbjct	329		ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	388	
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420		
Sbjct	389		ATCACATTATGGTCCTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	448	

Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	449	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	508
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	509	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	568
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	569	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	628
Query	601	CACATCATTTTTTTGATCCTTCAGGAGG-AGGAGATCCC-ATTTTATATCAACACTTATTT	658
Sbjct	629	TACATCATTTTTTTGATCCTTCAGGGGGGAGGAGATCCAAATTTTATATCAACTTTTATTT	688

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S943 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426020.1 Length: 812
Range 1: 2 to 644

Score:1038 bits(562), Expect:0.0,
Identities:616/643(96%), Gaps:0/643(0%), Strand: Plus/Plus

Query	16	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	75
Sbjct	2	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	61
Query	76	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	135
Sbjct	62	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	121
Query	136	TGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTG	195
Sbjct	122	TGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	181
Query	196	ATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	255
Sbjct	182	ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	241
Query	256	ATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGG	315
Sbjct	242	ATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGG	301
Query	316	AGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCC	375
Sbjct	302	AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTCC	361
Query	376	ATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGC	435
Sbjct	362	TTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	421

Query	436	AATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAAT	495
Sbjct	422	AATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	481
Query	496	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGT	555
Sbjct	482	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT	541
Query	556	ATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGA	615
Sbjct	542	ATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGA	601
Query	616	TCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	602	TCCTTCAGGGGAGGAGATCCAATTTTATATCAACATTTATTT	644

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S337 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426010.1 Length: 824
Range 1: 1 to 648

Score:1037 bits(561), Expect:0.0,
Identities:619/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	120
Query	131	GCACATGCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGA	190
Sbjct	121	GCACATGCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTAC CCCCCTCATTATTTTTATTGATTA ACTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTTTAC CTCTTCACTATTTTTATTAATTA ACTCTTCATTAATTGAA	300
Query	311	TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCTCTATCTTCAAATTTATCACATTAT	360
Query	371	GGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA	430

Sbjct	361	GGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA	550
Sbjct	481	CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTA	540
Query	551	CCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAAACTTTAACACATCATTT	610
Sbjct	541	CCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAATACATCATTT	600
Query	611	TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TTTGATCCTTCAGGGGAGGAGATCCAATTTTATATCAACATTTATTT	648

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S344 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426011.1 Length: 809
Range 1: 3 to 644

Score:1031 bits(558), Expect:0.0,
Identities:614/642(96%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	3	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	62
Query	77	GGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	63	GGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAC	122
Query	137	GCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	123	GCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	182
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	183	TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	242
Query	257	TTTTGACTTTTAC CCCCCTCATTATTTTTATTGATTA ACTCTTCATTAATTGAATCCGGA	316
Sbjct	243	TTTTGACTTTTAC CTCTTCACTATTTTTATTAATTA ACTCTTCATTAATTGAATCTGGA	302
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	303	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	362
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436

Sbjct	363		TCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	422
Query	437		ATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	423		ATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	482
Query	497		CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	483		CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	542
Query	557		TTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGAT	616
Sbjct	543		TTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGAT	602
Query	617		CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658	
Sbjct	603		CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S475 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426014.1 Length: 649
Range 1: 28 to 649

Score:1022 bits(553), Expect:0.0,
Identities:599/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	28	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	87
Query	61	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	88	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	147
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	148	AATCGTAACAGCACATGCATTTATTATAATTTT TTTATAGTTATACCAATCATAATCGG	207
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	208	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	267
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCTCATTATTTTTATTGATTA ACTCTTC	300
Sbjct	268	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTA ACTCTTC	327
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCTCTATCTTCAAATTT	360
Sbjct	328	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	387

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	388	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	447
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	448	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	507
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	508	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	567
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	568	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	627
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	628	TACATCATTTTTTTGATCCTTCA	649

>Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383818.1 Length: 768

>Rhipicephalus sanguineus isolate LIC5554A cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383819.1 Length: 768

Range 1: 1 to 642

Score:1020 bits(552), Expect:0.0,

Identities:612/642(95%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300

Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATTAAC TTTATTACA ACTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	481	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557	TTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGAT	616
Sbjct	541	TTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGAT	600
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTTATATCAACACTTATTT 658	
Sbjct	601	CCTTCAGGGGGAGGAGATCCAATTTTTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1568
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426000.1 Length: 635
Range 1: 14 to 635

Score:1016 bits(550), Expect:0.0,
Identities:598/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTAT ATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCAT ATTTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTAC CCCCCTCATTATTTTTATTGATTAAC TCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTAC CTTCTTCACTATTTTTATTAATTAAC TCTTC	313

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	613
Query	601	CACATCATTTTTTGATCCTTCA	622
Sbjct	614	TACATCATTTTTTGATCCTTCA	635

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SF3003
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425988.1 Length: 654
Range 1: 1 to 640

Score:1016 bits(550), Expect:0.0,
Identities:610/640(95%), Gaps:0/640(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGA	316

Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA 	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA 	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA 	496
Sbjct	421	ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA 	556
Sbjct	481	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557	TTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTGAT 	616
Sbjct	541	TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGAT	600
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTAT	656
Sbjct	601	CCTTCAGGGGGAGGACATCCAATTTTATATCACCATTTAT	640

Score:1013 bits(548), Expect:0.0,
Identities:608/638(95%), Gaps:0/638(0%), Strand: Plus/Plus

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Sbjct  181  TCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT  240
Query  261  GACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTG  320
          ||||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  241  GACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTG  300
Query  321  GAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAG  380
          | ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  301  GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG  360
Query  381  TAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA  440
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  361  TAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA  420
Query  441  ACTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCAT  500
          |||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  421  ACTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCAT  480
Query  501  TATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAG  560
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  481  TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG  540
Query  561  CAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTT  620
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  541  CAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTT  600
Query  621  CAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
          |||| ||||| ||||| ||||| |||||
Sbjct  601  CAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  638

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>Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383807.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383808.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736F cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383810.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5535C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383813.1 Length: 763

Range 1: 1 to 637

Score:1011 bits(547), Expect:0.0,

Identities:607/637(95%), Gaps:0/637(0%), Strand: Plus/Plus

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Query  22  AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA  81
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  1    AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA  60

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Query	82	ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT	141
Sbjct	61	ACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT	120
Query	142	TATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	CCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	ACTTTTACCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGG	321
Sbjct	241	ACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGG	300
Query	322	AACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGT	381
Sbjct	301	TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA	441
Sbjct	361	AGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA	420
Query	442	CTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	CTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATT	480
Query	502	ATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGC	561
Sbjct	481	ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC	540
Query	562	AGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTC	621
Sbjct	541	AGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTC	600
Query	622	AGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	AGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	637

>Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial

Sequence ID: KU568516.1 Length: 656

Range 1: 27 to 656

Score:1009 bits(546), Expect:0.0,

Identities:602/630(96%), Gaps:0/630(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	27	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	86

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	87	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	146
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	147	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	206
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	207	AGGATTTGGAAATTGATTAATCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	266
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	267	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	326
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	327	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	386
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	387	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	446
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	447	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	506
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	507	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	566
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	567	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	626
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGG	630
Sbjct	627	TACATCATTTTTTTGACCCTTCAGGAGGAGG	656

>Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383809.1 Length: 762
 Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
 Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82

Sbjct	1	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142
Sbjct	61	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143	ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT	202
Sbjct	121	ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA	322
Sbjct	241	CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA	382
Sbjct	301	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	GATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA	502
Sbjct	421	TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA	562
Sbjct	481	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540
Query	563	GGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCA	622
Sbjct	541	GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT	636

>Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383806.1 Length: 714
Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
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Sbjct	1	 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83	CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142
Sbjct	61	 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143	ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT	202
Sbjct	121	 ATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	 CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA	322
Sbjct	241	 CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA	382
Sbjct	301	 ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	 GATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA	502
Sbjct	421	 TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA	562
Sbjct	481	 TTTGTGTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540
Query	563	GGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCA	622
Sbjct	541	 GGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	 GGGGGAGGAGATCCAATTTTATATCAACATTATTT	636

>Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383805.1 Length: 761
 Range 1: 1 to 635

Score:1007 bits(545), Expect:0.0,
 Identities:605/635(95%), Gaps:0/635(0%), Strand: Plus/Plus

Query	24	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	83
Sbjct	1	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAAC	60
Query	84	CTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	143
Sbjct	61	CTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	120
Query	144	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTC	203
Sbjct	121	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	180
Query	204	CTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	263
Sbjct	181	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	240
Query	264	TTTTACCCCTCATTATTTTATTGATTAACCTTTCATTAATTGAATCCGGAGCTGGAA	323
Sbjct	241	TTTTACCTCCTCACTATTTTATTAATTAACCTTTCATTAATTGAATCTGGAGCTGGTA	300
Query	324	CAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAG	383
Sbjct	301	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	360
Query	384	ATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	443
Sbjct	361	ATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	444	TCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTAT	503
Sbjct	421	TTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTAT	480
Query	504	TTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAG	563
Sbjct	481	TTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	540
Query	564	GTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTGATCCTTCAG	623
Sbjct	541	GTGCCATTACAATATTGTTAACCTGATCGAACTTTAATACATCATTTTTTGATCCTTCAG	600
Query	624	GAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	GGGGAGGAGATCCAATTTTATATCAACATTTATTT	635

>Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630347.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTGGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	619
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	620	TACATCATTTTTTTGATCCTTCA	641

>Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630346.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,

Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 20 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 80 AATTGGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 140 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 199

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| ||
Sbjct 200 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
|||||
Sbjct 260 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 319

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 320 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 380 ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 440 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 500 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 559

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
| |||||
Sbjct 560 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAAGTATCGAAACTTTAA 619

Query 601 CACATCATTTTTTTGATCCTTCA 622
|||||
Sbjct 620 TACATCATTTTTTTGATCCTTCA 641
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>Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519712.1 Length: 654
Range 1: 3 to 628

Score:1002 bits(542), Expect:0.0,
Identities:598/626(96%), Gaps:0/626(0%), Strand: Plus/Plus

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Query 33 GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT 92
|||||
Sbjct 3 GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT 62

Query 93 TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT 152
|||||
Sbjct 63 TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT 122

Query 153 TCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATAT 212
| |||||
Sbjct 123 TTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT 182

Query 213 TAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCC 272
| |||||
Sbjct 183 TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC 242

Query 273 CCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAA 332
| ||| |||||
Sbjct 243 CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA 302

Query 333 CAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTA 392
||||| || |||||
Sbjct 303 CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA 362

Query 393 TTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAA 452
||||| |||||
Sbjct 363 TTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAA 422

Query 453 CTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGAT 512
||||| |||||
Sbjct 423 CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT 482

Query 513 CTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTA 572
||||| |||||
Sbjct 483 CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA 542

Query 573 CAATATTATTAACGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAG 632
||||| |||||
Sbjct 543 CAATATTGTTAACGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG 602

Query 633 ATCCCATTTTATATCAACACTTATTT 658
|||| |||||
Sbjct 603 ATCCAATTTTATATCAACATTTATTT 628
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1575
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426002.1 Length: 639
Range 1: 1 to 628

Score:1000 bits(541), Expect:0.0,
Identities:599/628(95%), Gaps:0/628(0%), Strand: Plus/Plus

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Query 31 AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC 90
|||||
Sbjct 1 AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC 60

Query 91 TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT 150
|||||
Sbjct 61 TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT 120

Query 151 TTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTAT 210
||| |||||
Sbjct 121 TTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT 180

Query 211 ATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC 270
||| |||||
Sbjct 181 ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC 240

Query 271 CCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATG 330
|| ||| |||||
Sbjct 241 TCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATG 300

Query 331 AACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGC 390
|||||| || |||||
Sbjct 301 AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC 360

Query 391 TATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCAC 450
||| |||||
Sbjct 361 TATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTAC 420

Query 451 AACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTG 510
|||||| |||||
Sbjct 421 AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG 480

Query 511 ATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCAT 570
|||||| |||||
Sbjct 481 ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT 540

Query 571 TACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGG 630
|||||| |||||
Sbjct 541 TACAATATTGTTAAGTATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGG 600

Query 631 AGATCCCATTTTATATCAACACTTATTT 658
|||||
Sbjct 601 AGATCCAATTTTATATCAACATTTATTT 628
```

>Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855658.1 Length: 630

Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial

Sequence ID: MG855657.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
        |||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
        |||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
        |||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
        |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
        |||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
        |||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
        |||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
        |||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
        |||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
        |||
Sbjct   541  TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA   600

Query   639  TTTTATATCAACACTTATTT   658
        |||
Sbjct   601  TTTTATATCAACATTTATTT   620
```

>Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase subunit I (cox1)

gene, partial cds; mitochondrial
Sequence ID: MG855656.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
|||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
|||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
|||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
|||||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
|||||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
| ||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
|||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
|||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
|||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
| ||
Sbjct 541 TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
|||||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757910.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757904.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
          |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
          |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
          |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
          |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
          |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
          |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
          |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
          |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
          |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
          |||
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
          |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757902.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757896.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
      |||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      |||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      |||
Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      |||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      |||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      |||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      |||
Sbjct 541 TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
      |||
Sbjct 601 TTTTATATCAACATTTATTT 620
```

>Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757889.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

```
Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
          |||||||||||||||||||||||| || |||||||||||| |||| |||| ||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
          |||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
          ||||||||| ||||||||||||||||||||| ||||||| |||||||||||||||
Sbjct 241 TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
          | || ||||||||||||||||||||||||| || |||||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTG 458
          ||||||| ||||||||||||||||||||||||| || ||||||||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATTACAAGTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
          |||| ||||||||||||||||||||||||| |||||||||||||||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
          |||||||||||||||| |||| |||||||||||||||||||||||||||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
          | ||||||||||||||||| ||||||||||||||||||||| ||||||||| |
Sbjct 541 TGTTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
          |||||||||||| |||||
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Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Rovind cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757887.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
      ||||||||||||||||||||| || |||||||||||| |||| |||| ||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
      ||||||||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
      ||||||||| ||||||||||||||||||||| ||||||| |||||||||||||||
Sbjct 241 TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
      | || |||||||||||||||||||||||||||| || |||||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
      ||||||| ||||||||||||||||||||||||||||||||||||| || |||||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
      ||||| |||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
      |||||||||||||||| ||||| |||||||||||||||||||||||||||||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
      | ||||||||||||||||| ||||||||||||||||||||| ||||||||| |
Sbjct 541 TGTTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
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Sbjct 601 ||||| |||||
TTTTATATCAACATTTATT 620

>Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757879.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	 TGTTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600


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Query   639  TTTTATATCAACACTTATTT  658
        |||||
Sbjct   601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519711.1 Length: 636
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  98
        |||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
        |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
        |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
        |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTGATTAACCTCTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
        |||||
Sbjct   241  TATTTTTATTAATTAACCTCTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
        |||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG  458
        |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
        |||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        |||||
Sbjct   541  TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600

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Query   639   TTTTATATCAACACTTATTT   658
          |||||
Sbjct   601   TTTTATATCAACATTTATTT   620

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>Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135448.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
          |||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
          |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
          |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
          |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
          |||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
          |||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
          |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
          |||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
          |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAACGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
          |||||

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Sbjct 541 TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
 |||||

Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757905.1 Length: 630
 Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
 Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
 |||||

Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
 |||||

Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
 |||||

Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
 |||||

Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
 |||||

Sbjct 241 TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
 |||||

Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
 |||||

Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
 |||||

Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
 |||||

Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAACGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638

[illegible]

>Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757895.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTCATCACAAC TATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTATTACAAC TATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540

Query	579	TATTA	ACTGATCGAA	ACTTTA	ACATCAT	TTTTTT	GATCCTTC	AGGAGG	AGGAGAT	CCCA	638
Sbjct	541	TGTTA	ACTGATCGAA	ACTTTA	ATACAT	TTTTTT	GATCCTTC	AGGGGG	AGGAGAT	CCAA	600
Query	639	TTTTAT	ATCAAC	ACTTAT	TTT	658					
Sbjct	601	TTTTAT	ATCAAC	ATTTAT	TTT	620					

>Rhipicephalus sanguineus isolate Zadar cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757892.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAAC	TTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158	
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120	
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218	
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180	
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278	
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240	
Query	279	TATTTTTATTGATTA	ACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398	
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360	
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	ACTTCATCACAACTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	ACTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518	
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480	
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578	
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540	

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Query    579  TATTAAGTATCGAAACTTTAACACATCATTTTTTATCCTTCAGGAGGAGGAGATCCCA  638
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    541  TGTTAAGTATCGAAACTTTAATACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAA  600

Query    639  TTTTATATCAACACTTATTT  658
      |||||||||||||||
Sbjct    601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757890.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 	578

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757888.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCACAACTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus


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Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        |||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        | |||
Sbjct   541  TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600

Query   639  TTTTATATCAACACTTATTT  658
        |||
Sbjct   601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519708.1 Length: 629
Range 1: 4 to 620

Score:985 bits(533), Expect:0.0,
Identities:589/617(95%), Gaps:0/617(0%), Strand: Plus/Plus

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Query   42   GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA  101
        |||
Sbjct    4   GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA  63

Query   102  ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAG  161
        |||
Sbjct   64   ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAG  123

Query   162  TTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCC  221
        |||
Sbjct   124  TTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCC  183

Query   222  CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCTCATTAT  281
        |||
Sbjct   184  CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT  243

Query   282  TTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATC  341
        |||
Sbjct   244  TTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC  303

Query   342  CCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTC  401
        | |||
Sbjct   304  CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTC  363

Query   402  TTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAATATTGTAA  461
        |||
Sbjct   364  TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAATATTGTAA  423

Query   462  ATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAA  521
        | |||
Sbjct   424  ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA  483

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Query	522	TTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTAT	581
Sbjct	484	TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	543
Query	582	TAACTGATCGAAACTTTAACACATCATTTTTTGTATCCTTCAGGAGGAGGAGATCCCATT	641
Sbjct	544	TAACTGATCGAAACTTTAATACATCATTTTTTGTATCCTTCAGGGGGAGGAGATCCAATT	603
Query	642	TATATCAACACTTATTT	658
Sbjct	604	TATATCAACATTATTT	620

>Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135447.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518

Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGACCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519707.1 Length: 626
Range 1: 1 to 616

Score:983 bits(532), Expect:0.0,
Identities:588/616(95%), Gaps:0/616(0%), Strand: Plus/Plus

Query	43	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAA	102
Sbjct	1	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAA	60
Query	103	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGT	162
Sbjct	61	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT	120
Query	163	TATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCC	222
Sbjct	121	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	180
Query	223	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATT	282
Sbjct	181	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	240
Query	283	TTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC	342
Sbjct	241	TTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCC	300
Query	343	CCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT	402
Sbjct	301	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTTCTCT	360
Query	403	TCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTGTAAG	462
Sbjct	361	TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTGTAAG	420
Query	463	TATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT	522

Sbjct	421		CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523		TACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT	582
Sbjct	481		TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583		AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	642
Sbjct	541		AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	600
Query	643		ATATCAACACTTATTT 658	
Sbjct	601		ATATCAACATTATTT 616	

>Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757901.1 Length: 630
Range 1: 1 to 620

Score:979 bits(530), Expect:0.0,
Identities:590/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1		TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61		GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159		TAGTTATACCAATCATAATCGGAGGGTTCGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121		TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181		CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279		TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241		TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339		ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301		ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTT	360
Query	399		CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420

Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:974 bits(527), Expect:0.0,
Identities:589/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	422	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	481
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	482	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	541
Query	579	TATTAAC TGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	542	TGTTAAC TGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	601
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	602	TTTTATATCAACATTTATTT	621

>Rhipicephalus sanguineus isolate LIC4723B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX714599.1 Length: 723
>Rhipicephalus sanguineus isolate LIC4750B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX714600.1 Length: 723
Range 1: 1 to 597

Score:937 bits(507), Expect:0.0,
Identities:567/597(95%), Gaps:0/597(0%), Strand: Plus/Plus

Query	62	ATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTA	121
Sbjct	1	ATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTA	60
Query	122	ATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGA	181
Sbjct	61	ATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATTGGA	120
Query	182	GGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGA	241
Sbjct	121	GGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGA	180
Query	242	ATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCA	301
Sbjct	181	ATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCA	240
Query	302	TTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTA	361
Sbjct	241	TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA	300
Query	362	TCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCT	421
Sbjct	301	TCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCT	360

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Query  422  TCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATA  481
        |||
Sbjct  361  TCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATA  420

Query  482  ACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTT  541
        |||
Sbjct  421  ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT  480

Query  542  CTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAAC  601
        |||
Sbjct  481  TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAAT  540

Query  602  ACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        |||
Sbjct  541  ACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT  597

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>Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519713.1 Length: 580
Range 1: 1 to 580

Score:933 bits(505), Expect:0.0,
Identities:555/580(96%), Gaps:0/580(0%), Strand: Plus/Plus

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Query  43   ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA  102
        |||
Sbjct  1     ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA  60

Query  103  TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGT  162
        |||
Sbjct  61   TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT  120

Query  163  TATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCC  222
        |||
Sbjct  121  TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC  180

Query  223  AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATT  282
        |||
Sbjct  181  AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT  240

Query  283  TTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC  342
        |||
Sbjct  241  TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC  300

Query  343  CCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT  402
        |||
Sbjct  301  TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTTCTCT  360

Query  403  TCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAA  462
        |||

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Sbjct  361  TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAA  420
Query  463  TATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT  522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT  480
Query  523  TACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT  582
          |||||||||||||| |||| |||||||||||||||||||||||||||||| ||
Sbjct  481  TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT  540
Query  583  AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCA  622
          |||||||||||||| ||||||||||||||||||
Sbjct  541  AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA  580

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>Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519706.1 Length: 595
Range 1: 1 to 570

Score:898 bits(486), Expect:0.0,
Identities:542/570(95%), Gaps:0/570(0%), Strand: Plus/Plus

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Query  89  ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA  148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1  ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA  60
Query  149  ATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATT  208
          ||||| |||||||||||||||||||||||||| || |||||||||||| |||||
Sbjct  61  ATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATC  120
Query  209  ATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA  268
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA  180
Query  269  CCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGA  328
          || || || || || || || || || || || || || || || || || || || || ||
Sbjct  181  CCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGA  240
Query  329  TGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTA  388
          |||||||||| || |||||||||||||||||||||| || ||||||||||||
Sbjct  241  TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA  300
Query  389  GCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATC  448
          |||||||||||||| |||||||||||||||||||||||||||||||||| ||
Sbjct  301  GCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATT  360
Query  449  ACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTT  508
          |||||||||||||| |||||||||||||||||||||||||| ||||||||||||
Sbjct  361  ACAACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT  420
Query  509  TGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCC  568

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Sbjct	421		TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	480
Query	569		ATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGA	628
Sbjct	481		ATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGA	540
Query	629		GGAGATCCCATTTTATATCAACACTTATTT 658	
Sbjct	541		GGAGATCCAATTTTATATCAACACTTATTT 570	

>Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase subunit 1 gene,
partial cds; mitochondrial
Sequence ID: KY678135.1 Length: 790
Range 1: 18 to 675

Score:883 bits(478), Expect:0.0,
Identities:599/659(91%), Gaps:2/659(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	18	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	77
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	78	AATTCGTATAGAATTAGGCCAACCTGGAACCCTAATTGGTAATGATCAAATTTATAATGT	137
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	138	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	197
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	198	TGGATTTGGAAACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTCCCACG	257
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGACTTCTCCTCCCTCATTATTTATATTAATTAATTCTTC	317
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC-CCCTCTATCTTCAAATT	359
Sbjct	318	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCT-TATCCTCAAATT	376
Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTT	419
Sbjct	377	TATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTT	436
Query	420	CTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAA	479
Sbjct	437	CTTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAA	496

Query	480	TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	497	TAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAC	556
Query	540	TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTA	599
Sbjct	557	TATTATCTTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCGATCGAAATTTTA	616
Query	600	ACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	617	ACACTTCATTTTTTGACCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	675

>Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800313.1 Length: 673
Range 1: 8 to 665

Score:883 bits(478), Expect:0.0,
Identities:598/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCTATTATAATTGG	187
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTCATTATTTCTATTAATTAACCTCTTC	307
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCAGGAGCAGGAACAGGATGAAGTGTATCCCCCTTTATCCTCAAATTT	367
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAAT	487

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Query  481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT  540
        ||||||||||||||||||||||||||||||||||||||||||||| || || ||||| ||
Sbjct  488  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT  547

Query  541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA  600
        ||||||||||||| ||||||||| ||||||||||||||||||||||||| || ||
Sbjct  548  CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAAGTATCGAAATTTCAA  607

Query  601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        || ||||||||||||||||| ||||| ||||| ||||||| ||||||||| ||
Sbjct  608  TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATTT  665

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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SC3005
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425987.1 Length: 574
Range 1: 1 to 561

Score:881 bits(477), Expect:0.0,
Identities:533/561(95%), Gaps:0/561(0%), Strand: Plus/Plus

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Query  98  GGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTT  157
        ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Sbjct  1  GGAAATGATCAGATTTATAATGTAATCGTAACAGCACACGCATTTATTATAATTTTTTTT  60

Query  158  ATAGTTATACCAATCATAATCGGAGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGT  217
        ||||||||||||||||||||||||| || ||||||||||||| ||||||||||||| ||
Sbjct  61  ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATTATATTAGGT  120

Query  218  GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCA  277
        ||||||||||||||||||||||||||||||||||||||||||||| || ||||
Sbjct  121  GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA  180

Query  278  TTATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTT  337
        ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||
Sbjct  181  CTATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT  240

Query  338  TATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTT  397
        || || ||||||||||||||||||||||||| || ||||||||||||||||| |||
Sbjct  241  TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTT  300

Query  398  TCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATT  457
        ||||||| ||||||||||||||||||||||||||||||||||||||||| || |||||||||
Sbjct  301  TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATT  360

Query  458  GTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTT  517
        ||||| ||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  361  GTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTT  420

Query  518  TTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATA  577
        ||||||||||||||||| ||||| ||||||||||||||||||||||||||||| ||

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Sbjct	421	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	480
Query	578	TTATTAAGTATGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCC	637
Sbjct	481	TTGTTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCA	540
Query	638	ATTTTATATCAACACTTATTT	658
Sbjct	541	ATTTTATATCAACACTTATTT	561

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (CO1) gene, partial cds;
mitochondrial
Sequence ID: KU214592.1 Length: 829
Range 1: 1 to 648

Score:876 bits(474), Expect:0.0,
Identities:590/648(91%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGCCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGTAATTGTTACA	120
Query	131	GCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGA	190
Sbjct	121	GCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGTGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTCTTCCTCCCTCATTATTTATATTAATTAATTCTTCATTAATTGAG	300
Query	311	TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCAGGAGCAGGTACAGGATGGACAGTTTATCCTCCCCTATCCTCAAATTTATCACATTAT	360
Query	371	GGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA	550

Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACTATTATCTTTA	540
Query	551	CCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTT	610
Sbjct	541	CCTGTTTTAGCAGGTGCCATTACAATATTATTAACCGATCGAAATTTAACACTTCATTT	600
Query	611	TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	648

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	487	AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCCTATTTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAAGTATCGAAATTTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	ATTTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTATTT	652

>Rhipicephalus sanguineus isolate GY34 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MN862754.1 Length: 678
Range 1: 1 to 652

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCG	60
Query	67	TATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTT	186
Sbjct	121	AACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	CGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181	TGGAAACTGGTTAGTTCCTATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAAGTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACA	366
Sbjct	301	TGAATCTGGGGCAGGGACAGGTGAAGTGTATCCTCCTTATCCTCAAATTTATCCCA	360
Query	367	TTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAAGTTCATCACAAGTATTGTAAATATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTCAATACAAGTATTGTAAACATACGATCTATTGGAATAACAAT	480

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Query 487 AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC 546
          |||
Sbjct 481 AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCTTCTATC 540
          |||

Query 547 TTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATC 606
          |||
Sbjct 541 TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAAGTATCGAAATTTTAACACTTC 600
          |||

Query 607 ATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||
Sbjct 601 ATTTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTATTT 652
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>Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome oxidase subunit 1
gene, complete cds; mitochondrial
Sequence ID: KM494916.1 Length: 1539
Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||
Sbjct 45 AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT 104
          |||

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||
Sbjct 105 AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT 164
          |||

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
          |||
Sbjct 165 AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG 224
          |||

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          |||
Sbjct 225 TGGATTTGGAAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 284
          |||

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
          |||
Sbjct 285 AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC 344
          |||

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||
Sbjct 345 ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCTCAAATTT 404
          |||

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||
Sbjct 405 ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 464
          |||

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||

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Sbjct  465  TTCAATTTTAGGTGCAATTAATTTTATTACAACACTATTGTGAATATACGATCTATTGGAAT  524
Query  481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT  540
        ||||||||||||||||||||||||||| ||||||||||||||| || ||||||| ||||
Sbjct  525  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT  584
Query  541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA  600
        ||||||||||||||| ||||||||||| ||||||| ||||||| ||||||| ||||
Sbjct  585  ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA  644
Query  601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT  658
        ||| ||||||||||| ||||||||||| |||| ||||||||||| |||||||
Sbjct  645  CACTTCATTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT  702

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>Rhipicephalus sanguineus isolate Tehran cytochrome oxidase subunit 1 gene,
complete cds; mitochondrial
Sequence ID: KM494915.1 Length: 1539
Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT  60
        ||||||||||||||||||||||||||| || ||||||||| | || ||||||||| |
Sbjct  45    AACAAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT  104
Query  61    AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT  120
        ||||||||||||||||| ||||||||||| ||||||| ||||||| |||||||||
Sbjct  105   AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT  164
Query  121   AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG  180
        ||| || ||||| ||||||||||||||||| ||||||| ||||||| ||||| ||
Sbjct  165   AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG  224
Query  181   AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG  240
        || || ||||| ||||||| ||||||||| |||| || ||||||||||||| |||||
Sbjct  225   TGGATTTGGAAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  284
Query  241   AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC  300
        ||||||||||||||||||||||||| || ||||||||||| |||| ||||| |||||
Sbjct  285   AATAAATAATATAAGATTTTGACTTCTCCTCCCTCATTATTTATATTAATTAATTCTTC  344
Query  301   ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT  360
        ||||||||| || ||||| || ||||||||||||||||||| || ||||| |||||||
Sbjct  345   ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCCTCAAATTT  404
Query  361   ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC  420
        ||||||||||||| ||||||||||||||||||||||||||||| |||||||||||||
Sbjct  405   ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC  464
Query  421   TTCAATTTTAGGTGCAATTAACCTTCATCACAACACTATTGTAAATATACGATCAATTGGAAT  480

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Sbjct	465	 TTCAATTTTAGGTGCAATTAATTTTATTACAACATTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	525	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	585	 ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	645	 CACTTCATTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800314.1 Length: 673
Range 1: 8 to 664

Score:870 bits(471), Expect:0.0,
Identities:595/657(91%), Gaps:0/657(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	 AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	 AATTCGCATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128	 AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCCATTATAATTGG	187
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	 TGGATTTGGAAATTGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	248	 TATAAATAACATAAGATTTTGATTACTTCCTCCTCATTATTTCTATTAATTAACCTCTC	307
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	308	 ATTAATTGAATCGGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	 ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	427

Query	421	TTCAATTTTAGGTGCAATTA	AACTTCATCACA	ACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTA	AATTTTATTACA	ACTATTGTAAACATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540		
Sbjct	488	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547		
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAAACTTTAA	600	
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTA	ACTGATCGAAATTTCAA	607	
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATT	657		
Sbjct	608	TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATT	664		

>Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KY606303.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60	
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125	
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120	
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	185	
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180	
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245	
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240	
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305	
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA	ACTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365	
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360	
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCTCCTTTATCTTCAAATTT	425	
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420	
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485	

Query	421	TTCAATTTTAGGTGCAATTA	AACTTCATCACA	ACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTA	AATTTTCATTACA	ACTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540		
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605		
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAACTTTAA	600	
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAAATTTCAA	665	
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658		
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723		

>Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KY606302.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60	
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125	
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120	
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	185	
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180	
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245	
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240	
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305	
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA	ACTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCCTTATTAATTAATTCTTC	365	
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360	
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425	
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420	

Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTCATTACA ACTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACC GCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTA ACTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KY606301.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAAC TTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCAT TATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA ACTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420

Sbjct	426	 ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAAC TATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTT CATTACAAC TATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACC GCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAC TGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTTAGCAGGTGCCATTACAATATTATTAAC TGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACG 	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATTATGTTAGGAGCTCCAGACATAGCATTTCACG	305
Query	241	AATAAATAATATAAGATTTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 	300
Sbjct	306	AATAAATAATATAAGATTTTTGATTACTTCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCCTCTTTATCTTCAAATTT	425

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTATTT	723

>Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606299.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACGTCTACCCTCCTTTATCTTCAAATTT	425

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTATTT	723

>Rhipicephalus camicasi isolate SC0126 mitochondrion, complete genome

Sequence ID: NC_061616.1 Length: 14725

>Rhipicephalus camicasi isolate SC0126 mitochondrion, complete genome

Sequence ID: MZ323229.1 Length: 14725

Range 1: 45 to 702

Score:861 bits(466), Expect:0.0,

Identities:595/659(90%), Gaps:2/659(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATACTTAATTTTTGGAGCATGATCTGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGACCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATGATTGG	224
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTCGGAAATTGATTAGTCCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGATTACTTCCTCCTTCATTATTTTTATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC-CCCTCTATCTTCAAATT	359

Sbjct	345	 ATTAATTGAATCAGGAGCAGGGACAGGATGAACAGTTTACCCTCCCT-TATCATCAAATT	403
Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTT	419
Sbjct	404	 TATCACACTATGGTCCATCAGTAGATCTAGCTATTTTTCTCTTCATCTTGCTGGTGCTT	463
Query	420	CTTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTGTAAATATACGATCAATTGGAA	479
Sbjct	464	 CTTCAATTTTAGGCGCAATTAATTTTCATTACAACCATTGTAAACATACGATCTATTGGAA	523
Query	480	TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	524	 TAACAATAGAACGAATACCTTTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAT	583
Query	540	TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTTA	599
Sbjct	584	 TATTATCTTTACCAGTTTTAGCTGGTGCAATTACAATATTATTA ACTGATCGAAATTTTA	643
Query	600	ACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	644	 ATACCTCGTTCTTTGATCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305547.1 Length: 658
Range 1: 1 to 658

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	 AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	 AATTCGAATAGAGTTAGGACAACCTGGGACTTTAATTGGAAATGATCAAATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	 AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAACTGATTAGTGCCCAT TATGTTAGGAGCTCCAGACATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA ACTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	300

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	658

>Rhipicephalus turanicus isolate Xinjiang-WQIA cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: MF002581.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002580.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300

Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-BC cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002579.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300

Sbjct	314	 AATAAAATACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	 ATTAATTGAATCAGGAGCAGGAACGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	 ATCACACTATGGACCATCAGTAGATTTAGCTATTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	 TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	 AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGT TACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	 TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCC TTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	 CACTTCATTTTTTGATCC TTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-YC cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002578.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAAATTTTTTTCATAGTAATACCAATTATAAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313

Query	241	AATAAATAATATAAGATTTTGA	CTTTTACCCCCCTCATTATTTT	TATTGATTA	AACTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGA	TACTTCCCCCTCATTATTTCT	ATTAATTA	ATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGA	ACAGGATGAACAGTTTATCCC	CCTCTATCTT	CAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGA	ACTGGATGAACTGTTTATCCG	CCTTTATCAT	CAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTA	GATTTAGCTATTTTTTCTCTT	CACCTTGCTGGT	GCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTA	GATTTAGCTATTTTTCTCTCT	TTCATCTTGCTGGT	GCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAAC	TTTCATCACA	ACTATTGTAA	TATACGATCA	ATTGGAAT
Sbjct	494	TTCAATTTTAGGTGCAATCAAT	TTTATTACGACTATTATAAA	TATACGATCTATTGGAAT		553
Query	481	AACAATAGAACGAATACCATT	ATTTGTTTGATCTGTTTTA	ATTACAGCTATTTT	ACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACT	ATTTGTTTGATCTGTTTTA	ATTACTGCTATTTT	GTTACT	613
Query	541	TCTATCTTTACCTGTATTAGC	AGGTGCCATTACAATATTAT	TAACTGATCGAA	ACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGC	AGGAGCCATTACAATATTAT	TAACTGATCGAA	ATTTCAA	673
Query	601	CACATCATTTTTT	GATCCTTCAGGAGGAGGAGAT	CCCCATTTTATATCA	AACTTATTT	658
Sbjct	674	CACTTCATTTTTT	GATCCTTCAGGAGGGGTGAT	CCAATTTTATACCA	ACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-PS cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: MF002577.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGG	GAGCATGATCAGGTATATTAGG	ACTTAGTATAAGA	ATATT	60
Sbjct	74	AACAATATATTTAATTTTTGG	GGGCATGATCAGGAATATTAGG	ACTAAGAATAAGA	ATATT	133
Query	61	AATTCGTATAGAATTAGGACA	ACCTGGAACTTTAATTGGAA	ATGATCAGATTTATA	AATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCA	ACCTGGAACTTTAATTGGAA	ATGATCAAATTTATA	AATGT	193
Query	121	AATCGTAACAGCACATGCAT	TTTATTATAATTTTCTTTAT	AGTTATACCAATCA	TAAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCAT	TTTATTATAATTTTTTCTA	GTAAATACCAATTAT	AATTGG	253
Query	181	AGGGTTCGGAAATTGATTAG	TTCCTATTATATTAGGTGCC	CCAGATATAGCAT	TTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGT	ACCTATTATATTAGGAGCT	CCAGATATAGCAT	TTCCACG	313

Query	241	AATAAATAATATAAGATTTT	GACTTTTACCCCCCTCATTATTTT	TATTGATTA	AACTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTT	GATTACTTCCCCCTTCATTATTT	CTATTAATTA	AATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	ATCCCCCTCTATCTTCAAATTT			360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAACTGTTT	ATCCGCCTTTATCATCAAATTT			433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTT	TCTCTTCACCTTGCTGGTGCTTC			420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTT	TCTCTCTTCATCTTGCTGGTGCTTC			493
Query	421	TTCAATTTTAGGTGCAATTA	AACTTCATCACA	ACTATTGTAAATATACGATCAATTGGAAT		480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTT	ATTACGACTATTATAAAATATACGATCTATTGGAAT			553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTT	ACTACT			540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTT	GTTACT			613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	AACTGATCGAAACTTTAA			600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTA	AACTGATCGAAATTTCAA			673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	TATATCAACACTTATTT			658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTT	TATACCAACATTTATTT			731

>Rhipicephalus turanicus isolate SHZ cytochrome oxidase subunit I (C01) gene, partial cds; mitochondrial
Sequence ID: KY069271.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTT	TGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTT	TGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAAC	TTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTT	CTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTT	TCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG		240

Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAACCTGATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate FK-1 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KY606291.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACTTTAATTGGAAATGATCAAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAAATTGG	253

Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTCATTATTTCTATTAATTAATTCTCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAAGTGTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAACTTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate YN2 cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606289.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253

Query	181	AGGGTTTCGGAAATTGATTAGTTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAACGGATGAAGTGTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Sequences producing significant alignments:

Rhipicephalu... NA MF425993.1	2138177	1216	1216	100%	0.0	100.00	702
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA MF425992.1	2138177	1216	1216	100%	0.0	100.00	693
Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...							
Rhipicephalu... brown dog tick KT906183.1	34632	1216	1216	100%	0.0	100.00	690
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...							
Rhipicephalu... brown dog tick KT906182.1	34632	1216	1216	100%	0.0	100.00	690
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...							
Rhipicephalu... brown dog tick OM368327.1	34632	1216	1216	100%	0.0	100.00	14711
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...							
Rhipicephalu... brown dog tick OM368323.1	34632	1216	1216	100%	0.0	100.00	14714
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...							
Rhipicephalu... brown dog tick OM368322.1	34632	1216	1216	100%	0.0	100.00	14713
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...							
Rhipicephalu... brown dog tick JQ737084.1	34632	1216	1216	100%	0.0	100.00	707
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...							
Rhipicephalu... brown dog tick KF437543.1	34632	1216	1216	100%	0.0	100.00	658
Rhipicephalus linnaei isolate LA032-2 clone JS5930...							
Rhipicephalu... NA MW429383.1	2138177	1216	1216	100%	0.0	100.00	14715
Rhipicephalus linnaei mitochondrion, complete sequence							
Rhipicephalu... NA NC_060409.1	2138177	1216	1216	100%	0.0	100.00	14711
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,... Ixodidae							
sp.... NA KX053537.1	1901042	1210	1210	100%	0.0	99.85	658
Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...							
Rhipicephalu... brown dog tick KT906185.1	34632	1210	1210	100%	0.0	99.85	690
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...							
Rhipicephalu... brown dog tick KT906184.1	34632	1210	1210	100%	0.0	99.85	690
Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...							
Rhipicephalu... brown dog tick KF200113.1	34632	1210	1210	100%	0.0	99.85	658
Rhipicephalus linnaei isolate SC931-1 clone JS5927...							
Rhipicephalu... NA MW429382.1	2138177	1210	1210	100%	0.0	99.85	14717
Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase...							
Rhipicephalu... brown dog tick KX360367.1	34632	1205	1205	99%	0.0	99.85	658
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...							
Rhipicephalu... brown dog tick KT906186.1	34632	1205	1205	100%	0.0	99.70	690
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...							

Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	658
KF200112.1							
Rhipicephalus sanguineus mitochondrion, complete genome							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	14714
JX416325.1							
Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	100.00	661
MZ401443.1							
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	100.00	661
MZ401441.1							
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	99.85	664
MZ401440.1							
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1190	1190	97%	0.0	100.00	664
MG969507.1							
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1188	1188	98%	0.0	99.69	649
KF200084.1							
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	768
KX383817.1							
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	657
MZ401442.1							
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	661
MZ401438.1							
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969506.1							
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969505.1							
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969504.1							
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	644
KF200096.1							
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1177	1177	100%	0.0	98.94	658
OM984983.1							
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416302.1							
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416298.1							
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1177	1177	97%	0.0	99.69	670
HM193873.1							
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...							

Rhipicephalu... brown dog tick	34632	1175	1175	97%	0.0	99.69	768
KX383820.1							
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	97%	0.0	99.53	724
KX383816.1							
Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984984.1							
Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984974.1							
Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984973.1							
Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416308.1							
Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416304.1							
Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416300.1							
Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416299.1							
Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416297.1							
Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416296.1							
Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416293.1							
Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	100.00	650
MZ401439.1							
Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	763
KX383802.1							
Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658
OM984979.1							
Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658
OM984968.1							
Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416295.1							
Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416294.1							
Rhipicephalus sanguineus isolate sanguineus0926 cytochrome...							

Rhipicephalu... brown dog tick	34632	1162	1162	99%	0.0	98.77	658
MH513252.1							
Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984985.1							
Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984978.1							
Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984977.1							
Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984975.1							
Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984971.1							
Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984970.1							
Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984969.1							
Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	802
JX416301.1							
Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrom...							
Rhipicephalu... brown dog tick	34632	1155	1155	95%	0.0	99.68	642
MT010523.1							
Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984988.1							
Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984976.1							
Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1155	1155	96%	0.0	99.37	802
JX416303.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA	2138177	1153	1153	98%	0.0	98.77	826
MF426003.1							
Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1146	1146	96%	0.0	99.21	665
HM193874.1							
Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
KX757914.1							
Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1136	1136	97%	0.0	98.60	768
KX383800.1							
Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1131	1131	93%	0.0	99.68	744
KX383796.1							
Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase...							

Rhipicephalu... brown dog tick	34632	1127	1127	96%	0.0	98.59	698
KX383798.1							
Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1125	1125	97%	0.0	98.29	768
KX383814.1							
Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1122	1122	96%	0.0	98.43	763
KX383801.1							
Rhipicephalus sanguineus isolate 400 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1120	1120	97%	0.0	98.28	657
MW558150.1							
Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726445.1							
Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726444.1							
Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726443.1							
Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726442.1							
Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726441.1							
Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726440.1							
Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726439.1							
Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726438.1							
Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726437.1							
Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726436.1							
Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726435.1							
Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726434.1							
Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726433.1							
Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726432.1							
Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subun...							

Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726431.1							
Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726430.1							
Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726449.1							
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726429.1							
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726428.1							
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726427.1							
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726426.1							
Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1092	1092	91%	0.0	99.33	638
KX360338.1							

Alignments:

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425994.1 Length: 703

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425996.1 Length: 703

Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	560	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	200	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome
Sequence ID: OM368327.1 Length: 14711
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	1364

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome
Sequence ID: OM368323.1 Length: 14714
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	1364

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome
Sequence ID: OM368322.1 Length: 14713
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	1364

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 24 to 681

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	24	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	83
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	84	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	143
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	144	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	203
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	204	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	263
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	264	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	323
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	324	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	383
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	384	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	443
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	444	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	503
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	504	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	563
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	564	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	623
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	624	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	681

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome

Sequence ID: MW429383.1 Length: 14715

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	105	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	405	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	585	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus linnaei mitochondrion, complete sequence

Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome

Sequence ID: MW429381.1 Length: 14711

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAAATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053537.1 Length: 658

Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
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Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KF200113.1 Length: 658
 Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome

Sequence ID: MW429382.1 Length: 14717

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 45 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 104

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 105 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 164

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 165 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 224

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 225 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 284

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 285 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 344

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 345 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 404

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 405 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC 464

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 465 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 524

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 525 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 584

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 585 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 644

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 645 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 702
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>Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360367.1 Length: 658
Range 1: 4 to 658

Score:1205 bits(652), Expect:0.0,
Identities:654/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

```
Query 4 AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT 63
      |||
Sbjct 4 AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT 63

Query 64 CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT 123
      |||
Sbjct 64 CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT 123

Query 124 TGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGG 183
      |||
Sbjct 124 TGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGG 183

Query 184 ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAAT 243
      |||
Sbjct 184 ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAAT 243

Query 244 AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT 303
      |||
Sbjct 244 AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT 303

Query 304 AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATC 363
      |||
Sbjct 304 AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATC 363

Query 364 ACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTC 423
      |||
Sbjct 364 ACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTC 423

Query 424 AATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAAC 483
      |||
Sbjct 424 AATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAAC 483

Query 484 AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT 543
      |||
Sbjct 484 AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT 543

Query 544 ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC 603
      |||
Sbjct 544 ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC 603

Query 604 ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 604 ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I
(COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690

Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 498 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 558 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KF200112.1 Length: 658

>Rhipicephalus sanguineus voucher D0-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX360403.1 Length: 658

Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,

Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus mitochondrion, complete genome
Sequence ID: JX416325.1 Length: 14714
Range 1: 1185 to 1842

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCCTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT	1842

>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

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Query 14  ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 73
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 60

Query 74  TTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 120

Query 134  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  CATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 180

Query 194  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 240

Query 254  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 300

Query 314  GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA 373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA 360

Query 374  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 420

Query 434  GCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  GCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 480

Query 494  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 540

Query 554  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT 613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT 600

Query 614  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          ||||||||||||||||||||||||||||||||||||||||||
Sbjct 601  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645
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>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401441.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

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Query 14  ATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 73
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   ATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 60

Query 74  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 133
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 120

Query 134  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 193
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 180

Query 194  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 253
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 240

Query 254  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 313
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 300

Query 314  GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA 373
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA 360

Query 374  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 433
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 420

Query 434  GCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 493
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  GCAATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 480

Query 494  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 553
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 540

Query 554  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT 613
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT 600

Query 614  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||||||||||||||||||||||||||||||||||||||
Sbjct 601  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645
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>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,
Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	1	TTAATTTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	60
Query	71	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	61	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	120
Query	131	GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	121	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	241	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	300
Query	311	TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	301	TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	360
Query	371	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTA	430
Sbjct	361	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550
Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	540
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAATACATCATTC	610
Sbjct	541	CCAGTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAATACATCATTC	600
Query	611	TTTGACCCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

Sbjct 601 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 648

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1190 bits(644), Expect:0.0,
Identities:644/644(100%), Gaps:0/644(0%), Strand: Plus/Plus

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Query 15  TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1    TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query 75  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query 135  ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query 195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query 255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query 315  GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query 375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query 435  CAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  CAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query 495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query 555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

Query 615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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Sbjct  601 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644
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>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 1 to 649

Score:1188 bits(643), Expect:0.0,
Identities:647/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

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Query  10  CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT 69
          |||
Sbjct   1  CTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCAT 60

Query  70  AGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 129
          |||
Sbjct  61  AGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 120

Query  130  AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG 189
          |||
Sbjct  121  AGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGG 180

Query  190  AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA 249
          |||
Sbjct  181  AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA 240

Query  250  TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 309
          |||
Sbjct  241  TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 300

Query  310  ATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTA 369
          |||
Sbjct  301  ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA 360

Query  370  CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 429
          |||
Sbjct  361  CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 420

Query  430  AGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGA 489
          |||
Sbjct  421  AGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGA 480

Query  490  ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 549
          |||
Sbjct  481  ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 540

Query  550  ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 609
          |||
Sbjct  541  ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 600
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Query	610	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	649

>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC	600

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Query   617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||
Sbjct   601 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642

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>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

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Query   17  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
        |||
Sbjct   1  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query   77  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
        |||
Sbjct   61  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query   137 GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
        |||
Sbjct   121 GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query   197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
        |||
Sbjct   181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query   257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
        |||
Sbjct   241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query   317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
        |||
Sbjct   301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query   377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 436
        |||
Sbjct   361 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 420

Query   437 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
        |||
Sbjct   421 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query   497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
        |||
Sbjct   481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query   557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 616
        |||

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Sbjct	541	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642	

>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76	
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60	
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136	
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120	
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196	
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180	
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256	
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240	
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316	
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300	
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376	
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360	
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	436	
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	420	
Query	437	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496	
Sbjct	421	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480	
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556	
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540	
Query	557	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	616

Sbjct	541		TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	600
Query	617		CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601		CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642	

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540

Query	555	TCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644	

>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540

Query	555	TCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644	

>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene, partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554

Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	6	TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC	65
Sbjct	1	TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC	60
Query	66	GCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTG	125
Sbjct	61	GCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTG	120
Query	126	TAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGAT	185
Sbjct	121	TAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGAT	180
Query	186	TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAA	245
Sbjct	181	TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCACGAATAA	240
Query	246	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	305
Sbjct	241	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	300
Query	306	TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCAC	365
Sbjct	301	TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCAC	360
Query	366	ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	425
Sbjct	361	ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	420
Query	426	TTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAA	485
Sbjct	421	TTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAA	480
Query	486	TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	545

Sbjct	481		TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	540
Query	546		CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT	605
Sbjct	541		CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT	600
Query	606		CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA	649
Sbjct	601		CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA	644

>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 1 to 658

Score:1177 bits(637), Expect:0.0,
Identities:651/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361		ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATTAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT

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Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
        |||
Sbjct   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
        |||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT  658

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>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416302.1 Length: 802

>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416305.1 Length: 802

>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416306.1 Length: 802

>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416307.1 Length: 802

Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,

Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

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Query   22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
        |||
Sbjct   1  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query   82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
        |||
Sbjct   61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query   142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
        |||
Sbjct   121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query   202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
        |||
Sbjct   181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query   262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
        |||
Sbjct   241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query   322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
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Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGT	381

Sbjct	301		TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442		TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421		TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 1 to 642

Score:1177 bits(637), Expect:0.0,
Identities:642/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGG-CATGATCCGG-ATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	58
Query	75	TAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	59	TAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	118
Query	135	ATGCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	119	ATGCATTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	178
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	179	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	238
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	239	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	298

Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	299	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	358
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	359	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	418
Query	435	CAATCAATTTTATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	419	CAATCAATTTTATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	478
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	479	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	538
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	539	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	598
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	599	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383820.1 Length: 768
Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,
Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300

Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTACATCTTGAGGTGCTTCTTCAATTTAGGTGCA	420
Query	437	ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383816.1 Length: 724
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316

Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAAATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAAATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGTGAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACAACATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416304.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT	120
Query	142	TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT	180

Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416299.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180

Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416297.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201

Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTACTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416296.1 Length: 802

Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,

Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201

Sbjct	121		180
		TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120

Query	142	TATTATAA		201
Sbjct	121	TATTATAA		180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG		321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG		300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT		381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT		360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA		441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA		420
Query	442	TTTCATTACAAC		501
Sbjct	421	TTTCATTACAAC		480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC		561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC		540
Query	562	TGGCGCAATTACAATATTATTA		621
Sbjct	541	TGGCGCAATTACAATATTATTA		600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		637

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MZ401439.1 Length: 650
 Range 1: 1 to 634

Score:1171 bits(634), Expect:0.0,
 Identities:634/634(100%), Gaps:0/634(0%), Strand: Plus/Plus

Query	25	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC		84
Sbjct	1	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC		60
Query	85	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT		144
Sbjct	61	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT		120

Query	145	TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	204
Sbjct	121	TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	180
Query	205	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	264
Sbjct	181	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	240
Query	265	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	324
Sbjct	241	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	300
Query	325	AGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	384
Sbjct	301	AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	360
Query	385	TTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT	444
Sbjct	361	TTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT	420
Query	445	CATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	504
Sbjct	421	CATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	480
Query	505	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	564
Sbjct	481	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	540
Query	565	CGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	624
Sbjct	541	CGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	600
Query	625	AGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGTGACCCAATTCTATATCAACATTTATTT	634

>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383802.1 Length: 763
 >Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383803.1 Length: 763
 >Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383804.1 Length: 763
 Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
 Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGGGGTGAACCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984979.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,

Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAACCTGATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416295.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
|||||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
|||||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
|||||
Sbjct 301 TACAGGGTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
|||||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
|||||
Sbjct 421 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
|||||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
|||||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT 637
```

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      ||||||||||||||||||||||||||||||||||||
Sbjct  601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637
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>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1
(COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658

Range 1: 6 to 658

Score:1162 bits(629), Expect:0.0,
Identities:645/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 6 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 65

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 66 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 125

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 126 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 185

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 186 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 245

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 246 AATAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 305

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 306 ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 365

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 366 ATCACACTACGGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTC 425

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 426 TTCAATTTTAGGCGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 485

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 486 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 545

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 546 ATTATCTTTACAGTCTTAGCTGGTGAATACAATATTGTAACTGATCGAACTTTAA 605

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT 653
      |||
Sbjct 606 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT 658
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>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: OM984985.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: OM984978.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGAATACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984977.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| |||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| |||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| |||||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||| |||||||||||||||| |||||||||||||||| ||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATGGTAAATATACGATCCATTGGGAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      ||||||||||||| ||||||||||||||||||||| || ||||||||||| |||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      ||||||||||||| ||||||||||||| || ||||||||||||| |||||||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||| ||||||||||||| ||||||||||||| |||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||| ||||||||||||| ||||||||||||| |||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||| ||||||||||||| ||||||||||||| |||||||||||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||| ||||||||||||| ||||||||||||| |||||||||||||
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Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416301.1 Length: 802

Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,

Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT  141
      |||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT  120

Query  142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||
Sbjct  241  GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||
Sbjct  421  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||
Sbjct  541  TGGCGCTATTACAATATTATTAAGTATCGAACTTTAATACATTATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
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Sbjct 601 ||||| AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT010523.1 Length: 642
Range 1: 1 to 631

Score:1155 bits(625), Expect:0.0,
Identities:629/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

Query	28	ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG	87
Sbjct	1	ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG	60
Query	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Sbjct	61	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	120
Query	148	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Sbjct	121	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	180
Query	208	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267
Sbjct	181	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	240
Query	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Sbjct	241	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	300
Query	328	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	387
Sbjct	301	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	360
Query	388	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA	447
Sbjct	361	AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA	420
Query	448	TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Sbjct	421	TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	480
Query	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	567
Sbjct	481	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	540
Query	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Sbjct	541	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	600

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Query  628  AGGTGACCCAATTCTATATCAACATTTATTT  658
        ||||||||||||||||||||||||||||
Sbjct  601  GGGTGACCCAATTCTATATCAACATTTATTT  631

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>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query  61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121   AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  121   AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  181   AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT  360
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT  360

Query  361   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC  420
        ||||||||||| ||||||||||||||||| || ||||||||||| |||||||||
Sbjct  361   ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC  420

Query  421   TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480
        ||||||||||||||||| ||||||||||||||||| |||||||||||||||||
Sbjct  421   TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480

Query  481   AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  481   AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query  541   ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
        ||||||||||||||||| ||||||||||||||||| |||||||||||||||||
Sbjct  541   ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

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Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||
Sbjct   601  TACATCATTTTTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

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>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
        |||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
        |||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
        |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
        |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
        |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
        |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query   361  ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC 420
        |||
Sbjct   361  ATCACAACACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query   421  TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT 480
        |||
Sbjct   421  TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT 480

Query   481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
        |||
Sbjct   481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query   541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
        |||

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Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
 |||

Sbjct 601 TACATCATTTTTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,
 partial cds; mitochondrial
 Sequence ID: JX416303.1 Length: 802
 Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,
 Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
 |||

Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
 |||

Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
 |||

Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
 |||

Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
 |||

Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
 |||

Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
 |||

Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA 420

Query 442 TTTCAATACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
 |||

Sbjct 421 TTTCAATACAACTATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
 |||

Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621

Sbjct	541		TGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637	

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1153 bits(624), Expect:0.0,
Identities:640/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	3	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATA	62
Query	71	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	63	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	122
Query	131	GCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	123	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	182
Query	191	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	183	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAAT	242
Query	251	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	243	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	302
Query	311	TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	303	TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	362
Query	371	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA	430
Sbjct	363	GGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA	422
Query	431	GGTGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	423	GGCGCAATCAATTTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA	482
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550
Sbjct	483	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	542

Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTC	610
Sbjct	543	CCAGTCTTAGCTGGTGAATTACAATATTGT	TAAGTATCGAAACTTTAATACATCATTC	602
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCT	TATATCAACATTTATTT	658
Sbjct	603	TTTGACCCTTCAGGAGGAGGTGACCCAATTCT	GTATCAACATTTATTT	650

>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1146 bits(620), Expect:0.0,
Identities:631/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	31	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	90
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	91	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	150
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	151	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	210
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	211	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	270
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	271	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	330
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	331	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	390
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	391	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	450
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	451	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	510
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	511	AACAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	570


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Query    541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
      |||
Sbjct    571  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAATATTAAGTATCGAAACTTTAA  630

Query    601  TACATCATTCTTTGACCCCTTCAGGAGGAGGTGACCC  636
      |||
Sbjct    631  TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC  665

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>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG	98
Sbjct	1	TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG	60
Query	99	GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttA	158
Sbjct	61	GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAATTTTTTTTA	120
Query	159	TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG	218
Sbjct	121	TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG	180
Query	219	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC	278
Sbjct	181	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC	240
Query	279	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	338
Sbjct	241	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	300
Query	339	AccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAACATTG	458
Sbjct	361	CTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAACATTG	420
Query	459	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	518
Sbjct	421	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	480
Query	519	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	578

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Sbjct  481  TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT  540
Query  579  TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA  638
        |||
Sbjct  541  TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA  600
Query  639  TTCTATATCAACATTTATTT  658
        |||
Sbjct  601  TTCTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383800.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383815.1 Length: 768
Range 1: 1 to 642

Score:1136 bits(615), Expect:0.0,
Identities:633/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

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Query  17  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA  76
        |||
Sbjct  1  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA  60
Query  77  GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT  136
        |||
Sbjct  61  GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT  120
Query  137  GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA  196
        |||
Sbjct  121  GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA  180
Query  197  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA  256
        |||
Sbjct  181  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA  240
Query  257  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA  316
        |||
Sbjct  241  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA  300
Query  317  GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA  376
        |||
Sbjct  301  GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA  360
Query  377  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA  436
        |||
Sbjct  361  TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGCGCA  420
Query  437  ATCAATTTTATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATA  496
        |||

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Sbjct  421  ATCAATTTCACTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA  480
Query  497  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC  556
          |||
Sbjct  481  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACAGTC  540
Query  557  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC  616
          |||
Sbjct  541  TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC  600
Query  617  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
          |||
Sbjct  601  CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT  642

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>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383796.1 Length: 744
Range 1: 1 to 618

Score:1131 bits(612), Expect:0.0,
Identities:616/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

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Query  41  GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA  100
          |||
Sbjct  1  GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA  60
Query  101  AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAatttttttATA  160
          |||
Sbjct  61  AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATA  120
Query  161  GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT  220
          |||
Sbjct  121  GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT  180
Query  221  CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA  280
          |||
Sbjct  181  CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA  240
Query  281  TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAc  340
          |||
Sbjct  241  TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAC  300
Query  341  cccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT  400
          |||
Sbjct  301  CCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT  360
Query  401  CTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTA  460
          ||
Sbjct  361  CTACATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTA  420
Query  461  AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA  520

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Sbjct	421	 AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	480
Query	521	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	580
Sbjct	481	 ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	540
Query	581	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT	640
Sbjct	541	 TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATT	600
Query	641	CTATATCAACATTTATTT 658	
Sbjct	601	 CTATATCAACATTTATTT 618	

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KX383798.1 Length: 698
Range 1: 1 to 637

Score:1127 bits(610), Expect:0.0,
Identities:628/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420

Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383814.1 Length: 768
Range 1: 1 to 642

Score:1125 bits(609), Expect:0.0,
Identities:631/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA	60
Query	77	GGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAA TCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTT AccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTT ACCCCCCCTTATCATCAAATTTATCACACTACGGATCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGCGCA	420

Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441

Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGC AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW558150.1 Length: 657
Range 1: 1 to 639

Score:1120 bits(606), Expect:0.0,
Identities:628/639(98%), Gaps:0/639(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCAGGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAA ttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199
Sbjct	121	TTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATGGATTA	180
Query	200	GTTCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259
Sbjct	181	GTTCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	240
Query	260	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	319
Sbjct	241	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	300
Query	320	GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA	379
Sbjct	301	GGTACAGGGGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCA	360
Query	380	GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	439

Sbjct	361	GTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC	420
Query	440	AATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	499
Sbjct	421	AATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	480
Query	500	TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	559
Sbjct	481	TTATTTGTAGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	540
Query	560	GCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAATACATCATTCTTTGACCCT	619
Sbjct	541	GCTGGTGCAATTACAATATTATTAACCTGATCGAAACTTTAATACATCATTCTTTGACCCT	600
Query	620	TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	639

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726444.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial

Sequence ID: MZ726441.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttTATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726440.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACGATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACGATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726438.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726437.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726434.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726433.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726432.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726430.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121		AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601		TACA 604	
Sbjct	601		TACA 604	

>Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726449.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT

Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACGGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726429.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MZ726428.1 Length: 604
 Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
 Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604 	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726426.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus sanguineus voucher D0-306 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX360338.1 Length: 638
 Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
 Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60

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Query  80  CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA  139
      |||
Sbjct  61  CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA  120

Query  140  TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  199
      |||
Sbjct  121  TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  180

Query  200  GTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  259
      |||
Sbjct  181  GTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  240

Query  260  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  319
      |||
Sbjct  241  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  300

Query  320  GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA  379
      ||
Sbjct  301  GGNACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCA  360

Query  380  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  439
      |||
Sbjct  361  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  420

Query  440  AATTTCAATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  499
      |||
Sbjct  421  AATTTCAATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  480

Query  500  TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA  559
      |||
Sbjct  481  TTATTTGTATGATCTGTTTTAATTACNGCAATTTTATTATTATTATCTTTACCAGTCTTA  540

Query  560  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  619
      |||
Sbjct  541  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  600

Query  620  T      620
      |
Sbjct  601  T      601

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Query #11: TKCJJ083-19|TKCJ012018G11|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26773 Length: 571

Sequences producing significant alignments:

Common		Max	Total Query	E	Per.	Acc.	Scientific
Description	Taxid	Score	Score	cover	Value	Ident	Name
Name						Len	Accession

Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...							
Rhipicephalu... brown dog tick 34632	1055	1055	100%	0.0	100.00	658	
KF200113.1							
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick 34632	1055	1055	100%	0.0	100.00	664	
MZ401440.1							
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	664	
MG969507.1							
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	664	
MG969506.1							
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	664	
MG969505.1							
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	664	
MG969504.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA 2138177	1050	1050	100%	0.0	99.82	688	
MF425995.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA 2138177	1050	1050	100%	0.0	99.82	703	
MF425994.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA 2138177	1050	1050	100%	0.0	99.82	702	
MF425993.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA 2138177	1050	1050	100%	0.0	99.82	693	
MF425992.1							
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	768	
KX383817.1							
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	690	
KT906184.1							
Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	690	
KT906183.1							
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	690	
KT906182.1							
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	14711	
OM368327.1							
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	14714	
OM368323.1							
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	14713	
OM368322.1							
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick 34632	1050	1050	100%	0.0	99.82	802	

JX416302.1
Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 802
JX416299.1
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 802
JX416298.1
Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 802
JX416293.1
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 707
JQ737084.1
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 658
KF437543.1
Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 661
MZ401443.1
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 657
MZ401442.1
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 661
MZ401441.1
Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 650
MZ401439.1
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 661
MZ401438.1
Rhipicephalus linnaei isolate LA032-2 clone JS5930...
Rhipicephalu... NA 2138177 1050 1050 100% 0.0 99.82 14715
MW429383.1
Rhipicephalus linnaei mitochondrion, complete sequence
Rhipicephalu... NA 2138177 1050 1050 100% 0.0 99.82 14711
NC_060409.1
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidas...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 99.82 670
HM193873.1
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,... Ixodidae
sp.... NA 1901042 1044 1044 100% 0.0 99.65 658
KX053537.1
Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 630
KX757914.1
Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 658
KX360367.1
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 690
KT906186.1
Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 690

KT906185.1
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 658
KF200112.1
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 649
KF200084.1
Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 802
JX416308.1
Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 802
JX416304.1
Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 802
JX416300.1
Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 802
JX416297.1
Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 802
JX416296.1
Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1044 1044 100% 0.0 99.65 802
JX416294.1
Rhipicephalus linnaei isolate SC931-1 clone JS5927...
Rhipicephalu... NA 2138177 1044 1044 100% 0.0 99.65 14717
MW429382.1
Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrom...
Rhipicephalu... brown dog tick 34632 1038 1038 100% 0.0 99.47 642
MT010523.1
Rhipicephalus sanguineus isolate LIC4030B cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1038 1038 100% 0.0 99.47 723
KX714597.1
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1038 1038 100% 0.0 99.47 768
KX383820.1
Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1038 1038 100% 0.0 99.47 763
KX383802.1
Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1038 1038 100% 0.0 99.47 744
KX383796.1
Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1038 1038 100% 0.0 99.47 802
JX416295.1
Rhipicephalus sanguineus mitochondrion, complete genome
Rhipicephalu... brown dog tick 34632 1038 1038 100% 0.0 99.47 14714
JX416325.1
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1035 1035 100% 0.0 99.30 724
KX383816.1
Rhipicephalus sanguineus isolate LIC4668G cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1033 1033 100% 0.0 99.30 723

KX714598.1								
Rhipicephalus sanguineus isolate LIC6664A cytochrome oxidase...								
Rhipicephalu...	brown dog tick	34632	1033	1033	100%	0.0	99.30	736
KX383797.1								
Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1033	1033	100%	0.0	99.30	802
JX416301.1								
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...								
Rhipicephalu...	brown dog tick	34632	1027	1027	98%	0.0	99.64	644
KF200096.1								
Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subun...								
Rhipicephalu...	brown dog tick	34632	1027	1027	100%	0.0	99.12	802
JX416303.1								
Rhipicephalus sanguineus isolate RS5 cytochrome c oxidase...								
Rhipicephalu...	brown dog tick	34632	1022	1022	100%	0.0	98.95	716
OK576083.1								
Rhipicephalus sanguineus isolate RS1 cytochrome c oxidase...								
Rhipicephalu...	brown dog tick	34632	1022	1022	100%	0.0	98.95	716
OK576079.1								
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1016	1016	100%	0.0	98.77	658
OM984983.1								
Rhipicephalus sanguineus isolate RS6 cytochrome c oxidase...								
Rhipicephalu...	brown dog tick	34632	1016	1016	100%	0.0	98.77	716
OK576084.1								
Rhipicephalus sanguineus isolate RS4 cytochrome c oxidase...								
Rhipicephalu...	brown dog tick	34632	1016	1016	100%	0.0	98.77	716
OK576082.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu...	NA	2138177	1011	1011	100%	0.0	98.60	826
MF426003.1								
Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1011	1011	100%	0.0	98.60	658
OM984984.1								
Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1011	1011	100%	0.0	98.60	658
OM984974.1								
Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase...								
Rhipicephalu...	NA	2138177	1011	1011	100%	0.0	98.60	658
OM984973.1								
Rhipicephalus sanguineus isolate RS2 cytochrome c oxidase...								
Rhipicephalu...	brown dog tick	34632	1011	1011	100%	0.0	98.60	716
OK576080.1								
Rhipicephalus sanguineus isolate LIC6545A cytochrome oxidase...								
Rhipicephalu...	brown dog tick	34632	1005	1005	100%	0.0	98.42	723
KX714594.1								
Rhipicephalus sanguineus isolate LIC4528B cytochrome oxidase...								
Rhipicephalu...	brown dog tick	34632	1005	1005	100%	0.0	98.42	723
KX714593.1								
Rhipicephalus leporis isolate Bas-Sassandra-A cytochrome oxida...								
Rhipicephalu...	NA	669982	1005	1005	100%	0.0	98.42	630
KX757912.1								
Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase...								
Rhipicephalu...	brown dog tick	34632	1005	1005	100%	0.0	98.42	768

KX383800.1							
Rhipicephalus sanguineus isolate LIC5958C	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1005	1005	100%	0.0	98.42	720
KX383799.1							
Rhipicephalus sanguineus isolate LIC5958B	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1005	1005	100%	0.0	98.42	698
KX383798.1							
Rhipicephalus leporis voucher INHM:TC1338	cytochrome oxidase...						
Rhipicephalu... NA	669982	1005	1005	100%	0.0	98.42	632
KM235720.1							
Rhipicephalus linnaei voucher P1/22_16-1	cytochrome c oxidase...						
Rhipicephalu... NA	2138177	1005	1005	100%	0.0	98.42	658
OM984979.1							
Rhipicephalus linnaei voucher P1/22_1-1	cytochrome c oxidase...						
Rhipicephalu... NA	2138177	1005	1005	100%	0.0	98.42	658
OM984968.1							
Rhipicephalus sanguineus isolate RS8	cytochrome c oxidase...						
Rhipicephalu... brown dog tick	34632	1005	1005	100%	0.0	98.42	716
OK576086.1							
Rhipicephalus sanguineus isolate sanguineus0926	cytochrome...						
Rhipicephalu... brown dog tick	34632	1002	1002	99%	0.0	98.59	658
MH513252.1							
Rhipicephalus sanguineus isolate LIC3635G	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1000	1000	100%	0.0	98.25	723
KX714601.1							
Rhipicephalus sanguineus isolate LIC5273D	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1000	1000	100%	0.0	98.25	723
KX714596.1							
Rhipicephalus sanguineus isolate LIC6120A	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1000	1000	100%	0.0	98.25	723
KX714595.1							
Rhipicephalus leporis isolate Bas-Sassandra-C	cytochrome oxida...						
Rhipicephalu... NA	669982	1000	1000	100%	0.0	98.25	630
KX757917.1							
Rhipicephalus leporis isolate Bas-Sassandra-B	cytochrome oxida...						
Rhipicephalu... NA	669982	1000	1000	100%	0.0	98.25	630
KX757913.1							
Rhipicephalus leporis isolate Turkana-A	cytochrome oxidase...						
Rhipicephalu... NA	669982	1000	1000	100%	0.0	98.25	633
KX757911.1							
Rhipicephalus sanguineus isolate LIC5755	cytochrome oxidase...						
Rhipicephalu... brown dog tick	34632	1000	1000	100%	0.0	98.25	763
KX383801.1							
Rhipicephalus linnaei voucher P1/22_19-1	cytochrome c oxidase...						
Rhipicephalu... NA	2138177	1000	1000	100%	0.0	98.25	658
OM984985.1							
Rhipicephalus linnaei voucher P1/22_14-1	cytochrome c oxidase...						
Rhipicephalu... NA	2138177	1000	1000	100%	0.0	98.25	658
OM984978.1							
Rhipicephalus linnaei voucher P1/22_13-1	cytochrome c oxidase...						
Rhipicephalu... NA	2138177	1000	1000	100%	0.0	98.25	658
OM984977.1							
Rhipicephalus linnaei voucher P1/22_10-1	cytochrome c oxidase...						
Rhipicephalu... NA	2138177	1000	1000	100%	0.0	98.25	658

OM984975.1
Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1000 1000 100% 0.0 98.25 658
OM984971.1
Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1000 1000 100% 0.0 98.25 658
OM984970.1
Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1000 1000 100% 0.0 98.25 658
OM984969.1
Rhipicephalus sanguineus isolate 400 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1000 1000 100% 0.0 98.25 657
MW558150.1
Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 994 994 100% 0.0 98.07 768
KX383814.1
Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 994 994 100% 0.0 98.07 658
OM984988.1
Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 994 994 100% 0.0 98.07 658
OM984976.1
Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidas...
Rhipicephalu... brown dog tick 34632 979 979 96% 0.0 98.91 665
HM193874.1
Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 972 972 93% 0.0 99.44 638
KX360338.1
Rhipicephalus sanguineus isolate A3657 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 963 963 91% 0.0 99.81 535
MN223692.1

Alignments:

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200113.1 Length: 658
Range 1: 88 to 658

Score:1055 bits(571), Expect:0.0,
Identities:571/571(100%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC TTTAATTG GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	AAC TTTAATTG GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	208	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267

Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	327
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	387
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	567
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628	AGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 78 to 648

Score:1055 bits(571), Expect:0.0,
Identities:571/571(100%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	78	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	137
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	138	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	197
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	198	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	257
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240

Sbjct	258	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	317
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	318	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	377
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	378	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	437
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	438	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	497
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	498	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	557
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	558	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	617
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	618	AGGTGACCCAATTCTATATCAACATTTATTT	648

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 74 to 644

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	74	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	133
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	134	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	193
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	194	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT	253
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	254	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	313
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300

Sbjct	314		GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	373
Query	301		AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	374		AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	433
Query	361		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	434		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	493
Query	421		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	494		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	553
Query	481		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	554		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	613
Query	541		AGGTGACCCAATTCTATATCAACATTTATTT 571	
Sbjct	614		AGGTGACCCAATTCTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 74 to 644

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC	TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	74	AAC	TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	133
Query	61	AAt	tttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	134	AAT	TTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	193
Query	121	TATA	CTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	194	TATA	CTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	253
Query	181	TCCT	CTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	254	TCCT	CTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	313
Query	241	GTGA	ACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	314	GTGA	ACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	373

Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	374	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	433
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	434	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	493
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	494	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	553
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	554	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	613
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	614	AGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 74 to 644

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	74	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	133
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	134	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	193
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	194	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	253
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	254	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	313
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	314	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	373
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	374	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	433

Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	434	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	493
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	494	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	553
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	554	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	613
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	614	AGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 74 to 644

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	74	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	133
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	134	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	193
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	194	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	253
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	254	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	313
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	314	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	373
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	374	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	433
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420

Sbjct	434	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	493
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	494	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	553
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	554	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	613
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	614	AGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 105 to 675

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	105	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	164
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	165	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	224
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	225	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	284
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	285	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	344
Query	241	GTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	345	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	404
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	405	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	464
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	465	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	524
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480

Sbjct	525	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	584
Query	481	AATTACAATATTATTAAC TGATCGAACTTTAATACATCATTCCTTTGACCCTTCAGGAGG	540
Sbjct	585	 AATTACAATATTATTAAC TGATCGAACTTTAATACATCATTCCTTTGACCCTTCAGGAGG	644
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	645	 AGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425994.1 Length: 703

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425996.1 Length: 703

Range 1: 107 to 677

Score:1050 bits(568), Expect:0.0,

Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC TTTTAATTGGAAACGATCAAATTTATAATGTAAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	107	AAC TTTTAATTGGAAACGATCAAATTTATAATGTAAATTGTAACAGCACATGCATTTATTAT	166
Query	61	AA ttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	167	AA TTTT TTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	226
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	227	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	286
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	287	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	346
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	347	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	406
Query	301	AGCTATTTTTTCTCTGCATCTTG CAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT CAT	360
Sbjct	407	AGCTATTTTTTCTCTGCATCTTG CAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT CAT	466
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	467	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	526
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480

Sbjct	527		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	586
Query	481		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	587		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	646
Query	541		AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	647		AGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 107 to 677

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC	TTTAATTG	GAAACG	ATCAA	ATTTATA	ATGTA	ATTGTA	ACAGCA	CATGC	ATTTAT	60		
Sbjct	107	AAC	TTTAATTG	GAAACG	ATCAA	ATTTATA	ATGTA	ATTGTA	ACAGCA	CATGC	ATTTAT	166		
Query	61	AAt	tttttt	tATAG	TTATA	ACCA	ATTATA	ATCGG	AGGAT	TTGG	AAATTG	ATTAG	TTCTAT	120
Sbjct	167	AAT	TTTTTT	TATAG	TTATA	ACCA	ATTATA	ATCGG	AGGAT	TTGG	AAATTG	ATTAG	TTCTAT	226
Query	121	TATA	CTAGG	AGCTC	CAGAT	ATAG	CATTT	CCACG	AATAA	ATAA	TAAAG	ATTTT	GGTTACT	180
Sbjct	227	TATA	CTAGG	AGCTC	CAGAT	ATAG	CATTT	CCACG	AATAA	ATAA	TAAAG	ATTTT	GGTTACT	286
Query	181	TCCT	CTTCT	CTATTT	CTACT	AATTA	ATTCT	TCATTA	ATCGA	ATCAG	GAGCAG	GAACAG	240	
Sbjct	287	TCCT	CTTCT	CTATTT	CTACT	AATTA	ATTCT	TCATTA	ATCGA	ATCAG	GAGCAG	GTACAG	346	
Query	241	GTGA	ACAGT	TTTAc	cccccc	TTAT	CATCA	AAATTT	ATCACA	CTACG	GACCAT	CAGTAG	ATTT	300
Sbjct	347	GTGA	ACAGT	TTTAc	cccccc	TTAT	CATCA	AAATTT	ATCACA	CTACG	GACCAT	CAGTAG	ATTT	406
Query	301	AGCT	ATTTTT	TTCT	CTGC	ATCTT	GCAGG	TGCTT	CTTCA	ATTTT	AGGTG	CAATCA	ATTT	360
Sbjct	407	AGCT	ATTTTT	TTCT	CTGC	ATCTT	GCAGG	TGCTT	CTTCA	ATTTT	AGGTG	CAATCA	ATTT	466
Query	361	TACA	ACTAT	TGTAA	ATATA	CGATC	CATTG	GAA	AACA	ATAGA	ACGA	ATAC	ATTAT	420
Sbjct	467	TACA	ACTAT	TGTAA	ATATA	CGATC	CATTG	GAA	AACA	ATAGA	ACGA	ATAC	ATTAT	526
Query	421	ATG	ATCTG	TTTTA	ATTACT	GCAAT	TTTAT	TATTAT	TATCT	TTTACC	AGTCT	TAGCT	GGCGC	480
Sbjct	527	ATG	ATCTG	TTTTA	ATTACT	GCAAT	TTTAT	TATTAT	TATCT	TTTACC	AGTCT	TAGCT	GGCGC	586

Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	587	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	646
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571	
Sbjct	647	AGGTGACCCAATTCTATATCAACATTTATTT	677	

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 107 to 677

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC	TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	107	AAC	TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	166
Query	61	AAt	tttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	167	AAT	TTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	226
Query	121	TATA	CTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	227	TATA	CTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT	286
Query	181	TCCT	CCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	287	TCCT	CCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	346
Query	241	GTGA	ACAGTTTACccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	347	GTGA	ACAGTTTACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	406
Query	301	AGCT	ATTTTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA	360
Sbjct	407	AGCT	ATTTTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA	466
Query	361	TACA	ACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	467	TACA	ACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	526
Query	421	ATGA	TCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	527	ATGA	TCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	586
Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	587	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	646

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Query   541  AGGTGACCCAATTCTATATCAACATTTATTT  571
        |||||||||||||||||||||||||||||||
Sbjct   647  AGGTGACCCAATTCTATATCAACATTTATTT  677

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>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768
Range 1: 72 to 642

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query    1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATTTATTAT  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   72  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATTTATTAT  131

Query   61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  132  AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  191

Query  121  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  192  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  251

Query  181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG  311

Query  241  GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  312  GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  371

Query  301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  431

Query  361  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  432  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  491

Query  421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  492  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  551

Query  481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  552  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  611

Query  541  AGGTGACCCAATTCTATATCAACATTTATTT  571
        |||||||||||||||||||||||||||||||

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Sbjct 612 AGGTGACCCAATTCTATATCAACATTTATTT 642

>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 105 to 675

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 105 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 164

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 165 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 224

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 225 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 284

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 285 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 344

Query 241 GTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 345 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 404

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 405 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 464

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 465 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 524

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 525 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 584

Query 481 AATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 585 AATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 644

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||||||||||||||||||||||||||||||
Sbjct 645 AGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 105 to 675

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 105 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 164

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 165 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 224

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 225 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 284

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 285 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 344

Query 241 GTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 345 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 404

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||
Sbjct 405 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 464

Query 361 TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 465 TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 524

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 525 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 584

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 585 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 644

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 645 AGGTGACCCAATTCTATATCAACATTTATTT 675
```

>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I

(COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 105 to 675

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
|||||
Sbjct 105 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 164

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
|||||
Sbjct 165 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 224

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
|||||
Sbjct 225 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 284

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
|||||
Sbjct 285 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 344

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
|||||
Sbjct 345 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 404

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
|||||
Sbjct 405 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 464

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
|||||
Sbjct 465 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 524

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
|||||
Sbjct 525 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 584

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
|||||
Sbjct 585 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 644

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
|||||
Sbjct 645 AGGTGACCCAATTCTATATCAACATTTATTT 675
```

>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome
Sequence ID: OM368327.1 Length: 14711
Range 1: 1272 to 1842

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1      AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
          |||
Sbjct 1272   AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 1331

Query 61     AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
          |||
Sbjct 1332   AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 1391

Query 121    TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
          |||
Sbjct 1392   TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 1451

Query 181    TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
          |||
Sbjct 1452   TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 1511

Query 241    GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
          |||
Sbjct 1512   GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 1571

Query 301    AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
          |||
Sbjct 1572   AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 1631

Query 361    TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
          |||
Sbjct 1632   TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 1691

Query 421    ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
          |||
Sbjct 1692   ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 1751

Query 481    AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
          |||
Sbjct 1752   AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 1811

Query 541    AGGTGACCCAATTCTATATCAACATTTATTT 571
          |||
Sbjct 1812   AGGTGACCCAATTCTATATCAACATTTATTT 1842
```

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome
Sequence ID: OM368323.1 Length: 14714
Range 1: 1272 to 1842

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1      AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
```

Sbjct	1272	 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	1331
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	1332	 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	1391
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	1392	 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	1451
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	1452	 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	1511
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	1512	 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	1571
Query	301	AGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	1572	 AGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	1631
Query	361	TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	1632	 TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	1691
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	1692	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	1751
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	1752	 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	1811
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT 571	
Sbjct	1812	 AGGTGACCCAATTCTATATCAACATTTATTT 1842	

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome
Sequence ID: OM368322.1 Length: 14713
Range 1: 1272 to 1842

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	1272	 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	1331
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120

Sbjct	1332	 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	1391
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	1392	 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	1451
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	1452	 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	1511
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	1512	 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	1571
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA	360
Sbjct	1572	 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA	1631
Query	361	TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	1632	 TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	1691
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	1692	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	1751
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	1752	 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	1811
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	1812	 AGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416302.1 Length: 802

>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416305.1 Length: 802

>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416306.1 Length: 802

>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416307.1 Length: 802

Range 1: 67 to 637

Score:1050 bits(568), Expect:0.0,

Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416299.1 Length: 802
Range 1: 67 to 637

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60

Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 67 to 637

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120

Sbjct	127	 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	 TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	 TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	 AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 67 to 637

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186

Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 111 to 681

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	111	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	170
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	171	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	230
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	231	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	290

Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	291	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	350
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	351	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	410
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	411	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	470
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	471	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	530
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	531	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	590
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	591	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	650
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	651	AGGTGACCCAATTCTATATCAACATTTATTT	681

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 88 to 658

Score:1050 bits(568), Expect:0.0,

Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	208	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267

Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	387
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	567
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628	AGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661
Range 1: 75 to 645

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	75	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	134
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	135	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	194
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	195	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	254
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240

Sbjct	255	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	314
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	315	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	374
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	375	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	434
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	435	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	494
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	495	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	554
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	555	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	614
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	615	AGGTGACCCAATTCTATATCAACATTTATTT	645

>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 72 to 642

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	72	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	131
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	132	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	191
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	192	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT	251
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	252	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	311
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300

Sbjct	312		GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	371
Query	301		AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	372		AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	431
Query	361		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	432		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	491
Query	421		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	492		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	551
Query	481		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	552		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	611
Query	541		AGGTGACCCAATTCTATATCAACATTTATTT 571	
Sbjct	612		AGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401441.1 Length: 661
Range 1: 75 to 645

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60	
Sbjct	75		AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	134
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120	
Sbjct	135		AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	194
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180	
Sbjct	195		TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	254
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240	
Sbjct	255		TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	314
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300	
Sbjct	315		GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	374

Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	375	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	434
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	435	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	494
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	495	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	554
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	555	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	614
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	615	AGGTGACCCAATTCTATATCAACATTTATTT	645

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401439.1 Length: 650
Range 1: 64 to 634

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	64	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	123
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	124	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	183
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	184	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	243
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	244	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	303
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	304	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	363
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	364	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	423

Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	424	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	483
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	484	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	543
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	544	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	603
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	604	AGGTGACCCAATTCTATATCAACATTTATTT	634

>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 72 to 642

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	72	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	131
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	132	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	191
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	192	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	251
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	252	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	311
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	312	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	371
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	372	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	431
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420

Sbjct	432	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	491
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	492	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	551
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	552	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	611
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	612	AGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome

Sequence ID: MW429383.1 Length: 14715

Range 1: 132 to 702

Score:1050 bits(568), Expect:0.0,

Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	132	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	191
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	192	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	251
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	252	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	311
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	312	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	371
Query	241	GTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	372	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	431
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	432	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	491
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	492	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	551
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480

Sbjct	552	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAAGTCTTAGCTGGCGC	611
Query	481	AATTACAATATTATTAAGTGATCGAACTTTAATACATCATTCCTTTGACCCTTCAGGAGG	540
Sbjct	612	 AATTACAATATTATTAAGTGATCGAACTTTAATACATCATTCCTTTGACCCTTCAGGAGG	671
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	672	 AGGTGACCCAATTCTATATCAACATTTATTT	702

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>Rhipicephalus linnaei mitochondrion, complete sequence
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Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome

Sequence ID: MW429381.1 Length: 14711

Range 1: 132 to 702

Score:1050 bits(568), Expect:0.0,

Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

[illegible]


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Sbjct  552  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  611
Query  481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  612  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  671
Query  541  AGGTGACCCAATTCTATATCAACATTTATTT  571
          ||||||||||||||||||
Sbjct  672  AGGTGACCCAATTCTATATCAACATTTATTT  702

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>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 72 to 642

Score:1050 bits(568), Expect:0.0,
Identities:570/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query   1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  72  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  131
Query  61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  132  AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  191
Query  121  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  192  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  251
Query  181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG  311
Query  241  GTGAACAGTTTAcCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  312  GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  371
Query  301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA  431
Query  361  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  432  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  491
Query  421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  492  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  551
Query  481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  540

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Sbjct	552		AATTACAATATTATTA	ACTGATCGAAACTTTA	AATACATCATTCTTTG	ACCCTTCAGGAGG	611
Query	541		AGGTGACCCAATTCT	TATATCAACATTTATT	571		
Sbjct	612		AGGTGACCCAATTCT	TATATCAACATTTATT	642		

>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial
Sequence ID: KX053537.1 Length: 658
Range 1: 88 to 658

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC	TTTAATTG	GAAACGATCAA	ATTTATAATG	AATTGTAACAG	CACATGCATTT	ATTAT	60
Sbjct	88	AAC	TTTAATTG	GAAACGATCAA	ATTTATAATG	AATTGTAACAG	CACATGCATTT	ATTAT	147
Query	61	AAt	ttttttt	tATAGTTATA	CCAATTATAA	TCGGAGGATTT	GGAAATTGATT	AGTTCCTAT	120
Sbjct	148	AAT	TTTTTTT	TATAGTTATA	CCAATTATAA	TCGGAGGATTT	GGAAATTGATT	AGTTCCTAT	207
Query	121	TATA	CTAGGAGCT	CCAGATATAG	CATTTCCAC	GAATAAATAA	TATAAGATTTT	TGGTTACT	180
Sbjct	208	TATA	CTAGGAGCT	CCAGATATAG	CATTTCCAC	GAATAAATAA	TATAAGATTTT	TGGTTACT	267
Query	181	TCCT	CCTTCTCT	ATTTCTACTA	ATTAATTCTT	CATTAATCGA	ATCAGGAGCAG	GAACAGG	240
Sbjct	268	TCCT	CCTTCTCT	ATTTCTACTA	ATTAATTCTT	CATTAATCGA	ATCAGGAGCAG	GTACAGG	327
Query	241	GTGA	ACAGTTTA	Acccccccc	TTATCATCAA	ATTTATCACAC	TACGGACCATC	AGTAGATTT	300
Sbjct	328	GTGA	ACAGTTTA	ACCCCCCCT	TATCATCAA	ATTTATCACAC	TACGGACCATC	AGTAGATCT	387
Query	301	AGCT	ATTTTTTT	CTCTGCATCT	TGCAGGTGCT	TCTTCAATTTT	AGGTGCAATCA	ATTTTCAT	360
Sbjct	388	AGCT	ATTTTTTT	CTCTGCATCT	TGCAGGTGCT	TCTTCAATTTT	AGGTGCAATCA	ATTTTCAT	447
Query	361	TACA	ACTATTGT	AAATATACG	ATCCATTGGA	ATAACAATAGA	ACGAATACCATT	ATTTTGT	420
Sbjct	448	TACA	ACTATTGT	AAATATACG	ATCCATTGGA	ATAACAATAGA	ACGAATACCATT	ATTTTGT	507
Query	421	ATGA	TCTGTTTT	AATTACTGCA	ATTTTATTAT	TATTATTATCT	TTTACCAGTCTT	AGCTGGCGC	480
Sbjct	508	ATGA	TCTGTTTT	AATTACTGCA	ATTTTATTAT	TATTATTATCT	TTTACCAGTCTT	AGCTGGCGC	567
Query	481	AATT	ACAATATT	ATTA	ACTGATCGAA	ACTTTAATAC	ATCATTCTTTG	ACCCTTCAGG	540
Sbjct	568	AATT	ACAATATT	ATTA	ACTGATCGAA	ACTTTAATAC	ATCATTCTTTG	ACCCTTCAGG	627

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Query   541  AGGTGACCCAATTCTATATCAACATTTATTT  571
        ||||||||||||||||||||||||||||
Sbjct   628  AGGTGACCCAATTCTATATCAACATTTATTT  658

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>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 50 to 620

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query    1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   50  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  109

Query   61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  110  AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  169

Query  121  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  180
        ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170  TATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  229

Query  181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  230  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG  289

Query  241  GTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  290  GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  349

Query  301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  350  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  409

Query  361  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  410  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  469

Query  421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  470  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  529

Query  481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  530  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  589

Query  541  AGGTGACCCAATTCTATATCAACATTTATTT  571
        ||||||||||||||||||||||||||||
Sbjct  590  AGGTGACCCAATTCTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus voucher D0-311 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360367.1 Length: 658
Range 1: 88 to 658

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 88 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 148 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 208 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 268 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 328 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 387

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 388 AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 447

Query 361 TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 448 TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 508 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 567

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 568 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      ||||||||||||||||||||||||||||
Sbjct 628 AGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 105 to 675

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
          |||
Sbjct 105 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 164

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
          |||
Sbjct 165 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 224

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT 180
          |||
Sbjct 225 TATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT 284

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
          |||
Sbjct 285 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 344

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
          |||
Sbjct 345 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 404

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
          |||
Sbjct 405 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 464

Query 361 TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
          |||
Sbjct 465 TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 524

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
          |||
Sbjct 525 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 584

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
          |||
Sbjct 585 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 644

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
          |||
Sbjct 645 AGGTGACCCAATTCTATATCAACATTTATTT 675
```

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial

Sequence ID: KT906185.1 Length: 690
Range 1: 105 to 675

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 105 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 164

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 165 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 224

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 225 TATACTGGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 284

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 285 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 344

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 345 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 404

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||
Sbjct 405 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 464

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 465 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 524

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 525 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 584

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 585 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 644

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 645 AGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200112.1 Length: 658
>Rhipicephalus sanguineus voucher D0-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX360403.1 Length: 658
Range 1: 88 to 658

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 88 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 148 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 208 TATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 268 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327

Query 241 GTGAACAGTTTAcCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 328 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 387

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||
Sbjct 388 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 447

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 448 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 508 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 567

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 568 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 628 AGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 79 to 649

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
|||||
Sbjct 79 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 138

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
|||||
Sbjct 139 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 198

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
|||||
Sbjct 199 TATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 258

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
|||||
Sbjct 259 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 318

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
|||||
Sbjct 319 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 378

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 360
|||||
Sbjct 379 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 438

Query 361 TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
|||||
Sbjct 439 TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 498

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
|||||
Sbjct 499 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 558

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
|||||
Sbjct 559 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 618

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
|||||
Sbjct 619 AGGTGACCCAATTCTATATCAACATTTATTT 649
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>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 67 to 637

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACAACATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416304.1 Length: 802

Range 1: 67 to 637

Score:1044 bits(565), Expect:0.0,

Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATTTATTAT	126

Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 67 to 637

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120

Sbjct	127	AATTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416297.1 Length: 802

Range 1: 67 to 637

Score:1044 bits(565), Expect:0.0,

Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	AATTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180

Sbjct	187		TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181		TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247		TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241		GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307		GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301		AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367		AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487		ATGATCTGTTTTAATTACTGCAATTTTATTATTACTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541		AGGTGACCCAATTCTATATCAACATTTATTT 571	
Sbjct	607		AGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 67 to 637

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67		AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127		GATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187		TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT

Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416294.1 Length: 802

Range 1: 67 to 637

Score:1044 bits(565), Expect:0.0,

Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	AATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306

Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome
Sequence ID: MW429382.1 Length: 14717
Range 1: 132 to 702

Score:1044 bits(565), Expect:0.0,
Identities:569/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	132	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	191
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	192	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	251
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	252	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	311
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	312	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	371
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300

Sbjct	372	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	431
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	432	AGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	491
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	492	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	551
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	552	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	611
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	612	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	671
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	672	AGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT010523.1 Length: 642
Range 1: 61 to 631

Score:1038 bits(562), Expect:0.0,
Identities:568/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC TTTAATTG GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	61	AAC TTTAATTG GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	120
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	121	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	180
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	181	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT	240
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	241	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	300
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	301	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	360
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360

Sbjct	361		AGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	420
Query	361		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	421		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	480
Query	421		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	481		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	540
Query	481		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	541		AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	600
Query	541		AGGTGACCCAATTCTATATCAACATTTATTT 571	
Sbjct	601		GGGTGACCCAATTCTATATCAACATTTATTT 631	

>Rhipicephalus sanguineus isolate LIC4030B cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KX714597.1 Length: 723
>Rhipicephalus sanguineus isolate 8 cytochrome c oxidase subunit I gene, partial cds; mitochondrial
Sequence ID: MH765337.1 Length: 723
Range 1: 27 to 597

Score:1038 bits(562), Expect:0.0,
Identities:568/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC	TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	27	AAC	TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	86
Query	61	AAt	tttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	87	AAT	TTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	146
Query	121	TATA	CTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	147	TATA	CTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	206
Query	181	TCCT	CTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	207	TCCT	CTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	266
Query	241	GTGA	ACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	267	GTGA	ACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	326
Query	301	AGCT	ATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360

Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	432	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	491
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	492	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	551
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	552	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	611
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	612	GGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383802.1 Length: 763
>Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383803.1 Length: 763
>Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383804.1 Length: 763
Range 1: 67 to 637

Score:1038 bits(562), Expect:0.0,
Identities:568/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTACccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTCAT	360

Sbjct	367	 AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCCTTCAGGAGG	540
Sbjct	547	 AATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	 GGGTGACCCAATTCTATATCAACATTTATTT	637

Score:1038 bits(562), Expect:0.0,
Identities:568/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	408	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	467
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	468	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	527
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	528	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	587
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	588	GGGTGACCCAATTCTATATCAACATTTATTT	618

>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416295.1 Length: 802
Range 1: 67 to 637

Score:1038 bits(562), Expect:0.0,
Identities:568/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486

Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTATATCGACATTTATTT	637

>Rhipicephalus sanguineus mitochondrion, complete genome
Sequence ID: JX416325.1 Length: 14714
Range 1: 1272 to 1842

Score:1038 bits(562), Expect:0.0,
Identities:568/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	1272	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	1331
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	1332	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	1391
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	1392	TATACTAGGAGCTCCAGATGTAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	1451
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	1452	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	1511
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	1512	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	1571
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	1572	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	1631
Query	361	TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	1632	TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	1691
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	1692	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	1751

Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	1752	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	1811
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571	
Sbjct	1812	AGGTGACCCAATTCTATATCAACGTTTATTT	1842	

>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383816.1 Length: 724
Range 1: 72 to 642

Score:1035 bits(560), Expect:0.0,
Identities:567/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC	TTTAATTG	GAAACGATCAA	ATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	72	AAC	TTTAATTG	GAAACGATSAA	ATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	131
Query	61	AAt	tttttttt	tATAGTTATA	CCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	132	AAT	TTTTTTTT	TATAGTTATA	CCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	191
Query	121	TATA	CTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180		
Sbjct	192	TATA	CTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	251		
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240			
Sbjct	252	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	311			
Query	241	GTGAACAGTTTA	AccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300		
Sbjct	312	GTGAACAGTTTA	ACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	371		
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360			
Sbjct	372	AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	431			
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420			
Sbjct	432	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	491			
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480			
Sbjct	492	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	551			
Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540		

Sbjct 552 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 611

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
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Sbjct 612 GGGTGACCCAATTCTATATCAACATTTATTT 642

>Rhipicephalus sanguineus isolate LIC4668G cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX714598.1 Length: 723
 Range 1: 27 to 597

Score:1033 bits(559), Expect:0.0,
 Identities:567/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATTTATTAT 60
 |||

Sbjct 27 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATTTATTAT 86

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
 |||

Sbjct 87 GATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 146

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
 |||

Sbjct 147 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 206

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
 |||

Sbjct 207 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 266

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
 |||

Sbjct 267 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 326

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 360
 |||

Sbjct 327 AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 386

Query 361 TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
 |||

Sbjct 387 TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 446

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
 |||

Sbjct 447 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 506

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
 |||

Sbjct 507 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 566

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571

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      ||||||||||||||||||||
Sbjct  567  GGGTGACCCAATTCTATATCAACATTTATTT  597

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>Rhipicephalus sanguineus isolate LIC6664A cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383797.1 Length: 736
Range 1: 40 to 610

Score:1033 bits(559), Expect:0.0,
Identities:567/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

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Query   1   AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   40   AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  99

Query   61   AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  100   AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  159

Query   121   TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  160   TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT  219

Query   181   TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG  240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  220   TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG  279

Query   241   GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  280   GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  339

Query   301   AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  360
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  340   AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  399

Query   361   TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  400   TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  459

Query   421   ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  460   ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  519

Query   481   AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  520   AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  579

Query   541   AGGTGACCCAATTCTATATCAACATTTATTT  571
      ||||||||||||||||||||
Sbjct  580   GGGTGACCCAATTCTATATCAACATTTATTT  610

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>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416301.1 Length: 802

Range 1: 67 to 637

Score:1033 bits(559), Expect:0.0,

Identities:567/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 67  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 126

Query 61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 127  AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 186

Query 121  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 187  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 246

Query 181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
          |||||||||||| |||||||||||||||||||||||||||||||||||| |||||
Sbjct 247  TCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 306

Query 241  GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 307  GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 366

Query 301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 367  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 426

Query 361  TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 427  TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 486

Query 421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 487  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 546

Query 481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct 547  TATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 606

Query 541  AGGTGACCCAATTCTATATCAACATTTATTT 571
          |||||||||||||||||||||||||||||
Sbjct 607  AGGTGACCCAATTCTATATCAACATTTATTT 637
```

>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 83 to 644

Score:1027 bits(556), Expect:0.0,
Identities:560/562(99%), Gaps:0/562(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 83 AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 142

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 143 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 202

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 203 TATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 262

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 263 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 322

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 323 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 382

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||
Sbjct 383 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 442

Query 361 TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 443 TACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 502

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 503 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 562

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 563 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 622

Query 541 AGGTGACCCAATTCTATATCAA 562
      |||
Sbjct 623 AGGTGACCCAATTCTATATCAA 644
```

>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416303.1 Length: 802

Range 1: 67 to 637

Score:1027 bits(556), Expect:0.0,
Identities:566/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 67 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 126

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 127 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGTTCCTAT 186

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 187 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 246

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 247 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 306

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 307 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 366

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||
Sbjct 367 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAATTTTCAT 426

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 427 TACAACTATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 486

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 487 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGCTGGCGC 546

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 547 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 606

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 607 AGGTGACCCAATTCTATATCAACATTTATTT 637
```

>Rhipicephalus sanguineus isolate RS5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OK576083.1 Length: 716
Range 1: 3 to 573

Score:1022 bits(553), Expect:0.0,

Identities:565/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 3 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 62

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 63 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 122

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 123 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT 182

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 183 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 242

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 243 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 302

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 360
      |||
Sbjct 303 AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCA 362

Query 361 TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 363 TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 422

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 423 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 482

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 483 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 542

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 543 AGGTGACCCAATTCTGTATCAACATTTATTT 573
```

>Rhipicephalus sanguineus isolate RS1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OK576079.1 Length: 716
>Rhipicephalus sanguineus isolate RS3 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OK576081.1 Length: 716
Range 1: 3 to 573

Score:1022 bits(553), Expect:0.0,

Identities:565/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 3 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 62

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 63 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 122

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 123 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT 182

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 183 TCCTCCTTCTCTATTTCTCTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 242

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 243 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 302

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 360
      |||
Sbjct 303 AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCA 362

Query 361 TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 363 TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 422

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 423 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 482

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 483 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 542

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 543 AGGTGACCCAATTCTATATCAACATTTATTT 573
```

>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 88 to 658

Score:1016 bits(550), Expect:0.0,
Identities:564/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
```

Sbjct	88		AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAtttttttt	ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148		AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT		180
Sbjct	208		TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	267
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG		240
Sbjct	268		TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGAACAGTTT	AccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328		GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301	AGCTATTTTTTCTCTGCATCTTGCTGGTCTTCTTCAATTTTAGGTGCAATCAATTTTCAT		360
Sbjct	388		AGCTATCTTTTCTCTGCATCTTGCTGGTCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT		420
Sbjct	448		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC		480
Sbjct	508		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568		AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT		571
Sbjct	628		AGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate RS6 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: OK576084.1 Length: 716

>Rhipicephalus sanguineus isolate RS7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: OK576085.1 Length: 716

Range 1: 3 to 573

Score:1016 bits(550), Expect:0.0,

Identities:564/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
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Sbjct	3	 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	62
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	63	 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAATTCCTAT	122
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	123	 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT	182
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	183	 TCCTCCTTCTCTATTTCTTCTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	242
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	243	 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	302
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	303	 AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	362
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	363	 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	422
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	423	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	482
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	483	 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	542
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT 571	
Sbjct	543	 AGGTGACCCAATTCTATATCAACATTTATTT 573	

>Rhipicephalus sanguineus isolate RS4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OK576082.1 Length: 716
Range 1: 3 to 573

Score:1016 bits(550), Expect:0.0,
Identities:564/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	3	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	62

Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	63	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAATTCCTAT	122
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	123	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAACAATATAAGATTTTGGTTACT	182
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	183	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	242
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	243	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	302
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	303	AGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	362
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	363	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	422
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	423	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	482
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	483	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGGGG	542
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	543	AGGTGACCCAATTCTATATCAACATTTATTT	573

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 80 to 650

Score:1011 bits(547), Expect:0.0,
Identities:563/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	80	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	139
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	140	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	199

Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	200	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAACAATATAAGATTTTGGTTACT	259
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	260	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCGGGTACAGG	319
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	320	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	379
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	380	AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	439
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	440	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	499
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	500	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	559
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	560	AATTACAATATTGTTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	619
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	620	AGGTGACCCAATTCTGTATCAACATTTATTT	650

>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658
Range 1: 88 to 658

Score:1011 bits(547), Expect:0.0,
Identities:563/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATTTATTAT	60
Sbjct	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180

Sbjct	208	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	AGCTATCTTTTCTCTGCATCTTGTGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628	GGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 88 to 658

Score:1011 bits(547), Expect:0.0,
Identities:563/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	208	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240

Sbjct	268	 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	 AGCTATCTTTTCTCTGCATCTTGTGCTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628	 GGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 88 to 658

Score:1011 bits(547), Expect:0.0,
Identities:563/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	 AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	208	 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	267
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327

Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	AGCTATCTTTCTCTGCATCTTGTGGTGTCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628	GGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate RS2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OK576080.1 Length: 716
Range 1: 3 to 573

Score:1011 bits(547), Expect:0.0,
Identities:563/571(99%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	3	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	62
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	63	AATTTTTTTTATAGTCATACCAATTATAATCGGAGGATTTGGAAATTGATTAATTCCTAT	122
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	123	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT	182
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	183	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	242
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	243	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	302

Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	303	AGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	362
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	363	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	422
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	423	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	482
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	483	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGGGG	542
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	543	AGGTGACCCAATTCTATATCAACATTTATTT	573

>Rhipicephalus sanguineus isolate LIC6545A cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX714594.1 Length: 723
Range 1: 27 to 597

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	27	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATTTATTAT	86
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	87	AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	146
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	147	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGTTACT	206
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	207	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	266
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	267	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	326
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360

Sbjct	327	AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	386
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	387	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	446
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	447	ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC	506
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	507	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	566
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	567	AGGTGACCCAATTCTGTATCAACATTTATTT	597

>Rhipicephalus sanguineus isolate LIC4528B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX714593.1 Length: 723
Range 1: 27 to 597

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	27	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATTTATTAT	86
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	87	AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	146
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	147	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT	206
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	207	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	266
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	267	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	326
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	327	AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	386
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420

Sbjct	387		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	446
Query	421		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	447		ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC	506
Query	481		AATTACAATATTATTAACATGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	507		AATTACAATATTATTAACATGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	566
Query	541		AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	567		AGGTGACCCAATTCTGTATCAACATTTATTT	597

>Rhipicephalus leporis isolate Bas-Sassandra-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757912.1 Length: 630
Range 1: 50 to 620

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1		AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	50		AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	109
Query	61		AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	110		AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	169
Query	121		TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	170		TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	229
Query	181		TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	230		TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	289
Query	241		GTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	290		GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	349
Query	301		AGCTATTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	350		AGCTATCTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	409
Query	361		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	410		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	469

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Query   421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   470  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC  529

Query   481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   530  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  589

Query   541  AGGTGACCCAATTCTATATCAACATTTATTT  571
        || |||||||||| ||||||||||||
Sbjct   590  GGGGGACCCAATTCTGTATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383800.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383815.1 Length: 768
Range 1: 72 to 642

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

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Query    1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   72  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATTTATTAT  131

Query    61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  120
        ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   132  AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  191

Query   121  TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   192  TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAACAATATAAGATTTTGGTTACT  251

Query   181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   252  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG  311

Query   241  GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   312  GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  371

Query   301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA  360
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   372  AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCA  431

Query   361  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   432  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  491

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Query   421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  480
          |||
Sbjct   492  ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC  551

Query   481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  540
          |||
Sbjct   552  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  611

Query   541  AGGTGACCCAATTCTATATCAACATTTATTT  571
          |||
Sbjct   612  AGGTGACCCAATTCTGTATCAACATTTATTT  642

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>Rhipicephalus sanguineus isolate LIC5958C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383799.1 Length: 720
Range 1: 24 to 594

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

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Query    1  AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT  60
          |||
Sbjct   24  AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATTTATTAT  83

Query    61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  120
          |||
Sbjct   84  AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT  143

Query   121  TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGTTACT  180
          |||
Sbjct  144  TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAACAATATAAGATTTTGTTACT  203

Query   181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG  240
          |||
Sbjct  204  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG  263

Query   241  GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  300
          |||
Sbjct  264  GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT  323

Query   301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT  360
          |||
Sbjct  324  AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT  383

Query   361  TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  420
          |||
Sbjct  384  TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT  443

Query   421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  480
          |||
Sbjct  444  ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC  503

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Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	504	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	563
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571	
Sbjct	564	AGGTGACCCAATTCTGTATCAACATTTATTT	594	

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383798.1 Length: 698
Range 1: 67 to 637

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60	
Sbjct	67	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATTTATTAT	126	
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120	
Sbjct	127	AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186	
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180	
Sbjct	187	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT	246	
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240	
Sbjct	247	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306	
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300	
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	366	
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360	
Sbjct	367	AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	426	
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420	
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486	
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480	
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC	546	
Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540

Sbjct 547 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 606

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
 |||||

Sbjct 607 AGGTGACCCAATTCTGTATCAACATTTATTT 637

>Rhipicephalus leporis voucher INHM:TC1338 cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KM235720.1 Length: 632
 Range 1: 53 to 623

Score:1005 bits(544), Expect:0.0,
 Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
 |||||

Sbjct 53 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 112

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
 |||||

Sbjct 113 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 172

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
 ||| |||||

Sbjct 173 TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 232

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
 |||||

Sbjct 233 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 292

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
 |||||

Sbjct 293 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT 352

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
 |||||

Sbjct 353 AGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT 412

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
 |||||

Sbjct 413 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 472

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
 |||||

Sbjct 473 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 532

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
 |||||

Sbjct 533 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 592

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571

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      |||||
Sbjct 593 GGGTGACCCAATTCTGTATCAACATTTATTT 623

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>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984979.1 Length: 658
Range 1: 88 to 658

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||||
Sbjct 88  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147

Query 61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||||
Sbjct 148  AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207

Query 121  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      ||| |||||
Sbjct 208  TATCCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267

Query 181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||||
Sbjct 268  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327

Query 241  GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||||
Sbjct 328  GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT 387

Query 301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      ||||| |||||
Sbjct 388  AGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT 447

Query 361  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||||
Sbjct 448  TACAACTATTGTAAATATACGATCCATTGGGATAACAATAGAACGAATACCATTATTTGT 507

Query 421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||||
Sbjct 508  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 567

Query 481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||||
Sbjct 568  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627

Query 541  AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||||
Sbjct 628  GGGTGACCCAATTCTGTATCAACATTTATTT 658

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>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658
Range 1: 88 to 658

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 88  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147

Query 61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 148 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 208 TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 268 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
          ||||||||||||||| ||||||||||||||||||||||||||||| |||||||||||
Sbjct 328 GTGAACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT 387

Query 301 AGCTATTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 360
          ||||||||| ||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct 388 AGCTATTTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCA 447

Query 361 TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 448 TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 508 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 567

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 568 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
          ||||||||||||||| |||||||||||||
Sbjct 628 AGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate RS8 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OK576086.1 Length: 716
Range 1: 3 to 573

Score:1005 bits(544), Expect:0.0,
Identities:562/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 3  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 62

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 63 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAATTCCTAT 122

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 123 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT 182

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 183 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 242

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 243 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 302

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||
Sbjct 303 AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT 362

Query 361 TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 363 TACAAC TATTATAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 422

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 423 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 482

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 483 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 542

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 543 GGGTGACCCAATTCTGTATCAACATTTATTT 573
```

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1
(COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658

Range 1: 93 to 658

Score:1002 bits(542), Expect:0.0,
Identities:558/566(99%), Gaps:0/566(0%), Strand: Plus/Plus

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Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 93 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 152

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 153 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 212

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 213 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT 272

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 273 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCGGGTACAGG 332

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 333 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 392

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||
Sbjct 393 AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT 452

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 453 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 512

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 513 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 572

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 573 AATTACAATATTGTAACTGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 632

Query 541 AGGTGACCCAATTCTATATCAACATT 566
      |||
Sbjct 633 AGGTGACCCAATTCTGTATCAACATT 658
```

>Rhipicephalus sanguineus isolate LIC3635G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX714601.1 Length: 723
Range 1: 27 to 597

Score:1000 bits(541), Expect:0.0,

Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 27 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATTTATTAT 86

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 87 AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 146

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 147 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT 206

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 207 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 266

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 267 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGTAGATTT 326

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 360
      |||
Sbjct 327 AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCA 386

Query 361 TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 387 TACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 446

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 447 ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC 506

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 507 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 566

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 567 AGGTGACCCAATTCTGTATCAACATTTATTT 597
```

>Rhipicephalus sanguineus isolate LIC5273D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX714596.1 Length: 723
Range 1: 27 to 597

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
```


Sbjct	27		86
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	87	AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	146
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	147	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT	206
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	207	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	266
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	267	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGTAGATTT	326
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	327	AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	386
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	387	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	446
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	447	ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC	506
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	507	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	566
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT 571	
Sbjct	567	AGGTGACCCAATTCTGTATCAACATTTATTT 597	

>Rhipicephalus sanguineus isolate LIC6120A cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX714595.1 Length: 723
 Range 1: 27 to 597

Score:1000 bits(541), Expect:0.0,
 Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC	60
Sbjct	27	AAC	86

Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	87	AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	146
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	147	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGGTTACT	206
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	207	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	266
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	267	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGTAGATTT	326
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	327	AGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	386
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	387	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	446
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	447	ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC	506
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	507	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	566
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	567	AGGTGACCCAATTCTGTATCAACATTTATTT	597

>Rhipicephalus leporis isolate Bas-Sassandra-C cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757917.1 Length: 630
Range 1: 50 to 620

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	50	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	109
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	110	AATTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	169

Sbjct	170	TATATTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	229
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	230	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAGTCAGGAGCAGGTACAGG	289
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	290	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	349
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	350	AGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	409
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	410	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	469
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	470	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	529
Query	481	AATTACAATATTATTAACATGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	530	AATTACAATATTATTAACATGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	589
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	590	GGGGGACCCAATTCTGTATCAACATTTATTT	620

>Rhipicephalus leporis isolate Turkana-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757911.1 Length: 633
Range 1: 53 to 623

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	53	AACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	112
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	113	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	172
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	173	TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	232
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240

Sbjct	233	 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	292
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	293	 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	352
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	353	 AGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	412
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	413	 TACAACTATTGTAAATATACGATCTATTGGAATAACAATAGAACGAATACCATTATTTGT	472
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	473	 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	532
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	533	 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	592
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT 571	
Sbjct	593	 AGGTGACCCAATTCTGTATCAACATTTATTT 623	

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 67 to 637

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	67	 AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATTTATTAT	126
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	127	 AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	186
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	187	 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTGTTACT	246
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	247	 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	306

Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	307	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGTAGATTT	366
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	367	AGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT	426
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	427	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	486
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	487	ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGCTGGTGC	546
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	547	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	606
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	607	AGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984985.1 Length: 658
Range 1: 88 to 658

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	208	TATGCTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	267
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGAACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387

Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	AGCTATCTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628	AGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984978.1 Length: 658
Range 1: 88 to 658

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	208	TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGAACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360

Sbjct	388	AGCTATCTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628	AGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984977.1 Length: 658
Range 1: 88 to 658

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	208	TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGAACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301	AGCTATTTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	AGCTATCTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420

Sbjct	448		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508		ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481		AATTACAATATTATTAACATGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568		AATTACAATATTATTAACATGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541		AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628		AGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 88 to 658

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1		AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88		AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61		AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148		AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121		TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	208		TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	267
Query	181		TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268		TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241		GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328		GTGAACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301		AGCTATTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388		AGCTATCTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448		TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507

Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571
Sbjct	628	AGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658
Range 1: 88 to 658

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	180
Sbjct	208	TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	267
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	AGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	TACAACTATGGTAAATATACGATCCATTGGGATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	567

Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540
Sbjct	568	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Query	541	AGGTGACCCAATTCTATATCAACATTTATTT	571	
Sbjct	628	GGGTGACCCAATTCTGTATCAACATTTATTT	658	

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984970.1 Length: 658
Range 1: 88 to 658

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query	1	AAC	TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	60
Sbjct	88	AAC	TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Query	61	AAt	tttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	148	AAT	TTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Query	121	TATA	CTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	208	TAT	GCTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	267
Query	181	TCCT	CCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	268	TCCT	CCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Query	241	GTGA	ACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	328	GTGA	ACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT	387
Query	301	AGCT	ATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	388	AGCT	ATCTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT	447
Query	361	TACA	ACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	448	TACA	ACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Query	421	ATGAT	CTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	508	ATGAT	CTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC	567
Query	481	AATTACAATATTATTA	AACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	540

Sbjct 568 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
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Sbjct 628 AGGTGACCCAATTCTGTATCAACATTTATTT 658

>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984969.1 Length: 658
 Range 1: 88 to 658

Score:1000 bits(541), Expect:0.0,
 Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
 |||

Sbjct 88 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
 |||

Sbjct 148 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
 |||

Sbjct 208 TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
 |||

Sbjct 268 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
 |||

Sbjct 328 GTGAACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT 387

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCA 360
 |||

Sbjct 388 AGCTATCTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCA 447

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
 |||

Sbjct 448 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
 |||

Sbjct 508 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 567

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
 |||

Sbjct 568 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571

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      |||||
Sbjct 628 AGGTGACCCAATTCTGTATCAACATTTATTT 658

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>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW558150.1 Length: 657
Range 1: 69 to 639

Score:1000 bits(541), Expect:0.0,
Identities:561/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

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Query 1  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||||
Sbjct 69  AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 128

Query 61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||||
Sbjct 129  AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATGGATTAGTTCCTAT 188

Query 121  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 189  TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 248

Query 181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||||
Sbjct 249  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 308

Query 241  GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |
Sbjct 309  GGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT 368

Query 301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||||
Sbjct 369  AGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 428

Query 361  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||||
Sbjct 429  TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 488

Query 421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |
Sbjct 489  AGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 548

Query 481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||||
Sbjct 549  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 608

Query 541  AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||||
Sbjct 609  GGGTGACCCAATTCTATATCAACATTTATTT 639

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>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383814.1 Length: 768
Range 1: 72 to 642

Score:994 bits(538), Expect:0.0,
Identities:560/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 72 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATTTATTAT 131

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 132 AATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 191

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 192 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGATTTTGGTTACT 251

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 252 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 311

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 312 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGTAGATTT 371

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 372 AGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAATTTTCAT 431

Query 361 TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 432 TACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 491

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 492 ATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTTTTAGCTGGTGC 551

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 552 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 611

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      ||||||||||||||| |||||||||||||||
Sbjct 612 AGGTGACCCAATTCTGTATCAACATTTATTT 642
```

>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 88 to 658

Score:994 bits(538), Expect:0.0,
Identities:560/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1  AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 88  AACTTTAATTGGAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147

Query 61  AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 148  AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207

Query 121  TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 208  TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267

Query 181  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct 268  TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327

Query 241  GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      ||||||||||||||| ||||||||||||||||||||||||||||| ||||||||||||
Sbjct 328  GTGAACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT 387

Query 301  AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      ||||| || ||||||||||||||| ||||||||||||||||||||||||| |||||||
Sbjct 388  AGCTATCTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT 447

Query 361  TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 448  TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507

Query 421  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      ||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct 508  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 567

Query 481  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct 568  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTTTTTTGACCCTTCAGGAGG 627

Query 541  AGGTGACCCAATTCTATATCAACATTTATTT 571
      ||||||||||||| |||||||||||||
Sbjct 628  AGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658

Range 1: 88 to 658

Score:994 bits(538), Expect:0.0,
Identities:560/571(98%), Gaps:0/571(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
      |||
Sbjct 88 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
      |||
Sbjct 148 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
      |||
Sbjct 208 TATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
      |||
Sbjct 268 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
      |||
Sbjct 328 GTGAACAGTTTACCCTCCCTTATCATCAAATTTATCACACTACGGGCCATCAGTAGATTT 387

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
      |||
Sbjct 388 AGCTATCTTCTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATTAATTTTCAT 447

Query 361 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
      |||
Sbjct 448 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
      |||
Sbjct 508 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGTGC 567

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
      |||
Sbjct 568 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627

Query 541 AGGTGACCCAATTCTATATCAACATTTATTT 571
      |||
Sbjct 628 AGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like
(COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 118 to 665

Score:979 bits(530), Expect:0.0,

Identities:543/549(99%), Gaps:1/549(0%), Strand: Plus/Plus

```
Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
|||||
Sbjct 118 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 177

Query 61 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 120
|||||
Sbjct 178 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 237

Query 121 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 180
|||||
Sbjct 238 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 297

Query 181 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 240
|||||
Sbjct 298 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 357

Query 241 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 300
|||||
Sbjct 358 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 417

Query 301 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 360
|||||
Sbjct 418 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 477

Query 361 TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 420
|||||
Sbjct 478 TACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATCCCATTATTTGT 537

Query 421 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 480
|||||
Sbjct 538 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 597

Query 481 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 540
|||||
Sbjct 598 AATTACAATAATATTAAGTATCGAACTTTAATACATCATTCTTTGACCAGCAGGAGG 657

Query 541 AGGTGACCC 549
||| |||||
Sbjct 658 AGG-GACCC 665
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>Rhipicephalus sanguineus voucher D0-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638
Range 1: 69 to 601

Score:972 bits(526), Expect:0.0,
Identities:530/533(99%), Gaps:0/533(0%), Strand: Plus/Plus

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Query 1 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 60
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Sbjct	69		128
Query	61	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	120
Sbjct	129		188
Query	121	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT	180
Sbjct	189		248
Query	181	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	240
Sbjct	249		308
Query	241	GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	300
Sbjct	309		368
Query	301	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	360
Sbjct	369		428
Query	361	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	420
Sbjct	429		488
Query	421	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	480
Sbjct	489		548
Query	481	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTT	533
Sbjct	549		601

>Rhipicephalus sanguineus isolate A3657 cytochrome c oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: MN223692.1 Length: 535
Range 1: 1 to 524

Score:963 bits(521), Expect:0.0,
Identities:523/524(99%), Gaps:0/524(0%), Strand: Plus/Plus

Query	48	ATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	107
Sbjct	1		60
Query	108	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	167
Sbjct	61		120

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Query 168 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 227
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 180

Query 228 GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 287
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 240

Query 288 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 347
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 300

Query 348 CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 407
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 360

Query 408 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 467
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 420

Query 468 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 527
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 480

Query 528 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 571
          |||||||||||||||||||||||||||||||||||||||
Sbjct 481 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 524

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Query #12: TKCJJ023-19|TKCJ012018B11|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26774 Length: 658

Sequences producing significant alignments:

							Scientific	
Common		Max	Total Query	E	Per.	Acc.		
Description							Name	
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession	
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00	688
MF425995.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00	703
MF425994.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00	702
MF425993.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00	693
MF425992.1								

Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	690
KT906183.1							
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	690
KT906182.1							
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14711
OM368327.1							
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14714
OM368323.1							
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14713
OM368322.1							
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	707
JQ737084.1							
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	658
KF437543.1							
Rhipicephalus linnaei isolate LA032-2 clone JS5930...							
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	14715
MW429383.1							
Rhipicephalus linnaei mitochondrion, complete sequence							
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	14711
NC_060409.1							
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,... Ixodidae							
sp.... NA	1901042	1210	1210	100%	0.0	99.85	658
KX053537.1							
Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690
KT906185.1							
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690
KT906184.1							
Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	658
KF200113.1							
Rhipicephalus linnaei isolate SC931-1 clone JS5927...							
Rhipicephalu... NA	2138177	1210	1210	100%	0.0	99.85	14717
MW429382.1							
Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1205	1205	99%	0.0	99.85	658
KX360367.1							
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	690
KT906186.1							
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	658
KF200112.1							
Rhipicephalus sanguineus mitochondrion, complete genome							
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	14714
JX416325.1							

Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	100.00	661
MZ401443.1							
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	100.00	661
MZ401441.1							
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1192	1192	98%	0.0	99.85	664
MZ401440.1							
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1190	1190	97%	0.0	100.00	664
MG969507.1							
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1188	1188	98%	0.0	99.69	649
KF200084.1							
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	768
KX383817.1							
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	657
MZ401442.1							
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	97%	0.0	100.00	661
MZ401438.1							
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969506.1							
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969505.1							
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969504.1							
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	644
KF200096.1							
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1177	1177	100%	0.0	98.94	658
OM984983.1							
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416302.1							
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416298.1							
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1177	1177	97%	0.0	99.69	670
HM193873.1							
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1175	1175	97%	0.0	99.69	768
KX383820.1							
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	97%	0.0	99.53	724
KX383816.1							

Rhipicephalus linnaei voucher P1/22_18-5	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658	
OM984984.1								
Rhipicephalus linnaei voucher P1/22_8-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658	
OM984974.1								
Rhipicephalus linnaei voucher P1/22_6-2	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658	
OM984973.1								
Rhipicephalus sanguineus isolate SZM2	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416308.1								
Rhipicephalus sanguineus isolate GTF3	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416304.1								
Rhipicephalus sanguineus isolate GBM1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416300.1								
Rhipicephalus sanguineus isolate GBF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416299.1								
Rhipicephalus sanguineus isolate CHF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416297.1								
Rhipicephalus sanguineus isolate DGM1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416296.1								
Rhipicephalus sanguineus isolate FSF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802	
JX416293.1								
Rhipicephalus sanguineus isolate T78D2	cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	100.00	650	
MZ401439.1								
Rhipicephalus sanguineus isolate LIC5762	cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	763	
KX383802.1								
Rhipicephalus linnaei voucher P1/22_16-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658	
OM984979.1								
Rhipicephalus linnaei voucher P1/22_1-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658	
OM984968.1								
Rhipicephalus sanguineus isolate DGF1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802	
JX416295.1								
Rhipicephalus sanguineus isolate FSM1	cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802	
JX416294.1								
Rhipicephalus sanguineus isolate sanguineus0926	cytochrome...							
Rhipicephalu... brown dog tick	34632	1162	1162	99%	0.0	98.77	658	
MH513252.1								
Rhipicephalus linnaei voucher P1/22_19-1	cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658	
OM984985.1								

Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726449.1								
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726429.1								
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726428.1								
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726427.1								
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726426.1								
Rhipicephalus sanguineus voucher D0-306 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1092	1092	91%	0.0	99.33	638	
KX360338.1								

Alignments:

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425994.1 Length: 703

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425996.1 Length: 703

Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	258	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome

Sequence ID: OM368327.1 Length: 14711

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome

Sequence ID: OM368323.1 Length: 14714

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome

Sequence ID: OM368322.1 Length: 14713

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 24 to 681

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	24	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	83
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	84	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	143
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	144	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	203
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	204	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	263

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	264	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	323
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	324	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	383
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	384	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	443
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	444	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	503
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	504	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	563
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	564	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	623
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	624	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	681

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGACGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGACGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome

Sequence ID: MW429383.1 Length: 14715

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	165	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus linnaei mitochondrion, complete sequence

Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome

Sequence ID: MW429381.1 Length: 14711

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAA	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	585	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial
Sequence ID: KX053537.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccCTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	78	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	 AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	 GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT	77

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KF200113.1 Length: 658
 Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
 Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome

Sequence ID: MW429382.1 Length: 14717

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus sanguineus voucher D0-311 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX360367.1 Length: 658
 Range 1: 4 to 658

Score:1205 bits(652), Expect:0.0,
 Identities:654/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

Query	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
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Sbjct	4	 AATATACTTAATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Query	64	CCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Sbjct	64	 CCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Query	124	TGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGG	183
Sbjct	124	 TGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGG	183
Query	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Sbjct	184	 ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Query	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Sbjct	244	 AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Query	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATC	363
Sbjct	304	 AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATC	363
Query	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTC	423
Sbjct	364	 ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTC	423
Query	424	AATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAAC	483
Sbjct	424	 AATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAAC	483
Query	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Sbjct	484	 AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Query	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC	603
Sbjct	544	 ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC	603
Query	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	604	 ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KF200112.1 Length: 658

>Rhipicephalus sanguineus voucher D0-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX360403.1 Length: 658

Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus mitochondrion, complete genome
Sequence ID: JX416325.1 Length: 14714
Range 1: 1185 to 1842

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1185 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 1244

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 1245 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 1304

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 1305 AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG 1364

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 1365 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG 1424

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 1425 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 1484

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 1485 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 1544

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 1545 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC 1604

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 1605 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 1664

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 1665 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 1724

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 1725 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 1784

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 1785 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT 1842
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>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661

Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,

Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

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Query 14  ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 73
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 60

Query 74  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 120

Query 134  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 193
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  CATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 180

Query 194  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 253
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 240

Query 254  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 313
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 300

Query 314  GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA 373
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA 360

Query 374  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 433
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 420

Query 434  GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 493
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 480

Query 494  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 540

Query 554  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT 613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT 600

Query 614  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645
```

>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: MZ401441.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

```
Query 14  ATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 73
          |||
Sbjct 1    ATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 60

Query 74  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 133
          |||
Sbjct 61  TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 120

Query 134  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 193
          |||
Sbjct 121  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 180

Query 194  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATA 253
          |||
Sbjct 181  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATA 240

Query 254  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 313
          |||
Sbjct 241  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 300

Query 314  GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA 373
          |||
Sbjct 301  GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA 360

Query 374  CCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 433
          |||
Sbjct 361  CCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 420

Query 434  GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 493
          |||
Sbjct 421  GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 480

Query 494  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 553
          |||
Sbjct 481  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 540

Query 554  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT 613
          |||
Sbjct 541  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT 600

Query 614  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 601  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645
```

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,
Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

```
Query 11 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 70
|||||
Sbjct 1 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 60

Query 71 GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 130
|||||
Sbjct 61 GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 120

Query 131 GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA 190
|||||
Sbjct 121 GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA 180

Query 191 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 250
|||||
Sbjct 181 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 240

Query 251 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 310
|||||
Sbjct 241 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 300

Query 311 TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC 370
|||||
Sbjct 301 TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC 360

Query 371 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA 430
|||||
Sbjct 361 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA 420

Query 431 GGTGCAATCAATTTCAATACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA 490
|||||
Sbjct 421 GGTGCAATCAATTTCAATACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA 480

Query 491 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 550
|||||
Sbjct 481 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 540

Query 551 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC 610
|||||
Sbjct 541 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC 600

Query 611 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 648
```

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1190 bits(644), Expect:0.0,
Identities:644/644(100%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 1 to 649

Score:1188 bits(643), Expect:0.0,
Identities:647/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

```
Query 10  CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT 69
          |||
Sbjct 1    CTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCAT 60

Query 70  AGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 129
          |||
Sbjct 61  AGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 120

Query 130 AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG 189
          |||
Sbjct 121 AGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGG 180

Query 190 AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA 249
          |||
Sbjct 181 AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA 240

Query 250 TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 309
          |||
Sbjct 241 TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 300

Query 310 ATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTA 369
          |||
Sbjct 301 ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA 360

Query 370 CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 429
          |||
Sbjct 361 CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 420

Query 430 AGGTGCAATCAATTTTCATTACAACATTGTAATATACGATCCATTGGAATAACAATAGA 489
          |||
Sbjct 421 AGGTGCAATCAATTTTCATTACAACATTGTAATATACGATCCATTGGAATAACAATAGA 480

Query 490 ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 549
          |||
Sbjct 481 ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 540

Query 550 ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 609
          |||
Sbjct 541 ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 600

Query 610 CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 601 CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 649
```

>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
          |||
Sbjct 1   TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
          |||
Sbjct 61  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
          |||
Sbjct 121 GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
          |||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
          |||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
          |||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 436
          |||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
          |||
Sbjct 421 ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
          |||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 616
          |||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 601 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
```

>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17  TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
          |||
Sbjct 1    TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
          |||
Sbjct 61  GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
          |||
Sbjct 121 GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
          |||
Sbjct 181  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
          |||
Sbjct 241  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317  GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
          |||
Sbjct 301  GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 436
          |||
Sbjct 361  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437  ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
          |||
Sbjct 421  ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
          |||
Sbjct 481  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 616
          |||
Sbjct 541  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 600

Query 617  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct 601  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
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>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
|||||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
|||||
Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
|||||
Sbjct 121 GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
|||||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
|||||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCA 376
|||||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA 436
|||||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
|||||
Sbjct 421 ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
|||||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 616
|||||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
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Sbjct 601 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query 15  TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
          || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query 75  TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query 135  ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121  ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query 195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query 255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query 315  GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query 375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query 435  CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421  CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query 495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query 555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

Query 615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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      |||||||||||||||||||||||||||||||||||||||
Sbjct  601 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644

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>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query   15  TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
      || |||||||||||||||||||||||||||||||||||||||
Sbjct   1  TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query   75  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
      |||||||||||||||||||||||||||||||||||||||
Sbjct   61  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query   135  ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
      |||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query   195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
      |||||||||||||||||||||||||||||||||||||||
Sbjct   181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query   255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
      |||||||||||||||||||||||||||||||||||||||
Sbjct   241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query   315  GAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGAC 374
      |||||||||||||||||||||||||||||||||||||||
Sbjct   301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query   375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
      |||||||||||||||||||||||||||||||||||||||
Sbjct   361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query   435  CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
      |||||||||||||||||||||||||||||||||||||||
Sbjct   421  CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query   495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
      |||||||||||||||||||||||||||||||||||||||
Sbjct   481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query   555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
      |||||||||||||||||||||||||||||||||||||||
Sbjct   541  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

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Query   615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   601  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644

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>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query   15  TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
        || ||||||||||||||||||||||||||||||||||||||||
Sbjct   1  TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query   75  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   61  TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query   135  ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query   195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query   255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query   315  GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query   375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query   435  CAATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CAATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query   495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query   555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
        ||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 600

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Query   615  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
Sbjct   601  ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644

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>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query    6   TATACTTAATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC 65
          |||
Sbjct    1   TATACTTAATTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCC 60

Query   66   GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG 125
          |||
Sbjct   61   GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG 120

Query   126   TAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGAT 185
          |||
Sbjct   121   TAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGAT 180

Query   186   TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAA 245
          |||
Sbjct   181   TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAA 240

Query   246   ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA 305
          |||
Sbjct   241   ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA 300

Query   306   TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCAC 365
          |||
Sbjct   301   TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCAC 360

Query   366   ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA 425
          |||
Sbjct   361   ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA 420

Query   426   TTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAA 485
          |||
Sbjct   421   TTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAA 480

Query   486   TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT 545
          |||
Sbjct   481   TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT 540

Query   546   CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT 605
          |||

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Sbjct  541  CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT  600
Query  606  CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA  649
          |||||
Sbjct  601  CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA  644

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>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 1 to 658

Score:1177 bits(637), Expect:0.0,
Identities:651/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121     AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG  180
          |||||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC  420
          |||||
Sbjct  361     ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC  420

Query  421     TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT  480
          |||||
Sbjct  421     TTCAATTTTAGGTGCAATTAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT  480

Query  481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||||
Sbjct  481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query  541     ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600

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Sbjct	541		ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416302.1 Length: 802
>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416305.1 Length: 802
>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416306.1 Length: 802
>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416307.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420

Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441

Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 1 to 642

Score:1177 bits(637), Expect:0.0,
Identities:642/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGG-CATGATCCGG-ATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	58
Query	75	TAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	59	TAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	118
Query	135	ATGCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	119	ATGCATTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	178
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	179	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	238
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	239	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	298
Query	315	GAGCAGGTACAGGGTGAACAGTTT AccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	299	GAGCAGGTACAGGGTGAACAGTTT ACCCCCCCTTATCATCAAATTTATCACACTACGGAC	358
Query	375	CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434

Sbjct	359		CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	418
Query	435		CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	419		CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	478
Query	495		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	479		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	538
Query	555		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	539		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	598
Query	615		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	599		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383820.1 Length: 768
Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,
Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360

Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383816.1 Length: 724
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360

Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCTGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttTATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300

Query	322	TACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416304.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321

Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321

Sbjct	241		GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322		TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301		TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382		AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361		AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442		TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421		TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416299.1 Length: 802

Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,

Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1		AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142		TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121		TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240

Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416297.1 Length: 802

Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,

Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAATTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAAATTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240

Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTATTATTACTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTAAC TATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401439.1 Length: 650
Range 1: 1 to 634

Score:1171 bits(634), Expect:0.0,
Identities:634/634(100%), Gaps:0/634(0%), Strand: Plus/Plus

Query	25	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	84
Sbjct	1	 ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	60
Query	85	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	144
Sbjct	61	 AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	120
Query	145	TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	204
Sbjct	121	 TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	180

Query	205	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	264
Sbjct	181	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	240
Query	265	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	324
Sbjct	241	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	300
Query	325	AGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	384
Sbjct	301	AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	360
Query	385	TTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTT	444
Sbjct	361	TTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTT	420
Query	445	CATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	504
Sbjct	421	CATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	480
Query	505	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	564
Sbjct	481	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	540
Query	565	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	624
Sbjct	541	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	600
Query	625	AGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGTGACCCAATTCTATATCAACATTTATTT	634

>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383802.1 Length: 763
 >Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383803.1 Length: 763
 >Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383804.1 Length: 763
 Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
 Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141

Sbjct	61		ACCAGGAAC	TTTAATTG	GAAACGAT	CAAATTTA	AATGTAATT	GTAACAGC	ACATGCATT	120
Query	142		TATTATAA	tttttttt	tATAGTTA	TACCAATT	AATAATCG	GAGGATTT	GGAATTGAT	201
Sbjct	121		TATTATAA	TTTTTTTT	TATAGTTA	TACCAATT	AATAATCG	GAGGATTT	GGAATTGAT	180
Query	202		TCCTATT	TATACTAG	GAGCTCC	AGATATAG	CATTTCC	ACGAATAA	ATAAGATTT	261
Sbjct	181		TCCTATT	TATACTAG	GAGCTCC	AGATATAG	CATTTCC	ACGAATAA	ATAAGATTT	240
Query	262		GTTACTT	CCTCCTT	CTCTATT	TTCTACTA	ATTAATTCT	TTCATTAAT	CGAATCAGG	321
Sbjct	241		GTTACTT	CCTCCTT	CTCTATT	TTCTACTA	ATTAATTCT	TTCATTAAT	CGAATCAGG	300
Query	322		TACAGGG	TGAACAG	TTTAc	cccccc	TTATCAT	CAAATTTAT	CACACTACG	381
Sbjct	301		TACAGGG	TGAACAG	TTTAC	CCCCCT	TATCAT	CAAATTTAT	CACACTACG	360
Query	382		AGATTTA	GCTATTT	TTTCTCT	GCATCTT	GCAGGTG	CTTCTTCA	ATTTTAGGT	441
Sbjct	361		AGATTTA	GCTATTT	TTTCTCT	ACATCTT	GCAGGTG	CTTCTTCA	ATTTTAGGT	420
Query	442		TTTCATT	ACAAC	TATTGTA	AATATAC	GATCCATT	GGAATAACA	ATAGAACGA	501
Sbjct	421		TTTCATT	ACAAC	TATTGTA	AATATAC	GATCCATT	GGAATAACA	ATAGAACGA	480
Query	502		ATTTGT	ATGATCT	GTTTTA	ATTACTG	CAATTTT	ATTATTAT	TCTTTACC	561
Sbjct	481		ATTTGT	ATGATCT	GTTTTA	ATTACTG	CAATTTT	ATTATTAT	TCTTTACC	540
Query	562		TGGCGCA	ATTACA	ATTATTA	ACTGATC	GAAACTTT	AATACATC	ATTCTTTG	621
Sbjct	541		TGGCGCA	ATTACA	ATTATTA	ACTGATC	GAAACTTT	AATACATC	ATTCTTTG	600
Query	622		AGGAGG	AGGTGAC	CCAATT	CTATAT	CAACATTT	TATTT	658	
Sbjct	601		AGGAGG	GGGTGAC	CCAATT	CTATAT	CAACATTT	TATTT	637	

>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984979.1 Length: 658
 Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
 Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984968.1 Length: 658
 Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
 Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416295.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81

Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT	637

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
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Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658
Range 1: 6 to 658

Score:1162 bits(629), Expect:0.0,
Identities:645/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	6	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	65
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	66	AATTCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	125
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	126	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	185
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	186	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	245
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	246	AATAAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	305
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	306	ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	365
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	366	ATCACACTACGGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTC	425
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	426	TTCAATTTTAGGCGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	485
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	486	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	545
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	546	ATTATCTTTACCACTCTTAGCTGGTGAATACAATATTGTAACTGATCGAAACTTTAA	605
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT	653
Sbjct	606	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT	658

>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984985.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984978.1 Length: 658
 Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,

Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984977.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||||| ||||||||
Sbjct 361 ATCACAACACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658

Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATGGTAAATATACGATCCATTGGGAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial

Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGAATACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416301.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCTATTACAATATTATTAAGTATCGAACTTTAATACATTATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT010523.1 Length: 642
Range 1: 1 to 631

Score:1155 bits(625), Expect:0.0,
Identities:629/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

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Query 28 ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG 87
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG 60

Query 88 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 120

Query 148 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 180

Query 208 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 240

Query 268 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 327
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 300

Query 328 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 387
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 360

Query 388 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 447
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct 361 AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 420

Query 448 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 480

Query 508 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 567
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 540

Query 568 AATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 AATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 600

Query 628 AGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||
Sbjct 601 GGGTGACCCAATTCTATATCAACATTTATTT 631
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>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||| |||||||||||||||||||| ||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416303.1 Length: 802
Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,
Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAAttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA  420

Query  442  TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCATTACAACATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC  621
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||||||||||||||||||||||||||||||||||
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Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1153 bits(624), Expect:0.0,
Identities:640/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

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Query 11  TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 70
          |||
Sbjct 3   TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATA 62

Query 71  GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 130
          |||
Sbjct 63  GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 122

Query 131  GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA 190
          |||
Sbjct 123  GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA 182

Query 191  AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 250
          |||
Sbjct 183  AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAAT 242

Query 251  ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 310
          |||
Sbjct 243  ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 302

Query 311  TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC 370
          |||
Sbjct 303  TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC 362

Query 371  GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA 430
          |||
Sbjct 363  GGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA 422

Query 431  GGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA 490
          ||
Sbjct 423  GGC GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA 482

Query 491  CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 550
          |||
Sbjct 483  CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 542

Query 551  CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTC 610
          |||
Sbjct 543  CCAGTCTTAGCTGGTGCAATTACAATATTGTAACTGATCGAAACTTTAATACATCATTC 602

Query 611  TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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|||||
Sbjct  603  TTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 650
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>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1146 bits(620), Expect:0.0,
Identities:631/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

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Query   1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct  31  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 90

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct   91  AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 150

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct   151  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 210

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct   211  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 270

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct   271  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 330

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct   331  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 390

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      |||
Sbjct   391  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 450

Query   421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct   451  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 510

Query   481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct   511  AACAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 570

Query   541  ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct   571  ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATAATATTAAGTATCGAAACTTTAA 630
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Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCC   636
        ||||||||||||||||| ||||||||| |||||
Sbjct   631  TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC   665

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>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG   98
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG   60

Query   99   GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttA   158
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAATTTTTTTTA   120

Query   159  TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG   218
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG   180

Query   219  CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC   278
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC   240

Query   279  TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT   338
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT   300

Query   339  AccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT   398
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTG   458
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTCAATACAATATTG   420

Query   459  TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT   518
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT   480

Query   519  TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT   578
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT   540

Query   579  TATTAACGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA   638
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TATTAACGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA   600

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Query 639 TTCTATATCAACATTTATTT 658
 |||||
 Sbjct 601 TTCTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383800.1 Length: 768
 >Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383815.1 Length: 768
 Range 1: 1 to 642

Score:1136 bits(615), Expect:0.0,
 Identities:633/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
 |||||
 Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
 |||||
 Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
 |||||
 Sbjct 121 GCATTTATTATAAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
 |||||
 Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
 |||||
 Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
 |||||
 Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGACGGTGCTTCTTCAATTTTAGGTGCA 436
 |||||
 Sbjct 361 TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGACGGTGCTTCTTCAATTTTAGGCGCA 420

Query 437 ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
 |||||
 Sbjct 421 ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
 |||||
 Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTC 540

Query	557	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642	

>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383796.1 Length: 744
Range 1: 1 to 618

Score:1131 bits(612), Expect:0.0,
Identities:616/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

Query	41	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA	100
Sbjct	1	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA	60
Query	101	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAttttttttATA	160
Sbjct	61	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAATTTTTTTTATA	120
Query	161	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	220
Sbjct	121	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	180
Query	221	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	280
Sbjct	181	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	240
Query	281	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAc	340
Sbjct	241	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAC	300
Query	341	ccccccTTATCATCAAATTTATCACA	400
Sbjct	301	CCCCCTTATCATCAAATTTATCACA	360
Query	401	CTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACA	460
Sbjct	361	CTACATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACA	420
Query	461	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	520
Sbjct	421	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	480
Query	521	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	580

Sbjct	481	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	540
Query	581	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT	640
Sbjct	541	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATT	600
Query	641	CTATATCAACATTTATTT	658
Sbjct	601	CTATATCAACATTTATTT	618

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383798.1 Length: 698
Range 1: 1 to 637

Score:1127 bits(610), Expect:0.0,
Identities:628/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561

Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383814.1 Length: 768
Range 1: 1 to 642

Score:1125 bits(609), Expect:0.0,
Identities:631/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480

Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480

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Query   502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
        |||
Sbjct   481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC  540

Query   562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
        |||
Sbjct   541  TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query   622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||
Sbjct   601  AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT  637

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>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW558150.1 Length: 657
Range 1: 1 to 639

Score:1120 bits(606), Expect:0.0,
Identities:628/639(98%), Gaps:0/639(0%), Strand: Plus/Plus

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Query   20   GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT  79
        |||
Sbjct    1   GGAGCAGGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT  60

Query   80   CAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA  139
        |||
Sbjct   61   CAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA  120

Query   140  TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  199
        |||
Sbjct   121  TTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATGGATTA  180

Query   200  GTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  259
        |||
Sbjct   181  GTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  240

Query   260  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  319
        |||
Sbjct   241  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  300

Query   320  GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA  379
        |||
Sbjct   301  GGTACAGGGGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCA  360

Query   380  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC  439
        |||
Sbjct   361  GTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC  420

Query   440  AATTTCAATACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCA  499
        |||

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Sbjct  421  AATTTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  480
Query   500  TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA  559
        |||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTATTTGTAGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA  540
Query   560  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  619
        |||||  |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  600
Query   620  TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||||||  |||||||||||||||||||||||||||||||
Sbjct  601  TCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT  639

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>Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726445.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
Query   61      AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT  120
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61      AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT  120
Query   121      AATTGTAACAGCACATGCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGG  180
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121      AATTGTAACAGCACATGCATTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGG  180
Query   181      AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181      AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query   241      AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241      AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query   301      ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT AccccccTTATCATCAAATTT  360
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301      ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT ACCCCCCCTTATCATCAAATTT  360
Query   361      ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
        |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361      ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
Query   421      TTCAATTTTAGGTGCAATCAATTTTATTACAAC TATTGTAAATATACGATCCATTGGAAT  480

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Sbjct	421		TTCAATTTTAGGTGCAATCAATTCATTACAAC	ATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT		540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT		540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA	600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA	600
Query	601		TACA	604	
Sbjct	601		TACA	604	

>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726444.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA	604	
Sbjct	601	TACA	604	

>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420

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Query  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
          |||
Sbjct  421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480

Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

Query  601  TACA  604
          |||
Sbjct  601  TACA  604

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>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
          |||

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Sbjct  361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC  420
Query  421  TTCAATTTTAGGTGCAATCAATTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
      |||
Sbjct  421  TTCAATTTTAGGTGCAATCAATTCATTACAACACTATTGTAAATATACGATCCATTGGAAT  480
Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
      |||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
      |||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601  TACA  604
      |||
Sbjct  601  TACA  604

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>Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726441.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
      |||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT  120
      |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
      |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
      |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
      |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
      |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360
Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC  420

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Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726440.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726438.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726437.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601		TACA 604	
Sbjct	601		TACA 604	

>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121		AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726434.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726433.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241		300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726432.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726430.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726449.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Query	601	TACA 604 	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726429.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726428.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726426.1 Length: 604

Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,

Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638
Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	 GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	 CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120

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Query  140  TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  199
          |||
Sbjct   121  TTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  180

Query  200  GTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  259
          |||
Sbjct   181  GTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  240

Query  260  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  319
          |||
Sbjct   241  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  300

Query  320  GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA  379
          || |||
Sbjct   301  GGNACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCA  360

Query  380  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  439
          |||
Sbjct   361  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  420

Query  440  AATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  499
          |||
Sbjct   421  AATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  480

Query  500  TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA  559
          |||
Sbjct   481  TTATTTGTATGATCTGTTTTAATTACNGCAATTTTATTATTATTATCTTTACCAGTCTTA  540

Query  560  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  619
          |||
Sbjct   541  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  600

Query  620  T    620
          |
Sbjct  601  T    601

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Query #13: TKCJJ056-19|TKCJ012018E08|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26775 Length: 658

Sequences producing significant alignments:

Common		Max	Total Query	E	Per.	Acc.	Scientific
Description							Name
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession
Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	658
KF200113.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							

Rhipicephalu... NA MF425995.1	2138177	1210	1210	100%	0.0	99.85	688
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA MF425994.1	2138177	1210	1210	100%	0.0	99.85	703
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA MF425993.1	2138177	1210	1210	100%	0.0	99.85	702
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA MF425992.1	2138177	1210	1210	100%	0.0	99.85	693
Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...							
Rhipicephalu... brown dog tick 34632 KT906183.1		1210	1210	100%	0.0	99.85	690
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...							
Rhipicephalu... brown dog tick 34632 KT906182.1		1210	1210	100%	0.0	99.85	690
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...							
Rhipicephalu... brown dog tick 34632 OM368327.1		1210	1210	100%	0.0	99.85	14711
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...							
Rhipicephalu... brown dog tick 34632 OM368323.1		1210	1210	100%	0.0	99.85	14714
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...							
Rhipicephalu... brown dog tick 34632 OM368322.1		1210	1210	100%	0.0	99.85	14713
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...							
Rhipicephalu... brown dog tick 34632 JQ737084.1		1210	1210	100%	0.0	99.85	707
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...							
Rhipicephalu... brown dog tick 34632 KF437543.1		1210	1210	100%	0.0	99.85	658
Rhipicephalus linnaei isolate LA032-2 clone JS5930...							
Rhipicephalu... NA MW429383.1	2138177	1210	1210	100%	0.0	99.85	14715
Rhipicephalus linnaei mitochondrion, complete sequence							
Rhipicephalu... NA NC_060409.1	2138177	1210	1210	100%	0.0	99.85	14711
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,...							
sp.... NA KX053537.1	1901042	1205	1205	100%	0.0	99.70	658
Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...							
Rhipicephalu... brown dog tick 34632 KT906185.1		1205	1205	100%	0.0	99.70	690
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...							
Rhipicephalu... brown dog tick 34632 KT906184.1		1205	1205	100%	0.0	99.70	690
Rhipicephalus linnaei isolate SC931-1 clone JS5927...							
Rhipicephalu... NA MW429382.1	2138177	1205	1205	100%	0.0	99.70	14717
Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase...							
Rhipicephalu... brown dog tick 34632 KX360367.1		1199	1199	99%	0.0	99.69	658
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...							

Rhipicephalu... brown dog tick	34632	1199	1199	100%	0.0	99.54	690
KT906186.1							
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1199	1199	100%	0.0	99.54	658
KF200112.1							
Rhipicephalus sanguineus mitochondrion, complete genome							
Rhipicephalu... brown dog tick	34632	1199	1199	100%	0.0	99.54	14714
JX416325.1							
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1197	1197	98%	0.0	100.00	664
MZ401440.1							
Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	98%	0.0	99.84	661
MZ401443.1							
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1186	1186	98%	0.0	99.84	661
MZ401441.1							
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969507.1							
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1182	1182	98%	0.0	99.54	649
KF200084.1							
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1181	1181	97%	0.0	99.84	768
KX383817.1							
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1181	1181	97%	0.0	99.84	657
MZ401442.1							
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1181	1181	97%	0.0	99.84	661
MZ401438.1							
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	664
MG969506.1							
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	664
MG969505.1							
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	664
MG969504.1							
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1173	1173	97%	0.0	99.53	644
KF200096.1							
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984983.1							
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416302.1							
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416298.1							
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidas...							

Rhipicephalu... brown dog tick	34632	1171	1171	97%	0.0	99.53	670
HM193873.1							
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1170	1170	97%	0.0	99.53	768
KX383820.1							
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1166	1166	97%	0.0	99.38	724
KX383816.1							
Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658
OM984984.1							
Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658
OM984974.1							
Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658
OM984973.1							
Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416308.1							
Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416304.1							
Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416300.1							
Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416299.1							
Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416297.1							
Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416296.1							
Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416293.1							
Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.84	650
MZ401439.1							
Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	763
KX383802.1							
Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984979.1							
Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984968.1							
Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	802
JX416295.1							
Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subun...							

Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	802
JX416294.1							
Rhipicephalus sanguineus isolate sanguineus0926 cytochrome...							
Rhipicephalu... brown dog tick	34632	1157	1157	99%	0.0	98.62	658
MH513252.1							
Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984985.1							
Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984978.1							
Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984977.1							
Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984975.1							
Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984971.1							
Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984970.1							
Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984969.1							
Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1155	1155	96%	0.0	99.37	802
JX416301.1							
Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrom...							
Rhipicephalu... brown dog tick	34632	1149	1149	95%	0.0	99.52	642
MT010523.1							
Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1149	1149	100%	0.0	98.18	658
OM984988.1							
Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1149	1149	100%	0.0	98.18	658
OM984976.1							
Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1149	1149	96%	0.0	99.22	802
JX416303.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA	2138177	1147	1147	98%	0.0	98.61	826
MF426003.1							
Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1140	1140	96%	0.0	99.06	665
HM193874.1							
Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1134	1134	94%	0.0	99.68	630
KX757914.1							
Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1131	1131	97%	0.0	98.44	768
KX383800.1							
Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase...							

Rhipicephalu... brown dog tick	34632	1125	1125	93%	0.0	99.51	744
KX383796.1							
Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1122	1122	96%	0.0	98.43	698
KX383798.1							
Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1120	1120	97%	0.0	98.13	768
KX383814.1							
Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1116	1116	96%	0.0	98.27	763
KX383801.1							
Rhipicephalus sanguineus isolate 400 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1114	1114	97%	0.0	98.12	657
MW558150.1							
Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726445.1							
Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726444.1							
Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726443.1							
Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726442.1							
Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726441.1							
Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726440.1							
Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726439.1							
Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726438.1							
Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726437.1							
Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726436.1							
Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726435.1							
Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726434.1							
Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726433.1							
Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subun...							

Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726432.1							
Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726431.1							
Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726430.1							
Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604
MZ726449.1							
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604
MZ726429.1							
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604
MZ726428.1							
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604
MZ726427.1							
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604
MZ726426.1							
Rhipicephalus sanguineus voucher D0-306 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1092	1092	91%	0.0	99.33	638
KX360338.1							

Alignments:

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KF200113.1 Length: 658
 Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,
 Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425994.1 Length: 703
>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425996.1 Length: 703
Range 1: 20 to 677

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	140	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425992.1 Length: 693

Range 1: 20 to 677

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	140	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	380	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	560	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137

Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137

Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome

Sequence ID: OM368327.1 Length: 14711

Range 1: 1185 to 1842

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAA	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATT	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATT	1424
Query	241	AATAAATAATATAAGATTTTGGTTACT	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACT	1484
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGG	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGG	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAG	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAG	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTAT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTAT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAG	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAG	1842

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome
Sequence ID: OM368323.1 Length: 14714
Range 1: 1185 to 1842

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTGGAGCATGATCC	60
Sbjct	1185	GACAATATACTTAATTTTGGAGCATGATCC	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAAC	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAAC	1304

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAA	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome

Sequence ID: OM368322.1 Length: 14713

Range 1: 1185 to 1842

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAA	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 24 to 681

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	24	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	83
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	84	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	143
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	144	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	203
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	204	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	263
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	264	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	323
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	324	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	383
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	384	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	443
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	444	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	503
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	504	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	563
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	564	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	623
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	624	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	681

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome

Sequence ID: MW429383.1 Length: 14715

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
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Sbjct	45	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	585	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus linnaei mitochondrion, complete sequence

Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome

Sequence ID: MW429381.1 Length: 14711

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 45 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 104

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 105 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 164

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 165 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 224

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 225 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 284

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 285 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 344

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 345 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 404

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 405 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 464

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 465 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 524

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 525 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 584

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 585 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 644

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 645 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 702
```

>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053537.1 Length: 658

Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
```

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I
(COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 498 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 558 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I
(COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690

Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 498 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 558 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome

Sequence ID: MW429382.1 Length: 14717
Range 1: 45 to 702

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 45 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 104

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 105 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 164

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 165 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 224

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 225 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 284

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 285 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 344

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 345 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 404

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 405 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC 464

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 465 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 524

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 525 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 584

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 585 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 644

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 645 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 702
```

>Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase subunit 1 (COI)

gene, partial cds; mitochondrial
Sequence ID: KX360367.1 Length: 658
Range 1: 4 to 658

Score:1199 bits(649), Expect:0.0,
Identities:653/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

```
Query 4 AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT 63
      |||
Sbjct 4 AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT 63

Query 64 CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT 123
      |||
Sbjct 64 CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT 123

Query 124 TGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGG 183
      |||
Sbjct 124 TGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGG 183

Query 184 ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAAT 243
      |||
Sbjct 184 ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAAT 243

Query 244 AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT 303
      |||
Sbjct 244 AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT 303

Query 304 AATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATC 363
      |||
Sbjct 304 AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATC 363

Query 364 ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTC 423
      |||
Sbjct 364 ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTC 423

Query 424 AATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAAC 483
      |||
Sbjct 424 AATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAAC 483

Query 484 AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT 543
      |||
Sbjct 484 AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT 543

Query 544 ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC 603
      |||
Sbjct 544 ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC 603

Query 604 ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 604 ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 18 to 675

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
|||||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 498 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 558 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KF200112.1 Length: 658

>Rhipicephalus sanguineus voucher D0-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX360403.1 Length: 658

Range 1: 1 to 658

Score:1199 bits(649), Expect:0.0,

Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
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Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658

>Rhipicephalus sanguineus mitochondrion, complete genome

Sequence ID: JX416325.1 Length: 14714

Range 1: 1185 to 1842

Score:1199 bits(649), Expect:0.0,

Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
          |||
Sbjct 1185   GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 1244

Query 61     AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
          |||
Sbjct 1245   AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 1304

Query 121    AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG 180
          |||
Sbjct 1305   AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG 1364

Query 181    AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
          |||
Sbjct 1365   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG 1424

Query 241    AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
          |||
Sbjct 1425   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 1484

Query 301    ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT 360
          |||
Sbjct 1485   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTT 1544

Query 361    ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
          |||
Sbjct 1545   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 1604

Query 421    TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
          |||
Sbjct 1605   TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 1664

Query 481    AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
          |||
Sbjct 1665   AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 1724

Query 541    ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTTAA 600
          |||
Sbjct 1725   ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTTAA 1784

Query 601    TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          |||
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Sbjct 1785 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT 1842

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 1 to 648

Score:1197 bits(648), Expect:0.0,
Identities:648/648(100%), Gaps:0/648(0%), Strand: Plus/Plus

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Query 11 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 70
|||||
Sbjct 1 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA 60

Query 71 GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 130
|||||
Sbjct 61 GAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA 120

Query 131 GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA 190
|||||
Sbjct 121 GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA 180

Query 191 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 250
|||||
Sbjct 181 AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT 240

Query 251 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 310
|||||
Sbjct 241 ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA 300

Query 311 TCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC 370
|||||
Sbjct 301 TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC 360

Query 371 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA 430
|||||
Sbjct 361 GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA 420

Query 431 GGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA 490
|||||
Sbjct 421 GGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA 480

Query 491 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 550
|||||
Sbjct 481 CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA 540

Query 551 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTC 610
|||||
Sbjct 541 CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTC 600

Query 611 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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|||||
Sbjct 601 TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 648
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>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661
Range 1: 1 to 645

Score:1186 bits(642), Expect:0.0,
Identities:644/645(99%), Gaps:0/645(0%), Strand: Plus/Plus

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Query 14 ATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 73
|||||
Sbjct 1 ATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 60

Query 74 TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 133
|||||
Sbjct 61 TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 120

Query 134 CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 193
|||||
Sbjct 121 CATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 180

Query 194 TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 253
|||||
Sbjct 181 TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 240

Query 254 AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 313
|||||
Sbjct 241 AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 300

Query 314 GGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA 373
|||||
Sbjct 301 GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA 360

Query 374 CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 433
|||||
Sbjct 361 CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 420

Query 434 GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 493
|||||
Sbjct 421 GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 480

Query 494 ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 553
|||||
Sbjct 481 ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 540

Query 554 GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT 613
|||||
Sbjct 541 GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT 600
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Query   614  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645

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>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401441.1 Length: 661
Range 1: 1 to 645

Score:1186 bits(642), Expect:0.0,
Identities:644/645(99%), Gaps:0/645(0%), Strand: Plus/Plus

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Query   14   ATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 73
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct    1   ATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA 60

Query   74   TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 133
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA 120

Query   134  CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 193
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  CATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT 180

Query   194  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 253
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA 240

Query   254  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 313
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA 300

Query   314  GGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA 373
        ||||||| |||||||||||||||||||||||||||||||||||
Sbjct   301  GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA 360

Query   374  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 433
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT 420

Query   434  GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 493
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  GCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA 480

Query   494  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 553
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA 540

Query   554  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT 613
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT 600

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Query   614  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645

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>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

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Query   15   TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   1     TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60

Query   75   TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120

Query   135  ATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  ATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query   195  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 240

Query   255  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 300

Query   315  GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC 374
        ||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   301  GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 360

Query   375  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 434
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   361  CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG 420

Query   435  CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   421  CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 480

Query   495  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
        |||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 540

Query   555  TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
        |||||||||||||||||||||||||||||||||||||||||||

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Sbjct 541 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG 600

Query 615 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
 |||

Sbjct 601 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644

>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KF200084.1 Length: 649
 Range 1: 1 to 649

Score:1182 bits(640), Expect:0.0,
 Identities:646/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

Query 10 CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT 69
 |||

Sbjct 1 CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT 60

Query 70 AGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 129
 |||

Sbjct 61 AGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC 120

Query 130 AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG 189
 |||

Sbjct 121 AGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGG 180

Query 190 AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA 249
 |||

Sbjct 181 AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA 240

Query 250 TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 309
 |||

Sbjct 241 TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA 300

Query 310 ATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTA 369
 |||

Sbjct 301 ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA 360

Query 370 CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 429
 |||

Sbjct 361 CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT 420

Query 430 AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA 489
 |||

Sbjct 421 AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA 480

Query 490 ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 549
 |||

Sbjct 481 ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT 540

Query 550 ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT 609

[illegible]

Score:1181 bits(639), Expect:0.0,
Identities:641/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	557	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642	

>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1181 bits(639), Expect:0.0,
Identities:641/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGACGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGACGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540

Query	557	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642	

>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1181 bits(639), Expect:0.0,
Identities:641/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556

Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554

Sbjct	481		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480

Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480

Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1173 bits(635), Expect:0.0,
Identities:641/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	6	TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC	65
Sbjct	1	TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC	60
Query	66	GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG	125
Sbjct	61	GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG	120
Query	126	TAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGAT	185
Sbjct	121	TAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGAT	180
Query	186	TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAA	245
Sbjct	181	TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAA	240
Query	246	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	305
Sbjct	241	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	300
Query	306	TCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCAC	365
Sbjct	301	TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCAC	360
Query	366	ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	425
Sbjct	361	ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	420
Query	426	TTTtagGTGCAATCAATTTTATTACAACATTGTAATATACGATCCATTGGAATAACAA	485

Sbjct	421	TTT TAGGTGCAATCAATTT CATTACA ACTATTGTAAATATACGATCCATTGGAATAACAA	480
Query	486	TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	545
Sbjct	481	TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	540
Query	546	CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA ACTGATCGAAACTTTAATACAT	605
Sbjct	541	CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA ACTGATCGAAACTTTAATACAT	600
Query	606	CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA	649
Sbjct	601	CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA	644

>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTT CATTACA ACTATTGTAAATATACGATCCATTGGAAT	480

Sbjct	421		TTCAATTTTAGGTGCAATTAATTTTCATTACAAC	ATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540		
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	600	
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658		
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658	

>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416302.1 Length: 802
>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416305.1 Length: 802
>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416306.1 Length: 802
>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416307.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300

Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321

Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:641/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGG-CATGATCCGG-ATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	58
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	59	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	118
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	119	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	178
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	179	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	238
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314

Sbjct	239		GATTTTGGTTACTTCCTCCTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	298
Query	315		GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	299		GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	358
Query	375		CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	359		CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	418
Query	435		CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	419		CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	478
Query	495		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	479		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	538
Query	555		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	539		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	598
Query	615		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	599		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383820.1 Length: 768
Range 1: 1 to 642

Score:1170 bits(633), Expect:0.0,
Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240

Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383816.1 Length: 724
Range 1: 1 to 642

Score:1166 bits(631), Expect:0.0,
Identities:638/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240

Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGAGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGAGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180

Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
 partial cds; mitochondrial
 Sequence ID: JX416304.1 Length: 802
 Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
 Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201

Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201

Sbjct	121		TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT	180
Query	202		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	261
Sbjct	181		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	240
Query	262		GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241		GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322		AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301		TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442		TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421		TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416299.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1		AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120

Query	142	TATTATAA		201
Sbjct	121	TATTATAA		180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG		321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG		300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT		381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT		360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA		441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA		420
Query	442	TTTCATTACAAC		501
Sbjct	421	TTTCATTACAAC		480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC		561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC		540
Query	562	TGGCGCAATTACAATATTATTA		621
Sbjct	541	TGGCGCAATTACAATATTATTA		600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		637

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416297.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA		81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA		60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT		141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT		120

Query	142	TATTATAA		201
Sbjct	121	TATTATAA		180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG		240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG		321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG		300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT		381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT		360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA		441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA		420
Query	442	TTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT		501
Sbjct	421	TTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT		480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC		561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTACTATCTTTACCAGTCTTAGC		540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC		621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC		600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		637

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA		81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA		60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT		141

Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141

Sbjct	61	 ACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MZ401439.1 Length: 650
 Range 1: 1 to 634

Score:1166 bits(631), Expect:0.0,
 Identities:633/634(99%), Gaps:0/634(0%), Strand: Plus/Plus

Query	25	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	84
Sbjct	1	 ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	60

Query	85	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	144
Sbjct	61	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	120
Query	145	TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	204
Sbjct	121	TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	180
Query	205	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	264
Sbjct	181	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	240
Query	265	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAAC	324
Sbjct	241	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	300
Query	325	AGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	384
Sbjct	301	AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	360
Query	385	TTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTT	444
Sbjct	361	TTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTT	420
Query	445	CATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	504
Sbjct	421	CATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	480
Query	505	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	564
Sbjct	481	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	540
Query	565	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	624
Sbjct	541	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	600
Query	625	AGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGTGACCCAATTCTATATCAACATTTATTT	634

>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383802.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383803.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383804.1 Length: 763
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
|||||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
|||||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
|||||
Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
|||||
Sbjct 361 AGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
|||||
Sbjct 421 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
|||||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
|||||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 AGGAGGGGGTGAACCAATTCTATATCAACATTTATTT 637
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>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984979.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC 420
      |||||||||| |||||||||||||||||| |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||| |||||||||||||||||||||||||||||||||| ||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGGAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||||||||||||| |||||||||||||| ||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658

Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||||| |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGAATACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416295.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
      |||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
      |||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
      |||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
      |||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
      |||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
      |||
Sbjct 301 TACAGGGTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
      |||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
      |||
Sbjct 421 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
      |||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
      |||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT 637
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>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene,

partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658
Range 1: 6 to 658

Score:1157 bits(626), Expect:0.0,
Identities:644/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 6 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 65

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 66 AATTCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 125

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 126 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 185

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 186 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 245

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 246 AATAAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 305

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 306 ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 365

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 366 ATCACACTACGGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTC 425

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 426 TTCAATTTTAGGCGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 485

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 486 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 545

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 546 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTGTTAAGTATCGAACTTTAA 605

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT 653
      |||
Sbjct 606 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT 658
```

>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984985.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||||| || |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984978.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||| |||||||||||||||||| || |||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984977.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||| |||||||||||||||||| || |||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||| |||||||||||||||||| ||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||||||||||||||||||||||||||||| ||||||||||||||||
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Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACAACACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAACATTTGTAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAACATATGGTAAATATACGATCCATTGGGAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
```

Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGAATACAATATTATTAAGTATCGAAACTTTAA	600

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Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

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>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416301.1 Length: 802
Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,
Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query   22   AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
        |||
Sbjct   1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query   82   ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
        |||
Sbjct   61   ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query   142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
        |||
Sbjct   121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query   202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
        |||
Sbjct   181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query   262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
        |||
Sbjct   241  GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query   322  AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
        |||
Sbjct   301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query   382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
        |||
Sbjct   361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query   442  TTTCAATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
        |||
Sbjct   421  TTTCAATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query   502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
        |||
Sbjct   481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query   562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
        |||

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Sbjct 541 TGGCGCTATTACAATATTATTAAGTATCGAACTTTAATACATTATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
 |||

Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
 Sequence ID: MT010523.1 Length: 642
 Range 1: 1 to 631

Score:1149 bits(622), Expect:0.0,
 Identities:628/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

Query 28 ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG 87
 |||

Sbjct 1 ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG 60

Query 88 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 147
 |||

Sbjct 61 AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT 120

Query 148 AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 207
 |||

Sbjct 121 AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT 180

Query 208 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 267
 |||

Sbjct 181 TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACT 240

Query 268 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG 327
 |||

Sbjct 241 TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG 300

Query 328 GTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 387
 |||

Sbjct 301 GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT 360

Query 388 AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 447
 |||

Sbjct 361 AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT 420

Query 448 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 507
 |||

Sbjct 421 TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT 480

Query 508 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 567
 |||

Sbjct 481 ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC 540

Query 568 AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG 627

Sbjct	541		AATTACAATATTATTA	ACTGATCGAACTTTA	AATACATCATTCTTT	GACCCTTCAGGAGG	600
Query	628		AGGTGACCCAATTCT	TATATCAACATTTATT			658
Sbjct	601		GGGTGACCCAATTCT	TATATCAACATTTATT			631

>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 1 to 658

Score:1149 bits(622), Expect:0.0,
Identities:646/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTTTTTACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1149 bits(622), Expect:0.0,
Identities:646/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTA	ACTGATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	TACATCATTTTTTGGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658	

>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416303.1 Length: 802
Range 1: 1 to 637

Score:1149 bits(622), Expect:0.0,
Identities:632/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561

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Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC  540
Query  562  TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC  621
          |||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC  600
Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
          |||
Sbjct  601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637

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>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1147 bits(621), Expect:0.0,
Identities:639/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

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Query  11  TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA  70
          |||
Sbjct  3    TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA  62
Query  71  GAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA  130
          |||
Sbjct  63  GAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA  122
Query  131  GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA  190
          |||
Sbjct  123  GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA  182
Query  191  AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT  250
          |||
Sbjct  183  AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAAT  242
Query  251  ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA  310
          |||
Sbjct  243  ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA  302
Query  311  TCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC  370
          |||
Sbjct  303  TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC  362
Query  371  GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA  430
          |||
Sbjct  363  GGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA  422
Query  431  GGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA  490
          ||
Sbjct  423  GGCAGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAA  482
Query  491  CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA  550

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Sbjct	483		CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	542
Query	551		CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTC	610
Sbjct	543		CCAGTCTTAGCTGGTGCAATTACAATATTGTAACTGATCGAAACTTTAATACATCATTC	602
Query	611		TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	603		TTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	650

>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1140 bits(617), Expect:0.0,
Identities:630/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	31	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	90
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	91	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	150
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	151	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	210
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	211	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	270
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	271	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	330
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	331	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	390
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	391	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	450
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	451	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	510

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Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   511  AACAAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 570

Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   571  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAATATTAAGTATCGAAACTTTAA 630

Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCC 636
        ||||||||||||||| ||||||||| |||||
Sbjct   631  TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC 665

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>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1134 bits(614), Expect:0.0,
Identities:618/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG 98
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   1     TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG 60

Query   99   GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttA 158
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   61   GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAATTTTTTTTA 120

Query   159  TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG 218
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   121  TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG 180

Query   219  CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC 278
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   181  CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC 240

Query   279  TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTT 338
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   241  TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT 300

Query   339  AccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT 398
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   301  ACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT 360

Query   399  CTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTG 458
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   361  CTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTG 420

Query   459  TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT 518
        ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   421  TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT 480

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Query   519  TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT  578
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT  540

Query   579  TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA  638
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA  600

Query   639  TTCTATATCAACATTTATTT  658
        ||||||||||||||||
Sbjct   601  TTCTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383800.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383815.1 Length: 768
Range 1: 1 to 642

Score:1131 bits(612), Expect:0.0,
Identities:632/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

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Query   17   TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA  76
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1   TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA  60

Query   77   GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT  136
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT  120

Query   137  GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA  196
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA  180

Query   197  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA  256
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA  240

Query   257  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA  316
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA  300

Query   317  GCAGGAACAGGGTGAACAGTTTAcCCCCCTTATCATCAAATTTATCACACTACGGACCA  376
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA  360

Query   377  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA  436
        |||||||||||||||| |||||||||||||||| ||||||||||||| |||
Sbjct   361  TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGCGCA  420

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Query	437	ATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556	
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTC	540	
Query	557	TTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642	

>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383796.1 Length: 744
Range 1: 1 to 618

Score:1125 bits(609), Expect:0.0,
Identities:615/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

Query	41	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAAC	TTTAATTGGA	100
Sbjct	1	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAAC	TTTAATTGGA	60
Query	101	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAA	tttttttttATA	160
Sbjct	61	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAA	TTTTTTTTTATA	120
Query	161	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	220	
Sbjct	121	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	180	
Query	221	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	280	
Sbjct	181	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	240	
Query	281	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAc	340	
Sbjct	241	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAC	300	
Query	341	ccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	400	
Sbjct	301	CCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	360	
Query	401	CTGCATCTTGCAAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTA	460

Sbjct	361	CTACATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTA	420
Query	461	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	520
Sbjct	421	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	480
Query	521	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	580
Sbjct	481	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	540
Query	581	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT	640
Sbjct	541	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATT	600
Query	641	CTATATCAACATTTATTT	658
Sbjct	601	CTATATCAACATTTATTT	618

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383798.1 Length: 698
Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAA	441

Sbjct	361	 AGATTTAGCTATCTTTTCTCTGCATCTTG CAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTA AACTGATCGAAACTTTAATACATCATTCCTTTGACCCTTC 	621
Sbjct	541	TGGT GCAATTACAATATTATTA AACTGATCGAAACTTTAATACATCATTCCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658 	
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 637	

Score:1120 bits(606), Expect:0.0,
Identities:630/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 1 to 637

Score:1116 bits(604), Expect:0.0,
Identities:626/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360

Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW558150.1 Length: 657
Range 1: 1 to 639

Score:1114 bits(603), Expect:0.0,
Identities:627/639(98%), Gaps:0/639(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCAGGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199
Sbjct	121	TTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	180
Query	200	G TTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259
Sbjct	181	G TTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	240
Query	260	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	319
Sbjct	241	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	300
Query	320	GGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA	379

Sbjct	301	GGTACAGGGGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCA	360
Query	380	GTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	439
Sbjct	361	GTAGATTTAGCTATCTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC	420
Query	440	AATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	499
Sbjct	421	AATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	480
Query	500	TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	559
Sbjct	481	TTATTTGTAGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	540
Query	560	GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	619
Sbjct	541	GCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	600
Query	620	TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	639

>Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726445.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATT TAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATT TAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTT CATTACA ACTATT GTAAATATA CGATCCATT GGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTT CATTACA ACTATT GTAAATATA CGATCCATT GGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA AACTGATCGAAA CTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA AACTGATCGAAA CTTTAA	600
Query	601	TACA 604 	
Sbjct	601	TACA 604	

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>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726444.1 Length: 604
Range 1: 1 to 604
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Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAattttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726441.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726440.1 Length: 604

Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,

Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726438.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726437.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301		ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726434.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726433.1 Length: 604

Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,

Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726432.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726430.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726449.1 Length: 604
Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604 	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MZ726429.1 Length: 604
 Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
 Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MZ726428.1 Length: 604
 Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
 Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60


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Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301     ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360
Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
          |||
Sbjct  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC  420
Query  421     TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480
          |||
Sbjct  421     TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480
Query  481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||
Sbjct  481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541     ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          |||
Sbjct  541     ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601     TACA  604
          |||
Sbjct  601     TACA  604

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>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726426.1 Length: 604
Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

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Sbjct	1	 GACAATATACTTAATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638
Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199
Sbjct	121	TTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	180
Query	200	GTTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259
Sbjct	181	GTTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	240
Query	260	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	319
Sbjct	241	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	300
Query	320	GGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA	379
Sbjct	301	GGNACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCA	360
Query	380	GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	439
Sbjct	361	GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	420
Query	440	AATTTCAATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	499
Sbjct	421	AATTTCAATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	480
Query	500	TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	559
Sbjct	481	TTATTTGTATGATCTGTTTTAATTACNGCAATTTTATTATTATTATCTTTACCAGTCTTA	540
Query	560	GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	619
Sbjct	541	GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	600
Query	620	T 620	
Sbjct	601	T 601	

Query #14: TKCJJ043-19|TKCJ012018D07|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26776 Length: 658

Sequences producing significant alignments:

Common	Max	Total Query	E	Per.	Acc.	Scientific
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Description	Name	Taxid	Score	Score	cover	Value	Ident	Len	Name	Accession
Rhipicephalus sanguineus mitochondrial DNA, complete genome										
Rhipicephalu... brown dog tick		34632		1216	1216	100%	0.0	100.00	14710	
	AF081829.1									
Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase...										
Rhipicephalu... brown dog tick		34632		1140	1140	94%	0.0	99.84	629	
	KX757893.1									
Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase...										
Rhipicephalu... brown dog tick		34632		1129	1129	94%	0.0	99.52	630	
	KX757903.1									
Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidas...										
Rhipicephalu... brown dog tick		34632		1112	1112	94%	0.0	99.03	630	
	KX757909.1									
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...										
Rhipicephalu... brown dog tick		34632		1072	1072	100%	0.0	96.05	692	
	MF426015.1									
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...										
Rhipicephalu... brown dog tick		34632		1066	1066	100%	0.0	95.90	675	
	MF426018.1									
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...										
Rhipicephalu... brown dog tick		34632		1066	1066	100%	0.0	95.90	680	
	MF426016.1									
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...										
Rhipicephalu... brown dog tick		34632		1066	1066	100%	0.0	95.90	693	
	MF426013.1									
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...										
Rhipicephalu... brown dog tick		34632		1066	1066	100%	0.0	95.90	679	
	MF426009.1									
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...										
Rhipicephalu... brown dog tick		34632		1066	1066	100%	0.0	95.90	686	
	MF426007.1									
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...										
Rhipicephalu... brown dog tick		34632		1061	1061	100%	0.0	95.74	697	
	MF426019.1									
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...										
Rhipicephalu... brown dog tick		34632		1061	1061	100%	0.0	95.74	705	
	MF426006.1									
Rhipicephalus sanguineus haplotype III cytochrome oxidase...										
Rhipicephalu... brown dog tick		34632		1061	1061	100%	0.0	95.74	713	
	KU556745.1									
Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidas...										
Rhipicephalu... brown dog tick		34632		1061	1061	100%	0.0	95.74	710	
	MN593344.1									
Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidas...										
Rhipicephalu... brown dog tick		34632		1061	1061	100%	0.0	95.74	710	
	MN593343.1									
Rhipicephalus sanguineus isolate 11N cytochrome oxidase subuni...										
Rhipicephalu... brown dog tick		34632		1061	1061	100%	0.0	95.74	703	
	MN585197.1									
Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene,...										
Rhipicephalu... brown dog tick		34632		1061	1061	100%	0.0	95.74	793	

AF132839.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 680
MF426017.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 690
MF426008.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 684
MF426001.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 689
MF425998.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 695
MF425997.1
Rhipicephalus sanguineus haplotype IV cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1055 1113 100% 0.0 95.59 771
KU556746.1
Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 658
MZ305546.1
Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 658
MZ305545.1
Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 676
MW152145.1
Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 675
MW152144.1
Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 676
MW152143.1
Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1055 1055 100% 0.0 95.59 669
MW152142.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1050 1050 100% 0.0 95.44 684
MF426012.1
Rhipicephalus sanguineus haplotype I cytochrome oxidase subuni...
Rhipicephalu... brown dog tick 34632 1048 1048 98% 0.0 95.83 659
KU556743.1
Rhipicephalus sanguineus haplotype II cytochrome oxidase subun...
Rhipicephalu... brown dog tick 34632 1046 1046 100% 0.0 95.30 787
KU556744.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1038 1038 97% 0.0 95.80 812
MF426020.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1037 1037 98% 0.0 95.52 824
MF426010.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 1031 1031 97% 0.0 95.64 809

MF426011.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1022	1022	94%	0.0	96.30	649
MF426014.1							
Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1020	1020	97%	0.0	95.33	768
KX383818.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1016	1016	94%	0.0	96.14	635
MF426000.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1016	1016	97%	0.0	95.31	654
MF425988.1							
Rhipicephalus sanguineus isolate LIC5533B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1013	1013	96%	0.0	95.30	764
KX383811.1							
Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1011	1011	96%	0.0	95.29	763
KX383807.1							
Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subuni...							
Rhipicephalu... brown dog tick	34632	1009	1009	95%	0.0	95.56	656
KU568516.1							
Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1009	1009	96%	0.0	95.28	762
KX383809.1							
Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1009	1009	96%	0.0	95.28	714
KX383806.1							
Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1007	1007	96%	0.0	95.28	761
KX383805.1							
Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1005	1005	94%	0.0	95.82	644
MH630347.1							
Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1005	1005	94%	0.0	95.82	644
MH630346.1							
Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I...							
Rhipicephalu... brown dog tick	34632	1002	1002	95%	0.0	95.53	654
KX519712.1							
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...							
Rhipicephalu... brown dog tick	34632	1000	1000	95%	0.0	95.38	639
MF426002.1							
Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
MG855658.1							
Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
MG855657.1							
Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630
MG855656.1							
Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome...							
Rhipicephalu... brown dog tick	34632	990	990	94%	0.0	95.48	630

KX757910.1
Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 990 990 94% 0.0 95.48 630
KX757904.1
Rhipicephalus sanguineus isolate Malta-A cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 990 990 94% 0.0 95.48 630
KX757902.1
Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 990 990 94% 0.0 95.48 630
KX757896.1
Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 990 990 94% 0.0 95.48 630
KX757889.1
Rhipicephalus sanguineus isolate Rovind cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 990 990 94% 0.0 95.48 630
KX757887.1
Rhipicephalus sanguineus isolate Kajtasovo cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 990 990 94% 0.0 95.48 630
KX757879.1
Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I...
Rhipicephalu... brown dog tick 34632 990 990 94% 0.0 95.48 636
KX519711.1
Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 990 990 94% 0.0 95.48 630
MW135448.1
Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 985 985 94% 0.0 95.32 630
KX757905.1
Rhipicephalus sanguineus isolate Sibenik cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 985 985 94% 0.0 95.32 630
KX757895.1
Rhipicephalus sanguineus isolate Zadar cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 985 985 94% 0.0 95.32 630
KX757892.1
Rhipicephalus sanguineus isolate Zagreb-A cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 985 985 94% 0.0 95.32 630
KX757890.1
Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 985 985 94% 0.0 95.32 630
KX757888.1
Rhipicephalus sanguineus isolate Petnica cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 985 985 94% 0.0 95.32 630
KX757883.1
Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I...
Rhipicephalu... brown dog tick 34632 985 985 93% 0.0 95.46 629
KX519708.1
Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 985 985 94% 0.0 95.32 630
MW135447.1
Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I...
Rhipicephalu... brown dog tick 34632 983 983 93% 0.0 95.45 626
KX519707.1
Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 979 979 94% 0.0 95.16 630

KX757901.1
Rhipicephalus sanguineus clone #4 cytochrome oxidase subunit I...
Rhipicephalu... brown dog tick 34632 974 974 94% 0.0 95.00 635
KX519709.1
Rhipicephalus sanguineus isolate LIC4723B cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 937 937 90% 0.0 94.97 723
KX714599.1
Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I...
Rhipicephalu... brown dog tick 34632 933 933 88% 0.0 95.69 580
KX519713.1
Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I...
Rhipicephalu... brown dog tick 34632 898 898 86% 0.0 95.09 595
KX519706.1
Rhipicephalus sanguineus isolate Rsang2 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 883 883 100% 0.0 90.90 790
KY678135.1
Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c...
Rhipicephalu... NA 34633 883 883 100% 0.0 90.88 673
MT800313.1
Rhipicephalus sanguineus sensu lato 'temperate lineage' isolat...
Rhipicephalu... brown dog tick 34632 881 881 85% 0.0 95.01 574
MF425987.1
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (CO1)...
Rhipicephalu... brown dog tick 34632 876 876 98% 0.0 91.05 829
KU214592.1
Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase...
Rhipicephalu... NA 34633 872 872 99% 0.0 90.80 678
MT079206.1
Rhipicephalus sanguineus isolate GY34 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 872 872 99% 0.0 90.80 678
MN862754.1
Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome...
Rhipicephalu... brown dog tick 34632 872 872 100% 0.0 90.58 1539
KM494916.1
Rhipicephalus sanguineus isolate Tehran cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 872 872 100% 0.0 90.58 1539
KM494915.1
Rhipicephalus turanicus isolate COX1-18-Sheep cytochrome c...
Rhipicephalu... NA 34633 870 870 99% 0.0 90.56 673
MT800314.1
Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit...
Rhipicephalu... NA 34633 861 861 100% 0.0 90.27 873
KY606303.1
Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit...
Rhipicephalu... NA 34633 861 861 100% 0.0 90.27 873
KY606302.1
Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit...
Rhipicephalu... NA 34633 861 861 100% 0.0 90.27 873
KY606301.1
Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit...
Rhipicephalu... NA 34633 861 861 100% 0.0 90.27 873
KY606300.1
Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit...
Rhipicephalu... NA 34633 861 861 100% 0.0 90.27 873

KY606299.1
Rhipicephalus camicasi isolate SC0126 mitochondrion, complete...
Rhipicephalu... NA 669981 861 861 100% 0.0 90.29 14725
NC_061616.1
Rhipicephalus turanicus voucher CROBB808 cytochrome oxidase...
Rhipicephalu... NA 34633 861 861 100% 0.0 90.27 658
MZ305547.1
Rhipicephalus turanicus isolate Xinjiang-WQIA cytochrome oxida...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
MF002581.1
Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
MF002580.1
Rhipicephalus turanicus isolate Xinjiang-BC cytochrome oxidase...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
MF002579.1
Rhipicephalus turanicus isolate Xinjiang-YC cytochrome oxidase...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
MF002578.1
Rhipicephalus turanicus isolate Xinjiang-PS cytochrome oxidase...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
MF002577.1
Rhipicephalus turanicus isolate SHZ cytochrome oxidase subunit...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
KY069271.1
Rhipicephalus turanicus isolate FK-1 cytochrome oxidase subuni...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
KY606291.1
Rhipicephalus turanicus isolate YN3 cytochrome oxidase subunit...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
KY606290.1
Rhipicephalus turanicus isolate YN2 cytochrome oxidase subunit...
Rhipicephalu... NA 34633 850 850 100% 0.0 89.97 889
KY606289.1

Alignments:

>Rhipicephalus sanguineus mitochondrial DNA, complete genome

Sequence ID: AF081829.1 Length: 14710

Range 1: 1191 to 1848

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1191	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	1250
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	1251	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	1310
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180

Sbjct	1311	 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	1370
Query	181	AGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACG	240
Sbjct	1371	 AGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACG	1430
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	1431	 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	1490
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	1491	 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	1550
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	1551	 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	1610
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	1611	 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	1670
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	1671	 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	1730
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1731	 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	1790
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	1791	 CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	1848

>Rhipicephalus sanguineus isolate Zagreb-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757893.1 Length: 629
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120

Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTCATTAAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTCATTAAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTAACCTGATCGAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Italy-A cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757903.1 Length: 630
 Range 1: 1 to 620

Score:1129 bits(611), Expect:0.0,
 Identities:617/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120

Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAATTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTAAGTATCGAACTTTAACACATCATTTTTTTGACCCTTCAGGAGGAGGAGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus isolate Al-Hosema-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757909.1 Length: 630
Range 1: 1 to 620

Score:1112 bits(602), Expect:0.0,
Identities:614/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158

Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATAATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	240
Query	279	TATTTTTATTGATTAACCTCTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTGATTAACCTCTCATTAATTGAATCTGGAGCTGGAACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ATCCCCCTCTATCTTCAAATTTATCACATTATGGCCCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TATTGACTGATCGAACTTTAACACATCATTTTTTGACCCTTCAGGAGGAGGGGATCCCA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACACTTATTT	620

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S48 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426015.1 Length: 692
Range 1: 19 to 676

Score:1072 bits(580), Expect:0.0,
Identities:632/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120

Sbjct	79	 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	139	 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	259	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	319	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	379	 ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	439	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	499	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	559	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	618
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	619	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S58 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426018.1 Length: 675
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	11	 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	251	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	551	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	610
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S52 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426016.1 Length: 680
Range 1: 12 to 669

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	311
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	312	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	372	ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	432	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	491
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	492	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	552	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	611
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	612	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	669

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S37 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426013.1 Length: 693
Range 1: 20 to 677

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60

Sbjct	20	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	79
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	80	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	139
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	140	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	199
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	319
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	320	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	379
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	380	ATCACATTATGGTCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	500	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	559
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	560	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAACTTTAA	619
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	620	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	677

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S33 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426009.1 Length: 679
Range 1: 11 to 668

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
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Sbjct	11	 AACAATATATTTAATTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	70
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	71	 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	130
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	131	 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	190
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	191	 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	250
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	251	 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	310
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	311	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	370
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	371	 ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	430
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	431	 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	490
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	491	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	550
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	551	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	610
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	611	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	668

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S29 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426007.1 Length: 686
Range 1: 14 to 671

Score:1066 bits(577), Expect:0.0,
Identities:631/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGTCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	554	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S827 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426019.1 Length: 697
Range 1: 19 to 676

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	19	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	78
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	79	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	138
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	139	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	198
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	199	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	258
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	259	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	318
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	319	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	378
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	379	ATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	438
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	439	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	498
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	499	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	558
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	559	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	618
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	619	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	676

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S1060
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426006.1 Length: 705
Range 1: 28 to 685

Score:1061 bits(574), Expect:0.0,

Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 28 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 87

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 88 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 147

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 148 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 207

Query 181 AGGGTTCGGAATTTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 208 AGGATTTGGAAATTTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 267

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 268 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 327

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 328 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 387

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 388 ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 447

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 448 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATTAATTGGAAT 507

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 508 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 567

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 568 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAAGTATCGAAACTTTAA 627

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 628 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 685
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>Rhipicephalus sanguineus haplotype III cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556745.1 Length: 713
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 27 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 86

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 87 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 146

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 147 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 206

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 207 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 266

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC 300
      |||
Sbjct 267 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACTCTTC 326

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 327 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 386

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 387 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 446

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 447 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 506

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 507 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 566

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |||
Sbjct 567 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA 626

Query 601 CACATCATTTTTTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 627 TACATCATTTTTTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 684
```

>Rhipicephalus sanguineus isolate Arizona-1 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593344.1 Length: 710
Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 684 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 625

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 624 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 565

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 564 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 505

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 504 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 445

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||||||||||||||||||||||||||||| || || |||||||||| |||||||
Sbjct 444 AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTTATTAATTAACCTCTTC 385

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||||||||| |||||| |||||||||||||| || |||||||||||||||
Sbjct 384 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 325

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||||||||| || |||||||||||||||||||||||||| |||||||||||
Sbjct 324 ATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 265

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||||||||||||||||| || |||||||||| |||||||||||||||
Sbjct 264 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 205

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||||||||| |||||||||||||||||| |||||||||||||||
Sbjct 204 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 145

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
      | |||||||||||||||||||||||||| |||||||||||||||
Sbjct 144 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 85

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||||||||||||||||| |||||| |||||||||| |||||
Sbjct 84 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 27
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>Rhipicephalus sanguineus isolate Arizona-2 cytochrome c oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MN593343.1 Length: 710

Range 1: 27 to 684

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 684 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 625

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 624 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 565

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 564 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 505

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| ||
Sbjct 504 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 445

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
|||||
Sbjct 444 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 385

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 384 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 325

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 324 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 265

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 264 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 205

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 204 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 145

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
| |||||
Sbjct 144 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 85

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
|||||
Sbjct 84 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 27
```

>Rhipicephalus sanguineus isolate 11N cytochrome oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MN585197.1 Length: 703
Range 1: 22 to 679

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Minus

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Query 1   AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 679 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 620

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 619 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 560

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 559 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 500

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| ||
Sbjct 499 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 440

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
      |||
Sbjct 439 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 380

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 379 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 320

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 319 ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 260

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 259 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 200

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 199 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 140

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
      |
Sbjct 139 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 80

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 79  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 22
```

>Rhipicephalus sanguineus cytochrome c oxidase I (COI) gene, partial cds;

mitochondrial gene for mitochondrial product
Sequence ID: AF132839.1 Length: 793
Range 1: 42 to 699

Score:1061 bits(574), Expect:0.0,
Identities:630/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 42  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 101

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 102  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 161

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 162  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 221

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| || |||
Sbjct 222  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 281

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTT 300
      |||
Sbjct 282  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTT 341

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 342  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 401

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 402  ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 461

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 462  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 521

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 522  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 581

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      | |||
Sbjct 582  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 641

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 642  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 699
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S56 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426017.1 Length: 680
Range 1: 11 to 668

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 11 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 70

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 71 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 130

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 131 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 190

Query 181 AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      ||| ||
Sbjct 191 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 250

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTT 300
      |||
Sbjct 251 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTT 310

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 311 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 370

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 371 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 430

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 431 TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 490

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 491 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 550

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |
Sbjct 551 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 610

Query 601 CACATCATTTTTTGTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 611 TACATCATTTTTTGTATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 668
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S32 cytochrome
c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426008.1 Length: 690
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 14  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 74  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 134  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 193

Query 181  AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 194  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 253

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 254  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 313

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 314  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 374  ATCACATTATGGCCCTTCACTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 434  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 493

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 494  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 553

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
      |
Sbjct 554  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 613

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 614  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 671
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1570
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426001.1 Length: 684
Range 1: 14 to 671

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||
Sbjct 14  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 73

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||
Sbjct 74  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 133

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
          |||
Sbjct 134 AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 193

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          ||| || |||
Sbjct 194  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 253

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
          |||
Sbjct 254  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 313

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||
Sbjct 314  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 373

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||
Sbjct 374  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTC 433

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||
Sbjct 434  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 493

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          |||
Sbjct 494  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 553

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA 600
          | |||
Sbjct 554  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 613

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||
Sbjct 614  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 671
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1553
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425998.1 Length: 689
Range 1: 20 to 677

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 20  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 80  AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 140  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 199

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200  AGGATTTGGAAATTGATTAGTTCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 259

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTCACTATTTTATTAATTAACCTCTTC 319

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 380  ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 500  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 559

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 560  CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 619

Query 601  CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 620  TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 677
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>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1551
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425997.1 Length: 695
Range 1: 22 to 679

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 22  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 81

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 82  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 141

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 142  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 201

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          ||| || |||||||||||||| |||| |||| |||||||||||||||||||||||
Sbjct 202  AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 261

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
          |||||||||||||||||||||||||| || ||| |||||||||| |||||||||||
Sbjct 262  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC 321

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||||||||| |||||| |||||||||||||| || |||||||||||||||||||
Sbjct 322  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 381

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||||||||| || |||||||||||||| |||||||||| |||||||||||
Sbjct 382  ATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 441

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||||||||||||||||| || |||||||||||||| |||||||||||||||||||
Sbjct 442  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 501

Query 481  AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          |||||||||| |||||||||||||||||||||||||||||||||||||| ||||
Sbjct 502  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 561

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
          | |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct 562  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 621

Query 601  CACATCATTTTTTATGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||||||||||||||||| |||||||||| |||||||||| |||||||
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Sbjct 622 TACATCATTTTTTGGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 679

>Rhipicephalus sanguineus haplotype IV cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556746.1 Length: 771
Range 1: 90 to 747

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
|||||
Sbjct 90 AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 149

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT 120
|||||
Sbjct 150 AATTCGTATAGAATTAGGACAACCTGGAACTTAATTGGAAATGATCAGATTTATAATGT 209

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
|||||
Sbjct 210 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 269

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
||| || |||||
Sbjct 270 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 329

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
|||||
Sbjct 330 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 389

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
|||||
Sbjct 390 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTATCCTCCTCTATCTTCAAATTT 449

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
|||||
Sbjct 450 ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 509

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
|||||
Sbjct 510 TTCAATTTTAGGAGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 569

Query 481 AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
|||||
Sbjct 570 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 629

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
| |||||
Sbjct 630 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 689

Query 601 CACATCATTTTTTGGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
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Sbjct 690 |||||TACATCATTTTTTGGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 747

Range 2: 30 to 64

Score:58.4 bits(31), Expect:0.001,
 Identities:34/35(97%), Gaps:1/35(2%), Strand: Plus/Plus

Query 1 AACAAATATATTTAATTTTTGGAGCATGATCA-GGT 34
 |||||
 Sbjct 30 AACAAATATATTTAATTTTTGGAGCATGATCATGGT 64

>Rhipicephalus sanguineus voucher CROBB813 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: MZ305546.1 Length: 658
 Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
 Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
 |||||
 Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
 |||||
 Sbjct 61 AATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
 |||||
 Sbjct 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
 ||| ||
 Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
 |||||
 Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 300

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
 |||||
 Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
 |||||
 Sbjct 361 ATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 420

Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus voucher CROBB810 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MZ305545.1 Length: 658
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420

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Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
          |||
Sbjct 421 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          |||
Sbjct 481 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 540

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA 600
          |
Sbjct 541 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA 600

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
          |||
Sbjct 601 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 658

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>Rhipicephalus sanguineus isolate 5MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152145.1 Length: 676
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||
Sbjct 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120
          |||
Sbjct 61 AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT 120

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
          |||
Sbjct 121 AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          |||
Sbjct 181 AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC 300
          |||
Sbjct 241 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC 300

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          |||
Sbjct 301 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 360

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
          |||

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Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTTATATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate 1MSK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152144.1 Length: 675
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420

Sbjct	361		ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420	
Query	421	TTCAATTTTAGGTGCAATTA	ACTTCATCACA	ACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTA	ACTTTATTACA	ACTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT			540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT			540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA	ACTGATCGAACTTTAA		600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	TAACTGATCGAACTTTAA		600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTTATATCAACACTTATTT			658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGAGGAGATCCAATTTTTATATCAACATTTATTT			658

>Rhipicephalus sanguineus isolate RSN2SK cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MW152143.1 Length: 676
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAA	600
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	658

>Rhipicephalus sanguineus isolate RSN11SK cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW152142.1 Length: 669
Range 1: 1 to 658

Score:1055 bits(571), Expect:0.0,
Identities:629/658(96%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	121	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	180
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	360

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	658

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S358 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF426012.1 Length: 684

Range 1: 14 to 671

Score:1050 bits(568), Expect:0.0,

Identities:628/658(95%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	14	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	73
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	74	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	133
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	134	AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG	193
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	194	AGGATTTGGAAATTGATTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG	253
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	254	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	313
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	314	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	373
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	374	ATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC	433
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	434	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTATAAACATACGATCAATTGGAAT	493
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	494	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	553
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	554	CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	613
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	614	TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	671

>Rhipicephalus sanguineus haplotype I cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU556743.1 Length: 659
Range 1: 12 to 659

Score:1048 bits(567), Expect:0.0,
Identities:621/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	12	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	71
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	72	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	131
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	132	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	191
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	192	AGGATTTGGAAATTGATTAATCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG	251
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	252	AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTC	311
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	312	 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	371
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	372	 ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	431
Query	421	TTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTGTAAATATA CGATCAATTGGAAT	480
Sbjct	432	 TTCAATTTTAGGTGCAATTAAC TTTATTACA ACTATTGTAA ACATAC GATCAATTGGAAT	491
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	492	 AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	551
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA AACTGATCGAAACTTTAA	600
Sbjct	552	 TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAA	611
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCA	648
Sbjct	612	 TACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCA	659

Score:1046 bits(566), Expect:0.0,
Identities:629/660(95%), Gaps:2/660(0%), Strand: Plus/Plus

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	329	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	388
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	389	ATCACATTATGGTCCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	448
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	449	TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT	508
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	509	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT	568
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	569	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA	628
Query	601	CACATCATTTTTTTGATCCTTCAGGAGG-AGGAGATCCC-ATTTTATATCAACACTTATTT	658
Sbjct	629	TACATCATTTTTTTGATCCTTCAGGGGGGAGGAGATCCAAATTTTATATCAACTTTTATTT	688

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S943 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426020.1 Length: 812
Range 1: 2 to 644

Score:1038 bits(562), Expect:0.0,
Identities:616/643(96%), Gaps:0/643(0%), Strand: Plus/Plus

Query	16	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	75
Sbjct	2	TTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATT	61
Query	76	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	135
Sbjct	62	AGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACA	121
Query	136	TGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCTGGAAATTG	195
Sbjct	122	TGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTG	181
Query	196	ATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	255
Sbjct	182	ATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAG	241
Query	256	ATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGG	315
Sbjct	242	ATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGG	301

Query	316	AGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCC	375
Sbjct	302	AGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGTCC	361
Query	376	ATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGC	435
Sbjct	362	TTCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGC	421
Query	436	AATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAAT	495
Sbjct	422	AATTAAC TTTATTACA ACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTAT	481
Query	496	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGT	555
Sbjct	482	ACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGT	541
Query	556	ATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAACACATCATTTTTTTGA	615
Sbjct	542	ATTAGCAGGTGCCATTACAATATTGT TAACTGATCGAACTTTAATACATCATTTTTTTGA	601
Query	616	TCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	602	TCCTTCAGGGGAGGAGATCCAATTTTATATCAACATTTATTT	644

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S337 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426010.1 Length: 824
Range 1: 1 to 648

Score:1037 bits(561), Expect:0.0,
Identities:619/648(96%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	120
Query	131	GCACATGCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGA	190
Sbjct	121	GCACATGCATTTATTATAA TTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTAC CCCCCTCATTATTTTTATTGATTA ACTCTTCATTAATTGAA	310

Sbjct	241	ATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAA	300
Query	311	TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTAT	360
Query	371	GGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA	550
Sbjct	481	CGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTA	540
Query	551	CCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTT	610
Sbjct	541	CCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTT	600
Query	611	TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	TTTGATCCTTCAGGGGAGGAGATCCAATTTTATATCAACACTTATTT	648

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate S344 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426011.1 Length: 809
Range 1: 3 to 644

Score:1031 bits(558), Expect:0.0,
Identities:614/642(96%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	3	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	62
Query	77	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	63	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAC	122
Query	137	GCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTTCGGAAATTGA	196
Sbjct	123	GCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	182
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	183	TTAGTCCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	242
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGA	316

Sbjct	243	 TTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	302
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	303	 GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	362
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	363	 TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	422
Query	437	ATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	423	 ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	482
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	483	 CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	542
Query	557	TTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTGAT	616
Sbjct	543	 TTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGAT	602
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	603	 CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT	644

Score:1022 bits(553), Expect:0.0,
Identities:599/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Query	241	AATAAATAATATAAGATTTTGGACTTTTACCCCCCTCATTATTTTTATTGATTAAGTCTTC	300
Sbjct	268	AATAAATAATATAAGATTTTGGACTTTTACCTCCTTCACTATTTTTATTAATTAAGTCTTC	327
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	328	ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT	387
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	388	ATCACATTATGGTCTTCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	447
Query	421	TTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	448	TTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTGTAAACATACGATCAATTGGAAT	507
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	508	AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	567
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	568	TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTAAGTATCGAAACTTTAA	627
Query	601	CACATCATTTTTTTGATCCTTCA	622
Sbjct	628	TACATCATTTTTTTGATCCTTCA	649

>Rhipicephalus sanguineus isolate LIC5424B cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial

Sequence ID: KX383818.1 Length: 768

>Rhipicephalus sanguineus isolate LIC5554A cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial

Sequence ID: KX383819.1 Length: 768

Range 1: 1 to 642

Score:1020 bits(552), Expect:0.0,

Identities:612/642(95%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTA	60
Query	77	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	136
Sbjct	61	GGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACAT	120
Query	137	GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGA	180

Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA 	256
Sbjct	181	TTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCCCCTCATTATTTTTATTGATTA ACTCTTCATTAATTGAATCCGGA 	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTATTAATTA ACTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA 	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA 	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA 	496
Sbjct	421	ATTAAC TTTATTACA ACTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA 	556
Sbjct	481	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557	TTAGCAGGTGCCATTACAATATTATTA AACTGATCGAAACTTTAACACATCATTTTTTGAT 	616
Sbjct	541	TTAGCAGGTGCCATTACAATATTGT TAACTGATCGAAACTTTAATACATCATTTTTTGAT	600
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658 	
Sbjct	601	CCTTCAGGGGGAGGAGATCCAATTTTATATCAACATTTATTT 642	

Score:1016 bits(550), Expect:0.0,
Identities:598/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

Sbjct	121	GCATTTATTATAATTTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAAATTGA	180
Query	197	TTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTCCCTATCATATTAGGTGCCCCAGATATAGCATTTCACGAATAAATAATATAAGA	240
Query	257	TTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGA	316
Sbjct	241	TTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGA	300
Query	317	GCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCA	376
Sbjct	301	GCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCT	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATA	480
Query	497	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTA	556
Sbjct	481	CCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTA	540
Query	557	TTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTGAT	616
Sbjct	541	TTAGCAGGTGCCATTACAATATTGTTAACCTGATCGAAACTTTAATACATCATTTTTTGAT	600
Query	617	CCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTAT	656
Sbjct	601	CCTTCAGGGGGAGGACATCCAATTTTATATCACCATTAT	640

Score:1013 bits(548), Expect:0.0,
Identities:608/638(95%), Gaps:0/638(0%), Strand: Plus/Plus

Sbjct	61	AACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCAT	120
Query	141	TTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAG	200
Sbjct	121	TTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAG	180
Query	201	TTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	260
Sbjct	181	TCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTT	240
Query	261	GACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTG	320
Sbjct	241	GACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTG	300
Query	321	GAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAG	380
Sbjct	301	GTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAG	360
Query	381	TAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	440
Sbjct	361	TAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	420
Query	441	ACTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCAT	500
Sbjct	421	ACTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCAT	480
Query	501	TATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAG	560
Sbjct	481	TATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAG	540
Query	561	CAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTT	620
Sbjct	541	CAGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTT	600
Query	621	CAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	CAGGGGGAGGAGATCCAATTTTATATCAACATTATTT	638

>Rhipicephalus sanguineus isolate LIC4736B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383807.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383808.1 Length: 763

>Rhipicephalus sanguineus isolate LIC4736F cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383810.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5535C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383813.1 Length: 763

Range 1: 1 to 637

Score:1011 bits(547), Expect:0.0,
Identities:607/637(95%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA 81
|||||
Sbjct 1 AGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACA 60

Query 82 ACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATT 120

Query 142 TATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 CCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 ACTTTTACCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGG 321
|||||
Sbjct 241 ACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGG 300

Query 322 AACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGT 381
|||||
Sbjct 301 TACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGT 360

Query 382 AGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA 441
|||||
Sbjct 361 AGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAA 420

Query 442 CTTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATT 501
|||
Sbjct 421 CTTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATT 480

Query 502 ATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGC 561
|||||
Sbjct 481 ATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGC 540

Query 562 AGGTGCCATTACAATATTATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTC 621
|||||
Sbjct 541 AGGTGCCATTACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTC 600

Query 622 AGGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
|||
Sbjct 601 AGGGGGAGGAGATCCAATTTTATATCAACACTTATTT 637
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>Rhipicephalus sanguineus voucher Rs7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KU568516.1 Length: 656

Range 1: 27 to 656

Score:1009 bits(546), Expect:0.0,
Identities:602/630(96%), Gaps:0/630(0%), Strand: Plus/Plus

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Query 1 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 27 AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 86

Query 61 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 87 AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 146

Query 121 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 147 AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 206

Query 181 AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 207 AGGATTTGGAAATTGATTAATCCCTATCATATTAGGTGCCCCAGATATAGCATTTCCACG 266

Query 241 AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 267 AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 326

Query 301 ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 327 ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 386

Query 361 ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 387 ATCACATTATGGCCCTTCACTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTC 446

Query 421 TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 447 TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 506

Query 481 AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 507 AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACT 566

Query 541 TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 567 CTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAAACTTTAA 626

Query 601 CACATCATTTTTTTGATCCTTCAGGAGGAGG 630
      |||
Sbjct 627 TACATCATTTTTTTGACCCTTCAGGAGGAGG 656
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>Rhipicephalus sanguineus isolate LIC4736D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383809.1 Length: 762
Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

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Query 23 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA 82
      |||
Sbjct 1 GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA 60

Query 83 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT 142
      |||
Sbjct 61 CCTGGAACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT 120

Query 143 ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT 202
      |||
Sbjct 121 ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC 180

Query 203 CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA 262
      |||
Sbjct 181 CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA 240

Query 263 CTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA 322
      |||
Sbjct 241 CTTTTACCTCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT 300

Query 323 ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA 382
      |||
Sbjct 301 ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA 360

Query 383 GATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC 442
      |||
Sbjct 361 GATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC 420

Query 443 TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA 502
      |||
Sbjct 421 TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA 480

Query 503 TTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA 562
      |||
Sbjct 481 TTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA 540

Query 563 GGTGCCATTACAATATTATTAAGTATCGAAACTTTAATACATCATTTTTTATCCTTCA 622
      |||
Sbjct 541 GGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTATCCTTCA 600

Query 623 GGAGGAGGAGATCCCATTTTATATCAACACTTATTT 658
      |||
Sbjct 601 GGGGGAGGAGATCCAATTTTATATCAACACTTATTT 636
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>Rhipicephalus sanguineus isolate LIC4727D cytochrome oxidase subunit 1 (COI)

gene, partial cds; mitochondrial
Sequence ID: KX383806.1 Length: 714
Range 1: 1 to 636

Score:1009 bits(546), Expect:0.0,
Identities:606/636(95%), Gaps:0/636(0%), Strand: Plus/Plus

Query	23	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	82
Sbjct	1	GCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAA	60
Query	83	CCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	142
Sbjct	61	CCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTT	120
Query	143	ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTT	202
Sbjct	121	ATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTC	180
Query	203	CCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	262
Sbjct	181	CCTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGA	240
Query	263	CTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGA	322
Sbjct	241	CTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGT	300
Query	323	ACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTA	382
Sbjct	301	ACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTA	360
Query	383	GATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	442
Sbjct	361	GATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	443	TTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTA	502
Sbjct	421	TTTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTA	480
Query	503	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCA	562
Sbjct	481	TTTGTGTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCA	540
Query	563	GGTGCCATTACAATATTATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCA	622
Sbjct	541	GGTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA	600
Query	623	GGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	GGGGGAGGAGATCCAATTTTATATCAACATTTATTT	636

>Rhipicephalus sanguineus isolate LIC4727C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383805.1 Length: 761
Range 1: 1 to 635

Score:1007 bits(545), Expect:0.0,
Identities:605/635(95%), Gaps:0/635(0%), Strand: Plus/Plus

Query	24	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAAC	83
Sbjct	1	CATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAAC	60
Query	84	CTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	143
Sbjct	61	CTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTA	120
Query	144	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTC	203
Sbjct	121	TTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCC	180
Query	204	CTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	263
Sbjct	181	CTATCATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGAC	240
Query	264	TTTTACCCCCTCATTATTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAA	323
Sbjct	241	TTTTACCTCCTTCACTATTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTA	300
Query	324	CAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAG	383
Sbjct	301	CAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAG	360
Query	384	ATTTAGCTATTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	443
Sbjct	361	ATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC	420
Query	444	TCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTAT	503
Sbjct	421	TTATTACAACCTATTGTAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTAT	480
Query	504	TTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAG	563
Sbjct	481	TTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAG	540
Query	564	GTGCCATTACAATATTATTAACGATCGAAACTTTAACACATCATTTTTTGATCCTTCAG	623
Sbjct	541	GTGCCATTACAATATTGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAG	600
Query	624	GAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	GGGGAGGAGATCCAATTTTATATCAACACTTATTT	635

>Rhipicephalus sanguineus isolate Samont2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630347.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

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Query 1  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 20  AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 120
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 80  AATTGGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG 180
          |||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct 140  AATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATCATAATCGG 199

Query 181  AGGGTTCGGA AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
          ||| || |||||||||||| | ||| |||| ||||||||||||||||||
Sbjct 200  AGGATTTGGAA AATTGATTAGTCCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 259

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTA ACTCTTC 300
          |||||||||||||||||||||||| | || |||||||| | |||||||||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTTATTAATTA ACTCTTC 319

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
          ||||||||| ||||| ||||||||||||| || |||||||||||||||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC 420
          ||||||||| || ||||||||||||||||||||||||| |||||||||
Sbjct 380  ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421  TTCAATTTTAGGTGCAATTA ACTTTCATCACAACTATTGTAAATATACGATCAATTGGAAT 480
          |||||||||||||||||||| | |||||||||||| | |||||||||
Sbjct 440  TTCAATTTTAGGTGCAATTA ACTTTATTACA ACTATTGTAAACATACGATCAATTGGAAT 499

Query 481  AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
          ||||||||| ||||||||||||||||||||||||| ||||||||| |||
Sbjct 500  AACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 559

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAACTTTAA 600
          | ||||||||||||||||||||||||| ||||||||| |||||||||
Sbjct 560  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTTA ACTGATCGAACTTTAA 619

Query 601  CACATCATTTTTTTGATCCTTCA 622
          ||||||||||||||||
Sbjct 620  TACATCATTTTTTTGATCCTTCA 641
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>Rhipicephalus sanguineus isolate Samont1 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MH630346.1 Length: 644
Range 1: 20 to 641

Score:1005 bits(544), Expect:0.0,
Identities:596/622(96%), Gaps:0/622(0%), Strand: Plus/Plus

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Query 1  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 60
      |||
Sbjct 20  AACAAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT 79

Query 61  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 120
      |||
Sbjct 80  AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT 139

Query 121  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 180
      |||
Sbjct 140  AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG 199

Query 181  AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200  AGGATTTGGAAATTGATTAGTTCCTATCATATTGGGTGCCCCAGATATAGCATTTCCACG 259

Query 241  AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC 300
      |||
Sbjct 260  AATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATTTTATTAATTAACCTCTTC 319

Query 301  ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT 360
      |||
Sbjct 320  ATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTT 379

Query 361  ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC 420
      |||
Sbjct 380  ATCACATTATGGCCCTTCACTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC 439

Query 421  TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT 480
      |||
Sbjct 440  TTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAAT 499

Query 481  AACAAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 540
      |||
Sbjct 500  AACAAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT 559

Query 541  TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 560  TTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAA 619

Query 601  CACATCATTTTTTTGATCCTTCA 622
      |||
Sbjct 620  TACATCATTTTTTTGATCCTTCA 641
```

>Rhipicephalus sanguineus clone #7 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519712.1 Length: 654
Range 1: 3 to 628

Score:1002 bits(542), Expect:0.0,
Identities:598/626(96%), Gaps:0/626(0%), Strand: Plus/Plus

Query	33	GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT	92
Sbjct	3	GTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTT	62
Query	93	TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT	152
Sbjct	63	TAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTT	122
Query	153	TCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATAT	212
Sbjct	123	TTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATAT	182
Query	213	TAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCC	272
Sbjct	183	TGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTC	242
Query	273	CCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAA	332
Sbjct	243	CTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAA	302
Query	333	CAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTA	392
Sbjct	303	CAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTA	362
Query	393	TTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAA	452
Sbjct	363	TTTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAA	422
Query	453	CTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGAT	512
Sbjct	423	CTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGAT	482
Query	513	CTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTA	572
Sbjct	483	CTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTA	542
Query	573	CAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAG	632
Sbjct	543	CAATATTGTTAACCTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAG	602
Query	633	ATCCCATTTTATATCAACACTTATTT	658
Sbjct	603	ATCCAATTTTATATCAACATTTATTT	628

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate CR1575
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426002.1 Length: 639
Range 1: 1 to 628

Score:1000 bits(541), Expect:0.0,
Identities:599/628(95%), Gaps:0/628(0%), Strand: Plus/Plus

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Query 31  AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC 90
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   AGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC 60

Query 91  TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT 150
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  TTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT 120

Query 151 TTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTAT 210
          ||| |||||||||||||||||||||||||||| || |||||||||||| |||| ||
Sbjct 121 TTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT 180

Query 211 ATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC 270
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 ATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACC 240

Query 271 CCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATG 330
          || ||| ||||||||| ||||||||||||||||||||| ||||||| |||||||
Sbjct 241 TCCTTCACTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATG 300

Query 331 AACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGC 390
          |||||||| || |||||||||||||||||||||||||||| || |||||||||||||
Sbjct 301 AACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGC 360

Query 391 TATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCAC 450
          ||| ||||||||| |||||||||||||||||||||||||||| || ||||| |||
Sbjct 361 TATCTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTAC 420

Query 451 AACTATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTG 510
          ||||||||| |||||||||||||||||||||||||||| |||||||||||||||||
Sbjct 421 AACTATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTG 480

Query 511 ATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCAT 570
          ||||||||||||||||||||| |||| |||||||||||||||||||||||||||||
Sbjct 481 ATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCAT 540

Query 571 TACAATATTATTAACCTGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGG 630
          |||||||| |||||||||||||||||||| ||||||||||||||||||||| |||||
Sbjct 541 TACAATATTGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGG 600

Query 631 AGATCCCATTTTATATCAACACTTATTT 658
          ||||| ||||||||||||| |||||
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Sbjct 601 AGATCCAATTTTATATCAACATTTATTT 628

>Rhipicephalus sanguineus isolate Rsan-ML4 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855658.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 98
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
          ||||||||||||||||||||| || |||||||||||| |||| |||| ||||
Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
          ||||||||||||||||||||||||||||||||||||||||||||| || |||
Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
          ||||||||| ||||||||||||||||||||| ||||||| |||||||||||||
Sbjct 241 TATTTTTATTAATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
          | || ||||||||||||||||||||||||| || |||||||||||||||||
Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
          ||||| ||||||||||||||||||||||||||||| || |||||||||
Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
          |||| ||||||||||||||||||||||||| |||||||||||||||||
Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
          ||||||||||||| |||| |||||||||||||||||||||||||
Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAAGTATGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
          | ||||||||||||||||| ||||||||||||||||| ||||||||| |
Sbjct 541 TGTTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
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Sbjct 601 ||||| |||||
TTTTATATCAACATTTATT 620

>Rhipicephalus sanguineus isolate Rsan-ML3 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855657.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1		60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61		120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121		180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181		240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241		300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301		360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361		420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421		480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481		540
Query	579	TATTAAGTATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541		600

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Query   639   TTTTATATCAACACTTATTT   658
          |||||
Sbjct   601   TTTTATATCAACATTTATTT   620

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>Rhipicephalus sanguineus isolate Rsan-ML2 cytochrome oxidase subunit I (cox1)
gene, partial cds; mitochondrial
Sequence ID: MG855656.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   98
          |||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
          |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
          |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
          |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
          |||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
          |||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
          |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
          |||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
          |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAAC TGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
          |||||
Sbjct   541  TGTTAAC TGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA   600

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Query   639   TTTTATATCAACACTTATTT   658
          |||||
Sbjct   601   TTTTATATCAACATTTATTT   620

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>Rhipicephalus sanguineus isolate Kehf-Lagareb-A cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757910.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG   98
          |||||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG   60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA   158
          |||||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA   120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG   218
          |||||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG   180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT   278
          |||||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC   240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT   338
          |||||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT   300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT   398
          |||||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT   360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG   458
          |||||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG   420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT   518
          |||||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT   480

Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   578
          |||||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT   540

Query   579  TATTAACGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA   638
          |||||

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Sbjct 541 TGTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query 639 TTTTATATCAACACTTATTT 658
 |||||

Sbjct 601 TTTTATATCAACATTTATTT 620

>Rhipicephalus sanguineus isolate Italy-B cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX757904.1 Length: 630
 Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
 Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query 39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
 |||||

Sbjct 1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query 99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
 |||||

Sbjct 61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query 159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
 |||||

Sbjct 121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query 219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
 |||||

Sbjct 181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query 279 TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
 |||||

Sbjct 241 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query 339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
 |||||

Sbjct 301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query 399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG 458
 |||||

Sbjct 361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG 420

Query 459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
 |||||

Sbjct 421 TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT 480

Query 519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
 |||||

Sbjct 481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query 579 TATTAACGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638


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Sbjct  541  TGTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600
Query   639  TTTTATATCAACTTATTT  658
Sbjct  601  TTTTATATCAACATTTATTT  620

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Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	579	TATTA	ACTGATCGAA	ACTTTA	ACACATCAT	TTTTTT	GATCCTTC	CAGGAGG	GAGAGAT	CCCA	638
Sbjct	541	TGTTA	ACTGATCGAA	ACTTTA	ATACATCAT	TTTTTT	GATCCTTC	CAGGGGG	GAGAGAT	CCAA	600
Query	639	TTTTATATCA	AACTTATTT	658							
Sbjct	601	TTTTATATCA	AATTTATTT	620							

>Rhipicephalus sanguineus isolate Zagreb-C cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757896.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	TTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAAT	TTTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTAT	ATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCAT	ATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTAC	CCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTAC	CTCCTCAC	240
Query	279	TATTTTTATTGATTA	ACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAG	CTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAG	CTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	ACTTCATCACA	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	ACTTTATTACA	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTG	TTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTG	TTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCC	ATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	ATTACAATAT	540

Query	579	TATTA	ACTGATCGAA	ACTTTA	ACATCAT	TTTTTT	GATCCTTC	CAGGAGG	GAGAGAT	CCCA	638
Sbjct	541	TGTTA	ACTGATCGAA	ACTTTA	ATACATCAT	TTTTTT	GATCCTTC	CAGGGGG	GAGAGAT	CCAA	600
Query	639	TTTTATATCA	AACTTATTT	658							
Sbjct	601	TTTTATATCA	AATTTATTT	620							

>Rhipicephalus sanguineus isolate Pula-B cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757889.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAAC	TTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158	
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	120	
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218	
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180	
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278	
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240	
Query	279	TATTTTTATTGATTA	ACTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTA	ACTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398	
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360	
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	AACTTCATCACAACTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTA	AACTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518	
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480	
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578	

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Rovind cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757887.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCACAACTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578

Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
        |||
Sbjct   481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540

Query   579  TATTAAGTATGATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA  638
        | |||
Sbjct   541  TGTTAAGTATGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA  600

Query   639  TTTTATATCAACACTTATTT  658
        |||
Sbjct   601  TTTTATATCAACATTTATTT  620

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>Rhipicephalus sanguineus clone #6 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519711.1 Length: 636
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39   TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  98
        |||
Sbjct   1    TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG  60

Query   99   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  158
        |||
Sbjct   61   GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  120

Query   159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
        |||
Sbjct   121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180

Query   219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
        |||
Sbjct   181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240

Query   279  TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
        |||
Sbjct   241  TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300

Query   339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
        | ||
Sbjct   301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360

Query   399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG  458
        |||
Sbjct   361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG  420

Query   459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518
        |||
Sbjct   421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480

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Query   519 TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 578
        |||
Sbjct   481 TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT 540

Query   579 TATTAAGTATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA 638
        | |||
Sbjct   541 TGTTAAGTATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA 600

Query   639 TTTTATATCAACACTTATTT 658
        |||
Sbjct   601 TTTTATATCAACATTTATTT 620

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>Rhipicephalus sanguineus isolate SV4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135448.1 Length: 630
Range 1: 1 to 620

Score:990 bits(536), Expect:0.0,
Identities:592/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 98
        |||
Sbjct   1 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG 60

Query   99 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 158
        |||
Sbjct   61 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA 120

Query   159 TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG 218
        |||
Sbjct   121 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG 180

Query   219 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT 278
        |||
Sbjct   181 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC 240

Query   279 TATTTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT 338
        |||
Sbjct   241 TATTTTTATTGATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT 300

Query   339 ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT 398
        | |||
Sbjct   301 ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT 360

Query   399 CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTG 458
        |||
Sbjct   361 CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAAGTATTG 420

Query   459 TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT 518
        |||

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Sbjct  421  TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT  480
Query   519  TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  578
          |||
Sbjct  481  TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT  540
Query   579  TATTAAGTATCGAACTTTAACAACATCATTCTTTGATCCTTCAGGAGGAGGAGATCCCA  638
          |||
Sbjct  541  TGTTAAGTATCGAACTTTAATACATCATTCTTTGATCCTTCAGGGGGAGGAGATCCAA  600
Query   639  TTTTATATCAACACTTATTT  658
          |||
Sbjct  601  TTTTATATCAACATTATTT  620

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>Rhipicephalus sanguineus isolate Boka-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757905.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

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Query   39  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  98
          |||
Sbjct   1  TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG  60
Query   99  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA  158
          |||
Sbjct  61  GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA  120
Query  159  TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG  218
          |||
Sbjct 121  TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG  180
Query  219  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT  278
          |||
Sbjct 181  CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC  240
Query  279  TATTTTATTGATTAAGTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT  338
          |||
Sbjct 241  TATTTTATTGATTAAGTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT  300
Query  339  ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT  398
          |||
Sbjct 301  ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT  360
Query  399  CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAACCTATTG  458
          |||
Sbjct 361  CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAGTTCATCACAACCTATTG  420
Query  459  TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT  518

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Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTCTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTCTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Zadar cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757892.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420

Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACTGATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATTACAACATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate Pula-A cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757888.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAATTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACATTG	458

Sbjct	361		420
		CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus isolate Petnica cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757883.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAGTTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAATGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTCAGTAGATTTAGCTATTTTTT	360

Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAACCTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAACCTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus clone #3 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519708.1 Length: 629
Range 1: 4 to 620

Score:985 bits(533), Expect:0.0,
Identities:589/617(95%), Gaps:0/617(0%), Strand: Plus/Plus

Query	42	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	101
Sbjct	4	GACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAA	63
Query	102	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAG	161
Sbjct	64	ATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAG	123
Query	162	TTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCC	221
Sbjct	124	TTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCC	183
Query	222	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTAT	281
Sbjct	184	CAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTAT	243
Query	282	TTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATC	341
Sbjct	244	TTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACC	303
Query	342	CCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTC	401
Sbjct	304	CTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTC	363

Query	402	TTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAA	461
Sbjct	364	TTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAA	423
Query	462	ATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAA	521
Sbjct	424	ACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAA	483
Query	522	TTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTAT	581
Sbjct	484	TTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGT	543
Query	582	TAACTGATCGAAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATT	641
Sbjct	544	TAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATT	603
Query	642	TATATCAACACTTATTT	658
Sbjct	604	TATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate SV2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW135447.1 Length: 630
Range 1: 1 to 620

Score:985 bits(533), Expect:0.0,
Identities:591/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	61	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300
Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398

Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGACCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTATTT	620

>Rhipicephalus sanguineus clone #2 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519707.1 Length: 626
Range 1: 1 to 616

Score:983 bits(532), Expect:0.0,
Identities:588/616(95%), Gaps:0/616(0%), Strand: Plus/Plus

Query	43	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	102
Sbjct	1	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAA	60
Query	103	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGT	162
Sbjct	61	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT	120
Query	163	TATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCC	222
Sbjct	121	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	180
Query	223	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATT	282
Sbjct	181	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	240
Query	283	TTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC	342
Sbjct	241	TTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	300
Query	343	CCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT	402

Sbjct	301	 TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTCTCT	360
Query	403	TCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAA	462
Sbjct	361	 TCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTATTACAACCTATTGTAAA	420
Query	463	TATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT	522
Sbjct	421	 CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT	480
Query	523	TACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT	582
Sbjct	481	 TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT	540
Query	583	AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTT	642
Sbjct	541	 AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTT	600
Query	643	ATATCAACACTTATTT 658	
Sbjct	601	 ATATCAACATTTATTT 616	

>Rhipicephalus sanguineus isolate Szekszard cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: KX757901.1 Length: 630
Range 1: 1 to 620

Score:979 bits(530), Expect:0.0,
Identities:590/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	1	 TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	60
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTA	158
Sbjct	61	 GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	121	 TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	180
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	181	 CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	240
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	241	 TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	300

Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTT	360
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTG	458
Sbjct	361	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTG	420
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	421	TAAACATACGGTCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	480
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	481	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAACACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	541	TGTTAAGTATCGAACTTTAATACATCATTTTTTTGATCCTTCAGGGGGAGGAGATCCAA	600
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	601	TTTTATATCAACATTTATTT	620

>Rhipicephalus sanguineus clone #4 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519709.1 Length: 635
Range 1: 2 to 621

Score:974 bits(527), Expect:0.0,
Identities:589/620(95%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	98
Sbjct	2	TAGGACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTG	61
Query	99	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTTA	158
Sbjct	62	GAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCTTTTATTATAATTTTCTTTA	121
Query	159	TAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTG	218
Sbjct	122	TAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTG	181
Query	219	CCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCAT	278
Sbjct	182	CCCCGGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCAC	241
Query	279	TATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTT	338
Sbjct	242	TATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTT	301

Query	339	ATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	302	ACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGGAGATTTAGCTATTTTTT	361
Query	399	CTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTCATCACAACTATTG	458
Sbjct	362	CTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAAC TTTATTACAAC TATTG	421
Query	459	TAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTT	518
Sbjct	422	TAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTT	481
Query	519	TAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	578
Sbjct	482	TAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATAT	541
Query	579	TATTAAC TGATCGAAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCA	638
Sbjct	542	TGTTAAC TGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAA	601
Query	639	TTTTATATCAACACTTATTT	658
Sbjct	602	TTTTATATCAACATTTATTT	621

Score:937 bits(507), Expect:0.0,
Identities:567/597(95%), Gaps:0/597(0%), Strand: Plus/Plus

Query	302	TTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTA	361
Sbjct	241	TTAATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCCTCCTCTATCTTCAAATTTA	300
Query	362	TCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCT	421
Sbjct	301	TCACATTATGGCCCTTCAGTAGATTTAGCTATCTTTCTCTTCATCTTGCTGGTGCTTCT	360
Query	422	TCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATA	481
Sbjct	361	TCAATTTTAGGTGCAATTAACCTTTATTACAACCTATTGTAAACATACGATCAATTGGAATA	420
Query	482	ACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTT	541
Sbjct	421	ACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTATTACTT	480
Query	542	CTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAAC	601
Sbjct	481	TTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTAACTGATCGAACTTTAAT	540
Query	602	ACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	541	ACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCAATTTTATATCAACACTTATTT	597

>Rhipicephalus sanguineus clone #8 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519713.1 Length: 580
Range 1: 1 to 580

Score:933 bits(505), Expect:0.0,
Identities:555/580(96%), Gaps:0/580(0%), Strand: Plus/Plus

Query	43	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAA	102
Sbjct	1	ACTTAGTATAAGAATATTAATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAA	60
Query	103	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGT	162
Sbjct	61	TGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTTTTTATAGT	120
Query	163	TATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCC	222
Sbjct	121	TATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATCATATTGGGTGCCCC	180
Query	223	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATT	282
Sbjct	181	AGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCACTATT	240
Query	283	TTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCC	342

Sbjct	241	TTTATTAATTA	ACTCTTCATTA	AATTGAATCTGGAGCTGGTACAGGATGAACAGTTTACCC	300
Query	343	CCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCT			402
Sbjct	301	TCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATTTTTTCTCT			360
Query	403	TCACCTTGCTGGTGTCTTCTTCAATTTTAGGTGCAATTA	ACTTCATCACA	ACTATTGTAAA	462
Sbjct	361	TCATCTTGCTGGTGTCTTCTTCAATTTTAGGTGCAATTA	ACTTTATTACA	ACTATTGTAAA	420
Query	463	TATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAAT			522
Sbjct	421	CATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTTTTAAT			480
Query	523	TACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATT			582
Sbjct	481	TACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTGTT			540
Query	583	AACTGATCGAAACTTTAACACATCATTTTTTTGATCCTTCA		622	
Sbjct	541	AACTGATCGAAACTTTAATACATCATTTTTTTGATCCTTCA		580	

>Rhipicephalus sanguineus clone #1 cytochrome oxidase subunit I (COI) gene,
partial cds; mitochondrial
Sequence ID: KX519706.1 Length: 595
Range 1: 1 to 570

Score:898 bits(486), Expect:0.0,
Identities:542/570(95%), Gaps:0/570(0%), Strand: Plus/Plus

Query	89	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA			148
Sbjct	1	ACTTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATA			60
Query	149	ATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATT			208
Sbjct	61	ATTTTTTTTATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATC			120
Query	209	ATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA			268
Sbjct	121	ATATTGGGTGCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTA			180
Query	269	CCCCCTCATTATTTTTATTGATTA	ACTCTTCATTA	AATTGAATCCGGAGCTGGAACAGGA	328
Sbjct	181	CCTCCTTCACTATTTTTATTAATTA	ACTCTTCATTA	AATTGAATCTGGAGCTGGTACAGGA	240
Query	329	TGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTA			388
Sbjct	241	TGAACAGTTTACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTA			300
Query	389	GCTATTTTTTCTCTTCACCTTGCTGGTGTCTTCTTCAATTTTAGGTGCAATTA	ACTTCATC		448

Sbjct	301	GCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACTTTATT	360
Query	449	ACAAC TATTGTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTT	508
Sbjct	361	ACAAC TATTGTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTT	420
Query	509	TGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCC	568
Sbjct	421	TGATCTGTTTTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCC	480
Query	569	ATTACAATATTATTAAC TGATCGAAACTTTAACACATCATTTTTTGATCCTTCAGGAGGA	628
Sbjct	481	ATTACAATATTGTTAACTGATCGAAACTTTAATACATCATTTTTTGATCCTTCAGGGGGA	540
Query	629	GGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	541	GGAGATCCAATTTTATATCAACATTTATTT	570

Score:883 bits(478), Expect:0.0,
Identities:599/659(91%), Gaps:2/659(0%), Strand: Plus/Plus

Query	360	TATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTT	419
Sbjct	377	TATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTT	436
Query	420	CTTCAATTTTAGGTGCAATTAACCTTCATCACAACATTGTAAATATACGATCAATTGGAA	479
Sbjct	437	CTTCAATTTTAGGTGCAATTAATTTTATTACAACATTGTAAATATACGATCTATTGGAA	496
Query	480	TAACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTAC	539
Sbjct	497	TAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTAC	556
Query	540	TTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTA	599
Sbjct	557	TATTATCTTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCGATCGAAATTTTA	616
Query	600	ACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	617	ACACTTCATTTTTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	675

>Rhipicephalus turanicus isolate COX1-225-Goat cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT800313.1 Length: 673
Range 1: 8 to 665

Score:883 bits(478), Expect:0.0,
Identities:598/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	8	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTGAGAATAAGAATACT	67
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	68	AATTCGCATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAAATTTATAACGT	127
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	128	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATGGTAATACCTATTATAATTGG	187
Query	181	AGGGTTCGGAATGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	188	TGGATTTGGAAATGATTAGTTCCTATTATATTAGGGGCTCCAGATATAGCATTTCCACG	247
Query	241	AATAAATAATATAAGATTTTGACTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	248	TATAAATAACATAAGATTTTGATTACTTCCTCCTCATTATTTCTATTAATTAACCTCTTC	307
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCAGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTTATCCTCAAATTT	367

Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAACCTGATCGAAATTTCAA	607
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	608	TACTTCATTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATTT	665

>Rhipicephalus sanguineus sensu lato 'temperate lineage' isolate SC3005
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425987.1 Length: 574
Range 1: 1 to 561

Score:881 bits(477), Expect:0.0,
Identities:533/561(95%), Gaps:0/561(0%), Strand: Plus/Plus

Query	98	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACATGCATTTATTATAATTTTCTTT	157
Sbjct	1	GGAAATGATCAGATTTATAATGTAATCGTAACAGCACACGCATTTATTATAATTTTTTTT	60
Query	158	ATAGTTATACCAATCATAATCGGAGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGT	217
Sbjct	61	ATAGTTATACCAATCATAATCGGAGGATTTGGAAATTGATTAGTCCCTATTATATTAGGT	120
Query	218	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCCCCCTCA	277
Sbjct	121	GCCCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGACTTTTACCTCCTTCA	180
Query	278	TTATTTTTATTGATTAACCTCTTCATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTT	337
Sbjct	181	CTATTTTTATTAATTAACCTCTTCATTAATTGAATCTGGAGCTGGTACAGGATGAACAGTT	240
Query	338	TATCCCCCTCTATCTTCAAATTTATCACATTATGGTCCATCAGTAGATTTAGCTATTTTT	397
Sbjct	241	TACCCTCCTCTATCTTCAAATTTATCACATTATGGCCCTTCAGTAGATTTAGCTATCTTT	300
Query	398	TCTCTTCACCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATT	457

Sbjct	301	TCTCTTCATCTTGCTGGTGCTTCTTCAATTTTAGGTGCAATTAACCTTTATTACAACCTATT	360
Query	458	GTAAATATACGATCAATTGGAATAACAATAGAACGAATACCATTATTTGTTTGATCTGTT	517
Sbjct	361	GTAAACATACGATCAATTGGAATAACAATAGAACGTATACCATTATTTGTTTGATCTGTT	420
Query	518	TTAATTACAGCTATTTTACTACTTCTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	577
Sbjct	421	TTAATTACAGCTATTTTATTACTTTTATCTTTACCTGTATTAGCAGGTGCCATTACAATA	480
Query	578	TTATTAACCTGATCGAACTTTAACACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCC	637
Sbjct	481	TTGTTAACCTGATCGAACTTTAATACATCATTTTTTGATCCTTCAGGGGGAGGAGATCCA	540
Query	638	ATTTTATATCAACACTTATTT	658
Sbjct	541	ATTTTATATCAACATTTATTT	561

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (CO1) gene, partial cds;
mitochondrial
Sequence ID: KU214592.1 Length: 829
Range 1: 1 to 648

Score:876 bits(474), Expect:0.0,
Identities:590/648(91%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCGTATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACTAATTCGTATA	60
Query	71	GAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGTAATCGTAACA	130
Sbjct	61	GAATTAGGCCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGTAATTGTTACA	120
Query	131	GCACATGCATTTATTATAAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTTCGGA	190
Sbjct	121	GCTCATGCATTTATTATAAATTTTTTTTATAGTAATACCAATCATAATTGGTGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AACTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAATTGAA	310
Sbjct	241	ATAAGATTTTGACTTCTTCCCTCCCTCATTATTTATATTAATTAATTCTTCATTAATTGAG	300
Query	311	TCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACATTAT	370
Sbjct	301	TCAGGAGCAGGTACAGGATGGACAGTTTATCCTCCCCTATCCTCAAATTTATCACATTAT	360
Query	371	GGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTCTTCAATTTTA	430

Sbjct	361		GGGCCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTCTTCAATTTTA	420
Query	431		GGTGCAATTAAC TTCATCACA ACTATTGTAAATATACGATCAATTGGAATAACAATAGAA	490
Sbjct	421		GGTGCAATTAATTTTATTACA ACTATTGTAAATATACGATCTATTGGAATAACAATAGAA	480
Query	491		CGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATCTTTA	550
Sbjct	481		CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACTATTATCTTTA	540
Query	551		CCTGTATTAGCAGGTGCCATTACAATATTATTA ACTGATCGAAACTTTAACACATCATTT	610
Sbjct	541		CCTGTTTTAGCAGGTGCCATTACAATATTATTAACCGATCGAAATTTTAACACTTCATTT	600
Query	611		TTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601		TTTGACCCTTCAGGGGGAGGGGATCCAATTTTATATCAACATTTATTT	648

>Rhipicephalus turanicus isolate GY34-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MT079206.1 Length: 678
Range 1: 1 to 652

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7		ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCG	66
Sbjct	1		ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCG	60
Query	67		TATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61		AATAGAATTAGGACAACCTGGAAC TTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127		AACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGGAGGGTT	186
Sbjct	121		AACAGCTCATGCATTTATTATAATTTTCTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187		CGGAAATTGATTAGTTCTTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181		TGGAAACTGGTTAGTTCCAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247		TAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACTCTTCATTAAT	306
Sbjct	241		TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307		TGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACA	366
Sbjct	301		TGAATCTGGGGCAGGGACAGGGTGAAC TTTATCCTCCTTTATCCTCAAATTTATCCCA	360

Query	367	TTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTCAATACAACCTATTGTAAACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCTGATCGAAATTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	ATTTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTATTT	652

>Rhipicephalus sanguineus isolate GY34 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MN862754.1 Length: 678
Range 1: 1 to 652

Score:872 bits(472), Expect:0.0,
Identities:592/652(91%), Gaps:0/652(0%), Strand: Plus/Plus

Query	7	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATTAATTCG	66
Sbjct	1	ATATTTAATTTTTGGAGCATGATCAGGTATATTAGGATTAAGAATAAGAATATTAATTCG	60
Query	67	TATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGTAATCGT	126
Sbjct	61	AATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGTAATTGT	120
Query	127	AACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGGAGGGTT	186
Sbjct	121	AACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGGAGGATT	180
Query	187	CGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACGAATAAA	246
Sbjct	181	TGGAAACTGGTTAGTTCCAATTATATTAGGAGCTCCAGACATAGCATTTCCACGAATAAA	240
Query	247	TAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTCATTAAT	306
Sbjct	241	TAATATAAGATTTTGATTACTTCCCCCTCATTATTCTTATTAATTAATTCTTCACTGAT	300
Query	307	TGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTTATCACA	366
Sbjct	301	TGAATCTGGGGCAGGGACAGGGTGAACGTGTTTATCCTCCTTTATCCTCAAATTTATCCCA	360

Query	367	TTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTCTTCAAT	426
Sbjct	361	TTATGGACCATCAGTAGATTTAGCTATCTTCTCTTCATCTTGCTGGTGCTTCTTCAAT	420
Query	427	TTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAATAACAAT	486
Sbjct	421	TTTAGGCGCAATTAATTTTCATTACAACCTATTGTAAACATACGATCTATTGGAATAACAAT	480
Query	487	AGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACTTCTATC	546
Sbjct	481	AGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCTTCTATC	540
Query	547	TTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAACACATC	606
Sbjct	541	TTTACCTGTTTTAGCAGGTGCCATTACAATACTATTAACCTGATCGAAATTTTAACACTTC	600
Query	607	ATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	ATTTTTTGACCCTTCAGGAGGAGGTGACCCAATTTTATATCAACATTATTT	652

>Rhipicephalus sanguineus isolate Gilan-e Gharb cytochrome oxidase subunit 1 gene, complete cds; mitochondrial
Sequence ID: KM494916.1 Length: 1539
Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

Sbjct	345	ATTAATTGAGTCAGGAGCAGGTACAGGATGAACAGTTTATCCTCCCCTATCCTCAAATTT	404
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	405	ATCACATTATGGGCCATCAGTAGATTTAGCTATTTTTTCTCTTCATCTTGCTGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTGAATATACGATCTATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTACT	584
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCTGTTTTAGCAGGTGCTATTACAATACTATTAACCGATCGAAATTTTAA	644
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	645	CACTTCATTTTTTGACCCTTCAGGAGGAGGGGATCCAATTTTATATCAACATTTATTT	702

>Rhipicephalus sanguineus isolate Tehran cytochrome oxidase subunit 1 gene,
complete cds; mitochondrial
Sequence ID: KM494915.1 Length: 1539
Range 1: 45 to 702

Score:872 bits(472), Expect:0.0,
Identities:596/658(91%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	45	AACAATATATTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATACT	104
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	105	AATTCGTATAGAATTAGGTCAACCTGGAACCTCTAATTGGTAATGATCAAATTTATAATGT	164
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	165	AATTGTTACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATTATAATTGG	224
Query	181	AGGGTTCGGAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	225	TGGATTTGGAACTGATTAGTACCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGACTTCTTCTCCCTCATTATTTATATTAATTAATTCTTC	344
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360

[illegible]

Score:870 bits(471), Expect:0.0,
Identities:595/657(91%), Gaps:0/657(0%), Strand: Plus/Plus

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	308	ATTAATTGAATCGGGAGCAGGAACAGGATGAACTGTTTATCCCCCTTATCTCAAATTT	367
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	368	ATCACATTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	427
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	428	TTCAATTCTAGGTGCAATTAATTTTATTACAACCTATTGTAAACATACGATCTATTGGAAT	487
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	488	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACCGCCATCTTACTTCT	547
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	548	CTTATCTTTACCTGTTTTAGCAGGTGCTATTACAATATTATTAACCTGATCGAAATTTCAA	607
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATT	657
Sbjct	608	TACTTCATTTTTTTGATCCTTCAGGGGGAGGTGATCCAATTTTATACCAACACTTATT	664

>Rhipicephalus turanicus isolate 31X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606303.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365

Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTCATTACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 19X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606302.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTCAATACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 19C cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606301.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATTTATGTTAGGAGCTCCAGACATAGCATTTCCACG	305
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300

Sbjct	306	 AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAACTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTCAATACAACCTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAACCTGATCGAAATTTCAA	665
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

>Rhipicephalus turanicus isolate 12X cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606300.1 Length: 873
Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,
Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAGCATGATCCGGGATATTAGGATTAAGAATAAGAATATT	125
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTATTATAATTTTTTTTATAGTAATACCAATCATAATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTGCCCATTTATGTTAGGAGCTCCAGACATAGCATTTCCACG	305

Query	241	AATAAATAATATAAGATTTTGA	CTTTTACCCCCCTCATTATTTT	TATTGATTA	AACTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGA	TACTTCTCCCTCATTATTCTT	ATTAATTA	AATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGA	ACAGGATGAACAGTTTATCCC	CCTCTATCTT	CAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGG	ACAGGATGAACTGTCTACCCT	CCTTTATCTT	CAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTA	GATTTAGCTATTTTTTCTCTT	CACCTTGCTGGT	GCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTA	GATTTAGCTATCTTCTCTCTT	CATCTCGCTGGT	GCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAAC	TTTCATCACA	ACTATTGTAA	TATACGATCA	ATTGGAAT
Sbjct	486	TTCAATTTTAGGTGCAATTAAT	TTTCATTACA	ACTATTGTAA	ACATACGATCT	ATTGGAAT
Query	481	AACAATAGAACGAATACCATTAT	TTGTTTGATCTGTTTTAATTAC	AGCTATTTTACT	ACT	540
Sbjct	546	AACAATAGAACGAATACCATTAT	TCGTTTGATCTGTTTTAATCAC	CGCTATTTTATT	GCT	605
Query	541	TCTATCTTTACCTGTATTAGCAG	GTGCCATTACAATATTATTAAC	TGATCGAA	ACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAG	GTGCCATTACAATATTATTAAC	TGATCGAA	ATTTCAA	665
Query	601	CACATCATTTTTT	GATCCTTCAGGAGGAGGAGAT	CCCCATTTTATATCA	AACTTATTT	658
Sbjct	666	CACTTCATTTTTT	GACCCTTCAGGAGGAGGTGACC	CTATTTTATATCA	AATTTATTT	723

>Rhipicephalus turanicus isolate 12C cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial

Sequence ID: KY606299.1 Length: 873

Range 1: 66 to 723

Score:861 bits(466), Expect:0.0,

Identities:594/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAG	CATGATCAGGTATATTAGGACTT	AGTATAAGA	AATATT	60
Sbjct	66	AACAATATATTTAATTTTTGGAG	CATGATCCGGGATATTAGGATTA	AGAATAAGA	AATATT	125
Query	61	AATTCGTATAGAATTAGGACAAC	CTGGAACTTTAATTGGAAATGA	TCA	GATCAGATTTATAATGT	120
Sbjct	126	AATTCGAATAGAGTTAGGACAAC	CTGGAACTTTAATTGGAAATGA	CA	AATTTATAATGT	185
Query	121	AATCGTAACAGCACATGCATTTA	TATAATTTTCTTTATAGTTATA	ACCAATCATA	ATCGG	180
Sbjct	186	AATTGTAACAGCTCATGCATTTA	TATAATTTTTTTTATAGTAATA	ACCAATCATA	AATTGG	245
Query	181	AGGGTTCGGAAATTGATTAGTTC	CTATTATATTAGGTGCCCCAG	ATATAGCATTTCC	CACG	240
Sbjct	246	AGGATTTGGAAACTGATTAGTG	CCCATTATGTTAGGAGCTCCAG	ACATAGCATTTCC	CACG	305

Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	306	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	365
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	366	ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCTCCTTTATCTTCAAATTT	425
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	426	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	485
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACATTGTAAATATACGATCAATTGGAAT	480
Sbjct	486	TTCAATTTTAGGTGCAATTAATTTTATTACAACTATTGTAAACATACGATCTATTGGAAT	545
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	546	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCCTATTTTATTGCT	605
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	606	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	665
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	666	CACTTCATTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	723

Score:861 bits(466), Expect:0.0,
Identities:595/659(90%), Gaps:2/659(0%), Strand: Plus/Plus

Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAACTGATTAGTGCCATTATGTTAGGAGCTCCAGACATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGATTACTTCCTCCCTCATTATTCTTATTAATTAATTCTTC	300
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	301	ACTGATTGAATCTGGAGCAGGGACAGGATGAAGTGTCTACCCTCCTTTATCTTCAAATTT	360
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	361	ATCGCATTATGGACCATCAGTAGATTTAGCTATCTTCTCTCTTCATCTCGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAACCTATTGTAAATATACGATCTATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	481	AACAATAGAACGAATACCATTATTCGTTTGATCTGTTTTAATCACCGCTATTTTATTGCT	540
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	TCTATCTTTACCTGTTTTAGCAGGTGCCATTACAATATTATTAAGTATCGAAATTTCAA	600
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	601	CACTTCATTTTTTTGACCCTTCAGGAGGAGGTGACCCTATTTTATATCAACATTTATTT	658

>Rhipicephalus turanicus isolate Xinjiang-WQIA cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: MF002581.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTCATAGTAATACCAATTATAATTGG	253

Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAAGTGTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-WS cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002580.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180

Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGA AATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAAGTGTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAACTTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate Xinjiang-BC cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: MF002579.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180

Sbjct	194	 AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCACG	240
Sbjct	254	 TGGATTTGGAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	314	 AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	 ATTAATTGAATCAGGAGCAGGAAGTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	 ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	 TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	 AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	 TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	 CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	121	AATCGTAACAGCACATGCATTTATTATAAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAAATTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCTCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAAGTGTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	121	AATCGTAACAGCACATGCATTTATTATAATTTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTGATCCTTCAGGAGGGGGTGATCCAATTTTATACCAACATTTATTT	731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133
Query	61	AATTCGTATAGAATTAGGACAACCTGGAACTTTAATTGGAAATGATCAGATTTATAATGT	120

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTATTGATTAACCTCTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

>Rhipicephalus turanicus isolate YN2 cytochrome oxidase subunit 1 (COI) gene,
partial cds; mitochondrial
Sequence ID: KY606289.1 Length: 889
Range 1: 74 to 731

Score:850 bits(460), Expect:0.0,
Identities:592/658(90%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	AACAATATATTTAATTTTTGGAGCATGATCAGGTATATTAGGACTTAGTATAAGAATATT	60
Sbjct	74	AACAATATATTTAATTTTTGGGGCATGATCAGGAATATTAGGACTAAGAATAAGAATATT	133

Query	61	AATTCGTATAGAATTAGGACAACCTGGAACCTTTAATTGGAAATGATCAGATTTATAATGT	120
Sbjct	134	AATTCGAATAGAATTAGGCCAACCTGGAACCTTTAATTGGAAATGATCAAATTTATAATGT	193
Query	121	AATCGTAACAGCACATGCATTTATTATAATTTCTTTATAGTTATACCAATCATAATCGG	180
Sbjct	194	AATTGTAACAGCCCATGCATTTATTATAATTTTTTCATAGTAATACCAATTATAATTGG	253
Query	181	AGGGTTCGGAAATTGATTAGTTCCTATTATATTAGGTGCCCCAGATATAGCATTTCCACG	240
Sbjct	254	TGGATTTGGAAACTGATTAGTACCTATTATATTAGGAGCTCCAGATATAGCATTTCCACG	313
Query	241	AATAAATAATATAAGATTTTGACTTTTACCCCCCTCATTATTTTTATTGATTAACCTCTTC	300
Sbjct	314	AATAAATAACATAAGATTTTGATTACTTCCCCCTTCATTATTTCTATTAATTAATTCCTC	373
Query	301	ATTAATTGAATCCGGAGCTGGAACAGGATGAACAGTTTATCCCCCTCTATCTTCAAATTT	360
Sbjct	374	ATTAATTGAATCAGGAGCAGGAAGCTGGATGAACTGTTTATCCGCCTTTATCATCAAATTT	433
Query	361	ATCACATTATGGTCCATCAGTAGATTTAGCTATTTTTCTCTTCACCTTGCTGGTGCTTC	420
Sbjct	434	ATCACACTATGGACCATCAGTAGATTTAGCTATTTTTCTCTCTTCATCTTGCTGGTGCTTC	493
Query	421	TTCAATTTTAGGTGCAATTAACCTTCATCACAACCTATTGTAAATATACGATCAATTGGAAT	480
Sbjct	494	TTCAATTTTAGGTGCAATCAATTTTATTACGACTATTATAAATATACGATCTATTGGAAT	553
Query	481	AACAATAGAACGAATACCATTATTTGTTTGATCTGTTTTAATTACAGCTATTTTACTACT	540
Sbjct	554	AACAATAGAACGAATGCCACTATTTGTTTGATCTGTTTTAATTACTGCTATTTTGTTACT	613
Query	541	TCTATCTTTACCTGTATTAGCAGGTGCCATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	614	TTTATCTTTGCCTGTTTTAGCAGGAGCCATTACAATATTATTAAGTATCGAAATTTCAA	673
Query	601	CACATCATTTTTTTGATCCTTCAGGAGGAGGAGATCCCATTTTATATCAACACTTATTT	658
Sbjct	674	CACTTCATTTTTTTGATCCTTCAGGAGGGGTGATCCAATTTTATACCAACATTTATTT	731

Query #15: TKCJJ065-19|TKCJ012018F05|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26777 Length: 658

Sequences producing significant alignments:

Common		Max	Total Query	E	Per.	Acc.	Scientific
Description	Taxid	Score	Score	cover	Value	Ident	Name
Name						Len	Accession

Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	688	
MF425995.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	703	
MF425994.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	702	
MF425993.1								
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	693	
MF425992.1								
Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...								
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	690	
KT906183.1								
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...								
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	690	
KT906182.1								
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...								
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14711	
OM368327.1								
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...								
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14714	
OM368323.1								
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...								
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	14713	
OM368322.1								
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	707	
JQ737084.1								
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...								
Rhipicephalu... brown dog tick	34632	1216	1216	100%	0.0	100.00	658	
KF437543.1								
Rhipicephalus linnaei isolate LA032-2 clone JS5930...								
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	14715	
MW429383.1								
Rhipicephalus linnaei mitochondrion, complete sequence								
Rhipicephalu... NA	2138177	1216	1216	100%	0.0	100.00	14711	
NC_060409.1								
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,...								
Ixodidae sp.... NA	1901042	1210	1210	100%	0.0	99.85	658	
KX053537.1								
Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...								
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690	
KT906185.1								
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...								
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	690	
KT906184.1								
Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1210	1210	100%	0.0	99.85	658	
KF200113.1								
Rhipicephalus linnaei isolate SC931-1 clone JS5927...								
Rhipicephalu... NA	2138177	1210	1210	100%	0.0	99.85	14717	

MW429382.1							
Rhipicephalus sanguineus voucher D0-311 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1205	1205	99%	0.0	99.85 658
KX360367.1							
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...							
Rhipicephalu...	brown dog tick	34632	1205	1205	100%	0.0	99.70 690
KT906186.1							
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1205	1205	100%	0.0	99.70 658
KF200112.1							
Rhipicephalus sanguineus mitochondrion, complete genome							
Rhipicephalu...	brown dog tick	34632	1205	1205	100%	0.0	99.70 14714
JX416325.1							
Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...							
Rhipicephalu...	brown dog tick	34632	1192	1192	98%	0.0	100.00 661
MZ401443.1							
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...							
Rhipicephalu...	brown dog tick	34632	1192	1192	98%	0.0	100.00 661
MZ401441.1							
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...							
Rhipicephalu...	brown dog tick	34632	1192	1192	98%	0.0	99.85 664
MZ401440.1							
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1190	1190	97%	0.0	100.00 664
MG969507.1							
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1188	1188	98%	0.0	99.69 649
KF200084.1							
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1186	1186	97%	0.0	100.00 768
KX383817.1							
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...							
Rhipicephalu...	brown dog tick	34632	1186	1186	97%	0.0	100.00 657
MZ401442.1							
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...							
Rhipicephalu...	brown dog tick	34632	1186	1186	97%	0.0	100.00 661
MZ401438.1							
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1184	1184	97%	0.0	99.84 664
MG969506.1							
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1184	1184	97%	0.0	99.84 664
MG969505.1							
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1184	1184	97%	0.0	99.84 664
MG969504.1							
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...							
Rhipicephalu...	brown dog tick	34632	1179	1179	97%	0.0	99.69 644
KF200096.1							
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...							
Rhipicephalu...	NA	2138177	1177	1177	100%	0.0	98.94 658
OM984983.1							
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...							
Rhipicephalu...	brown dog tick	34632	1177	1177	96%	0.0	100.00 802

JX416302.1							
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416298.1							
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1177	1177	97%	0.0	99.69	670
HM193873.1							
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1175	1175	97%	0.0	99.69	768
KX383820.1							
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	97%	0.0	99.53	724
KX383816.1							
Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984984.1							
Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984974.1							
Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984973.1							
Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416308.1							
Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416304.1							
Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416300.1							
Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416299.1							
Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416297.1							
Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416296.1							
Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416293.1							
Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	100.00	650
MZ401439.1							
Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	763
KX383802.1							
Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658
OM984979.1							
Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658

OM984968.1									
Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subun...									
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		
JX416295.1									
Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subun...									
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		
JX416294.1									
Rhipicephalus sanguineus isolate sanguineus0926 cytochrome...									
Rhipicephalu... brown dog tick	34632	1162	1162	99%	0.0	98.77	658		
MH513252.1									
Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984985.1									
Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984978.1									
Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984977.1									
Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984975.1									
Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984971.1									
Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984970.1									
Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984969.1									
Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subun...									
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	802		
JX416301.1									
Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrom...									
Rhipicephalu... brown dog tick	34632	1155	1155	95%	0.0	99.68	642		
MT010523.1									
Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984988.1									
Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase...									
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984976.1									
Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subun...									
Rhipicephalu... brown dog tick	34632	1155	1155	96%	0.0	99.37	802		
JX416303.1									
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...									
Rhipicephalu... NA	2138177	1153	1153	98%	0.0	98.77	826		
MF426003.1									
Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidas...									
Rhipicephalu... brown dog tick	34632	1146	1146	96%	0.0	99.21	665		
HM193874.1									
Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase...									
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630		

KX757914.1
Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1136 1136 97% 0.0 98.60 768
KX383800.1
Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1131 1131 93% 0.0 99.68 744
KX383796.1
Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1127 1127 96% 0.0 98.59 698
KX383798.1
Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1125 1125 97% 0.0 98.29 768
KX383814.1
Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1122 1122 96% 0.0 98.43 763
KX383801.1
Rhipicephalus sanguineus isolate 400 cytochrome c oxidase...
Rhipicephalu... brown dog tick 34632 1120 1120 97% 0.0 98.28 657
MW558150.1
Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726445.1
Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726444.1
Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726443.1
Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726442.1
Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726441.1
Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726440.1
Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726439.1
Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726438.1
Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726437.1
Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726436.1
Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726435.1
Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604

MZ726434.1
Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726433.1
Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726432.1
Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726431.1
Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1116 1116 91% 0.0 100.00 604
MZ726430.1
Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1110 1110 91% 0.0 99.83 604
MZ726449.1
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1110 1110 91% 0.0 99.83 604
MZ726429.1
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1110 1110 91% 0.0 99.83 604
MZ726428.1
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...
Rhipicephalu... NA 2138177 1110 1110 91% 0.0 99.83 604
MZ726427.1
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...
Rhipicephalu... NA 2138177 1110 1110 91% 0.0 99.83 604
MZ726426.1
Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase...
Rhipicephalu... brown dog tick 34632 1092 1092 91% 0.0 99.33 638
KX360338.1

Alignments:

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425994.1 Length: 703

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425996.1 Length: 703

Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	139

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAA	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	80	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	380	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	20	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	79
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	80	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	139
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	140	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	199
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	200	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	259
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	260	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	319
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	320	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	379
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	380	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	439
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	440	 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	499
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	500	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	559
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	560	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	619
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	620	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	677

>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 275

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome

Sequence ID: OM368327.1 Length: 14711

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome

Sequence ID: OM368323.1 Length: 14714

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome

Sequence ID: OM368322.1 Length: 14713

Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI)
 gene, partial cds; mitochondrial
 Sequence ID: JQ737084.1 Length: 707
 Range 1: 24 to 681

Score:1216 bits(658), Expect:0.0,
 Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAAATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Sbjct	24	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	83
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	84	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	143
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	144	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	203
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	204	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	263
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	264	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	323
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	324	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	383
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	384	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	443
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	444	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	503
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	504	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	563
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	564	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	623
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	624	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	681

>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome

Sequence ID: MW429383.1 Length: 14715

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 45 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 104

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 105 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 164

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 165 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 224

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 225 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 284

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 285 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 344

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 345 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 404

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 405 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 464

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 465 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 524

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 525 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 584

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 585 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 644

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 645 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 702
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>Rhipicephalus linnaei mitochondrion, complete sequence

Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion,
complete genome

Sequence ID: MW429381.1 Length: 14711
Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 45 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 104

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 105 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 164

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 165 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 224

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 225 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 284

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 285 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 344

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 345 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 404

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 405 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 464

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 465 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 524

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 525 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 584

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 585 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 644

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 645 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 702
```

>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;

mitochondrial

Sequence ID: KX053537.1 Length: 658

Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
```

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
|||||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 498 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 558 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
|||||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 498 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 558 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200113.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome

Sequence ID: MW429382.1 Length: 14717

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAAGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360367.1 Length: 658
Range 1: 4 to 658

Score:1205 bits(652), Expect:0.0,
Identities:654/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

Query	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT 	63
Sbjct	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Query	64	CCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAAT 	123
Sbjct	64	CCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Query	124	TGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGG 	183
Sbjct	124	TGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGG	183
Query	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT 	243
Sbjct	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243
Query	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT 	303
Sbjct	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Query	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATC 	363
Sbjct	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATC	363
Query	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTC 	423
Sbjct	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAAGTGCTTCTTC	423
Query	424	AATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAAC 	483
Sbjct	424	AATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAAC	483
Query	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT 	543
Sbjct	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Query	544	ATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACGATCGAACTTTAATAC 	603
Sbjct	544	ATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACGATCGAACTTTAATAC	603
Query	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 	658

Sbjct 604 ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658

>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 378 ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAACATTTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAACATTTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 498 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 558 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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|||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675

>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200112.1 Length: 658
>Rhipicephalus sanguineus voucher D0-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360403.1 Length: 658
Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600

Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus mitochondrion, complete genome
Sequence ID: JX416325.1 Length: 14714
Range 1: 1185 to 1842

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600

Sbjct	1725		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	1784
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		658
Sbjct	1785		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT		1842

>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60
Query	74	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133
Sbjct	61	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120
Query	134	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300
Query	314	GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA	373
Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433
Sbjct	361	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434	GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540

Query	554	GTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	645	

>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401441.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60
Query	74	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133
Sbjct	61	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120
Query	134	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATA	253
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATA	240
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300
Query	314	GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA	373
Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433
Sbjct	361	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434	GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540

Query	554	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	645

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,
Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	60
Query	71	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	61	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	120
Query	131	GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	121	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	241	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	300
Query	311	TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	301	TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	360
Query	371	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550

Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	540
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC	610
Sbjct	541	CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC	600
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	648

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1190 bits(644), Expect:0.0,
Identities:644/644(100%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554

Sbjct	481		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 1 to 649

Score:1188 bits(643), Expect:0.0,
Identities:647/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

Query	10	CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT	69
Sbjct	1	CTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCAT	60
Query	70	AGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC	129
Sbjct	61	AGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC	120
Query	130	AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG	189
Sbjct	121	AGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGG	180
Query	190	AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA	249
Sbjct	181	AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA	240
Query	250	TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA	309
Sbjct	241	TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA	300
Query	310	ATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTA	369
Sbjct	301	ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA	360
Query	370	CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT	429
Sbjct	361	CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT	420
Query	430	AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA	489
Sbjct	421	AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA	480

Query	490	ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT	549
Sbjct	481	ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT	540
Query	550	ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATT	609
Sbjct	541	ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATT	600
Query	610	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	649

>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480

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Query   497  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC  556
        |||
Sbjct   481  CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC  540

Query   557  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC  616
        |||
Sbjct   541  TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC  600

Query   617  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||
Sbjct   601  CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  642

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>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

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Query   17   TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA  76
        |||
Sbjct    1   TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA  60

Query   77   GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT  136
        |||
Sbjct   61   GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT  120

Query   137  GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA  196
        |||
Sbjct   121  GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA  180

Query   197  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA  256
        |||
Sbjct   181  TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA  240

Query   257  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA  316
        |||
Sbjct   241  TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA  300

Query   317  GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA  376
        |||
Sbjct   301  GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA  360

Query   377  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA  436
        |||
Sbjct   361  TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA  420

Query   437  ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA  496
        |||

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Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496

Sbjct	421		ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497		CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481		CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557		TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541		TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617		CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420

Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	420

Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	434

Sbjct	361	CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	6	TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC	65
Sbjct	1	TATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCC	60
Query	66	GCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTG	125
Sbjct	61	GCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTG	120
Query	126	TAACAGCACATGCATTTATTATAAATTTTTATAGTTATACCAATTATAATCGGAGGAT	185
Sbjct	121	TAACAGCACATGCATTTATTATAAATTTTTATAGTTATACCAATTATAATCGGAGGAT	180
Query	186	TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAA	245
Sbjct	181	TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAA	240
Query	246	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	305
Sbjct	241	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	300
Query	306	TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACccccTTATCATCAAATTTATCAC	365
Sbjct	301	TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCAC	360
Query	366	ACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	425

Sbjct	361	 ACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	420
Query	426	TTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAA	485
Sbjct	421	 TTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAA	480
Query	486	TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	545
Sbjct	481	 TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	540
Query	546	CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT	605
Sbjct	541	 CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT	600
Query	606	CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA	649
Sbjct	601	 CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA	644

>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 1 to 658

Score:1177 bits(637), Expect:0.0,
Identities:651/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416302.1 Length: 802

>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416305.1 Length: 802

>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416306.1 Length: 802

>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416307.1 Length: 802

Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,

Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 1 to 642

Score:1177 bits(637), Expect:0.0,
Identities:642/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	 TTTTTGGG-CATGATCCGG-ATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	58
Query	75	TAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	59	 TAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	118
Query	135	ATGCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	119	 ATGCATTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	178

Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	179	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	238
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	239	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	298
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	299	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	358
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGAGTGCTTCTTCAATTTTAGGTG	434
Sbjct	359	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGAGTGCTTCTTCAATTTTAGGTG	418
Query	435	CAATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	419	CAATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	478
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	479	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	538
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	539	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	598
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	599	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383820.1 Length: 768
Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,
Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180

Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383816.1 Length: 724
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196

Sbjct	121	GCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141

Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAACATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416304.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141

Sbjct	61	 ACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT	120
Query	142	TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAA TTTTTTTT ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTT Acccccc TTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTT ACCCCCC TTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60

Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416299.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60

Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416297.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81

Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTACTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
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Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MZ401439.1 Length: 650
 Range 1: 1 to 634

Score:1171 bits(634), Expect:0.0,
 Identities:634/634(100%), Gaps:0/634(0%), Strand: Plus/Plus

Query	25	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	84
Sbjct	1	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	60
Query	85	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	144
Sbjct	61	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	120
Query	145	TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	204
Sbjct	121	TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	180
Query	205	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	264
Sbjct	181	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	240
Query	265	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	324
Sbjct	241	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	300
Query	325	AGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	384
Sbjct	301	AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	360
Query	385	TTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT	444
Sbjct	361	TTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT	420
Query	445	CATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	504
Sbjct	421	CATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	480
Query	505	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	564
Sbjct	481	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	540
Query	565	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	624
Sbjct	541	CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	600
Query	625	AGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGTGACCCAATTCTATATCAACATTTATTT	634

>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383802.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383803.1 Length: 763

>Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383804.1 Length: 763
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGGGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984979.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGGAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416295.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT	637

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC  621
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||||||||||||||||||||||||||||||||||
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Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658
Range 1: 6 to 658

Score:1162 bits(629), Expect:0.0,
Identities:645/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 6 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 65

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 66 AATTCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 125

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 126 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 185

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 186 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 245

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 246 AATAAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 305

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 306 ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 365

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 366 ATCACACTACGGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTC 425

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 426 TTCAATTTTAGGCGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 485

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 486 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 545

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 546 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTGTAAAGTATCGAAACTTTAA 605

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT 653
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|||||
Sbjct 606 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT 658
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>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984985.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
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Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

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>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984978.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
        |||||||||||| |||||||||||||||||| || |||||||||||| ||||||||
Sbjct   361  ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query   421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
        |||||||||||||||| |||||||||||||||||| |||||||||||||||||| ||
Sbjct   421  TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query   541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
        |||||||||||||||||| |||||||||||||||||| |||||||||||||||||| ||
Sbjct   541  ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

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Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

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>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984977.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```

Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
        |||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
        |||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
        |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
        |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
        |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
        |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query   361  ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC 420
        |||
Sbjct   361  ATCACAACACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC 420

Query   421  TTCAATTTTAGGTGCAATCAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT 480
        |||
Sbjct   421  TTCAATTTTAGGTGCAATTAATTTTATTACAACCTATTGTAAATATACGATCCATTGGAAT 480

Query   481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
        |||
Sbjct   481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query   541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
        |||

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Sbjct  541  ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA  600
Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
          |||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT  658

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>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1   GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||
Sbjct    1   GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query   61   AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct   61   AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121  AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT  360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC  420
          |||
Sbjct   361  ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC  420

Query   421  TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT  480
          |||
Sbjct   421  TTCAATTTTAGGTGCAATTAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT  480

Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||
Sbjct   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query   541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600

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Sbjct	541	 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCCGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTATTACAATATGGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

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Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
        |||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        |||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 658

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>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
        |||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
        |||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
        |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
        |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG 240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
        |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
        |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT 360

Query   361  ATCACAACACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
        |||
Sbjct   361  ATCACAACACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC 420

Query   421  TTCAATTTTAGGTGCAATCAATTTTATTACAACATTTGTAAATATACGATCCATTGGAAT 480
        |||
Sbjct   421  TTCAATTTTAGGTGCAATTAATTTTATTACAACATTTGTAAATATACGATCCATTGGAAT 480

Query   481  AACAAAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
        |||

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Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416301.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561

Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCTATTACAATATTATTAAGTATCGAACTTTAATACATTATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT010523.1 Length: 642
Range 1: 1 to 631

Score:1155 bits(625), Expect:0.0,
Identities:629/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

Query	28	ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG	87
Sbjct	1	ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG	60
Query	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Sbjct	61	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	120
Query	148	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Sbjct	121	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	180
Query	208	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	267
Sbjct	181	TATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTGGTTACT	240
Query	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Sbjct	241	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	300
Query	328	GTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	387
Sbjct	301	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	360
Query	388	AGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	447
Sbjct	361	AGCTATTTTTTCTCTACATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	420
Query	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Sbjct	421	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	480


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Query   508  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  567
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481  ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC  540

Query   568  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  627
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541  AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG  600

Query   628  AGGTGACCCAATTCTATATCAACATTTATTT  658
          ||||||||||||||||||||||||||||
Sbjct   601  GGGTGACCCAATTCTATATCAACATTTATTT  631

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>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT  360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC  420
          |||||||||||| |||||||||||||||||| || |||||||||||||| ||||||||
Sbjct   361  ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC  420

Query   421  TTCAATTTTAGGTGCAATCAATTTTATTACAACATTTGTAATATACGATCCATTGGAAT  480
          |||||||||||||| |||||||||||||||||| |||||||||||||||||| ||||||
Sbjct   421  TTCAATTTTAGGTGCAATTAATTTTATTACAACATTTGTAATATACGATCCATTGGAAT  480

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Query  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  541  ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

Query  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
          ||||||||| ||||||||||||||||||||||||||||| |||||||||||
Sbjct  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT  658

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>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT  360

Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC  420
          ||||||||||||| ||||||||||||||||||| || ||||||||||||||| |||||||
Sbjct  361     ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC  420

Query  421     TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT  480
          ||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||

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Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGAATTACAATATTATTAACCTGATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416303.1 Length: 802
Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,
Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501

Sbjct	421		TTTTATTACAACATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1153 bits(624), Expect:0.0,
Identities:640/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11		TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	3		TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATA	62
Query	71		GAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	63		GAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	122
Query	131		GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	123		GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	182
Query	191		AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	183		AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAAT	242
Query	251		ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	243		ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	302
Query	311		TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	303		TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	362
Query	371		GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	430
Sbjct	363		GGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	422

Query	431	GGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	423	GGCGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAA	482
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550	
Sbjct	483	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	542	
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTC	610
Sbjct	543	CCAGTCTTAGCTGGTGCAATTACAATATTGT	TAACTGATCGAAACTTTAATACATCATTC	602
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	603	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	650	

>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1146 bits(620), Expect:0.0,
Identities:631/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	31	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	90	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAAC	TTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	91	AATCCGCATAGAATTAGGTCAACCAGGAAC	TTAATTGGAAACGATCAAATTTATAATGT	150
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	151	AATTGTAACAGCACATGCATTTATTATAA	TTTTTTTTTATAGTTATACCAATTATAATCGG	210
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	211	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	270	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	271	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	330	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	331	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTT	390
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420
Sbjct	391	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	450

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	451	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	510
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Sbjct	511	AACAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	570	
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAA	600
Sbjct	571	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAATATTA	ACTGATCGAACTTTAA	630
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCC	636	
Sbjct	631	TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC	665	

>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAAC	TTTAATTG	98
Sbjct	1	TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAAC	TTTAATTG	60
Query	99	GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAA	ttttttttA	158
Sbjct	61	GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAA	TTTTTTTTTA	120
Query	159	TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG		218
Sbjct	121	TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG		180
Query	219	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC		278
Sbjct	181	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC		240
Query	279	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT		338
Sbjct	241	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT		300
Query	339	AccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT		398
Sbjct	301	ACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT		360
Query	399	CTCTGCATCTTGCAAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTG	458

Sbjct	361	CTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCATTACAACATTG	420
Query	459	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	518
Sbjct	421	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	480
Query	519	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	578
Sbjct	481	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA	638
Sbjct	541	TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA	600
Query	639	TTCTATATCAACATTTATTT	658
Sbjct	601	TTCTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383800.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383815.1 Length: 768
Range 1: 1 to 642

Score:1136 bits(615), Expect:0.0,
Identities:633/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376

Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383796.1 Length: 744
Range 1: 1 to 618

Score:1131 bits(612), Expect:0.0,
Identities:616/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

Query	41	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA	100
Sbjct	1	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA	60
Query	101	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttATA	160
Sbjct	61	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATA	120
Query	161	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	220
Sbjct	121	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	180
Query	221	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	280
Sbjct	181	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	240
Query	281	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAc	340
Sbjct	241	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAC	300
Query	341	ccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	400

Sbjct	301		CCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	360
Query	401		CTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTGTA	460
Sbjct	361		CTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTGTA	420
Query	461		AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	520
Sbjct	421		AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	480
Query	521		ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	580
Sbjct	481		ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	540
Query	581		TTAACTGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT	640
Sbjct	541		TTAACTGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATT	600
Query	641		CTATATCAACATTTATTT 658	
Sbjct	601		CTATATCAACATTTATTT 618	

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383798.1 Length: 698
Range 1: 1 to 637

Score:1127 bits(610), Expect:0.0,
Identities:628/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1		AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61		ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142		TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121		TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181		TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262		GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241		GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300

Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383814.1 Length: 768
Range 1: 1 to 642

Score:1125 bits(609), Expect:0.0,
Identities:631/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300

Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTAGGCGCA	420
Query	437	ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321

Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360
Query	382	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW558150.1 Length: 657
Range 1: 1 to 639

Score:1120 bits(606), Expect:0.0,
Identities:628/639(98%), Gaps:0/639(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCAGGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199
Sbjct	121	TTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	180
Query	200	GTTCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259
Sbjct	181	GTTCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	240
Query	260	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	319

Sbjct	241		TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	300
Query	320		GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA	379
Sbjct	301		GGTACAGGGGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCA	360
Query	380		GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	439
Sbjct	361		GTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC	420
Query	440		AATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	499
Sbjct	421		AATTTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	480
Query	500		TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	559
Sbjct	481		TTATTTGTAGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	540
Query	560		GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	619
Sbjct	541		GCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	600
Query	620		TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		TCAGGAGGGGGTGAACCAATTCTATATCAACATTTATTT 639	

>Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726445.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726444.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Query	601	TACA	604	
Sbjct	601		TACA	604

>Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ726441.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726440.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726438.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180

Sbjct	121		AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601		TACA 604	
Sbjct	601		TACA 604	

>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726437.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726434.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604 	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726433.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726432.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

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Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360
Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
          |||
Sbjct  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
Query  421     TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480
          |||
Sbjct  421     TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480
Query  481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||
Sbjct  481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541     ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          |||
Sbjct  541     ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601     TACA  604
          |||
Sbjct  601     TACA  604

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>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726430.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

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Sbjct	1	 GACAATATACTTAATTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726449.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACGGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726429.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726428.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,

Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
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>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACAACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACAACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726426.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638

Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

```
Query 20  GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT 79
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 1    GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT 60

Query 80  CAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA 139
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 61  CAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA 120

Query 140 TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA 199
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 121 TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA 180

Query 200  GTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT 259
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 181  GTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT 240

Query 260  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA 319
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 241  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA 300

Query 320  GGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCA 379
          || ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 301  GGNACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCA 360

Query 380  GTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC 439
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 361  GTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC 420

Query 440  AATTTCAATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA 499
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 421  AATTTCAATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA 480

Query 500  TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA 559
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 481  TTATTTGTATGATCTGTTTTAATTACNGCAATTTTATTATTATTATCTTTACCAGTCTTA 540

Query 560  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT 619
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 541  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT 600

Query 620  T 620
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Sbjct 601  T 601
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Query #16: TKCJJ071-19|TKCJ012018F11|Rhipicephalus sanguineus|COI-5P Query ID:

1cl|Query_26778 Length: 658

Sequences producing significant alignments:

Common		Max	Total Query	E	Per.	Acc.	Scientific
Description							Name
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession
Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...							
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00 658
KF200113.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA		2138177	1210	1210	100%	0.0	99.85 688
MF425995.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA		2138177	1210	1210	100%	0.0	99.85 703
MF425994.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA		2138177	1210	1210	100%	0.0	99.85 702
MF425993.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA		2138177	1210	1210	100%	0.0	99.85 693
MF425992.1							
Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 690
KT906183.1							
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 690
KT906182.1							
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 14711
OM368327.1							
Rhipicephalus sanguineus isolate C19 mitochondrion, complete...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 14714
OM368323.1							
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 14713
OM368322.1							
Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 707
JQ737084.1							
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...							
Rhipicephalu... brown dog tick		34632	1210	1210	100%	0.0	99.85 658
KF437543.1							
Rhipicephalus linnaei isolate LA032-2 clone JS5930...							
Rhipicephalu... NA		2138177	1210	1210	100%	0.0	99.85 14715
MW429383.1							
Rhipicephalus linnaei mitochondrion, complete sequence							
Rhipicephalu... NA		2138177	1210	1210	100%	0.0	99.85 14711
NC_060409.1							
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,... Ixodidae							
sp.... NA		1901042	1205	1205	100%	0.0	99.70 658
KX053537.1							

Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...								
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	690	
KT906185.1								
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...								
Rhipicephalu... brown dog tick	34632	1205	1205	100%	0.0	99.70	690	
KT906184.1								
Rhipicephalus linnaei isolate SC931-1 clone JS5927...								
Rhipicephalu... NA	2138177	1205	1205	100%	0.0	99.70	14717	
MW429382.1								
Rhipicephalus sanguineus voucher D0-311 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1199	1199	99%	0.0	99.69	658	
KX360367.1								
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...								
Rhipicephalu... brown dog tick	34632	1199	1199	100%	0.0	99.54	690	
KT906186.1								
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1199	1199	100%	0.0	99.54	658	
KF200112.1								
Rhipicephalus sanguineus mitochondrion, complete genome								
Rhipicephalu... brown dog tick	34632	1199	1199	100%	0.0	99.54	14714	
JX416325.1								
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	1197	1197	98%	0.0	100.00	664	
MZ401440.1								
Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	1186	1186	98%	0.0	99.84	661	
MZ401443.1								
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	1186	1186	98%	0.0	99.84	661	
MZ401441.1								
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664	
MG969507.1								
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1182	1182	98%	0.0	99.54	649	
KF200084.1								
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1181	1181	97%	0.0	99.84	768	
KX383817.1								
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	1181	1181	97%	0.0	99.84	657	
MZ401442.1								
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	1181	1181	97%	0.0	99.84	661	
MZ401438.1								
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	664	
MG969506.1								
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	664	
MG969505.1								
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	664	
MG969504.1								

Rhipicephalus sanguineus voucher CAS-T066	cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1173	1173	97%	0.0	99.53	644		
KF200096.1									
Rhipicephalus linnaei voucher P1/22_18-4	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658		
OM984983.1									
Rhipicephalus sanguineus isolate GHM1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802		
JX416302.1									
Rhipicephalus sanguineus isolate CHM1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802		
JX416298.1									
Rhipicephalus sanguineus voucher AMMS-RS-5	cytochrome c oxidas...								
Rhipicephalu... brown dog tick	34632	1171	1171	97%	0.0	99.53	670		
HM193873.1									
Rhipicephalus sanguineus isolate LIC6767D	cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1170	1170	97%	0.0	99.53	768		
KX383820.1									
Rhipicephalus sanguineus isolate LIC5766G	cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1166	1166	97%	0.0	99.38	724		
KX383816.1									
Rhipicephalus linnaei voucher P1/22_18-5	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658		
OM984984.1									
Rhipicephalus linnaei voucher P1/22_8-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658		
OM984974.1									
Rhipicephalus linnaei voucher P1/22_6-2	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658		
OM984973.1									
Rhipicephalus sanguineus isolate SZM2	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		
JX416308.1									
Rhipicephalus sanguineus isolate GTF3	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		
JX416304.1									
Rhipicephalus sanguineus isolate GBM1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		
JX416300.1									
Rhipicephalus sanguineus isolate GBF1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		
JX416299.1									
Rhipicephalus sanguineus isolate CHF1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		
JX416297.1									
Rhipicephalus sanguineus isolate DGM1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		
JX416296.1									
Rhipicephalus sanguineus isolate FSF1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802		

Rhipicephalus sanguineus isolate LIC5762	cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	763		
KX383802.1									
Rhipicephalus linnaei voucher P1/22_16-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984979.1									
Rhipicephalus linnaei voucher P1/22_1-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658		
OM984968.1									
Rhipicephalus sanguineus isolate DGF1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	802		
JX416295.1									
Rhipicephalus sanguineus isolate FSM1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	802		
JX416294.1									
Rhipicephalus sanguineus isolate sanguineus0926	cytochrome...								
Rhipicephalu... brown dog tick	34632	1157	1157	99%	0.0	98.62	658		
MH513252.1									
Rhipicephalus linnaei voucher P1/22_19-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984985.1									
Rhipicephalus linnaei voucher P1/22_14-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984978.1									
Rhipicephalus linnaei voucher P1/22_13-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984977.1									
Rhipicephalus linnaei voucher P1/22_10-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984975.1									
Rhipicephalus linnaei voucher P1/22_5-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984971.1									
Rhipicephalus linnaei voucher P1/22_4-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984970.1									
Rhipicephalus linnaei voucher P1/22_3-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658		
OM984969.1									
Rhipicephalus sanguineus isolate GHF1	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1155	1155	96%	0.0	99.37	802		
JX416301.1									
Rhipicephalus sanguineus isolate Tropical lineage RJ	cytochrom...								
Rhipicephalu... brown dog tick	34632	1149	1149	95%	0.0	99.52	642		
MT010523.1									
Rhipicephalus linnaei voucher P1/22_21-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1149	1149	100%	0.0	98.18	658		
OM984988.1									
Rhipicephalus linnaei voucher P1/22_12-1	cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1149	1149	100%	0.0	98.18	658		
OM984976.1									
Rhipicephalus sanguineus isolate GTF2	cytochrome oxidase subun...								
Rhipicephalu... brown dog tick	34632	1149	1149	96%	0.0	99.22	802		
JX416303.1									

Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA	2138177	1147	1147	98%	0.0	98.61	826	
MF426003.1								
Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	1140	1140	96%	0.0	99.06	665	
HM193874.1								
Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1134	1134	94%	0.0	99.68	630	
KX757914.1								
Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1131	1131	97%	0.0	98.44	768	
KX383800.1								
Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1125	1125	93%	0.0	99.51	744	
KX383796.1								
Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1122	1122	96%	0.0	98.43	698	
KX383798.1								
Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1120	1120	97%	0.0	98.13	768	
KX383814.1								
Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1116	1116	96%	0.0	98.27	763	
KX383801.1								
Rhipicephalus sanguineus isolate 400 cytochrome c oxidase...								
Rhipicephalu... brown dog tick	34632	1114	1114	97%	0.0	98.12	657	
MW558150.1								
Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726445.1								
Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726444.1								
Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726443.1								
Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726442.1								
Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726441.1								
Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726440.1								
Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726439.1								
Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726438.1								
Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726437.1								

Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726436.1								
Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726435.1								
Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726434.1								
Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726433.1								
Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726432.1								
Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726431.1								
Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604	
MZ726430.1								
Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604	
MZ726449.1								
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604	
MZ726429.1								
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604	
MZ726428.1								
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...								
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604	
MZ726427.1								
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...								
Rhipicephalu... NA	2138177	1105	1105	91%	0.0	99.67	604	
MZ726426.1								
Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase...								
Rhipicephalu... brown dog tick	34632	1092	1092	91%	0.0	99.33	638	
KX360338.1								

Alignments:

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KF200113.1 Length: 658
 Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,
 Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
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Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAAATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425994.1 Length: 703

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425996.1 Length: 703
Range 1: 20 to 677

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 500 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 560 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
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>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 500 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 560 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
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>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome
c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 20 to 677

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 500 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 560 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
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>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I
(COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690

Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 498 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 558 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I
(COX1) gene, partial cds; mitochondrial

Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 498 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 558 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
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>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome

Sequence ID: OM368327.1 Length: 14711
Range 1: 1185 to 1842

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome

Sequence ID: OM368323.1 Length: 14714
Range 1: 1185 to 1842

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhhipicephalus sanguineus isolate A44 mitochondrion, complete genome

Sequence ID: OM368322.1 Length: 14713
Range 1: 1185 to 1842

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI)

gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 24 to 681

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 24 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 83

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 84 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 143

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 144 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 203

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 204 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 263

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 264 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 323

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 324 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 383

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
|||||
Sbjct 384 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 443

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 444 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 503

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 504 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 563

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 564 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 623

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 624 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 681
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>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KF437543.1 Length: 658

>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053539.1 Length: 658

Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome

Sequence ID: MW429383.1 Length: 14715

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 45 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 104

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 105 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 164

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 165 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 224

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 225 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 284

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 285 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 344

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 345 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 404

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
|||||
Sbjct 405 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 464

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 465 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 524

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 525 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 584

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 585 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 644

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
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Sbjct 645 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 702

>Rhipicephalus linnaei mitochondrion, complete sequence

Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome

Sequence ID: MW429381.1 Length: 14711

Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,

Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	585	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	644

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Query    601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    645  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  702

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>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial

Sequence ID: KX053537.1 Length: 658

Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,

Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttTATAGTTATACCAATTATAATCGG 	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccCTTATCATCAAATTT 	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTGTAAATATACGATCCATTGGAAT 	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTGTAAATATACGATCCATTGGAAT 	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 	600

Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600

Sbjct	558	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	 GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	 AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	 TTCAATTTTAGGTGCAATCAATTTTATTACAACATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557

Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	558	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome
Sequence ID: MW429382.1 Length: 14717
Range 1: 45 to 702

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584

Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Rhipicephalus sanguineus voucher D0-311 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360367.1 Length: 658
Range 1: 4 to 658

Score:1199 bits(649), Expect:0.0,
Identities:653/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

Query	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Sbjct	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63
Query	64	CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Sbjct	64	CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT	123
Query	124	TGTAACAGCACATGCATTTATTATAA	183
Sbjct	124	TGTAACAGCACATGCATTTATTATAA	183
Query	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAAT	243
Sbjct	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAAT	243
Query	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Sbjct	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303
Query	304	AATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATC	363
Sbjct	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATC	363
Query	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTC	423
Sbjct	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTC	423
Query	424	AATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAAC	483
Sbjct	424	AATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAAC	483
Query	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543

Sbjct	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Query	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATAC	603
Sbjct	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATAC	603
Query	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 18 to 675

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

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Sbjct  498  |||||AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557
Query  541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
Sbjct  558  |||||ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 617
Query  601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
Sbjct  618  |||||TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675

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>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KF200112.1 Length: 658

>Rhipicephalus sanguineus voucher DO-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX360403.1 Length: 658

Range 1: 1 to 658

Score:1199 bits(649), Expect:0.0,

Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query  1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
Sbjct  1    |||||GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60
Query  61    AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
Sbjct  61    |||||AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
Query  121   AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
Sbjct  121   |||||AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180
Query  181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
Sbjct  181   |||||AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG 240
Query  241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
Sbjct  241   |||||AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
Query  301   ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
Sbjct  301   |||||ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360
Query  361   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
Sbjct  361   |||||ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
Query  421   TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT 480

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Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus mitochondrion, complete genome
Sequence ID: JX416325.1 Length: 14714
Range 1: 1185 to 1842

Score:1199 bits(649), Expect:0.0,
Identities:655/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245		AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305		AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	480

Sbjct	1605		TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT	1842

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 1 to 648

Score:1197 bits(648), Expect:0.0,
Identities:648/648(100%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	60
Query	71	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	61	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	120
Query	131	GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	121	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	241	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	300
Query	311	TCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	301	TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	360
Query	371	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTA	430
Sbjct	361	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTA	420

Query	431	GGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550	
Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	540	
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTC	610
Sbjct	541	CCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTC	600
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	648	

>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661
Range 1: 1 to 645

Score:1186 bits(642), Expect:0.0,
Identities:644/645(99%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73	
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60	
Query	74	TTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133	
Sbjct	61	TTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120	
Query	134	CATGCATTTATTATAA	tttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAA	tttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253	
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240	
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313	
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300	
Query	314	GGAGCAGGAACAGGGTGAACAGTTT	AccccccTTATCATCAAATTTATCACACTACGGA	373
Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433	
Sbjct	361	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420	

Query	434	GCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553	
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540	
Query	554	GTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	645	

>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401441.1 Length: 661
Range 1: 1 to 645

Score:1186 bits(642), Expect:0.0,
Identities:644/645(99%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73	
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60	
Query	74	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133	
Sbjct	61	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120	
Query	134	CATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAA	tttttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253	
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240	
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313	
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300	
Query	314	GGAGCAGGAACAGGGTGAACAGTTT	AccccccTTATCATCAAATTTATCACACTACGGA	373
Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTG	CAGGTGCTTCTTCAATTTTAGGT	433

Sbjct	361	CCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434	GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540
Query	554	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	645

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434

Sbjct	361		CATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTAGGTG	420
Query	435		CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421		CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 1 to 649

Score:1182 bits(640), Expect:0.0,
Identities:646/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

Query	10		CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT	69
Sbjct	1		CTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCAT	60
Query	70		AGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC	129
Sbjct	61		AGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC	120
Query	130		AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG	189
Sbjct	121		AGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGG	180
Query	190		AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA	249
Sbjct	181		AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA	240
Query	250		TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA	309
Sbjct	241		TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA	300
Query	310		ATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTA	369
Sbjct	301		ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA	360

Query	370	CGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT	429
Sbjct	361	CGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT	420
Query	430	AGGTGCAATCAATTTTATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA	489
Sbjct	421	AGGTGCAATCAATTTTATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA	480
Query	490	ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT	549
Sbjct	481	ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT	540
Query	550	ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT	609
Sbjct	541	ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT	600
Query	610	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	649

>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768
Range 1: 1 to 642

Score:1181 bits(639), Expect:0.0,
Identities:641/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360

Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1181 bits(639), Expect:0.0,
Identities:641/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376

Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1181 bits(639), Expect:0.0,
Identities:641/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCA	376

Sbjct	301		360
		GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300

Query	315	GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300

Query	315	GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314

Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1173 bits(635), Expect:0.0,
Identities:641/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	6	TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC	65
Sbjct	1	TATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCC	60
Query	66	GCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTG	125
Sbjct	61	GCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTG	120
Query	126	TAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGAT	185
Sbjct	121	TAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGAT	180
Query	186	TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAA	245
Sbjct	181	TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAA	240
Query	246	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	305

Sbjct	241		ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	300
Query	306		TCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCAC	365
Sbjct	301		TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCAC	360
Query	366		ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	425
Sbjct	361		ACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	420
Query	426		TTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAA	485
Sbjct	421		TTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAA	480
Query	486		TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	545
Sbjct	481		TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	540
Query	546		CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACAT	605
Sbjct	541		CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACAT	600
Query	606		CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA 649	
Sbjct	601		CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA 644	

>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984983.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAAATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAAATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416302.1 Length: 802

>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416305.1 Length: 802

>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416306.1 Length: 802

>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial

Sequence ID: JX416307.1 Length: 802

Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,

Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141

Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141

Sbjct	61	 ACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAA TTTTTTTT ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTT Acccccc TTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTT ACCCCCC TTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:641/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	 TTTTTGGG-CATGATCCGG-ATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	58

Query	75	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	59	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	118
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	119	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	178
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	179	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	238
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	239	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	298
Query	315	GAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	299	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	358
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	359	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG	418
Query	435	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	419	CAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	478
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	479	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	538
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	539	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	598
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	599	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383820.1 Length: 768
 Range 1: 1 to 642

Score:1170 bits(633), Expect:0.0,
 Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60

Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383816.1 Length: 724
 Range 1: 1 to 642

Score:1166 bits(631), Expect:0.0,
 Identities:638/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76

Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984984.1 Length: 658
 Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
 Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
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Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGTGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,

Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
|||||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
|||||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 AACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTTATCACACTACGGACCATCAGT 381
|||||
Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
|||||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
|||||
Sbjct 421 TTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
|||||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
|||||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637
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>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416304.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
|||||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
|||||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
|||||
Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
|||||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
|||||
Sbjct 421 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
|||||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
|||||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637
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>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```

Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      ||||||||||||||||||||||||||||||||
Sbjct  601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637

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>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416299.1 Length: 802

Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
      |||
Sbjct 1 AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
      |||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
      |||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
      |||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
      |||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
      |||
Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
      |||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
      |||
Sbjct 421 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
      |||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
      |||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637
```

>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416297.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
      |||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
      |||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
      |||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
      |||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
      |||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
      |||
Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
      |||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
      |||
Sbjct 421 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
      |||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTACTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
      |||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637
```

>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,

partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      |||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAA tttttttt ATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||
Sbjct  121  TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||
Sbjct  361  AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||
Sbjct  421  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct  601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637
```

>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||
Sbjct  1    AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      |||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||
Sbjct  421  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct  601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637
```

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401439.1 Length: 650
Range 1: 1 to 634

Score:1166 bits(631), Expect:0.0,
Identities:633/634(99%), Gaps:0/634(0%), Strand: Plus/Plus

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Query 25  ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC 84
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC 60

Query 85  AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT 144
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61  AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT 120

Query 145 TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC 204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC 180

Query 205 TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT 264
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT 240

Query 265 ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAAC 324
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC 300

Query 325 AGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA 384
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA 360

Query 385 TTTAGCTATTTTTTCTCTGCATCTTGCGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT 444
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 TTTAGCTATTTTTTCTCTGCATCTTGCGAGGTGCTTCTTCAATTTTAGGTGCAATCAATTT 420

Query 445 CATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT 504
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 CATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT 480

Query 505 TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG 564
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG 540

Query 565 CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG 624
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 CGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGG 600

Query 625 AGGAGGTGACCCAATTCTATATCAACATTTATTT 658
          ||||||||||||||||||||||||||||||||||||
Sbjct 601 AGGAGGTGACCCAATTCTATATCAACATTTATTT 634
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>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383802.1 Length: 763
 >Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383803.1 Length: 763
 >Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383804.1 Length: 763
 Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
 Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621

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Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600
Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
          ||||| ||||||||||||||||||||||||||||
Sbjct  601  AGGAGGGGGTGACCCAATTCTATATCAACATTTATTT  637

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>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984979.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

```

Query   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||||||||||||||||||||||||||||||||||||||
Sbjct   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT  60

Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||||||||||||||||||||||||||||||||||||||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120

Query  121     AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG  180
          |||||||||||||||||||||||||||||||||||||||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||||||||||||||||||||||||||||||||||||||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG  240

Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||||||||||||||||||||||||||||||||||||||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query  301     ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          ||||||||||||||||||| |||||||||||||||||||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC  420
          ||||||||||| ||||||||||||||||||| |||||||||||
Sbjct  361     ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCGGTGCTTC  420

Query  421     TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT  480
          ||||||||||||||| ||||||||||||||||||| |||||
Sbjct  421     TTCAATTTTAGGTGCAATTAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGGAT  480

Query  481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||||||||||||||||||||||||||||||||||||||
Sbjct  481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query  541     ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600

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Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCCGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416295.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540

Query	562	TGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT	637	

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561

Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658
Range 1: 6 to 658

Score:1157 bits(626), Expect:0.0,
Identities:644/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	6	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	65
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	66	AATTCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	125
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	126	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	185
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	186	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	245
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	246	AATAAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	305
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	306	ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	365
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	366	ATCACACTACGGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTC	425
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	426	TTCAATTTTAGGCGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	485
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540

Sbjct	486	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	545
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	546	 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTGTAACTGATCGAAACTTTAA	605
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT	653
Sbjct	606	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT	658

>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984985.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480

Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984978.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAACATTTGTAAATATACGATCCATTGGAAT	480

Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACATGATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAACATGATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480

Sbjct	421		TTCAATTTTAGGTGCAATTAATTTTCATTACAAC	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTA	600
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCGGTGCTTC	420

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAAC	TATGGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCA	ATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCA	ATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120	
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTG	CCCGGTGCTTC	420

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420

Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416301.1 Length: 802
Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,
Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441

Sbjct	361		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442		TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421		TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCTATTACAATATTATTAAGTATCGAACTTTAATACATTATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MT010523.1 Length: 642
Range 1: 1 to 631

Score:1149 bits(622), Expect:0.0,
Identities:628/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

Query	28	ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG	87
Sbjct	1	ATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGG	60
Query	88	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	147
Sbjct	61	AACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTAT	120
Query	148	AAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	207
Sbjct	121	AATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTAT	180
Query	208	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	267
Sbjct	181	TATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGTTACT	240
Query	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGG	327
Sbjct	241	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	300
Query	328	GTGAACAGTTTAccccccTTATCATCAAATTTATCACAACACGACCATCAGTAGATTT	387
Sbjct	301	GTGAACAGTTTACCCCCCTTATCATCAAATTTATCACAACACGACCATCAGTAGATTT	360

Query	388	AGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	447
Sbjct	361	AGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	420
Query	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Sbjct	421	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	480
Query	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	567
Sbjct	481	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	540
Query	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Sbjct	541	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	600
Query	628	AGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GGGTGACCCAATTCTATATCAACATTTATTT	631

>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 1 to 658

Score:1149 bits(622), Expect:0.0,
Identities:646/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTTTTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1149 bits(622), Expect:0.0,
Identities:646/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAACCTGATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTTTTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416303.1 Length: 802
Range 1: 1 to 637

Score:1149 bits(622), Expect:0.0,
Identities:632/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381

Sbjct	301		TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361		AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA	420
Query	442		TTTCATTACAACATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421		TTTCATTACAACATATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481		ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC	540
Query	562		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541		TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1147 bits(621), Expect:0.0,
Identities:639/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	3	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATA	62
Query	71	GAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	63	GAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	122
Query	131	GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	123	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	182
Query	191	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	183	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAAT	242
Query	251	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	243	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	302

Query	311	TCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	303	TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	362
Query	371	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	430
Sbjct	363	GGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	422
Query	431	GGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	423	GGCGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA	482
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550
Sbjct	483	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	542
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTC	610
Sbjct	543	CCAGTCTTAGCTGGTGCAATTACAATATTGTAACTGATCGAACTTTAATACATCATTC	602
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	603	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	650

>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1140 bits(617), Expect:0.0,
Identities:630/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	31	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	90
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	91	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	150
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	151	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	210
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	211	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	270
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	271	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	330

Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	331	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	390
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	391	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	450
Query	421	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	451	TTCAATTTTAGGTGCAATCAATTCATTACAACATTGTAAATATACGATCCATTGGAAT	510
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	511	AACAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	570
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	571	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAATATTAAGTATCGAACTTTAA	630
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCC	636
Sbjct	631	TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC	665

>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1134 bits(614), Expect:0.0,
Identities:618/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG	98
Sbjct	1	TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG	60
Query	99	GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG	218
Sbjct	121	TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG	180
Query	219	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC	278
Sbjct	181	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC	240
Query	279	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTT	338

Sbjct	241	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	300
Query	339	AccccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTG	458
Sbjct	361	CTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTG	420
Query	459	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	518
Sbjct	421	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	480
Query	519	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	578
Sbjct	481	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	540
Query	579	TATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA	638
Sbjct	541	TATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA	600
Query	639	TTCTATATCAACATTTATTT	658
Sbjct	601	TTCTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383800.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383815.1 Length: 768
Range 1: 1 to 642

Score:1131 bits(612), Expect:0.0,
Identities:632/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256

Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KX383796.1 Length: 744
Range 1: 1 to 618

Score:1125 bits(609), Expect:0.0,
Identities:615/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

Query	41	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA	100
Sbjct	1	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGA	60
Query	101	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttATA	160
Sbjct	61	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAATTTTTTTTATA	120
Query	161	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	220
Sbjct	121	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	180
Query	221	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	280

Sbjct	181	 CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	240
Query	281	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAc	340
Sbjct	241	 TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAC	300
Query	341	ccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	400
Sbjct	301	 CCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	360
Query	401	CTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTA	460
Sbjct	361	 CTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTA	420
Query	461	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	520
Sbjct	421	 AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	480
Query	521	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	580
Sbjct	481	 ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	540
Query	581	TTAACTGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT	640
Sbjct	541	 TTAACTGATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATT	600
Query	641	CTATATCAACATTTATTT 658	
Sbjct	601	 CTATATCAACATTTATTT 618	

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383798.1 Length: 698
Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	 TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180

Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383814.1 Length: 768
Range 1: 1 to 642

Score:1120 bits(606), Expect:0.0,
Identities:630/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAA TCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180

Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383801.1 Length: 763
Range 1: 1 to 637

Score:1116 bits(604), Expect:0.0,
Identities:626/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201

Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	AACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MW558150.1 Length: 657
Range 1: 1 to 639

Score:1114 bits(603), Expect:0.0,
Identities:627/639(98%), Gaps:0/639(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
Sbjct	1	GGAGCAGGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199

Sbjct	121		180
Query	200	GTTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259
Sbjct	181	GTTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	240
Query	260	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	319
Sbjct	241	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	300
Query	320	GGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA	379
Sbjct	301	GGTACAGGGGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCA	360
Query	380	GTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	439
Sbjct	361	GTAGATTTAGCTATCTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC	420
Query	440	AATTTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	499
Sbjct	421	AATTTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	480
Query	500	TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	559
Sbjct	481	TTATTTGTAGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	540
Query	560	GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	619
Sbjct	541	GCTGGTGAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	600
Query	620	TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	TCAGGAGGGGGTGAACCAATTCTATATCAACATTTATTT 639	

>Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726445.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726444.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Query	121	AATTGTAACAGCACATGCATTTATTATAA	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAA	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA	604
Sbjct	601	TACA	604

>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120

Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604 	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subunit I (COX1) gene,
 partial cds; mitochondrial
 Sequence ID: MZ726441.1 Length: 604
 Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
 Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

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Query   61   AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT   120
        |||
Sbjct   61   AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT   120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG   180
        |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG   180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG   240
        |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG   240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC   300
        |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC   300

Query   301  ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT   360
        |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT   360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC   420
        |||
Sbjct   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC   420

Query   421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT   480
        |||
Sbjct   421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT   480

Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT   540
        |||
Sbjct   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT   540

Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA   600
        |||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA   600

Query   601   TACA   604
        |||
Sbjct   601   TACA   604

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>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726440.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

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Query   1   GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT   60
        |||
Sbjct   1   GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT   60

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Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60

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Sbjct  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
Query  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||
Sbjct  61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT  120
Query  121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||
Sbjct  121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180
Query  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||
Sbjct  181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
Query  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||
Sbjct  241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
Query  301     ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||
Sbjct  301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360
Query  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
          |||
Sbjct  361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
Query  421     TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480
          |||
Sbjct  421     TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT  480
Query  481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||
Sbjct  481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query  541     ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          |||
Sbjct  541     ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query  601     TACA  604
          |||
Sbjct  601     TACA  604

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>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726438.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

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Query  1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

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Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	 TACA 604	

>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726437.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,

Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATTACAACCTATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATTACAACCTATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
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>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726434.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726433.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726432.1 Length: 604

Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene,

partial cds; mitochondrial
Sequence ID: MZ726430.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726449.1 Length: 604
Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726429.1 Length: 604
Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726428.1 Length: 604
Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726426.1 Length: 604
Range 1: 1 to 604

Score:1105 bits(598), Expect:0.0,
Identities:602/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||| |||||||||||||||||| ||||||||||||||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      ||||
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Sbjct 601 TACA 604

>Rhipicephalus sanguineus voucher D0-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638
Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

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Query  20  GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT  79
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Sbjct  1  GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT  60

Query  80  CAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCA  139
      ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  61  CAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCA  120

Query  140  TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  199
      ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  180

Query  200  GTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  259
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Sbjct  181  GTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  240

Query  260  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  319
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Sbjct  241  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  300

Query  320  GGAACAGGGTGAACAGTTTAccccccctTATCATCAAATTTATCACACTACGGACCATCA  379
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Sbjct  301  GGNACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCA  360

Query  380  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  439
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Query  500  TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA  559
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Query  560  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  619
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Sbjct  541  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT  600

Query  620  T  620
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Sbjct 601 T 601

Query #17: TKCJJ053-19|TKCJ012018E05|Rhipicephalus sanguineus|COI-5P Query ID: 1c1|Query_26779 Length: 658

Sequences producing significant alignments:

							Scientific	
Common		Max	Total Query	E	Per.	Acc.		
Description							Name	
Name	Taxid	Score	Score cover	Value	Ident	Len	Accession	
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...								
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00	688
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Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00	703
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Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c...								
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00	690
KT906183.1								
Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c...								
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KT906182.1								
Rhipicephalus sanguineus isolate Q3 mitochondrion, complete...								
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00	14711
OM368327.1								
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Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00	14714
OM368323.1								
Rhipicephalus sanguineus isolate A44 mitochondrion, complete...								
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00	14713
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Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase...								
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00	707
JQ737084.1								
Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI)...								
Rhipicephalu... brown dog tick		34632	1216	1216	100%	0.0	100.00	658
KF437543.1								
Rhipicephalus linnaei isolate LA032-2 clone JS5930...								
Rhipicephalu... NA		2138177	1216	1216	100%	0.0	100.00	14715
MW429383.1								
Rhipicephalus linnaei mitochondrion, complete sequence								

Rhipicephalu... NA NC_060409.1	2138177	1216	1216	100%	0.0	100.00	14711
Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene,... Ixodidae sp.... NA KX053537.1	1901042	1210	1210	100%	0.0	99.85	658
Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c...							
Rhipicephalu... brown dog tick KT906185.1	34632	1210	1210	100%	0.0	99.85	690
Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c...							
Rhipicephalu... brown dog tick KT906184.1	34632	1210	1210	100%	0.0	99.85	690
Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase...							
Rhipicephalu... brown dog tick KF200113.1	34632	1210	1210	100%	0.0	99.85	658
Rhipicephalus linnaei isolate SC931-1 clone JS5927...							
Rhipicephalu... NA MW429382.1	2138177	1210	1210	100%	0.0	99.85	14717
Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase...							
Rhipicephalu... brown dog tick KX360367.1	34632	1205	1205	99%	0.0	99.85	658
Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c...							
Rhipicephalu... brown dog tick KT906186.1	34632	1205	1205	100%	0.0	99.70	690
Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase...							
Rhipicephalu... brown dog tick KF200112.1	34632	1205	1205	100%	0.0	99.70	658
Rhipicephalus sanguineus mitochondrion, complete genome							
Rhipicephalu... brown dog tick JX416325.1	34632	1205	1205	100%	0.0	99.70	14714
Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase...							
Rhipicephalu... brown dog tick MZ401443.1	34632	1192	1192	98%	0.0	100.00	661
Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase...							
Rhipicephalu... brown dog tick MZ401441.1	34632	1192	1192	98%	0.0	100.00	661
Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick MZ401440.1	34632	1192	1192	98%	0.0	99.85	664
Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase...							
Rhipicephalu... brown dog tick MG969507.1	34632	1190	1190	97%	0.0	100.00	664
Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase...							
Rhipicephalu... brown dog tick KF200084.1	34632	1188	1188	98%	0.0	99.69	649
Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase...							
Rhipicephalu... brown dog tick KX383817.1	34632	1186	1186	97%	0.0	100.00	768
Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase...							
Rhipicephalu... brown dog tick MZ401442.1	34632	1186	1186	97%	0.0	100.00	657
Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase...							
Rhipicephalu... brown dog tick MZ401438.1	34632	1186	1186	97%	0.0	100.00	661
Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase...							

Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969506.1							
Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969505.1							
Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1184	1184	97%	0.0	99.84	664
MG969504.1							
Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1179	1179	97%	0.0	99.69	644
KF200096.1							
Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1177	1177	100%	0.0	98.94	658
OM984983.1							
Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416302.1							
Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1177	1177	96%	0.0	100.00	802
JX416298.1							
Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1177	1177	97%	0.0	99.69	670
HM193873.1							
Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1175	1175	97%	0.0	99.69	768
KX383820.1							
Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	97%	0.0	99.53	724
KX383816.1							
Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984984.1							
Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984974.1							
Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1171	1171	100%	0.0	98.78	658
OM984973.1							
Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416308.1							
Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416304.1							
Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416300.1							
Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416299.1							
Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416297.1							
Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subun...							

Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416296.1							
Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	99.84	802
JX416293.1							
Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1171	1171	96%	0.0	100.00	650
MZ401439.1							
Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	763
KX383802.1							
Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658
OM984979.1							
Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1166	1166	100%	0.0	98.63	658
OM984968.1							
Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416295.1							
Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1166	1166	96%	0.0	99.69	802
JX416294.1							
Rhipicephalus sanguineus isolate sanguineus0926 cytochrome...							
Rhipicephalu... brown dog tick	34632	1162	1162	99%	0.0	98.77	658
MH513252.1							
Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984985.1							
Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984978.1							
Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984977.1							
Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984975.1							
Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984971.1							
Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984970.1							
Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1160	1160	100%	0.0	98.48	658
OM984969.1							
Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1160	1160	96%	0.0	99.53	802
JX416301.1							
Rhipicephalus sanguineus isolate Tropical lineage RJ cytochrom...							
Rhipicephalu... brown dog tick	34632	1155	1155	95%	0.0	99.68	642
MT010523.1							
Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase...							

Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984988.1							
Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1155	1155	100%	0.0	98.33	658
OM984976.1							
Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subun...							
Rhipicephalu... brown dog tick	34632	1155	1155	96%	0.0	99.37	802
JX416303.1							
Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate...							
Rhipicephalu... NA	2138177	1153	1153	98%	0.0	98.77	826
MF426003.1							
Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidas...							
Rhipicephalu... brown dog tick	34632	1146	1146	96%	0.0	99.21	665
HM193874.1							
Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1140	1140	94%	0.0	99.84	630
KX757914.1							
Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1136	1136	97%	0.0	98.60	768
KX383800.1							
Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1131	1131	93%	0.0	99.68	744
KX383796.1							
Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1127	1127	96%	0.0	98.59	698
KX383798.1							
Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1125	1125	97%	0.0	98.29	768
KX383814.1							
Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1122	1122	96%	0.0	98.43	763
KX383801.1							
Rhipicephalus sanguineus isolate 400 cytochrome c oxidase...							
Rhipicephalu... brown dog tick	34632	1120	1120	97%	0.0	98.28	657
MW558150.1							
Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726445.1							
Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726444.1							
Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726443.1							
Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726442.1							
Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726441.1							
Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726440.1							
Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subun...							

Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726439.1							
Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726438.1							
Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726437.1							
Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726436.1							
Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726435.1							
Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726434.1							
Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726433.1							
Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726432.1							
Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726431.1							
Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1116	1116	91%	0.0	100.00	604
MZ726430.1							
Rhipicephalus linnaei isolate B9-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726449.1							
Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726429.1							
Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726428.1							
Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726427.1							
Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subun...							
Rhipicephalu... NA	2138177	1110	1110	91%	0.0	99.83	604
MZ726426.1							
Rhipicephalus sanguineus voucher DO-306 cytochrome oxidase...							
Rhipicephalu... brown dog tick	34632	1092	1092	91%	0.0	99.33	638
KX360338.1							

Alignments:

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3021 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425995.1 Length: 688

Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
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Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
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Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 498 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 558 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675
```

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3015 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425994.1 Length: 703

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3022 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: MF425996.1 Length: 703

Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccctTATCATCAAATTT 360
      |||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 500 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 560 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
```

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3014 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425993.1 Length: 702
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 500 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 560 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
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>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate A3013 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF425992.1 Length: 693
Range 1: 20 to 677

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 20 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 79

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 80 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 139

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 140 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 199

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 200 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 259

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 260 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 319

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 320 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 379

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      |||
Sbjct 380 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 439

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 440 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 499

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 500 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 559

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 560 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 619

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 620 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 677
```

>Rhipicephalus sanguineus haplotype RsanColSinSP cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906183.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
|||||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 498 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 558 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
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Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675

>Rhipicephalus sanguineus haplotype RsanColSanM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906182.1 Length: 690
Range 1: 18 to 675

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 18 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 77

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 78 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 137

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 138 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 197

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 198 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 257

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 258 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 317

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 318 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 377

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 378 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 437

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 438 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 497

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 498 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 557

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 558 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 617

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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|||||
Sbjct 618 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 675

>Rhipicephalus sanguineus isolate Q3 mitochondrion, complete genome
Sequence ID: OM368327.1 Length: 14711
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

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|||||
Sbjct  1785 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 1842
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>Rhipicephalus sanguineus isolate C19 mitochondrion, complete genome
Sequence ID: OM368323.1 Length: 14714
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query   1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
          |||
Sbjct  1185  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 1244

Query   61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
          |||
Sbjct  1245  AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 1304

Query   121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
          |||
Sbjct  1305  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 1364

Query   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
          |||
Sbjct  1365  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 1424

Query   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
          |||
Sbjct  1425  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 1484

Query   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
          |||
Sbjct  1485  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 1544

Query   361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
          |||
Sbjct  1545  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 1604

Query   421     TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
          |||
Sbjct  1605  TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 1664

Query   481     AACAAAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
          |||
Sbjct  1665  AACAAAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 1724

Query   541     ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
          |||
Sbjct  1725  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 1784

Query   601     TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
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|||||
Sbjct 1785 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 1842

>Rhipicephalus sanguineus isolate A44 mitochondrion, complete genome
Sequence ID: OM368322.1 Length: 14713
Range 1: 1185 to 1842

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1185	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	1245	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	1305	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	1365	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	1425	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	1485	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	1725	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

|||||
Sbjct 1785 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 1842

>Rhipicephalus sanguineus isolate Guangxi cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: JQ737084.1 Length: 707
Range 1: 24 to 681

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 24 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 83

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 84 AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT 143

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 144 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 203

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 204 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 263

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 264 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 323

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 324 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 383

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
|||||
Sbjct 384 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 443

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 444 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 503

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 504 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 563

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
|||||
Sbjct 564 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 623

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Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   624  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 681

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>Rhipicephalus sanguineus cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial
Sequence ID: KF437543.1 Length: 658
>Ixodidae sp. sc_00964 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial
Sequence ID: KX053539.1 Length: 658
Range 1: 1 to 658

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query    1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query   61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61      AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query   121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query   361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query   421     TTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAAT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421     TTCAATTTTAGGTGCAATCAATTTTATTACAACACTATTGTAAATATACGATCCATTGGAAT 480

Query   481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

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Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus linnaei isolate LA032-2 clone JS5930 mitochondrion, complete genome
Sequence ID: MW429383.1 Length: 14715
Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,
Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	164
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284
Query	241	AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	285	AATAAATAATATAAGATTTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	464
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584

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Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||
Sbjct   585  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 644

Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct   645  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 702

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>Rhipicephalus linnaei mitochondrion, complete sequence

Sequence ID: NC_060409.1 Length: 14711

>Rhipicephalus linnaei strain Coominya isolate AUS3 clone JS5929 mitochondrion, complete genome

Sequence ID: MW429381.1 Length: 14711

Range 1: 45 to 702

Score:1216 bits(658), Expect:0.0,

Identities:658/658(100%), Gaps:0/658(0%), Strand: Plus/Plus

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Query   1    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct   45    GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 104

Query   61    AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct   105   AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 164

Query   121   AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct   165   AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 224

Query   181   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct   225   AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 284

Query   241   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct   285   AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 344

Query   301   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct   345   ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 404

Query   361   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct   405   ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 464

Query   421   TTCAATTTTAGGTGCAATCAATTTTATTACAACATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct   465   TTCAATTTTAGGTGCAATCAATTTTATTACAACATTGTAAATATACGATCCATTGGAAT 524

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Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702

>Ixodidae sp. sc_01082 cytochrome oxidase subunit 1 (COI) gene, partial cds;
mitochondrial
Sequence ID: KX053537.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATCTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTTGTAAATATACGATCCATTGGAAT	480

Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColCorL cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906185.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTGGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAACATTTGTAAATATACGATCCATTGGAAT	480

Sbjct	438	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACATGATCGAAACTTTAA	600
Sbjct	558	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAACATGATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus haplotype RsanColTolC cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906184.1 Length: 690
Range 1: 18 to 675

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGGATACTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	378	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480

Sbjct	438		TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	ATTGTAAATATACGATCCATTGGAAT	497
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT		540
Sbjct	498		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT		557
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA	600
Sbjct	558		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA	617
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		658
Sbjct	618		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT		675

>Rhipicephalus sanguineus voucher CAS-T065 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Sequence ID: KF200113.1 Length: 658
Range 1: 1 to 658

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	

>Rhipicephalus linnaei isolate SC931-1 clone JS5927 mitochondrion, complete genome
Sequence ID: MW429382.1 Length: 14717
Range 1: 45 to 702

Score:1210 bits(655), Expect:0.0,
Identities:657/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	45	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	104	
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	105	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	164	
Query	121	AATTGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	165	AATTGTAACAGCACATGCATTTATTATAA	tttttttttTATAGTTATACCAATTATAATCGG	224
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	225	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	284	
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	285	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	344	
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT	360
Sbjct	345	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTT	404
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC	420
Sbjct	405	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTG	CAGGTGCTTC	464

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	465	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	524
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540	
Sbjct	525	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	584	
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAA	600
Sbjct	585	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAA	644
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	645	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	702	

>Rhipicephalus sanguineus voucher DO-311 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360367.1 Length: 658
Range 1: 4 to 658

Score:1205 bits(652), Expect:0.0,
Identities:654/655(99%), Gaps:0/655(0%), Strand: Plus/Plus

Query	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63	
Sbjct	4	AATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAAT	63	
Query	64	CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT	123	
Sbjct	64	CCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAAT	123	
Query	124	TGTAACAGCACATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGGAGG	183
Sbjct	124	TGTAACAGCACATGCATTTATTATAA	tttttttttTATAGTTATACCAATTATAATCGGAGG	183
Query	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243	
Sbjct	184	ATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAAT	243	
Query	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303	
Sbjct	244	AAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATT	303	
Query	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTTATC	363
Sbjct	304	AATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTTATC	363
Query	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTC	423	

Sbjct	364	ACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTACATCTTGCAGGTGCTTCTTC	423
Query	424	AATTTTAGGTGCAATCAATTTCACTACAATATTGTAAATATACGATCCATTGGAATAAC	483
Sbjct	424	AATTTTAGGTGCAATCAATTTCACTACAATATTGTAAATATACGATCCATTGGAATAAC	483
Query	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Sbjct	484	AATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATT	543
Query	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC	603
Sbjct	544	ATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATAC	603
Query	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	604	ATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus haplotype RsanColSamCM cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: KT906186.1 Length: 690
Range 1: 18 to 675

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	18	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	77
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	78	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	137
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	138	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	197
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	198	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	257
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	258	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	317
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	318	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	377
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420

Sbjct	378	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	437
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	438	 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	497
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	498	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	557
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	558	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	617
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	618	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	675

>Rhipicephalus sanguineus voucher GRP5-154 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200112.1 Length: 658
>Rhipicephalus sanguineus voucher D0-309 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360403.1 Length: 658
Range 1: 1 to 658

Score:1205 bits(652), Expect:0.0,
Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

>Rhipicephalus sanguineus mitochondrion, complete genome

Sequence ID: JX416325.1 Length: 14714

Range 1: 1185 to 1842

Score:1205 bits(652), Expect:0.0,

Identities:656/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60	
Sbjct	1185		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	1244
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120	
Sbjct	1245		AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	1304
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	180	
Sbjct	1305		AATTGTAACAGCACATGCATTTATTATAAAttttttATAGTTATACCAATTATAATCGG	1364
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240	
Sbjct	1365		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATGTAGCATTTCCACG	1424
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300	
Sbjct	1425		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	1484
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360	

Sbjct	1485	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	1544
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	1545	 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	1604
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	1605	 TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	1664
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	1665	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	1724
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	1725	 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	1784
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	1785	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACGTTTATTT	1842

>Rhipicephalus sanguineus isolate T95D15 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401443.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73
Sbjct	1	 ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60
Query	74	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133
Sbjct	61	 TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120
Query	134	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	 CATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253
Sbjct	181	 TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313
Sbjct	241	 AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300

Query	314	GGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGA	373
Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433
Sbjct	361	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434	GCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540
Query	554	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 645	

>Rhipicephalus sanguineus isolate T81D7 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401441.1 Length: 661
Range 1: 1 to 645

Score:1192 bits(645), Expect:0.0,
Identities:645/645(100%), Gaps:0/645(0%), Strand: Plus/Plus

Query	14	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	73
Sbjct	1	ATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAA	60
Query	74	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	133
Sbjct	61	TTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCA	120
Query	134	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	193
Sbjct	121	CATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAAT	180
Query	194	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	253
Sbjct	181	TGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATA	240
Query	254	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	313
Sbjct	241	AGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCA	300

Query	314	GGAGCAGGTACAGGGTGAACAGTTTAccccccCTTATCATCAAATTTATCACACTACGGA	373
Sbjct	301	GGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGA	360
Query	374	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	433
Sbjct	361	CCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGT	420
Query	434	GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	493
Sbjct	421	GCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGA	480
Query	494	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	553
Sbjct	481	ATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCA	540
Query	554	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT	613
Sbjct	541	GTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTT	600
Query	614	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	645

>Rhipicephalus sanguineus isolate T79D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401440.1 Length: 664
Range 1: 1 to 648

Score:1192 bits(645), Expect:0.0,
Identities:647/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	1	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	60
Query	71	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	61	GAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	120
Query	131	GCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	121	GCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	180
Query	191	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	181	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	240
Query	251	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310

Sbjct	241	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	300
Query	311	TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	301	TCAGGAGCAGGAACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	360
Query	371	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA	430
Sbjct	361	GGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTA	420
Query	431	GGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	421	GGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAA	480
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550
Sbjct	481	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	540
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAATACATCATTC	610
Sbjct	541	CCAGTCTTAGCTGGCGCAATTACAATATTATTAACCTGATCGAACTTTAATACATCATTC	600
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	648

>Rhipicephalus sanguineus isolate WZ004 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969507.1 Length: 664
Range 1: 1 to 644

Score:1190 bits(644), Expect:0.0,
Identities:644/644(100%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314

Sbjct	241		GATTTTGGTTACTTCCTCCTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315		GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301		GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375		CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361		CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	420
Query	435		CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421		CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481		TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	614
Sbjct	541		TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTG	600
Query	615		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601		ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 644	

>Rhipicephalus sanguineus voucher GRP5-150 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200084.1 Length: 649
Range 1: 1 to 649

Score:1188 bits(643), Expect:0.0,
Identities:647/649(99%), Gaps:0/649(0%), Strand: Plus/Plus

Query	10	CTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCAT	69
Sbjct	1	CTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCAT	60
Query	70	AGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC	129
Sbjct	61	AGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAC	120
Query	130	AGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGG	189
Sbjct	121	AGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGG	180
Query	190	AAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAA	249
Sbjct	181	AAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAA	240

Query	250	TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA	309
Sbjct	241	TATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGA	300
Query	310	ATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTA	369
Sbjct	301	ATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTA	360
Query	370	CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT	429
Sbjct	361	CGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTT	420
Query	430	AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA	489
Sbjct	421	AGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGA	480
Query	490	ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT	549
Sbjct	481	ACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTT	540
Query	550	ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT	609
Sbjct	541	ACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATT	600
Query	610	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	649

>Rhipicephalus sanguineus isolate LIC6084B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383817.1 Length: 768
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240

Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate T91D13 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: MZ401442.1 Length: 657
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256

Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	420
Query	437	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate T63D1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401438.1 Length: 661
Range 1: 1 to 642

Score:1186 bits(642), Expect:0.0,
Identities:642/642(100%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256

Sbjct	181		TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA		316
Sbjct	241		TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTT	AccccccctTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTT	ACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361		TCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTCTTCAATTTTAGGTGCA 420
Query	437	ATCAATTTCAATACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421		ATCAATTTCAATACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTT	ATTATTATTATCTTTACCAGTC	556
Sbjct	481		CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTT	ATTATTATTATCTTTACCAGTC 540
Query	557	TTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541		TTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAACTTTAATACATCATTCTTTGAC 600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601		CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	642

>Rhipicephalus sanguineus isolate WZ003 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969506.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74	
Sbjct	1		TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 60	
Query	75	TAGGTCAACCAGGAAC	TTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134	
Sbjct	61		TAGGTCAACCAGGAAC	TTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 120
Query	135	ATGCATTTATTATAA	tttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194	
Sbjct	121		ATGCATTTATTATAA	TTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 180

Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ002 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969505.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTATTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194
Sbjct	121	ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180

Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTCAATACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus isolate WZ001 cytochrome oxidase subunit I gene,
partial cds; mitochondrial
Sequence ID: MG969504.1 Length: 664
Range 1: 1 to 644

Score:1184 bits(641), Expect:0.0,
Identities:643/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	15	TTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	74
Sbjct	1	TTGTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT	60
Query	75	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	134
Sbjct	61	TAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC	120
Query	135	ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	194

Sbjct	121	ATGCATTTATTATAATTTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT	180
Query	195	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	254
Sbjct	181	GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA	240
Query	255	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	314
Sbjct	241	GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG	300
Query	315	GAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGAC	374
Sbjct	301	GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC	360
Query	375	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	434
Sbjct	361	CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTG	420
Query	435	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	494
Sbjct	421	CAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA	480
Query	495	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	554
Sbjct	481	TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG	540
Query	555	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	614
Sbjct	541	TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG	600
Query	615	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	644

>Rhipicephalus sanguineus voucher CAS-T066 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KF200096.1 Length: 644
Range 1: 1 to 644

Score:1179 bits(638), Expect:0.0,
Identities:642/644(99%), Gaps:0/644(0%), Strand: Plus/Plus

Query	6	TATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCC	65
Sbjct	1	TATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCC	60
Query	66	GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG	125
Sbjct	61	GCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTG	120
Query	126	TAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGAT	185

Sbjct	121	 TAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGAT	180
Query	186	TTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAA	245
Sbjct	181	 TTGGAAATTGATTAGTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCACGAATAA	240
Query	246	ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	305
Sbjct	241	 ATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAA	300
Query	306	TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCAC	365
Sbjct	301	 TCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCAC	360
Query	366	ACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	425
Sbjct	361	 ACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAA	420
Query	426	TTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAA	485
Sbjct	421	 TTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAA	480
Query	486	TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	545
Sbjct	481	 TAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTAT	540
Query	546	CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT	605
Sbjct	541	 CTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAT	600
Query	606	CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA 649	
Sbjct	601	 CATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAA 644	

>Rhipicephalus linnaei voucher P1/22_18-4 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: OM984983.1 Length: 658
 Range 1: 1 to 658

Score:1177 bits(637), Expect:0.0,
 Identities:651/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120


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Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
      |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
      |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
      |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
      |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGAGGTGCTTC  420
      |||
Sbjct   361  ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC  420

Query   421  TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480
      |||
Sbjct   421  TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT  480

Query   481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
      |||
Sbjct   481  AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600
      |||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA  600

Query   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||
Sbjct   601  TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT  658

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>Rhipicephalus sanguineus isolate GHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416302.1 Length: 802

>Rhipicephalus sanguineus isolate GPF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416305.1 Length: 802

>Rhipicephalus sanguineus isolate GPF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416306.1 Length: 802

>Rhipicephalus sanguineus isolate SZM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416307.1 Length: 802

Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,

Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
|||||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
|||||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
|||||
Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
|||||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
|||||
Sbjct 421 TTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
|||||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
|||||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637
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>Rhipicephalus sanguineus isolate CHM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416298.1 Length: 802
Range 1: 1 to 637

Score:1177 bits(637), Expect:0.0,
Identities:637/637(100%), Gaps:0/637(0%), Strand: Plus/Plus

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Query 22 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
|||||
Sbjct 1 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query 82 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
|||||
Sbjct 61 ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query 142 TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
|||||
Sbjct 121 TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query 202 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
|||||
Sbjct 181 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query 262 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
|||||
Sbjct 241 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query 322 TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
|||||
Sbjct 301 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query 382 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
|||||
Sbjct 361 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query 442 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
|||||
Sbjct 421 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query 502 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
|||||
Sbjct 481 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 540

Query 562 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
|||||
Sbjct 541 TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

Query 622 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
|||||
Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637
```

>Rhipicephalus sanguineus voucher AMMS-RS-5 cytochrome c oxidase subunit I-like
(COI) gene, partial sequence; mitochondrial
Sequence ID: HM193873.1 Length: 670
Range 1: 1 to 642

Score:1177 bits(637), Expect:0.0,
Identities:642/644(99%), Gaps:2/644(0%), Strand: Plus/Plus

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Query 15 TTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 74
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 1 TTTTGGGA-CATGATCCGG-ATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAAT 58

Query 75 TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 134
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 59 TAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCAC 118

Query 135 ATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 194
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 119 ATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATT 178

Query 195 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 254
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 179 GATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAA 238

Query 255 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 314
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 239 GATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAG 298

Query 315 GAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGAC 374
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 299 GAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGAC 358

Query 375 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG 434
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 359 CATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTG 418

Query 435 CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 494
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 419 CAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAA 478

Query 495 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 554
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 479 TACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAG 538

Query 555 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 614
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 539 TCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTG 598

Query 615 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct 599 ACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 642
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>Rhipicephalus sanguineus isolate LIC6767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383820.1 Length: 768

Range 1: 1 to 642

Score:1175 bits(636), Expect:0.0,
Identities:640/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

```
Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
      |||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
      |||
Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
      |||
Sbjct 121 GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
      |||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
      |||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAcCCCCcTTATCATCAAATTTATCACACTACGGACCA 376
      |||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 436
      |||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
      |||
Sbjct 421 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
      |||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 616
      |||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 CCTTCAGGAGGGGTGACCCAATTCTATATCAACATTTATTT 642
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>Rhipicephalus sanguineus isolate LIC5766G cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial

Sequence ID: KX383816.1 Length: 724
Range 1: 1 to 642

Score:1171 bits(634), Expect:0.0,
Identities:639/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

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Query 17 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 76
      |||
Sbjct 1 TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA 60

Query 77 GGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT 136
      |||
Sbjct 61 GGTCAACCAGGAACTTTAATTGGAAACGATSAAATTTATAATGTAATTGTAACAGCACAT 120

Query 137 GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 196
      |||
Sbjct 121 GCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA 180

Query 197 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 256
      |||
Sbjct 181 TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA 240

Query 257 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 316
      |||
Sbjct 241 TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA 300

Query 317 GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA 376
      |||
Sbjct 301 GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA 360

Query 377 TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 436
      |||
Sbjct 361 TCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTCTTCAATTTTAGGTGCA 420

Query 437 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 496
      |||
Sbjct 421 ATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA 480

Query 497 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 556
      |||
Sbjct 481 CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC 540

Query 557 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 616
      |||
Sbjct 541 TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC 600

Query 617 CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 CCTTCAGGAGGGGGTGACCCAATTCTATATCAACATTTATTT 642
```

>Rhipicephalus linnaei voucher P1/22_18-5 cytochrome c oxidase subunit I (COX1)

gene, partial cds; mitochondrial
Sequence ID: OM984984.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT 658
```

>Rhipicephalus linnaei voucher P1/22_8-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984974.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGAGGTGCTTC 420
      |||||||||||| |||||||||||||||||| |||||||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||||||||||||||||| |||||||||||||| ||||||||||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus linnaei voucher P1/22_6-2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984973.1 Length: 658
Range 1: 1 to 658

Score:1171 bits(634), Expect:0.0,
Identities:650/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC 420
      |||||||||||| |||||||||||||||||| |||||||||||||||||| ||||||||
Sbjct 361 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCTGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||||||||||||||||| |||||||||||||||||| |||||||||||||||||| ||||||||
Sbjct 421 TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||||||||||||||||| |||||||||||||||||| |||||||||||||||||| ||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      |||||||||||||||||| |||||||||||||||||| |||||||||||||||||| ||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658
      |||||||||||||||||| |||||||||||||| |||||||||||||| ||||||||
Sbjct 601 TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT 658
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>Rhipicephalus sanguineus isolate SZM2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416308.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

```
Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query  142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACAACATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
      |||||||||||||||||||||||||||||||||||
Sbjct  601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637
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>Rhipicephalus sanguineus isolate GTF3 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial

Sequence ID: JX416304.1 Length: 802

Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,

Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCTCATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate GBM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416300.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGGAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAcCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658

Sbjct 601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

>Rhipicephalus sanguineus isolate GBF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416299.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query  22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
      |||
Sbjct  1    AGCATGATCCGGGATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query  82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT  141
      |||
Sbjct  61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT  120

Query  142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
      |||
Sbjct  121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query  202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
      |||
Sbjct  181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query  262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
      |||
Sbjct  241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query  322  TACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
      |||
Sbjct  301  TACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query  382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
      |||
Sbjct  361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query  442  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
      |||
Sbjct  421  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query  502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
      |||
Sbjct  481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query  562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
      |||
Sbjct  541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

Query  622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
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      ||||||||||||||||||||||||||||||||||
Sbjct  601 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637

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>Rhipicephalus sanguineus isolate CHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416297.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query   22  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 81
      ||||||||||||||||||||||||||||||||||
Sbjct   1  AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 60

Query   82  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 141
      ||||||||||||||||||||||||||||||||||
Sbjct   61  ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 120

Query   142  TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 201
      ||||||||||||||||||||||||||||||||||
Sbjct   121  TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 180

Query   202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 261
      ||||||||||||||||||||||||||||||||||
Sbjct   181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 240

Query   262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 321
      ||||||||||||||||||||||||||||||||||
Sbjct   241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 300

Query   322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 381
      ||||||||||||||||||||||||||||||||||
Sbjct   301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 360

Query   382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 441
      ||||||||||||||||||||||||||||||||||
Sbjct   361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 420

Query   442  TTTCAATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 501
      ||||||||||||||||||||||||||||||||||
Sbjct   421  TTTCAATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 480

Query   502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC 561
      |||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct   481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTACTATCTTTACCAGTCTTAGC 540

Query   562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 621
      ||||||||||||||||||||||||||||||||||
Sbjct   541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC 600

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Query   622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||||||||||||||||||||||||||||||||||
Sbjct   601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637

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>Rhipicephalus sanguineus isolate DGM1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416296.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

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Query   22   AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  81
        |||||||||||||||||||||||||||||||||||
Sbjct    1   AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA  60

Query   82   ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  141
        |||||||||||||||||||||||||||||||||||
Sbjct   61   ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT  120

Query   142  TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  201
        ||||| |||||||||||||||||||||||||||||||
Sbjct   121  TATTATGATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT  180

Query   202  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  261
        |||||||||||||||||||||||||||||||||||
Sbjct   181  TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG  240

Query   262  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  321
        |||||||||||||||||||||||||||||||||||
Sbjct   241  GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG  300

Query   322  TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT  381
        |||||||||||||||||||||||||||||||||||
Sbjct   301  TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT  360

Query   382  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  441
        |||||||||||||||||||||||||||||||||||
Sbjct   361  AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA  420

Query   442  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  501
        |||||||||||||||||||||||||||||||||||
Sbjct   421  TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT  480

Query   502  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  561
        |||||||||||||||||||||||||||||||||||
Sbjct   481  ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC  540

Query   562  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  621
        |||||||||||||||||||||||||||||||||||
Sbjct   541  TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC  600

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Query    622  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  658
        |||||||||||||||||||||||||||||||||||
Sbjct    601  AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT  637

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>Rhipicephalus sanguineus isolate FSF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416293.1 Length: 802
Range 1: 1 to 637

Score:1171 bits(634), Expect:0.0,
Identities:636/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTACGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCGAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCGAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTGAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTGAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAACGATCGAAACTTTAATACATCATTCTTTGACCCTTC	621

Sbjct	541	TGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637	

>Rhipicephalus sanguineus isolate T78D2 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ401439.1 Length: 650
Range 1: 1 to 634

Score:1171 bits(634), Expect:0.0,
Identities:634/634(100%), Gaps:0/634(0%), Strand: Plus/Plus

Query	25	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	84	
Sbjct	1	ATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACC	60	
Query	85	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	144	
Sbjct	61	AGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTAT	120	
Query	145	TATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	204	
Sbjct	121	TATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCC	180	
Query	205	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	264	
Sbjct	181	TATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTT	240	
Query	265	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	324	
Sbjct	241	ACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTAC	300	
Query	325	AGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	384	
Sbjct	301	AGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGA	360	
Query	385	TTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTT	444	
Sbjct	361	TTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTT	420	
Query	445	CATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	504	
Sbjct	421	CATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATT	480	
Query	505	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	564	
Sbjct	481	TGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGG	540	
Query	565	CGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGACCCTTCAGG	624

Sbjct	541		CGCAATTACAATATTATTA	ACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGG	600
Query	625		AGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601		AGGAGGTGACCCAATTCTATATCAACATTTATTT	634	

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>Rhipicephalus sanguineus isolate LIC5762 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383802.1 Length: 763
>Rhipicephalus sanguineus isolate LIC5767C cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383803.1 Length: 763
>Rhipicephalus sanguineus isolate LIC5767D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383804.1 Length: 763
Range 1: 1 to 637
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Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA 	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT 	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT 	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG 	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG 	300
Query	322	TACAGGGTGAACAGTTTAcccccccTTATCATCAAATTTATCACACTACGGACCATCAGT 	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT 	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA 	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT 	501

Sbjct	421	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGGGGTGAACCAATTCTATATCAACATTTATTT	637

>Rhipicephalus linnaei voucher P1/22_16-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984979.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATCCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAAC TATTGTAAATATACGATCCATTGGAAT	480

Sbjct	421		TTCAATTTTAGGTGCAATTAATTTTCATTACAAC	ATTGTA	AATATACGATCCATTGGGAT	480
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT			540
Sbjct	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT			540
Query	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA		600
Sbjct	541		ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTA	AACTGATCGAAACTTTAA		600
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT			658
Sbjct	601		TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT			658

>Rhipicephalus linnaei voucher P1/22_1-1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial
Sequence ID: OM984968.1 Length: 658
Range 1: 1 to 658

Score:1166 bits(631), Expect:0.0,
Identities:649/658(99%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT			60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT			60
Query	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT			120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT			120
Query	121		AATTGTAACAGCACATGCATTTATTATAA	tttttttATAGTTATACCAATTATAATCGG		180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAA	tttttttATAGTTATACCAATTATAATCGG		180
Query	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG			240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG			240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC			300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC			300
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	AccccccTTATCATCAAATTT		360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	ACCCTCCCTTATCATCAAATTT		360
Query	361		ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC		420
Sbjct	361		ATCACACTACGGGCCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTG	CAGGTGCTTC		420

Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAAC	TATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTG	TTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAAT	ATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCA	ATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCA	ATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate DGF1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416295.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAAACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACGGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420

Query	442	TTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAAC	TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561	
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540	
Query	562	TGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTA	ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCGACATTTATTT	637	

>Rhipicephalus sanguineus isolate FSM1 cytochrome oxidase subunit I (cox1) gene, partial cds; mitochondrial
Sequence ID: JX416294.1 Length: 802
Range 1: 1 to 637

Score:1166 bits(631), Expect:0.0,
Identities:635/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81	
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGTATTAGGTCA	60	
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141	
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120	
Query	142	TATTATAA	tttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAA	TTTTTTTTTATAGTTATACCTATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261	
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240	
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321	
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300	
Query	322	TACAGGGTGAACAGTTTA	acccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTA	ACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441	

Sbjct	361	AGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate sanguineus0926 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial
Sequence ID: MH513252.1 Length: 658
Range 1: 6 to 658

Score:1162 bits(629), Expect:0.0,
Identities:645/653(99%), Gaps:0/653(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	6	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	65
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	66	AATTCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	125
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	126	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	185
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	186	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	245
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	246	AATAACAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	305
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	306	ATTAATCGAATCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	365
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420

Sbjct	366		ATCACACTACGGACCATCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTC	425
Query	421		TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	426		TTCAATTTTAGGCGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	485
Query	481		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	486		AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	545
Query	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	546		ATTATCTTTACCAGTCTTAGCTGGTGAATACAATATTGTAACTGATCGAAACTTTAA	605
Query	601		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATT	653
Sbjct	606		TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATT	658

>Rhipicephalus linnaei voucher P1/22_19-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984985.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1		GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61		AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121		AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121		AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181		AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181		AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241		AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301		ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_14-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984978.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360

Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_13-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984977.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_10-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984975.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360

Sbjct	301	 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	 ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	 TTCAATTTTAGGTGCAATTAATTTTCATTACAACACTATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	 ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	 TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_5-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984971.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	 GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	 AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATGGTAAATATACGATCCATTGGGAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_4-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984970.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_3-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984969.1 Length: 658
Range 1: 1 to 658

Score:1160 bits(628), Expect:0.0,
Identities:648/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300

Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GHF1 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416301.1 Length: 802
Range 1: 1 to 637

Score:1160 bits(628), Expect:0.0,
Identities:634/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321

Sbjct	241	 GTTACTTCCTCCTTCTCTAATTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAC TATCGAAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCTATTACAATATTATTAAC TATCGAAACTTTAATACATTATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

Score:1155 bits(625), Expect:0.0,
Identities:629/631(99%), Gaps:0/631(0%), Strand: Plus/Plus

Query	268	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	327
Sbjct	241	TCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGG	300
Query	328	GTGAACAGTTTAccccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	387
Sbjct	301	GTGAACAGTTTACCCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTT	360
Query	388	AGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	447
Sbjct	361	AGCTATTTTTTCTCTACATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTCAT	420
Query	448	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	507
Sbjct	421	TACAACTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGT	480
Query	508	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	567
Sbjct	481	ATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGC	540
Query	568	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	627
Sbjct	541	AATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGG	600
Query	628	AGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	GGGTGACCCAATTCTATATCAACATTTATTT	631

>Rhipicephalus linnaei voucher P1/22_21-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984988.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240

Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGTGAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTTTTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus linnaei voucher P1/22_12-1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: OM984976.1 Length: 658
Range 1: 1 to 658

Score:1155 bits(625), Expect:0.0,
Identities:647/658(98%), Gaps:0/658(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240

Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCTCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGGCCATCAGTAGATTTAGCTATCTTCTCTCTGCATCTTGCCGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATTAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGTGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TACATCATTTTTTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	658

>Rhipicephalus sanguineus isolate GTF2 cytochrome oxidase subunit I (cox1) gene,
partial cds; mitochondrial
Sequence ID: JX416303.1 Length: 802
Range 1: 1 to 637

Score:1155 bits(625), Expect:0.0,
Identities:633/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	120
Query	142	TATTATAAAttttttTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAGATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261

Sbjct	181	 TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	 GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	 TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	 AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATCTTAGGTGCAATCAA	420
Query	442	TTTCATTACAAC TATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	 TTTCATTACAAC TATTGTAAATACACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	 ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	 TGGCGCAATTACAATATTATTA ACTGATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	 AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 637	

>Rhipicephalus sanguineus sensu lato 'tropical lineage' isolate CV3042
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial
Sequence ID: MF426003.1 Length: 826
Range 1: 3 to 650

Score:1153 bits(624), Expect:0.0,
Identities:640/648(99%), Gaps:0/648(0%), Strand: Plus/Plus

Query	11	TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATA	70
Sbjct	3	 TTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATA	62
Query	71	GAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	130
Sbjct	63	 GAATTAGGTCAACCAGGAAC TTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACA	122
Query	131	GCACATGCATTTATTATAA ttttttttATAGTTATACCAATTATAATCGGAGGATTTGGA	190
Sbjct	123	 GCACATGCATTTATTATAA TTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGA	182

Query	191	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAAT	250
Sbjct	183	AATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAAT	242
Query	251	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	310
Sbjct	243	ATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAA	302
Query	311	TCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTAC	370
Sbjct	303	TCAGGAGCGGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTAC	362
Query	371	GGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	430
Sbjct	363	GGACCATCAGTAGATTTAGCTATCTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTA	422
Query	431	GGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA	490
Sbjct	423	GGCGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAATAACAATAGAA	482
Query	491	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	550
Sbjct	483	CGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTA	542
Query	551	CCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTC	610
Sbjct	543	CCAGTCTTAGCTGGTGCAATTACAATATTGTAAAGTATCGAAACTTTAATACATCATTC	602
Query	611	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	603	TTTGACCCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	650

>Rhipicephalus sanguineus voucher AMMS-RS-4 cytochrome c oxidase subunit I-like (COI) gene, partial sequence; mitochondrial
Sequence ID: HM193874.1 Length: 665
Range 1: 31 to 665

Score:1146 bits(620), Expect:0.0,
Identities:631/636(99%), Gaps:1/636(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	31	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	90
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	91	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	150
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	151	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	210

Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	211	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	270
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	271	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	330
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	331	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	390
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	391	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTCTCTGCATCTTGCAGGTGCTTC	450
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	451	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	510
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	511	AACAATAGAACGAATCCCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	570
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	571	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAATATTAAGTATCGAAACTTTAA	630
Query	601	TACATCATTCTTTGACCCTTCAGGAGGAGGTGACCC	636
Sbjct	631	TACATCATTCTTTGACCCAGCAGGAGGAGG-GACCC	665

>Rhipicephalus sanguineus isolate Abidjan cytochrome oxidase subunit I (COI)
gene, partial cds; mitochondrial
Sequence ID: KX757914.1 Length: 630
Range 1: 1 to 620

Score:1140 bits(617), Expect:0.0,
Identities:619/620(99%), Gaps:0/620(0%), Strand: Plus/Plus

Query	39	TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG	98
Sbjct	1	TAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTG	60
Query	99	GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAttttttttA	158
Sbjct	61	GAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAATTTTTTTTA	120
Query	159	TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAG	218

Sbjct	121	TAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGGG	180
Query	219	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC	278
Sbjct	181	CTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTC	240
Query	279	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	338
Sbjct	241	TATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTT	300
Query	339	AccccccTTATCATCAAATTTATCACAACACGACCATCAGTAGATTTAGCTATTTTTT	398
Sbjct	301	ACCCCCCTTATCATCAAATTTATCACAACACGACCATCAGTAGATTTAGCTATTTTTT	360
Query	399	CTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACATTTG	458
Sbjct	361	CTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAACATTTG	420
Query	459	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	518
Sbjct	421	TAAATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTT	480
Query	519	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	578
Sbjct	481	TAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATAT	540
Query	579	TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA	638
Sbjct	541	TATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAA	600
Query	639	TTCTATATCAACATTTATTT	658
Sbjct	601	TTCTATATCAACATTTATTT	620

>Rhipicephalus sanguineus isolate LIC5960 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383800.1 Length: 768
>Rhipicephalus sanguineus isolate LIC5766D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383815.1 Length: 768
Range 1: 1 to 642

Score:1136 bits(615), Expect:0.0,
Identities:633/642(99%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA	60
Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136

Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCACGAATAAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTC	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC5682B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383796.1 Length: 744
Range 1: 1 to 618

Score:1131 bits(612), Expect:0.0,
Identities:616/618(99%), Gaps:0/618(0%), Strand: Plus/Plus

Query	41	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGA	100
Sbjct	1	GGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGA	60
Query	101	AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAAAttttttttATA	160

Sbjct	61	 AACGATCAAATTTATAATGTAATTGTAACAGCACATGCATTTATTATAATTTTTTTTATA	120
Query	161	GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	220
Sbjct	121	 GTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCT	180
Query	221	CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	280
Sbjct	181	 CCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTA	240
Query	281	TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAc	340
Sbjct	241	 TTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAC	300
Query	341	ccccccTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	400
Sbjct	301	 CCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCT	360
Query	401	CTGCATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTA	460
Sbjct	361	 CTACATCTTGCAAGTGCTTCTTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTA	420
Query	461	AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	520
Sbjct	421	 AATATACGATCCATTGGAATAACAATAGAACGAATACCATTATTTGTATGATCTGTTTTA	480
Query	521	ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	580
Sbjct	481	 ATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTA	540
Query	581	TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGAGGTGACCCAATT	640
Sbjct	541	 TTAACTGATCGAAACTTTAATACATCATTCTTTGACCCTTCAGGAGGGGGTGACCCAATT	600
Query	641	CTATATCAACATTTATTT 658	
Sbjct	601	 CTATATCAACATTTATTT 618	

>Rhipicephalus sanguineus isolate LIC5958B cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383798.1 Length: 698
Range 1: 1 to 637

Score:1127 bits(610), Expect:0.0,
Identities:628/637(99%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81
Sbjct	1	 AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60

Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGCAATTACAATATTATTAAGTATCGAAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 637	

>Rhipicephalus sanguineus isolate LIC5584D cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX383814.1 Length: 768
Range 1: 1 to 642

Score:1125 bits(609), Expect:0.0,
Identities:631/642(98%), Gaps:0/642(0%), Strand: Plus/Plus

Query	17	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTA	76
Sbjct	1	TTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTA	60

Query	77	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACAT	136
Sbjct	61	GGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACAT	120
Query	137	GCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	196
Sbjct	121	GCATTTATTATAAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGA	180
Query	197	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGA	256
Sbjct	181	TTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAACAATATAAGA	240
Query	257	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	316
Sbjct	241	TTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGA	300
Query	317	GCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCA	376
Sbjct	301	GCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCA	360
Query	377	TCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCA	436
Sbjct	361	TCAGTAGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCA	420
Query	437	ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	496
Sbjct	421	ATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATA	480
Query	497	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTC	556
Sbjct	481	CCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTT	540
Query	557	TTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	616
Sbjct	541	TTAGCTGGTGAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGAC	600
Query	617	CCTTCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT 658	
Sbjct	601	CCTTCAGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT 642	

>Rhipicephalus sanguineus isolate LIC5755 cytochrome oxidase subunit 1 (COI)
 gene, partial cds; mitochondrial
 Sequence ID: KX383801.1 Length: 763
 Range 1: 1 to 637

Score:1122 bits(607), Expect:0.0,
 Identities:627/637(98%), Gaps:0/637(0%), Strand: Plus/Plus

Query	22	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGTCA	81

Sbjct	1	AGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATTCGCATAGAATTAGGTCA	60
Query	82	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCATT	141
Sbjct	61	ACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTGACAGCACATGCATT	120
Query	142	TATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	201
Sbjct	121	TATTATAATCTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTAGT	180
Query	202	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTTTG	261
Sbjct	181	TCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAACAATATAAGATTTTG	240
Query	262	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	321
Sbjct	241	GTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCAGG	300
Query	322	TACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCAGT	381
Sbjct	301	TACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGATCATCAGT	360
Query	382	AGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATCAA	441
Sbjct	361	AGATTTAGCTATCTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGCGCAATCAA	420
Query	442	TTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	501
Sbjct	421	TTTCATTACAACATTTGTAATATACGATCCATTGGAATAACAATAGAACGAATACCATT	480
Query	502	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTAGC	561
Sbjct	481	ATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTGTTATCTTTACCAGTCTTAGC	540
Query	562	TGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	621
Sbjct	541	TGGTGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCTTC	600
Query	622	AGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	AGGAGGAGGTGACCCAATTCTGTATCAACATTTATTT	637

>Rhipicephalus sanguineus isolate 400 cytochrome c oxidase subunit I (COX1)
 gene, partial cds; mitochondrial
 Sequence ID: MW558150.1 Length: 657
 Range 1: 1 to 639

Score:1120 bits(606), Expect:0.0,
 Identities:628/639(98%), Gaps:0/639(0%), Strand: Plus/Plus

Query	20	GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	79
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Sbjct	1		
		GGAGCAGGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT	60
Query	80	CAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	139
Sbjct	61	CAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA	120
Query	140	TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA	199
Sbjct	121	TTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATGGATTA	180
Query	200	GTTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	259
Sbjct	181	GTTTCCTATTATGCTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT	240
Query	260	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	319
Sbjct	241	TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA	300
Query	320	GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA	379
Sbjct	301	GGTACAGGGGGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGGCCATCA	360
Query	380	GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC	439
Sbjct	361	GTAGATTTAGCTATCTTTTCTCTGCATCTTGCCGGTGCTTCTTCAATTTTAGGTGCAATC	420
Query	440	AATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	499
Sbjct	421	AATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA	480
Query	500	TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	559
Sbjct	481	TTATTTGTAGGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA	540
Query	560	GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	619
Sbjct	541	GCTGGTGCATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT	600
Query	620	TCAGGAGGAGGTGACCCAATTCTATATCAACATTTATTT	658
Sbjct	601	TCAGGAGGGGGTACCCAATTCTATATCAACATTTATTT	639

>Rhipicephalus linnaei isolate C2-T1 cytochrome c oxidase subunit I (COX1) gene,
 partial cds; mitochondrial
 Sequence ID: MZ726445.1 Length: 604
 Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
 Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate C1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726444.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B15-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726443.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
|||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
|||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
|||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
|||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
|||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
|||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
|||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
|||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
|||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
|||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B12-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726442.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B8-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726441.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAcccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B7-T3 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726440.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B7-T2 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726439.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B7-T1 cytochrome c oxidase subunit I (COX1) gene,

partial cds; mitochondrial
Sequence ID: MZ726438.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Sbjct	541	ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA	600
Query	601	TACA 604	
Sbjct	601	TACA 604	

>Rhipicephalus linnaei isolate B6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726437.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B4-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726436.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate B3-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726435.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      |||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      |||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      |||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      |||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      |||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      |||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
      |||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      |||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      |||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      |||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      |||
Sbjct 601 TACA 604
```


>Rhipicephalus linnaei isolate B2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial

Sequence ID: MZ726434.1 Length: 604

Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,

Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      ||||
Sbjct 601 TACA 604
```

>Rhipicephalus linnaei isolate A7-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726433.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query 601 TACA 604
      ||||
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Sbjct 601 TACA 604

>Rhipicephalus linnaei isolate A6-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726432.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

```
Query 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT 120

Query 121 AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query 361 ATCACAACACGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 ATCACAACACGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC 420

Query 421 TTCAATTTTAGGTGCAATCAATTTCAATACAACATTTGTAAATATACGATCCATTGGAAT 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 TTCAATTTTAGGTGCAATCAATTTCAATACAACATTTGTAAATATACGATCCATTGGAAT 480

Query 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

Query 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA 600

Query 601 TACA 604
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||||
Sbjct 601 TACA 604

>Rhipicephalus linnaei isolate A5-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726431.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAAGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Query	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600
Sbjct	541	ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA	600

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Query   601  TACA   604
        ||||
Sbjct   601  TACA   604

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>Rhipicephalus linnaei isolate A2-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726430.1 Length: 604
Range 1: 1 to 604

Score:1116 bits(604), Expect:0.0,
Identities:604/604(100%), Gaps:0/604(0%), Strand: Plus/Plus

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Query    1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query   61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121     AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121     AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query   361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC  420

Query   421     TTCAATTTTAGGTGCAATCAATTTCAATACAACCTATTGTAAATATACGATCCATTGGAAT  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421     TTCAATTTTAGGTGCAATCAATTTCAATACAACCTATTGTAAATATACGATCCATTGGAAT  480

Query   481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481     AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query   541     ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   541     ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

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Sbjct 601 TACA 604

Range 1: 1 to 604

Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

|||||

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Sbjct  541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600
Query   601  TACA  604
          ||||
Sbjct   601  TACA  604

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>Rhipicephalus linnaei isolate B18-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726429.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

```

Query    1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    1      GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT  60

Query   61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61      AATCCGCATAGAATTAGGTCAACCAGGAACCTTAATTGGAAACGATCAAATTTATAATGT  120

Query   121     AATTGTAACAGCACATGCATTTATTATAAttttttttATAGTTATACCAATTATAATCGG  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   121     AATTGTAACAGCACATGCATTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGG  180

Query   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181     AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG  240

Query   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241     AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC  300

Query   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   301     ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT  360

Query   361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC  420
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct   361     ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC  420

Query   421     TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   421     TTCAATTTTAGGTGCAATCAATTTTCATTACAACCTATTGTAAATATACGATCCATTGGAAT  480

Query   481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   481     AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540

Query   541     ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA  600

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Sbjct	541		ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTA	600
Query	601	TACA	604	
Sbjct	601	TACA	604	

>Rhipicephalus linnaei isolate B17-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726428.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTATTACAATATTGTAAATATACGATCCATTGGAAT	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540
Sbjct	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT	540


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Query   541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600
        |||
Sbjct   541  ATTATCTTTACCACTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAA 600

Query   601  TACA 604
        |||
Sbjct   601  TACA 604

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>Rhipicephalus linnaei isolate B16-T1 cytochrome c oxidase subunit I (COX1)
gene, partial cds; mitochondrial
Sequence ID: MZ726427.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

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Query    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60
        |||
Sbjct    1  GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 60

Query   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120
        |||
Sbjct   61  AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 120

Query   121  AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 180
        |||
Sbjct   121  AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 180

Query   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240
        |||
Sbjct   181  AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 240

Query   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300
        |||
Sbjct   241  AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 300

Query   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 360
        |||
Sbjct   301  ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 360

Query   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGAGGTGCTTC 420
        |||
Sbjct   361  ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGAGGTGCTTC 420

Query   421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480
        |||
Sbjct   421  TTCAATTTTAGGTGCAATCAATTTCAATACAATATTGTAAATATACGATCCATTGGAAT 480

Query   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540
        |||
Sbjct   481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 540

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Query    541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600

Query    601  TACA  604
        ||||
Sbjct    601  TACA  604

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>Rhipicephalus linnaei isolate B1-T1 cytochrome c oxidase subunit I (COX1) gene,
partial cds; mitochondrial
Sequence ID: MZ726426.1 Length: 604
Range 1: 1 to 604

Score:1110 bits(601), Expect:0.0,
Identities:603/604(99%), Gaps:0/604(0%), Strand: Plus/Plus

Query	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 	60
Sbjct	1	GACAATATACTTAATTTTTGGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATT 	60
Query	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 	120
Sbjct	61	AATCCGCATAGAATTAGGTCAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGT 	120
Query	121	AATTGTAACAGCACATGCATTTATTATAAAttttttttATAGTTATACCAATTATAATCGG 	180
Sbjct	121	AATTGTAACAGCACATGCATTTATTATAAATTTTTTTTATAGTTATACCAATTATAATCGG 	180
Query	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 	240
Sbjct	181	AGGATTTGGAAATTGATTAGTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACG 	240
Query	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 	300
Sbjct	241	AATAAATAATATAAGATTTTGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTC 	300
Query	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTT 	360
Sbjct	301	ATTAATCGAATCAGGAGCAGGTACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTT 	360
Query	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTC 	420
Sbjct	361	ATCACACTACGGACCATCAGTAGATTTAGCTATTTTTTCTCTACATCTTGCAGGTGCTTC 	420
Query	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT 	480
Sbjct	421	TTCAATTTTAGGTGCAATCAATTTTCATTACAACATTGTAAATATACGATCCATTGGAAT 	480
Query	481	AACAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT 	540

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Sbjct  481  AACAAATAGAACGAATACCATTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATT  540
Query   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
        |||
Sbjct   541  ATTATCTTTACCAGTCTTAGCTGGCGCAATTACAATATTATTAAGTATCGAAACTTTAA  600
Query   601  TACA  604
        |||
Sbjct   601  TACA  604

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>Rhipicephalus sanguineus voucher D0-306 cytochrome oxidase subunit 1 (COI)
gene, partial cds; mitochondrial
Sequence ID: KX360338.1 Length: 638
Range 1: 1 to 601

Score:1092 bits(591), Expect:0.0,
Identities:597/601(99%), Gaps:0/601(0%), Strand: Plus/Plus

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Query   20  GGAGCATGATCCGGAATACTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT  79
        |||
Sbjct   1  GGAGCATGATCCGGAATATTAGGATTAAGAATAAGAATATTAATCCGCATAGAATTAGGT  60

Query   80  CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA  139
        |||
Sbjct   61  CAACCAGGAACTTTAATTGGAAACGATCAAATTTATAATGTAATTGTAACAGCACATGCA  120

Query   140  TTTATTATAAAttttttttATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  199
        |||
Sbjct   121  TTTATTATAATTTTTTTTATAGTTATACCAATTATAATCGGAGGATTTGGAAATTGATTA  180

Query   200  GTTCCTATTATACTAGGAGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  259
        |||
Sbjct   181  GTTCCTATTATACTAGGGGCTCCAGATATAGCATTTCCACGAATAAATAATATAAGATTT  240

Query   260  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  319
        |||
Sbjct   241  TGGTTACTTCCTCCTTCTCTATTTCTACTAATTAATTCTTCATTAATCGAATCAGGAGCA  300

Query   320  GGTACAGGGTGAACAGTTTAccccccTTATCATCAAATTTATCACACTACGGACCATCA  379
        || |||
Sbjct   301  GGNACAGGGTGAACAGTTTACCCCCCTTATCATCAAATTTATCACACTACGGACCATCA  360

Query   380  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  439
        |||
Sbjct   361  GTAGATTTAGCTATTTTTTCTCTGCATCTTGCAGGTGCTTCTTCAATTTTAGGTGCAATC  420

Query   440  AATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  499
        |||
Sbjct   421  AATTTCAATTACAACATTGTAAATATACGATCCATTGGAATAACAATAGAACGAATACCA  480

Query   500  TTATTTGTATGATCTGTTTTAATTACTGCAATTTTATTATTATTATCTTTACCAGTCTTA  559

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Sbjct  481  ||||||||||||||||||| ||||||||||||||||||| ||||||||||||||| 540
          TTATTTGTATGATCTGTTTTAATTACNGCAATTTTATTATTATTATCTTTACCAGTCTTA

Query  560  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT 619
          ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||
Sbjct  541  GCTGGCGCAATTACAATATTATTAAGTATCGAACTTTAATACATCATTCTTTGACCCT 600

Query  620  T    620
          |
Sbjct  601  T    601
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