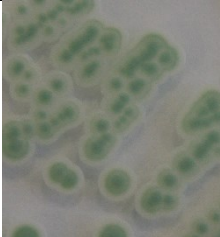

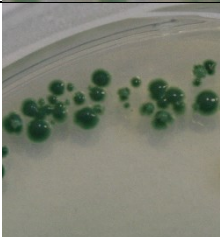
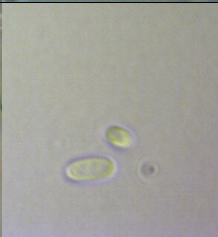


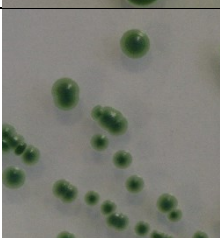
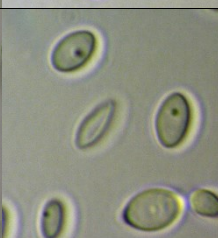
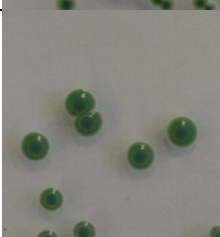

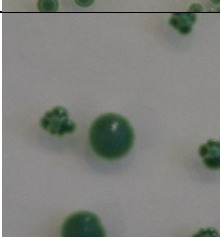
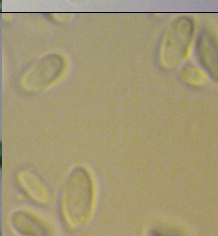
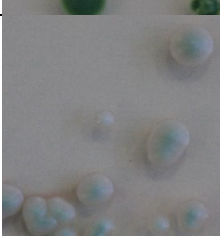
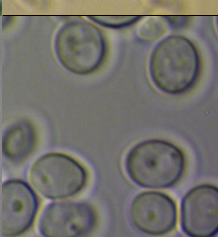
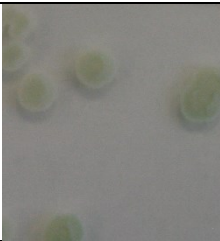
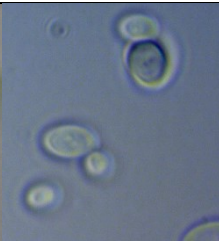

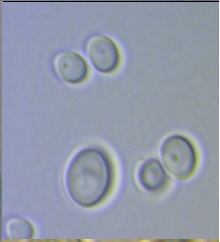
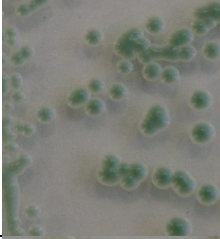
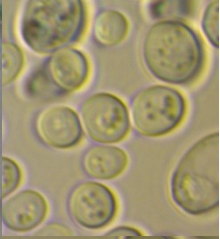

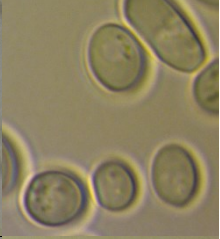

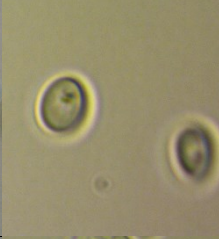
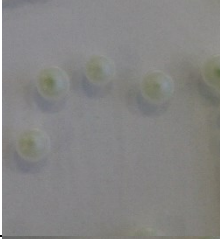

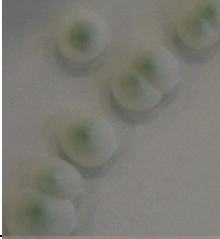


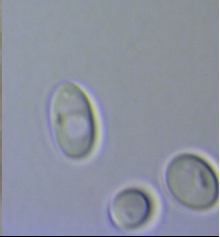


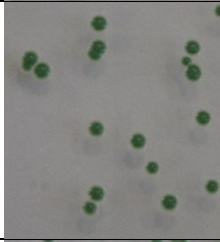
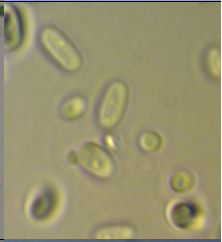
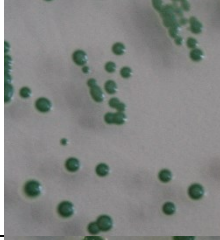
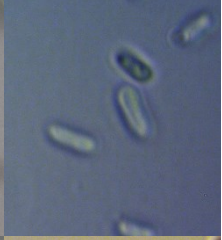


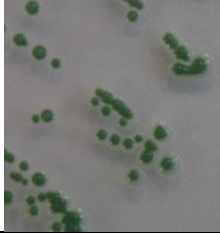
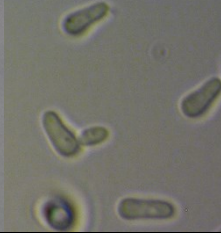


Table S1. Yeast strains isolated from red grape pomace and must and their morphological features.

Group	Code	Yeast strain	Morphology of the colony ¹	Morphology of the cell ²
1	C	<i>Candida californica</i> ³		
	H 1	<i>Hanseniaspora</i> spp.		
	H 2	<i>Hanseniaspora</i> spp.		
	H 3	<i>Hanseniaspora</i> spp. ³		
	H 4	<i>Hanseniaspora uvarum</i> ³		
2	H 5	<i>Hanseniaspora opuntiae</i> ³		
	M	<i>Metschnikowia fructicola</i> ³		
3				

4	P 1	<i>Pichia</i> spp.		
	P 2	<i>Pichia kluyveri</i> ³		
5	S 1	<i>Saccharomyces</i> spp.		
	S 2	<i>Saccharomyces cerevisiae</i> ³		
	S 3	<i>Saccharomyces</i> spp.		
	S 4	<i>Saccharomyces</i> spp.		
	S 5	<i>Saccharomyces cerevisiae</i> ³		
	S 6	<i>Saccharomyces</i> spp.		

6	S 7	<i>Saccharomyces</i> spp.		
	ST 1	<i>Starmerella bacillaris</i> ³		
	ST 2	<i>Starmerella bacillaris</i> ³		
	ST 3	<i>Starmerella</i> spp.		
	ST 4	<i>Starmerella</i> spp.		

¹ Grown on WL Nutrient Agar after incubation at 30°C for 48 hours

² Optical microscopy (magnification 100x)

³ Identification confirmed by PCR amplification and 26S rRNA sequencing

Table S2. Output of the complete alignment of the sequenced strains. Source: NCBI, Blast.

C

[Candida] californica isolate R9_7 large subunit ribosomal RNA gene, partial sequence

Sequence ID: MH681756.1Length: 559Number of Matches: 1

Range 1: 5 to 559GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Identities Gaps Strand

1014 bits(549) 0.0 554/556(99%) 2/556(0%) 2/556(0%) Plus/Plus

Query	3	GGA-TGCCTCAGTAGCGGGCGAGTGAAGCGGCAAGAGCTCAGATTTGAAATCGTGTTTTG	61
Sbjct	5	GGATTGCCTCAGTAGC-GGCGAGTGAAGCGGCAAGAGCTCAGATTTGAAATCGTGTTTTG	63
Query	62	GCACGAGTTGTAGAGTGTAGGTGGGAGTCTCTGCGGAGCACAGTGTCCAAGTCCCTTGGA	121
Sbjct	64	GCACGAGTTGTAGAGTGTAGGTGGGAGTCTCTGCGGAGCACAGTGTCCAAGTCCCTTGGA	123
Query	122	ACAGGGCGCCTGAGAGGGTGAGAGCCCCGTGGGGTGCTGTGCGAAGCTTTGAGGCCCTGC	181
Sbjct	124	ACAGGGCGCCTGAGAGGGTGAGAGCCCCGTGGGGTGCTGTGCGAAGCTTTGAGGCCCTGC	183
Query	182	TGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGCGGGTGGTAAATTCATCTAAGGCT	241
Sbjct	184	TGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGCGGGTGGTAAATTCATCTAAGGCT	243
Query	242	AAATATTGGCGAGAGACCGATAGCGAACAAGTACTGTGAAGGAAAGATGAAAAGCACTTT	301
Sbjct	244	AAATATTGGCGAGAGACCGATAGCGAACAAGTACTGTGAAGGAAAGATGAAAAGCACTTT	303
Query	302	GAAAAGAGAGTGAAACAGCACGTGAAATTGTTGAAAGGGAAGGGTATTGGGCCCGACATG	361
Sbjct	304	GAAAAGAGAGTGAAACAGCACGTGAAATTGTTGAAAGGGAAGGGTATTGGGCCCGACATG	363
Query	362	GGGAGTGCGCACCCTGTCTCTTGTAGGCGGCGCTCTGGGCGCTCTCTGGGCCAGCATCG	421
Sbjct	364	GGGAGTGCGCACCCTGTCTCTTGTAGGCGGCGCTCTGGGCGCTCTCTGGGCCAGCATCG	423
Query	422	GTTTCCTGCTGCGAGAGAAAGGGTTCCGGAAGTGGCTCTTCGGAGTGTTATAGCCGGGGC	481
Sbjct	424	GTTTCCTGCTGCGAGAGAAAGGGTTCCGGAAGTGGCTCTTCGGAGTGTTATAGCCGGGGC	483
Query	482	CAGATGTCGCGTGTGGGGACCGAGGACTGCGGCTTCTGTCTCGGATGCTGGCACAACGGC	541
Sbjct	484	CAGATGTCGCGTGTGGGGACCGAGGACTGCGGCTTCTGTCTCGGATGCTGGCACAACGGC	543
Query	542	GCAATACCGCCCGTCT	557
Sbjct	544	GCAATACCGCCCGTCT	559

H4

Hanseniaspora uvarum strain NS-EM-140 26S ribosomal RNA gene, partial sequence

Sequence ID: KT922411.1Length: 574Number of Matches: 1

Range 1: 11 to 574GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score Expect Identities Gaps Strand
1033 bits(559) 0.0 564/566(99%) 2/566(0%) Plus/Plus

Query	2	CCTTAGTAACGGGCGAGTGAAGCGGGTAAAAGCTCAAATTTGAAATCTGGTACTTTTCAGT	61
Sbjct	11	CCTTAGTAAC-GGCGAGTGAAGC-GGTAAAAGCTCAAATTTGAAATCTGGTACTTTTCAGT	68
Query	62	GCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTATGTTCCCTTGGA	121
Sbjct	69	GCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCCTTGTCTATGTTCCCTTGGA	128
Query	122	CAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGGATACCTTTTCTCTGTAAGACTT	181
Sbjct	129	CAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGGATACCTTTTCTCTGTAAGACTT	188
Query	182	TTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCAAAGTGGGTGGTAAATTCATCTAAA	241
Sbjct	189	TTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCAAAGTGGGTGGTAAATTCATCTAAA	248
Query	242	GCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAAC	301
Sbjct	249	GCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAAC	308
Query	302	TTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTGATCAGAC	361
Sbjct	309	TTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTGATCAGAC	368
Query	362	ATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCCTCTCAAAAATTTCACTGG	421
Sbjct	369	ATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCCTCTCAAAAATTTCACTGG	428
Query	422	GCCAACATCAATTCTGGCAGCAGGATAAATCATTAAGAATGTAGCTACTTCGGTAGTGTT	481
Sbjct	429	GCCAACATCAATTCTGGCAGCAGGATAAATCATTAAGAATGTAGCTACTTCGGTAGTGTT	488
Query	482	ATAGCTTTTTTGAATACTGTTAGCCGGGATTGAGGACTGCGCTTCGGCAAGGATGTTGGC	541
Sbjct	489	ATAGCTTTTTTGAATACTGTTAGCCGGGATTGAGGACTGCGCTTCGGCAAGGATGTTGGC	548
Query	542	ATAATGGTTAAATGCCGCCCGTCTAA	567
Sbjct	549	ATAATGGTTAAATGCCGCCCGTCTAA	574

Query	2	GGGA-T-CCTTAGTAACGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAAATCTGGTACTT	59
Sbjct	37	GGGATTACCTTAGTAACGGCGAGTGAAGCGGTAAAAGCTCAAATTTGAAATCTGGTACTT	96
Query	60	TCAGTGCCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCTTGCTCTATGTTCCCT	119
Sbjct	97	TCAGTGCCCCGAGTTGTAATTTGTAGAATTTGTCTTTGATTAGGTCTTGCTCTATGTTCCCT	156
Query	120	TGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGGATACCTTTTCTCTGTAA	179
Sbjct	157	TGGAACAGGACGTCATAGAGGGTGAGAATCCCGTTTGGCGAGGATACCTTTTCTCTGTAA	216
Query	180	GACTTTTTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCAAAGTGGGTGGTAAATTCCAT	239
Sbjct	217	GACTTTTTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCAAAGTGGGTGGTAAATTCCAT	276
Query	240	CTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAGATGAAA	299
Sbjct	277	CTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAGATGAAA	336
Query	300	AGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGAAGGGCATTTGAT	359
Sbjct	337	AGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGAAGGGCATTTGAT	396
Query	360	CAGACATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCCTCTCAAAAATTC	419
Sbjct	397	CAGACATGGTGTTTTTTGCATGCACTCGCCTCTCGTGGGCTTGGGCCTCTCAAAAATTC	456
Query	420	ACTGGGCCAACATCAATTCTGGCAGTAGGATAAATCATTAAGAATGTAGCTACCTCGGTA	479
Sbjct	457	ACTGGGCCAACATCAATTCTGGCAGTAGGATAAATCATTAAGAATGTAGCTACCTCGGTA	516
Query	480	GTGTTATAGCTTATTGGAATACTGCTAGCTGGGATTGAGGACTGCGCTTCGGCAAGGATG	539
Sbjct	517	GTGTTATAGCTTATTGGAATACTGCTAGCTGGGATTGAGGACTGCGCTTCGGCAAGGATG	576
Query	540	TTGGCATAATGGTTAAATGCCGCCCGTCTTGAACAACGGACCAAA	584
Sbjct	577	TTGGCATAATGGTTAAATGCCGCCCGTCTTGAACAACGGACCAAA	621

M**Metschnikowia fructicola isolate UASWS2493 JDP1 large subunit ribosomal RNA gene, partial sequence****Sequence ID: MW648802.1Length: 482Number of Matches: 1****Range 1: 1 to 476GenBankGraphicsNext MatchPrevious Match****Alignment statistics for match #1****Score Expect Identities Gaps Strand****880 bits(476) 0.0 476/476(100%) 0/476(0%) Plus/Plus**

Query	14	GAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGAATTGTAATTTGAAGAGATTT	73
Sbjct	1	GAGTGAAGCGGCAAAAGCTCAAATTTGAAATCCCCCGGAATTGTAATTTGAAGAGATTT	60
Query	74	GGGTCCGGCCGGCAGGGGTTAAGTCCACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCC	133
Sbjct	61	GGGTCCGGCCGGCAGGGGTTAAGTCCACTGGAAAGTGGCGCCACAGAGGGTGACAGCCCC	120
Query	134	GTGAACCCCTTTAACGCCTTCATCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAG	193
Sbjct	121	GTGAACCCCTTTAACGCCTTCATCCAGATCTCCAAGAGTCGAGTTGTTTGGGAATGCAG	180
Query	194	CTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCGAAC	253
Sbjct	181	CTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATACCGGCGAGAGACCGATAGCGAAC	240
Query	254	AAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAAAAAGTACGTGAAAT	313
Sbjct	241	AAGTACAGTGATGGAAAGATGAAAAGCACTTTGAAAAGAGAGTGAAAAAGTACGTGAAAT	300
Query	314	TGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCATCGGGGCGGCGGGA	373
Sbjct	301	TGTTGAAAGGGAAGGGCTTGCAAGCAGACACTTAACTGGGCCAGCATCGGGGCGGCGGGA	360
Query	374	AACAAAACCAACGGGGAATGTACCTTTCGAGGATTATAACCCCGGTCTCTATTTCCCTTGT	433
Sbjct	361	AACAAAACCAACGGGGAATGTACCTTTCGAGGATTATAACCCCGGTCTCTATTTCCCTTGT	420
Query	434	TGCCCCGAGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCCGTCT	489
Sbjct	421	TGCCCCGAGGCCTGCAATCTAAGGATGCTGGCGTAATGGTTGCAAGTCGCCCCGTCT	476

P2**Pichia kluyveri** culture CBS:7274 large subunit ribosomal RNA gene, partial sequence**Sequence ID: KY108823.1**Length: 909Number of Matches: 1**Range 1: 28 to 604**GenBankGraphicsNext MatchPrevious Match**Alignment statistics for match #1****Score** Expect Identities **Gaps** **Strand**
1053 bits(570) **0.0** **575/577(99%)** **2/577(0%)** **Plus/Plus**

Query	1	CCAA-AGGGA-TGCCTCAGTAGCGGCGAGTGAAGCGGCAAGAGCTCAGATTTGAAATCTC	58
Sbjct	28	CCAACAGGGATTGCCTCAGTAGCGGCGAGTGAAGCGGCAAGAGCTCAGATTTGAAATCTC	87
Query	59	ACCTAGTGTGCGAGTTGTAAATTGCAGGTTGGAGTCTCGGGTTAGACGTGTGTGCAAGTC	118
Sbjct	88	ACCTAGTGTGCGAGTTGTAAATTGCAGGTTGGAGTCTCGGGTTAGACGTGTGTGCAAGTC	147
Query	119	CCTTGGAAACAGGGTGCCACTGAGGGTGAGAGCCCCGTATCGTGCATGTCGACACCTGTGA	178
Sbjct	148	CCTTGGAAACAGGGTGCCACTGAGGGTGAGAGCCCCGTATCGTGCATGTCGACACCTGTGA	207
Query	179	GGCCCTTCTGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCAT	238
Sbjct	208	GGCCCTTCTGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCAT	267
Query	239	CTAAGGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACTGTGAAGGAAAGATGAAA	298
Sbjct	268	CTAAGGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACTGTGAAGGAAAGATGAAA	327
Query	299	AGCACTTTGAAAAGAGAGTGAAACAGCACGTGAAATTGTTGAAAGGGAAGGGTATTGGGC	358
Sbjct	328	AGCACTTTGAAAAGAGAGTGAAACAGCACGTGAAATTGTTGAAAGGGAAGGGTATTGGGC	387
Query	359	TCGACATGGGATTTACGCATCGTTGCCTCTCGTGGGCGGCGCTCTGGGTTTTTCCTGGGC	418
Sbjct	388	TCGACATGGGATTTACGCATCGTTGCCTCTCGTGGGCGGCGCTCTGGGTTTTTCCTGGGC	447
Query	419	CAGCATCGGTTTTTCGTTGCAGGATAAGGACAATTGGAATGTGGCTCCTCGGAGTGTATA	478
Sbjct	448	CAGCATCGGTTTTTCGTTGCAGGATAAGGACAATTGGAATGTGGCTCCTCGGAGTGTATA	507
Query	479	GCCTTTTGTAGATGCTGCGTATGGGGACCGAGGGCTGCGGCGGACTCGTTTCGTCTCGGA	538
Sbjct	508	GCCTTTTGTAGATGCTGCGTATGGGGACCGAGGGCTGCGGCGGACTCGTTTCGTCTCGGA	567
Query	539	TGCTGGCACAACGGCGCAATACCGCCCGTCTTGAAAC	575
Sbjct	568	TGCTGGCACAACGGCGCAATACCGCCCGTCTTGAAAC	604

S2

Saccharomyces cerevisiae strain JY4-1 26S ribosomal RNA gene, partial sequence

Sequence ID: JQ771733.1Length: 671Number of Matches: 1

Range 1: 8 to 581GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand		
1061 bits(574)	0.0	574/574(100%)	0/574(0%)	Plus/Plus		
Query	6	GGGGATGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCT				65
Sbjct	8	GGGGATGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGTACCT				67
Query	66	TCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCCTGTCTATGTTCC				125
Sbjct	68	TCGGTGCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTCCCTGTCTATGTTCC				127
Query	126	TTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCTTTGTA				185
Sbjct	128	TTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTCTTTGTA				187
Query	186	AAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCA				245
Sbjct	188	AAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCA				247
Query	246	TCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAA				305
Sbjct	248	TCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAA				307
Query	306	AAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTGA				365
Sbjct	308	AAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCATTGA				367
Query	366	TCAGACATGGTGTGTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACTG				425
Sbjct	368	TCAGACATGGTGTGTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATTTCACTG				427
Query	426	GGCCAGCATCAGTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTTGCCTCGGTAAGT				485
Sbjct	428	GGCCAGCATCAGTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTTGCCTCGGTAAGT				487
Query	486	ATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAGGACTGCGACGTAAGTCAAGGATG				545
Sbjct	488	ATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAGGACTGCGACGTAAGTCAAGGATG				547
Query	546	CTGGCATAATGGTTATATGCCGCCCGTCTTGAAC			579	
Sbjct	548	CTGGCATAATGGTTATATGCCGCCCGTCTTGAAC			581	

S5

Saccharomyces cerevisiae strain T14 26S ribosomal RNA gene, partial sequence

Sequence ID: JX141382.1Length: 606Number of Matches: 1

Range 1: 19 to 599GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand		
1061 bits(574)	0.0	579/581(99%)	1/581(0%)	Plus/Plus		
Query	1	CCAAAGGGGA-TGCCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTG	59			
Sbjct	19	CCAACGGGGATTGCCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTG	78			
Query	60	GTACCTTCGGTGCCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTTCCTTGTCTA	119			
Sbjct	79	GTACCTTCGGTGCCCCGAGTTGTAATTTGGAGAGGGCAACTTTGGGGCCGTTTCCTTGTCTA	138			
Query	120	TGTTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTC	179			
Sbjct	139	TGTTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCCGTGTGGCGAGGAGTGCGGTTC	198			
Query	180	TTTGTAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAA	239			
Sbjct	199	TTTGTAAGTGCCTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAA	258			
Query	240	ATTCCATCTAAAGCTAAATATTTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAA	299			
Sbjct	259	ATTCCATCTAAAGCTAAATATTTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAA	318			
Query	300	GATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGC	359			
Sbjct	319	GATGAAAAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGC	378			
Query	360	ATTTGATCAGACATGGTGTGTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATT	419			
Sbjct	379	ATTTGATCAGACATGGTGTGTTTGTGCCCTCTGCTCCTTGTGGGTAGGGGAATCTCGCATT	438			
Query	420	TCACTGGGCCAGCATCAGTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTTGCCTCG	479			
Sbjct	439	TCACTGGGCCAGCATCAGTTTGGTGGCAGGATAAATCCATAGGAATGTAGCTTGCCTCG	498			
Query	480	GTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAGGACTGCGACGTAAGTCA	539			
Sbjct	499	GTAAGTATTATAGCCTGTGGGAATACTGCCAGCTGGGACTGAGGACTGCGACGTAAGTCA	558			
Query	540	AGGATGCTGGCATAATGGTTATATGCCGCCCGTCTTGAAAC	580			
Sbjct	559	AGGATGCTGGCATAATGGTTATATGCCGCCCGTCTTGAAAC	599			

ST1**Starmerella bacillaris strain Fpc-1_KACC49637 large subunit ribosomal RNA gene, partial sequence****Sequence ID: MW171262.1Length: 517Number of Matches: 1****Range 1: 16 to 516GenBankGraphicsNext MatchPrevious Match****Alignment statistics for match #1****Score Expect Identities Gaps Strand**
913 bits(494) 0.0 499/501(99%) 2/501(0%) Plus/Plus

Query	1	CCAA-AGGGA-TGCCCTAGTAACGGCGAGTGAACAGGCAAGAGCTCAGATTTGAAAGGCA	58
Sbjct	16	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAACAGGCAAGAGCTCAGATTTGAAAGGCA	75
Query	59	CTTTTGTGCCGTTGTATTCTGAAGTTAGGGTCCTGAGAAACGATGCTTAAGTCTTCTGGA	118
Sbjct	76	CTTTTGTGCCGTTGTATTCTGAAGTTAGGGTCCTGAGAAACGATGCTTAAGTCTTCTGGA	135
Query	119	AAGGAGCGCCATGGAGGGTGATAGCCCCGTCTAGCATTGACCTCATATAGGATCTTAACA	178
Sbjct	136	AAGGAGCGCCATGGAGGGTGATAGCCCCGTCTAGCATTGACCTCATATAGGATCTTAACA	195
Query	179	TGGAGTCGAGTTGTTTGGGAATGCAGCTCAAATGGGTGGTATGCTCCATCTAAAGCTAAA	238
Sbjct	196	TGGAGTCGAGTTGTTTGGGAATGCAGCTCAAATGGGTGGTATGCTCCATCTAAAGCTAAA	255
Query	239	TATCTGCGAGAGACCGATAGTAAACAAGTACTGTGAGGGAAAGATGAAAAGAACTTTGAA	298
Sbjct	256	TATCTGCGAGAGACCGATAGTAAACAAGTACTGTGAGGGAAAGATGAAAAGAACTTTGAA	315
Query	299	AAGAGAGTGAAAAAGTACGTGAAATTGTTGAAATGGAAGGGTAGGCCGCTAACCATGTAG	358
Sbjct	316	AAGAGAGTGAAAAAGTACGTGAAATTGTTGAAATGGAAGGGTAGGCCGCTAACCATGTAG	375
Query	359	AGCCGTGTTTGGGGGAAGATAAATGCTGTAGAAATGTAGCTCCTCGGAGTATTATAGATG	418
Sbjct	376	AGCCGTGTTTGGGGGAAGATAAATGCTGTAGAAATGTAGCTCCTCGGAGTATTATAGATG	435
Query	419	CAGTTCATATTCCCACCCGAGCGCGAGGATCTCAGGTTCTACTAAATGGTGGTCTACCAC	478
Sbjct	436	CAGTTCATATTCCCACCCGAGCGCGAGGATCTCAGGTTCTACTAAATGGTGGTCTACCAC	495
Query	479	CCGTCTTGAACCACGGACCAA	499
Sbjct	496	CCGTCTTGAACCACGGACCAA	516

Starmerella bacillaris strain J16-7 large subunit ribosomal RNA gene, partial sequence

Sequence ID: MN337262.1Length: 529Number of Matches: 1

Range 1: 29 to 528[GenBank](#)[Graphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand	
900 bits	(487)	0.0	497/501(99%)	4/501(0%)	Plus/Plus

Query	1	CCAA-AGGGA-TGCCCTAGTAACGGCGAGTGAACAGGCAAGAGCTCAGATTTGAAAGGCA	58
Sbjct	29	CCAACAGGGATTGCCCTAGTAACGGCGAGTGAACAGGCAAGAGCTCAGATTTGAAAGGCA	88
Query	59	CTTTTGTGCCGTTGTATTCTGAAGTTAGGGTCCTGAGAAACGATGCTTAAGTCTTCTGGA	118
Sbjct	89	CTTTTGTGCCGTTGTATTCTGAAGTTAGGGTCCTGAGAAACGATGCTTAAGTCTTCTGGA	148
Query	119	AAGGAGCGCCATGGAGGGTGATAGCCCCGTCTAGCATTGACCTCATATAGGATCTTAACA	178
Sbjct	149	AAGGAGCGCCATGGAGGGTGATAGCCCCGTCTAGCATTGACCTCATATAGGATCTTAACA	208
Query	179	TGGAGTCGAGTTGTTTGGGAATGCAGCTCAAATGGGTGGTATGCTCCATCTAAAGCTAAA	238
Sbjct	209	TGGAGTCGAGTTGTTTGGGAATGCAGCTCAAATGGGTGGTATGCTCCATCTAAAGCTAAA	268
Query	239	TATCTGCGAGAGACCGATAGTAAACAAGTACTGTGAGGGAAAGATGAAAAGAACTTTGAA	298
Sbjct	269	TATCTGCGAGAGACCGATAGTAAACAAGTACTGTGAGGGAAAGATGAAAAGAACTTTGAA	328
Query	299	AAGAGAGTGAAAAAGTACGTGAAATTGTTGAAATGGAAGGGTAGGCCGCTAACCATGTAG	358
Sbjct	329	AAGAGAGTGAAAAAGTACGTGAAATTGTTGAAATGGAAGGGTAGGCCGCTAACCATGTAG	388
Query	359	AGCCGTGTTTGGGGGGAAGATAAATGCTGTAGAATGTAGCTCCTCGGAGTATTATAGATG	418
Sbjct	389	AGCCGTGTTTGGGGGGAAGATAAATGCTGTAGAATGTAGCTCCTCGGAGTATTATAGATG	448
Query	419	CAGTTCATATTCCCACCCGAGCGCGAGGATCTCAGGTTCTACTAAATGGTGGTCTACCAC	478
Sbjct	449	CAGTTCATATTCCCACCCGAGCGCGAGGATCTCAGGTTCTACTAAATGGTGGTCTACCAC	508
Query	479	CCGTCTTGAA-CAACCGGACC	498
Sbjct	509	CCGTCTTGAAACAAC-GGACC	528