

CTAAGCCTAAGC
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CTAAGACTAAGC
Nr of selected repeats 173 Similarity 0.987409
Consensus:
CTAAGCCTAAGC
>Cele-UNSB01_1:224582-224687 Satlength=106 Nr of Repeats=5 RepeatLength=15
seed=AGACCCATCG

AGACCCATCGTGGCGAGACATATCGTGGTGATATCCTTCGTGGCG
AGACCCATCGTGGTG
AGACCCATCGTGGCG
AGACCCATCGTGGTG
AGACCCATCGTGGTA

Nr of selected repeats 4 Similarity 0.911111

Consensus:

AGACCCATCGTGGtg

>Cele-UNSB01_1:282371-283239 Satlength=869 Nr of Repeats=23 RepeatLength=38
seed=AAATTTTAAT

AAATTTTAATTTTTTGAAAAATATTTTGGCGGGAATTTA
AAATTTTAATTTTTTGAAAAATATTTTGGCGGGAATTTA
AAATTTTAATTTTTTGAAAAATATTTTGGCGGGAATTTA
AAATTTTAATTTTTTGAAAAATATTTTGGCGGGAATTC
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AAATTTTAATTTTTTGAAAAATATTTTGACGGGAATTTA
AAATTTTAATTTCTGAAAAATATTTTGGCGGGAATTC
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AAATTTTAATTTCTGAAAAATATTTTGGCGGGAATTC
AAATTTTAATTTTTTGAAAAATATTTTGGCGGGAATTTA

Nr of selected repeats 17 Similarity 0.995872

Consensus:

AAATTTTAATTTTTTGAAAAATATTTTGGCGGGAATTTA

>Cele-UNSB01_1:283314-284124 Satlength=811 Nr of Repeats=52 RepeatLength=15
seed=TCGTGGTGAG

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TCGTGGTGAGACCCA
TCGTGGTGACACCCA
TCGTGGTGAGACCCCT
TCGTAGTGAGACCCCT
TCGTGGTGAGACCTT
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TCGTGGTGAGACCCA
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TCGTGGTGAGACCTT
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TCGTGGTGAGATCTT
TCGTGGTGAGCCCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACTTT
TCGTGGTGAGACCCA
TCGTGGTGAGACTTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT

Nr of selected repeats 48 Similarity 0.862569

Consensus:

TCGTGGTGAGACCca

>Cele-UNSB01_1:309874-309994 Satlength=121 Nr of Repeats=7 RepeatLength=15

seed=GAGACCCATC

GAGACCCATCGTGGC

GAGACCCATCGTGGC

GAGACCCATCGTGAC

GAGACCCATCGTGACGAGGCCTATCGTGGT

GAGACCCATCGTGGC

GAGACCCTCCGTTGA

GAGACCCATCGTGAT

Nr of selected repeats 6 Similarity 0.764583

Consensus:

GAGACCCATCGTGac

>Cele-UNSB01_1:336527-337247 Satlength=721 Nr of Repeats=18 RepeatLength=40

seed=AATTTTCTCG

AATTTTCTCGAAATTTTCAGAAGGTTCTAGAATATTTTCAG

GAATACAGAACACCAATTATGCCCGGAAAAAGATCCTACTCAGAATATAAACATATTCGAATTTATCGGATGTATAAA
GATTCCCGAAGACACTTTCCAATTACCCAAATTGTTTCATATTCTAAATGAAATTCCTTACTAGAACACTCTTGGCCAA
TGTACGCAGCCGAACGTATCATAAGT
GAATACAGAACACCAATTATGCCCGAGAAAAAGATCCAACTCAGAATATAAACATATTCGAATTTATCGGATGTATAAA
GATTCCCGAAGACACTTTCCAATTACCCAAATTGTTTCATATTCTAAATGAAATTCCTTACTAGAACACTCTTGGCCAA
TGTACGCAGCCGAACGTATCATAAGT

Nr of selected repeats 12 Similarity 0.974089

Consensus:

GAATACAGAACACCAATTATGCCCGAGAAAAAGATCCTACTCAGAATATAAACATAgTCgAATTTAtCGGATGTATAAA
GATTCCCGAAGACACTTTCCAATTACCCAAATTGTTTCATATTCTAAATGAAATTCCTTACTAGAACACTCTTGGCCAA
TGTACGCAGCCGAACGTATCATAAGT

>Cele-UNSB01_1:356425-357011 Satlength=587 Nr of Repeats=29 RepeatLength=19
seed=TATCGATTTT

TATCGATTTTTATG

TATCGAATTTACTGGAAAACTATCAAAAGTTTAGGAAAA

TATCGATTTTCCTGAAATT

TATCGATTTTCCTGAAATT

TATCGATTTTCCTGAAATT

TATCGATTTTCCTGAAATT

TATCGATTTTCTGGAATT

TATCGATTTTCTGGAATT

TATCGATTTTCCTGAAATT

TATCAATTTTCTGGAATT

TATCGATTTTCTGGAATT

TATCGATTTTCTGGAATT

TATCGATTTTCTGGAATT

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TATCGATTTTCCTGAAATT

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TATCGATTTTCCTGAAATT

TATCAATTTTCTGGAATT

TATCGATTTTCTGGAATT

TATCGATTTTCTGGAATT

TATCGATTTTCTGGAATT

TATCGATTTTCTGGAATA

TATCGATTTTCTGGAATTC

ATCGATTTTCTGGAATTCATCGAGTTTTCCGAGATT

Nr of selected repeats 25 Similarity 0.914854

Consensus:

TATCGATTTTtCTGgAATT

>Cele-UNSB01_1:360798-360950 Satlength=153 Nr of Repeats=8 RepeatLength=19
seed=GTACTACCTT

GTACTACCTTTTAATGTAT

GTACTACCTTTTAATGTAT

GTACTACCTTTTAATGTAT

GTACTACCTTTTAATGTAA

GTACTACCTTTTAATGTAT

GTACTACCTTTTAATGTAT

GTACTACCTTTTAATGTAT

GTACTACCTTTTAATGTAT

Nr of selected repeats 8 Similarity 0.982456

Consensus:

GTACTACCTTTTAATGTAT

>Cele-UNSB01_1:479600-479769 Satlength=170 Nr of Repeats=13 RepeatLength=12

seed=TAGGCTTAGG

TAGGCTTAGGTT

TAGGCCTAGGCT

TAGGCTTAGGCTA

AGGCTTAGGCT

TAGGCGTAGGCT

TAGGCATAGGCG

TAGGCTTTAGGTTTAGGCTAAAGCG

TAGGCTTAGGTT

TAGGCCTAGGCT

TAGGCTTAGGCTA

AGGCTTAGGCT

TAGGCGTAGGCT

TAGGCGTAGGCG

Nr of selected repeats 8 Similarity 0.813492

Consensus:

TAGGCnTAGGct

>Cele-UNSB01_1:558852-559000 Satlength=149 Nr of Repeats=8 RepeatLength=12

seed=CTAAGCCTAA

CTAAGCCTAAGC

CTAAGCCTAACCTAAATCGCGTCAGAGATAACGTTCCGCACTGACGCCAAGCCTCAAC

CTAAGCCTAAGC

CTAAGCCTAACA

CTAAGCCTAAGTA

TAAGCCTAAATCTAGGC

CTCAGCCTAATA

CTAAGCCTAAGC

Nr of selected repeats 5 Similarity 0.811111

Consensus:

CTaAGCCTAAgc

>Cele-UNSB01_1:564264-564319 Satlength=56 Nr of Repeats=5 RepeatLength=11

seed=GTACTCCTAC

GTACTCCTACC

GTACTCCTAAA

GTACTCCTACC

GTACTCCTACA

GTACTCCGACC

Nr of selected repeats 5 Similarity 0.830303

Consensus:

GTACTCCTAcc

>Cele-UNSB01_1:567454-567526 Satlength=73 Nr of Repeats=6 RepeatLength=12

seed=GCGTTGCGTG

GCGTTGCGTGCT

GCGTTGCGTGCC

GCGTTGCGTGCC

GCGTTGCGTGCT

GCGTTGCGGGCT

GCGTTGCGTGCC

Nr of selected repeats 6 Similarity 0.896296

Consensus :

GCGTTGCGTGCC

>Cele-UNSB01_1:568805-568943 Satlength=139 Nr of Repeats=8 RepeatLength=12

seed=AGGCTTAGGC

AGGCTTAGGCTTAGGTCTAGACTTAAGGCTACACTTAAATTT

AGGCCTAGGCTT

AGGCTTAGGCTT

AGGCTTAGGCTG

AGGCTTAGGCTG

AGGCTTAGGCTTATGCTC

AGACTTAGGCTT

AGGCTTACGCTTAGGCTT

Nr of selected repeats 5 Similarity 0.844444

Consensus :

AGgCtTAGGCTt

>Cele-UNSB01_1:625093-626033 Satlength=941 Nr of Repeats=22 RepeatLength=23

seed=AAAAAAAAATT

AAAAAAAAATTAGAGTTTGC GCGTCAAATATGATGTATGACCGGCAGTGTTCACACACATAGCCTAGACACGATAAAA

TACATCAGATTTTACGCGCAAACCTGGC

AAAAAAAAATTGATTTTTTGGCTTTTTCGGACTAAACATTAGAAAAAAGACTATACTCCAACAATTTTTTTTTCAGTTTTTTT

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AAAACGACGTATTCAGGCATCACATTTGACGCGCAATTTTTTTTTTAAAGAAGGATTTGCGCGTCAAATCTGGCGAATT

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AAAAAAAAATTAAATTTTTTCAAC

AAAAAAAAATTAAATTTTTTCAACA

AAAAAAAAATTAAATTTTTTCAACGA

AAAAAAAAATTAAATTTTTTCATCA

Nr of selected repeats 14 Similarity 0.950948

Consensus :

AAAAAAAAATTAAATTTTTTCAACa

>Cele-UNSB01_1:642767-642875 Satlength=109 Nr of Repeats=6 RepeatLength=12

seed=TAAGCCTAAG

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TAAGCCTAAGCCTGAGCCTATGCCTCAGCCTGAGAATAAGCG

TGAGCCTAAGCG

TGAGCCTAAGTC

GAATTCAAATTTTCAGAGAAAAATTTTGGCGG
GAATTCAAATTTTCTAAGAAAAATTTTGGCGG
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GAATTCAAATTTTCTGAGAAAAATTTAGGCG
GAATTCAAATTTTCTGAGAAAAATTTTGGCGG
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AATTCAAATTTTCTGAGAACATTTTGGCGG
GAATTCAAATTTTCTGAGAAAAATTTGGCGG
GAATTCAAATTTTCTGAGAAAAATTTAGGCGA
GAATTCAAATTTTCAGAGAAAAAATTTTGGCGG
Nr of selected repeats 192 Similarity 0.889807

Consensus:
GAATTCAAATTTTctgAGAAAAATTTtGGCGg
>Cele-UNSB01_1:685710-685978 Satlength=269 Nr of Repeats=6 RepeatLength=45
seed=TCTGATCCTT
TCTGATCCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT
TCTGATCCTTCAGATAAAGAAGGATCGTAAGGGTACCTCCTGATGG
TCTGATCCTTCAGATCCAAAGGATCACGAGGCTCTTCCTGATGT
TCTGATCCTTCAGCTCCGAAGGATCACATGGGCACCTTCTGATGA
TCTGATCCTTCAGATAAAGAAGGATCGTAAGGGTACCACTTGATGG
TCTGATCCTTCAGCTCCAAAGGATCACGAGGCTCTTCCTGATGT
Nr of selected repeats 4 Similarity 0.792593

Consensus:
TCTGATCCTTCAGaTaaGAAGGATCacAaGGGtACCTccTGATGg
>Cele-UNSB01_1:696260-697073 Satlength=814 Nr of Repeats=14 RepeatLength=44
seed=TTTGCCGGTT
TTTGCCGGTTTGCCGATTTGCCCGACATTTTCAATTTTCGGCAA
TTTGCCGGTTTGCCGATTTGCCCGAAATTTTCAATTTTCGGCAA
TTTGCCGGTTTGCCGATTTGCCCGACATTTTCAATTTTCGGCAA
TTTGCCGGTTTGCCGATTTGCCCGAAATTTTCAATTTTCGGCAA
TTTGCCGGTGTGCCGATTTGCCAAAAATTTTCAATTTTCGGCAA
TTTGCCGGTTTGCCGATTTGCCCGAAATTTTCAATTTTCGGCAA
TTTGCCGGTTTGCCGATTTGCCCGAAATTTTCAATTTTCGGCAA
TTTGCCGGTTTGCCGATTTGCCCGAATATTTCAATTTTCGGCAA

TTTGCCGGTTTGCCGATTTGCCCGAAGTTTTTCAATTTTCGGCAA
TTTGCCGGTTTGCCGATTTGTCGAAATTTTTCAATTTTCGGCAG
TTTGCCGGTTTGCCGATTTGCCCGAAATTTTTCAATTTTCGGCAG
TTTGCCGGTTTGCCGATTAGCCCGAAATTTTTAAATTTTCGGTAA
TTTGCCGGTTTGCTGATTTGCCAGAAATTTTTCAATTTTCAGCAATTTGTGCGATTTGCCATTTGCCGGAAGTGTTTCAGAA
GGATTTTTTTATAATAAGGAACCACTTAAACTGTGCCGTTTTGAACTTTTCCCGTTTTTTTTAAGATGATTTTCATAG
AATTTGCTTACTTGGTTTGCCGAATTGCCAGAAGTTTTTCAATTCCTACAAGTTGCCAATTTGCCGGAACTTTTTAAT
TATGGCAA

TTTGCCGGTTTGCCGATTTGCCAGAAATTTTTCAATTTTCGGCAA

Nr of selected repeats 9 Similarity 0.920875

Consensus:

TTTGCCGGTTTGCCGATTTGCCCGAaATTTTTCAATTTTCGGCAA

>Cele-UNSB01_1:698928-699108 Satlength=181 Nr of Repeats=12 RepeatLength=15

seed=GGTGAGACCC

GGTGAGACCCATCGT

GGTGAGACACATCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCTTCGT

GGTGAGACCCATAGT

GGTGAGACCCATCGA

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCATCGA

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

Nr of selected repeats 12 Similarity 0.900337

Consensus:

GGTGAGACCCaTCGT

>Cele-UNSB01_1:733992-734160 Satlength=169 Nr of Repeats=4 RepeatLength=42

seed=TTTGATCTAC

TTTGATCTACAAAAAATGCGGGAGTTTTCCCAGCATTGCTCA

TTTGATCTACAAAAAATGCGGGAAATTTCCCAGCATTGCTCA

TTTGATCTACAAAAAATGCGGGAAATTTCCCAGCATTGCTCA

TTTGATCTACAAAAAATGCGGGAAATTTCCCAGCATTGCTCA

Nr of selected repeats 4 Similarity 0.968254

Consensus:

TTTGATCTACAAAAAATGCGGGAaTTtCCCAGCATTGCTCA

>Cele-UNSB01_1:736250-736486 Satlength=237 Nr of Repeats=5 RepeatLength=12

seed=GCTTAGGCTT

GCTTAGGCTTAA

GCTTAGGCCTGG

GCTTAGTCTTAGGTTTATGCTTAAATTTGAAAAAAAAAATTTCTAATTTTTTCCAGATTTTTCCGTTTTTTTTTTTCAGA

GAAAATCTAAAATTTTCGATTTCTACCTGTTTTTCAAAAAAAGTTAAAAAACATTTTCGCAAATTTTGTAGAAATTT

TTCTTTTTTTTTTCTTAAAATTAG

GCTTAGGCTTAG

GCTTATGCTTAGGCTTAG

Nr of selected repeats 3 Similarity 0.777778

Consensus:

GCTTAGGCTtag

>Cele-UNSB01_1:742856-743285 Satlength=430 Nr of Repeats=11 RepeatLength=12

seed=GCAGGTAGGT

GCAGGTAGGTAG

GTAGGTAGGTAG

GTAGGTAGGTAG
GTAGGTAGGTAG
GTAGGTAGGTAGGTAAGTAGGTAAGCGAGACACGGTGCATCGATCTGACTTTAAAAATCTCAATCTCGTATCTTAAGC
GTCTTTGGTTCTGTCAGGGAA
GCAGGTAGGGGG
GAGGTAGGTGTGATCAGGCAGAGCACCGGAGTTAATATCTGGTGGATTGTGGGCTGCTAATAGGTAGGTAGGCAGGTAA
GCAAGCAAGCAA
GCAGGCAGGTAG
GTAGGTAGGTAGGTAG
GCAGGCAGGTATCAGTTGACAACCTTTTGTATGAACTAAACGGAGCCGAGTTATAAGGTGCCAAAGTTGCACTAGACAT
GGTGCATCGACCTAACTTGAACAACCTCGTATCTCAAGTGTCTTTGGTTCTATTTGGGAG
GCAGGTAGGTAG

Nr of selected repeats 7 Similarity 0.841270

Consensus:

GcAGGTAGGTAG

>Cele-UNSB01_1:758474-759042 Satlength=569 Nr of Repeats=35 RepeatLength=16

seed=TTTCAGGCTT

TTTCAGGCTTTTCAGGC

TTTCAGGCTTTTCAGGCTTTCAAAC

TTTCAGGCTTTTCAGGC

TTTCAGACTTTTCAGGC

TTTCAGGCTTTTCAGGC

Nr of selected repeats 34 Similarity 0.947564

Consensus:

TTTCAGGCTTTCAGGC

>Cele-UNSB01_1:768290-768741 Satlength=452 Nr of Repeats=13 RepeatLength=34
seed=TTTCTCAGAA

TTTCTCAGAAAATTTGAATTTCCCGCCAAAATTT
TTTATCAGAAAATTTGAATTTCCACCAAATTT
TTTATCAGAAAGATTTGAATTTCCACCAAATTT
TTTCTCAGAAAATTTGAATTTCCACCAAATTT
TTTCTCAGAAAATTTGAATTTCCCGCCAAAATTT
TTTCTCAGAAAATTTGAATTTCCCGCCAAAATTT
TTTCTCAGAAAATTTGAATTTCCCGCTAAAAATG
TTTCTCAGAAAATTTGAATTTCCCGCTAAAAATTT
TTTCTCAGAAAATTTAAAAATCCCGCCAAAATTT
TTTCTCAGAGAATTTGAATTTGCCGCCAAAATTTGT
TTTCTCATAAAATCTGAATTTCCACCAAATTT
TTTCTCAGAAAATTTGAATTTCCCGCTAAAAATTT
TTTCTCAGAAAATTTGAATTTCCCGCCAAAATTTGT
TTTCTCATAAAATCTGAATTTCCACCAAATTT

Nr of selected repeats 8 Similarity 0.787245

Consensus:

TTTtTCagAAaATtTGAAtTTCCCaCCAAAAtTT

>Cele-UNSB01_1:774871-775189 Satlength=319 Nr of Repeats=26 RepeatLength=12
seed=TCTAGGTCTA

TCTAGGTCTAAG
TCTAGGTTTAGG
TCTAGGTCTAAG
TCTAGGTCTAGG
TCTAGGTCTATG
TCTAGGTCTAGG
TCTATGTCTAGG
TCTAGGTCTAGGTCTAGG

Nr of selected repeats 25 Similarity 0.948148

Consensus:

TCTAGGTCTAGG

>Cele-UNSB01_1:787252-787531 Satlength=280 Nr of Repeats=6 RepeatLength=40
seed=GAACCTTCTG

GAACCTTCTGGAATATTTGAGAAACTCTAGAATGTTCTA

GAACCTTCTGAAAAATTCGAAAAAGTCTAGAATGTTCTAGAGCCTTTTGGAAAAATTCGAAAAAATCTGGAATATTCT
A

GAACCTTTTGGAAATTTTGGAGAAAATTCGGAATGTTTTG
GAACCTTCTGGAAAATTCGAGAAAATTCGGAATGTTCTA
GAACCTTCTGAAAAATTTGAGAAAATTCGGAATGTTCTA
GACCCTTCTGGAAATCCGAGAAAATTCGGAATGTTCTG

Nr of selected repeats 4 Similarity 0.850000

Consensus:

GAACCTTcTGgAAaaTTtGAGAAAAtTCTgGAATGTTcTa

>Cele-UNSB01_1:788353-788527 Satlength=175 Nr of Repeats=12 RepeatLength=12

seed=GCCTAAGCCT

GCCTAAGCCTAA

GCCTAAGCCTAA

GCCTAAGCCTAA

GCCTAAGCCTAA

GCCTAAGCCTAA

GCTTAAGCCTAA

GCCTAAGCCTAA

GCCTAAGCCTAG

GCCTAAGCCTAA

GTCTAAGCCTAAGCCTGAGCTTAAGCTTAA

GCCAAAGCCTAA

GCCTAAGCCTACTCCTATGCCTGA

Nr of selected repeats 10 Similarity 0.933333

Consensus:

GCCTAAGCCTAA

>Cele-UNSB01_1:789928-790208 Satlength=281 Nr of Repeats=7 RepeatLength=40

seed=TCTAGAACAT

TCTAGAACATTCCAGAATTTTCTCGAATTTTCCAAAAGT

TCTAGAACATTCCAAACTTTTCTCAAAGTTTCCAAAAGAC

TCTAGAACATTCCAGAATATTTCTCGAATTTTCCAGAAGT

TCTAGAACATTCCCTGAATTTTCTCGAATTTTCCAAAAGT

TCTAGAACATTTCCAGAATTTTCTCAAATTTTCCAAAAGT

TCTAGAACATTCCAGAATTTTCTCGAATTTTCCAAAAGAT

TCTAGAACATTCCAGAATATTTCTCGAATTTTCCAGAAGC

Nr of selected repeats 7 Similarity 0.838095

Consensus:

TCTAGAACATTCCAGAATtTTCTCgAATTTTcCAaAAGgt

>Cele-UNSB01_1:815618-815840 Satlength=223 Nr of Repeats=16 RepeatLength=12

seed=GCCTAAGCCT

GCCTAAGCCTGAACTTAAGTTTAA

GCCAAAGCCTGA

GCCTAAGCCTAA

GCCTAACCTAA

GCCTCAGCCTCA

GCCTAAGCCTAA

GCCTAAGCATAAG

GCTAAGCCTAA

GCCTAAGCCTGA

GCCTAAGCTTTAGTCTAA

GCGTAAGCCTAG

GCCTAACCTAACCTAA

GCTTAAGCCTAA

GCCTAACCTAA

GCCTAACCTAA
GCCTGAGCCTAAGCCTAA
Nr of selected repeats 10 Similarity 0.782716
Consensus:
GCcTAAgCCTaA
>Cele-UNSB01_1:817628-817952 Satlength=325 Nr of Repeats=8 RepeatLength=22
seed=TTAAAATTTT
TTAAAATTTTGTAGTTTGACC
TTAAAATTTTGTGTCAGTTTGACA
TTAAAATTTTGTGTCAGTTTGACC
TTAAAATTTTGTGTCAGACATATAATTTTTTTGTGTTTTTTGGTTAAAAAATTGAAGTTTTTCGCGATATTTAACACATT
ACATGGAAAAATTCTTTTGATCGAGTTTTCTAATTTGTTTCGTGTAGCAAGTCGATGCACCATGTCCAATTTT
TTAAAATTTTACTTTTTTTAAATTTTGTCCAGTTTGACC
TTAAAATTTTGTCAATTTTACC
TTAAAATTTTGTGTCAGTTTACC
TTAAAATTTTGTGTCAGTTTGACC
Nr of selected repeats 6 Similarity 0.886869
Consensus:
TTAAAATTTTGTGTCAGTTTgACC
>Cele-UNSB01_1:823660-823840 Satlength=181 Nr of Repeats=13 RepeatLength=12
seed=GCTTAGGCTT
GCTTAGGCTTAG
GTTTAGGCTTAGACTTAA
GCTTAGGCTTAG
GCTTAGGCTTAG
GCTTAGGCTTAGA
CTTAGGCTTAAGCTTATTCTTGA
GCTTAGGCTTAA
GCTTAGGCTTAA
GCTTAGGCTTCG
GCTTGGGCTTAG
GCTTAGGCTTAG
GCTTAGGCTTAA
GCTTAGGATTAGGCTTAG
Nr of selected repeats 9 Similarity 0.895062
Consensus:
GCTTAGGCTTAg
>Cele-UNSB01_1:833000-833653 Satlength=654 Nr of Repeats=29 RepeatLength=21
seed=TGGCCTAGAT
TGGCCTAGATTCTCTATAGGG
TGGCCTACATTTTTACACTGGTTGTCTAGATTCTTAAACAGGG
TGGCCTCGATTCTGTACAGGG
TGGCCTAGATTTTCTACACGG
TGGTCTAGATTTTCACTGG
TGGCCTAGATTCTCACACTAGG
TGGCCTAGATTTTTTCCACTAA
TAGCCTAGATTCTTTACAGGG
TGTCCCTAGATTTTCACTGG
TGTCCCTAGATTCTACACAGGG
TGACCTAGATTTTTTACACTGG
TGGCCTAGATTCTCTACAGGG
TGGCCTAAATTCCTTATAGGA
TGACCTAGATTCTTAAACAGGA
TGACCTAGATCTTGACACTAG

TGGCCTTGATTTTTTACAGGG
TGGCCTAGATTTTTCTACAA
TGGTCTAGATTTTTTGCAGGGTGGCTTGGATTCTTAAACAAGG
TGGCCTAGATTTTTTACAGGG
TGGCCTAGATTTTTATAACAGGG
TGGTCTAGATTTTTTACACTGG
TGGCCTAGATTCTTTACAGGT
TGGCCTAGATTTTTCTATAGGA
TGGCCTAGATTCTTAAACAGGG
TGGCCTAGATTCTTTACAGGG
TAGCCTAGATTCTTCACAGGG
TAGCCTAGATTTTTTACACTGG
TGGCCTAGATTTTTCTAAAGGG
TGGTCTAGATTTTTGCACTGG

Nr of selected repeats 21 Similarity 0.658586

Consensus:

TGGCCTAGATTnTttACAgGG

>Cele-UNSB01_1:842713-843650 Satlength=938 Nr of Repeats=48 RepeatLength=12
seed=CTTAGGCTTA

CTTAGGCTTAAGCTTAGGCCTTTT

CTCAGGCTTAGG

CTTAGGCTTATG

CTCAGGCTTAGGCCTTTT

CTTAGGCTTATG

CTTGGGCTTAGG

CTTAGGCGTAGG

CTTAGGCTTAGG

CTTAGGCTTATG

CTTAGACTTAGTCTCACTATCAGT

CTTAGGCTTAGG

CTTAGACTTAGG

CTTAAGCTTAGG

CTTAAGCTTAGA

CTTAGGCTTAGG

CTTAGGCTTAGG

CTTAGGCTTAGGTTTGGG

CTTAGGCTTAGGCTTAAC

CTCAGGCTTAGG

CTTAGGTTTAGG

CTCAGGCTTAAA

CTTAGGCTTAGGCCAGG

CTTAGGCTTAGGCTCACACGTTCTCACGTTCTTAACCATACAAAATCAGCTAAGAACTCTGCGTCTTTTCTCCCGCATT

TTTTGTAGATCTACGTAGATCAAACCGAAATGAGGCACTTTCTGAATCCACGAG

CTAGGCTTAAG

CTTAGGCTTAAGCTTAGGCCTTTT

CTCAGGCTTAGG

CTTAGGCTTATGCCAGGCTTAGGCCTTTT

CTTAGGCTTATG

CTTGGGCTTAGG

CTTAGGCGTAGG

CTTAGGCTTAGG

CTTAGGCTTATG

CTTAGACTTAGTCTCACTATCAGT

CTTAGGCTTAGG

CTTAGACTTAGG
CTTAAGCTTAGG
CTTAAGCTTAGA
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CTTAGGCTTAGG
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CTTAGGCTTAGGCTTAAC
CTCAGGCTTAGG
CTTAGGTTTAGG
CTCAGGCTTAAA
CTTAGGCTTAGGCCAGG
CTTAGGCTTAGGCTCACACGTTCTCACGTTCTTAACCATACAAAATCAGCTAAGAACTCTGCGTCTTTTCTCTCGCATT
TTTTGTAGATCAACGAAGATCGAGCCGAAATGAGGCACTCTGACATCACGTGGGCTAAGA
CTTAGGCTTAGG
CTTAGGCTTAGGCTTAGG

Nr of selected repeats 32 Similarity 0.819668

Consensus:

CTTAGGCTTAGG

>Cele-UNSB01_1:855372-855570 Satlength=199 Nr of Repeats=12 RepeatLength=12

seed=GCTTAGGCTT

GCTTAGGCTTAG

GCTTAGACTTAG

GCTTAGGCTTAGTCTTCG

GCTTAGGCTTAG

GCTTAGGCTTAG

GCTTAGGCTTAG

GCTTAGGCTTAG

GCTTAGGCTTAG

GCTTAGGCTTGGGACTGG

GCTTAGGCTTAGGCTTTGGCCTAA

GCTTAGGCTTAGGCTTACGCTCAGGCGTAGGATTAGGCTCTG

GCTTTGGCTTTG

Nr of selected repeats 8 Similarity 0.888889

Consensus:

GCTTAGGCTTAG

>Cele-UNSB01_1:907957-908415 Satlength=459 Nr of Repeats=21 RepeatLength=22

seed=TTTTAGCCAA

TTTTAGCCAAAAAATTCGCTA

TTTTAACCAAAAAATCCGTTGA

TTTTAGTCAAAAAATTCGCTAT

TTTTAGCCAAAAAATTCGCTAT

TTTTAGCCAAAAAATCCGTTAA

TTTTAGCCAAAAAATTCGCTAT

TTTTAGCCAAAAAATCCGTTAA

TTTTAGGCAAAAAATCCGTTAA

TTTTAGTCAAAAAATCCGCTA

TTTTAACCAAAAAATCCGCTA

TTTTAACCAAAAAATCCGTTAA

TTTTAGCCAAAAAATTCGCTAT

TTTTAGCCAAAAAATCCGTTAA

TTTTAGCCAAAAAATTCGCTAT

TTTTAGCCAAAAAATCCGTTAA

TTTTAGCCAAAAAATTCGCTAT

TTTTAGCCAAAAAATCCGTTAA

TTTTAGCCAAAAAATTCGCTAT
TTTTAGCCAAAAAATTCGCTAT
TTTTAGCCAAAAAATCCGTTAA
TTTTAGCCAAAAAATTCGCTAT

Nr of selected repeats 17 Similarity 0.862299

Consensus:

TTTTAGCCAAAAAATcCGtTAa

>Cele-UNSB01_1:911764-911915 Satlength=152 Nr of Repeats=8 RepeatLength=15

seed=ATCTTCTTTT

ATCTTCTTTTTCGTAGATTTTCAGAATGTAG

ATCTTCTTTTGGTAA

ATCTTCTTTTCGTAG

ATCTTCTTTTTCGTATCTTCAAAATGTAG

ATCTTCTTTTGGTAA

ATCTTCTTTTCGTAG

ATCTTCTTTTCGTAG

ATCTTCTTTTTCGTAG

Nr of selected repeats 5 Similarity 0.911111

Consensus:

ATCTTCTTTTcGTAg

>Cele-UNSB01_1:927465-927693 Satlength=229 Nr of Repeats=6 RepeatLength=32

seed=GAAAATTTGA

GAAAATTTGAATTCCTCGCCAAAAATGTTTCTTT

GAAAGTTTGAATTCCTCGCCAAAAACATTCTCAGAAAATTCAGTTCCCGCCAAAAATGTTTCTTT

GAAAATTTGAATTCCTCGCCAAAGATTTTTTACA

GAAAATTTGAATTTCCGCTAAAATATTCTCG

GAAAATTTGAATTCCTCGCCAAAAATTTTTCTTT

GAAAATTTGAACTCTCGCCAAAAATGTTTTTTTTTTT

Nr of selected repeats 4 Similarity 0.727941

Consensus:

GAAAATTTGAATTCCTCGCCAAaATtTTcTtt

>Cele-UNSB01_1:932742-934750 Satlength=2009 Nr of Repeats=89 RepeatLength=21

seed=AATTTCTAGG

AATTTCTAGGCCATCAAG

AATTTCTAGGCCACATCAGACTACTTTGAA

AATTTCTAGGCCACAATGGGAACATAATTTCTGAACCTAATTTCTGA

AATTTCTTGGCCACGATCTGAAAATTTTGAAGCCATAATTTGA

AATTTCTAGGCCACGATCTGA

AATTTCTAGACCATCAAC

AATTTCTAGGCCACGATTTGA

AATTTCTAGGCCACGATTTGA

AATTTGTAGGTCAAGTTTGA

AATTTCTAAGCCACGATTTGA

AATTTCTAGGCCACGATCTGA

AATTTTCTAGGCCACGATTTGA

AATTTCTAGGCCACGATTTGA

AATTTTCTAGGCCACGATCTGAAGTTTTTAGGTCATCAAA

AATTTCTAGGCCACGATTTGA

AATTTCTAGGCCACGATCTGA

AATTTCTAGGCCACGATTTGA

AATTTCTAGGCCACGATTTGA

AATTTTCTAGGCCACGATCTGA

AATTTCTAGGCCATCAAA

AATTTATAGGCCACGATTTGA

AATTTCTAGGCCACGATTTGA
AATTTCTGGGCCACGATCTGA
AATTTCTAGGTCATCAAA
AATTTCTAGGCCACGATTTGA
AATTTCTAGGCCACGATTTGA
AATTTCTAGGCCGCGATCTGA
AATTTCTAAGCCATCAAA
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AATTTTTAGGCCACGATCTGA
AATTTCTAGGCCATCAAA
AATTTATAGGCCACGATTTGA
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TTTTACTCTCTGTGGCTTCACCAACTA
TTTTACTCTCTGTGGCTTCACCAATTATCTTTCTCTCTGTGGCTTCCCCTATA
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TTTTACTCTCTGTGGCTTCCCCTATA
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TTTTACTCTCTGTGGCTTCCCACTATA
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TTTTACTCTCTGTGGCTTCCCACTATA
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TTTTACTCTCTGTGGCTTCACCAATA

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TTTTACTCTCTGTGGCTTCCCCTACTATA
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TTTTACTCTCTGTGGCTTCACAGTATA
TTTTATTCTCTGTGGCATCACAATATA
TTTTACTCTTTGGCTTCGCAGAATA
TTTTACTCTTTGGCTTCGCAGAATA
TTTTACTCTCTGTGGCTTCGCAGAATA

Nr of selected repeats 309 Similarity 0.884164

Consensus:

TTTTACTCTCTGTGGCTTCCCACtATa

>Cele-UNSB01_1:961004-961082 Satlength=79 Nr of Repeats=6 RepeatLength=12

seed=AGCCTAAGCC

AGCCTAAGCCTA

AGCCTAAGCCTA

AGCCTCAGCCTA

AGCTTAAGCCTA

AGCCTAAGCCTC

AGCCTAAGCCTAAGCCTA

Nr of selected repeats 5 Similarity 0.866667

Consensus:

AGCcTaAGCCTa

>Cele-UNSB01_1:961195-961471 Satlength=277 Nr of Repeats=23 RepeatLength=12

seed=CTAAGTCTAA

CTAAGTCTAAGT

Nr of selected repeats 23 Similarity 1.000000

Consensus:

CTAAGTCTAAGT

>Cele-UNSB01_1:961002-961808 Satlength=807 Nr of Repeats=44 RepeatLength=12

seed=TAAGCCTAAG

CCGGAAATTTTAAAAACCGGCAATTGCCGAAATTGCCGACTC
CCGGAAATTTTAAAAACCGGCAATTGCCGAAGTTGCCGACTC
CCGGAAATTTTAAAAACCGGCAATTGCCGAAATTGCCGATTG
CCGGAAATTTTAAAAACCGGCAATTGCCGAAATTGCCGCTTG
CCGGAAATTTTAAAAACCGGCAATTGCCGAAATTGCCGATTG
CCGGAAATTTTAAAAACCGGCAATTGCCGAAATTGCCATTG
CCGGAAATTTTAAAAACCGGCAATTGCCGAAATTGCCGCTTG
CCGGAAATTTTAAAAACCGGCAATTGCCGAACTGCCCTTTG
CCGGAAATTTTAAAAACCGGCAATTGCCGAAGTTGCCGACTC
CCGGAAATTTTAAAAACCGGCAATTGCCAAAATTGCCGATTG
CCGGAAATTTTAAAAACCGGCCACTGCCGAAATTGCCGACTC
CCGGAAATTTTAAAAACCGGCCACTGCCGAAATTGCCGACTC
CCGGAAATTTTAAAAACCGGCAATTGCCGAAATTGTCGATTG

Nr of selected repeats 16 Similarity 0.888889

Consensus:

CCGGAAATTTcAAAAACCGGCAATTGCCGAAATTGCCgatTg

>Cele-UNSB01_1:995161-995964 Satlength=804 Nr of Repeats=5 RepeatLength=162
seed=ATCATATGAA

ATCATATGAAGCGATTATTTTTTCTTTTATAAACCTGTTTcAGGATTTGCATTATTATGAGAAAATCCTAGGCCAATTAG
GCTAGCATGTACGGAAGTATTTTTTAAAAATTTATAAAAGTAATGAAAAGCTGATATTTTCAAATTCAGAATGACGG
AAAA

ATCATATGAAATGCTTTTTTTCTTTTTTAAACCTATTTAGAAATTGTCAAACTACCAGAAAATACTAAACAAAATAG
CTTAGCTTGACCGGAAATATTTTTTAAAAATTTGATAAAAATAATGAAAAGCTGATATTTTCAAATTCAGAATGACGG
AAAA

ATCATATGAAGCGATTCTTTTTTCTTTTATAAACCTCTTTAGAAATTGTCAAACTACCAGAAAATACTAAACAAAGTAG
GTTAGCTTAACCGGAAGTAATTTTTTACAAATTTGATAAAAATAATAAAAAGATGATTTTTTCAAATTCAAAATGACTG
AAAA

ATCATATGAAGCGATTTCGTTTTTCTTTCATAAAATAGTTTAGAAATTGGAATAATGATCAGAAAATACTAAACAAAGTAG
GTTAGCTTGACCGGAAGTATTTTTTAAAAATTTGATTAAAAAACTGATTTTTTAAAAATTCAGAATGACGGAAAA
ATCATATGAAGCGATTCTTTTTTCTTTTATAAAAGTAGTTTcAGAATTAGCATTATTATGAGAAAATCCTAGGCCAATAAG
GCTAGCATGTACGAAAGTATTTTAAAAATTTATAAAAGTAATGAAAAGCTGATTTTTTAAAAATTCAGAATGACGG
AAAA

Nr of selected repeats 4 Similarity 0.781893

Consensus:

ATCATATGAAGcGaTtTcTTTTTCTTTTaTAAAcctgTtAGaATTggCAaaAcTAccAGAAAATaCTAaaCaAAttAG
gcTAGCaTgaaCGgAAgTAtTtTtAaAAATtgATAAAAaTAATgAAAAGcTGATaTTTTcAAAATTCAGaAATGACgG
AAAA

>Cele-UNSB01_1:1009660-1009762 Satlength=103 Nr of Repeats=8 RepeatLength=12
seed=GGTCTAGGTCTC

GGTCTAGGTCTA

GGTCTAGGTCTA

GGTCTAGGTCTA

GGTCTAGGTCTA

GGTCTTGGTCTA

GGTCTAGGTCTA

GGTCTAGGTCTT

GGTCTAGGTCTAGTTCTA

Nr of selected repeats 7 Similarity 0.936508

Consensus:

GGTCTAGGTCTA

>Cele-UNSB01_1:1012680-1013098 Satlength=419 Nr of Repeats=4 RepeatLength=32
seed=CAAAATTTTT

CAAAATTTTTGACGTGGAAGAATTTTAAGATTTTCGAGGCCAAGAGGTGGCCTAGAATTCACATTTATTGGCAATTCT
TATCTAGATCCCGAACCCCGACCAGTCAGTTTTTAATTTCCGGTGTCTGAATTTTTTAATTAATAAATTTATTTTTGGGAGG

AGCTCCTGTTTTTTTTTCGTCAAAAAATGAAGGTGGCCTAGCTTTCTCATTTTAAGGCCACGAATTCTAGTTAATTTTT
TGTTGGCTCATTTTTTTGTTTCAAAAAACGAAAGTTAGTCAAAAACTTTTCTGCATATCAAATGCTCTTTTTGAGGTTTT
TTCCTG

CAAATTTTTCTAAGAAAATTTGAATTCCTGC
CAAATTTTTCTCAGAAAATTTGAATCGCCGC
CAAATTTTTCTCTGAAAATTTGAATCGCCGC

Nr of selected repeats 3 Similarity 0.88889

Consensus:

CAAATTTTTCTcaGAAAATTTGAATcgCCGC

>Cele-UNSB01_1:1018800-1018890 Satlength=91 Nr of Repeats=5 RepeatLength=12
seed=AGCCTAAGCC

AGCCTAAGCCTAAGCCTAAGTTTGAGCATA

AGCATAAGCCTA

AGCCTATGCCTA

AGCCTACGCCTC

AGCCTAAGCCAAATGCGGAGCCTA

Nr of selected repeats 3 Similarity 0.740741

Consensus:

AGCCTAnGCCTa

>Cele-UNSB01_1:1018801-1019027 Satlength=227 Nr of Repeats=14 RepeatLength=12
seed=GCCTAAGCCT

GCCTAAGCCTAAGCCTAAGTTTGAGCATAA

GCATAAGCCTAA

GCCTATGCCTAA

GCCTACGCCTCA

GCCTAAGCCAAATGCGGA

GCCTAAGCCTAA

GCCTAAGTCTAAGTCTAAGTCTAA

GTCTAAGCCTAA

GCCTAAGCCTAA

GCCTAAGCCTGCGGAGCCTAAGTATAA

GCCTAAGCCTAA

GCCTAAGCCTAA

GCCTAAGCCTAT

GCCTAAGCCTAAGCCGAT

Nr of selected repeats 9 Similarity 0.854938

Consensus:

GCCTAaGCCTAA

>Cele-UNSB01_1:1031726-1032601 Satlength=876 Nr of Repeats=25 RepeatLength=35
seed=ATTTTCAATT

ATTTTCAATTCCGGCAATTTTCCGATTTGCCGGAA

ATTTTCAATTCCGGCAATTTGCCGATTTGCCGGAA

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCGGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCGGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGAAA

ATTTTCAATTCCGGCAATTTTCCGATTTGCCGGAT

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGGAA

ATTTTCAATTCCTGCAGTTTGCCGATTTGCCGAAA

ATTTTCAATTCCGGCAATTTTCCGATTTGCCGGAT
ATTTTCAATTCCGGCAGTTTGCCGATTTGCCGGAA
ATTTTCAATTCCGGATATTTGCCGATTTGCCGGAA
ATTTTCAATTCCGGCAATTTGCTGATTCGCCGGAA
ATTTTCAATTCCAGCAGTTTGCCGATTTGCCGGAA
ATTTTCAATTCCGGATATTTGCCGATTTGCCGGAA
ATTTTCAATTCCGGCAATTTTCCGATTTGCCGGAA
ATTTTCAATTCCGGCAGTTTGCCGATTTGCCGGGA
ATTTTCAATTCCGGCAATTTGCCGATTTGCCGGAA
ATTTTCAATTCCGGCATTTTGCCGATTTGCCGGAA
ATTTTCAATTCCGGCAATTTGCCGATTTGCCGGAA

Nr of selected repeats 25 Similarity 0.921397

Consensus:

ATTTTCAATTCCGGCAgTTTGCCGATTTGCCGGAA

>Cele-UNSB01_1:1103105-1103421 Satlength=317 Nr of Repeats=8 RepeatLength=35
seed=CGGCAAAATCG

CGGCAAATCGGCATTTTGCCGGAATTGAAAATATC
CGGCAAATCGGTATTTTGCCGGAATTGAAAATTTT
CGGCAAATCGGCAATTTGTGCGAATCGAAAATTTT
CGGCAAATCGGCATTTTGCCGGAATTGAAAATATC
CGGCAAATCGGTATTTTGCCGGAATTGAAAATTTT
CGGCAAATCGGCAATTTGTGCGAATCGAAAATTTT
CGGCAAATCGGCATTTTGCCGGAATTGAAAATATC
CGGCAAATCGGCAATTTGTGCGAATCGAAAATTTT
CGGCAAATCGGCATTTTGCCGGAATTGAAAATATC

Nr of selected repeats 7 Similarity 0.873016

Consensus:

CGGCAAATCGGcAtTTTGcCGGAATTGAAAATtTc

>Cele-UNSB01_1:1117625-1118154 Satlength=530 Nr of Repeats=23 RepeatLength=23
seed=GGCCTAGAAA

GGCCTAGAAATACTAAAACGTGAT
GGCCTAGAAATACTGAAAAGTGGT
GGCCTAGAAATACTGAGCGTGGT
GGCCTAGAAATTCTAAAAGTGGT
GGCCTAGAAATACTGAACGTGGT
GGCCTAGAAATACTGAACGTGGT
GACCTAGAAAAACTAAAACGTGGT
GGCCTAGAAATACTGAGCGTGGT
GGCCTAGAAATACCGAGCGTGGT
GGCCTAGAAATTCTAAAAGTGGT
GGCCTAGAAATACTGAACGTGGT
GGCCTAGAAATTCTGAAAATGGT
GGCCTAGAAATACTGAATGTGGG
GGCCTAGAAATGCTGAACGTGAT
GGCCTAGAAATACTGAAAATGGT
GACCTAGAAATACTGAATGTGGG
GGCCTAGAAATGCTGAACGTGAT
GGCCTAGAAATACTGAGCGTGGT
GGCCTAGAAATTCTAAAAGTGGT
GGCCTAGAAATACTGAAAATGGT
GGCCTAGAAACACTGAATGTGGG
GGCCTAGAAATGCTGAACGTGAT
GGCCTAGAAATACTGAACGGGAT

Nr of selected repeats 23 Similarity 0.818525

Consensus:

GGCCTAGAAATaCTgAAcGTGgT

>Cele-UNSB01_1:1127917-1128577 Satlength=661 Nr of Repeats=21 RepeatLength=20
seed=ATTTCTAGGC

ATTTCTAGGCCATCAATATAAAATTTCTAGGTTATATTTCAAATATCTAGGGGACCAATGATGCTTCTATGTTATATATTA
A

ATTTCTAGGCTATCGATGAG

ATTTCTAGGCCATGTTTCAGA

ATTTCTAGGCTATCAATAAAAT

TTTCTAGGCTATCGATGAG

ATTTCTAGGCCATATTCAGA

ATTTCTAGGTAATCCATAAA

ATTTCTAGGCCATCGATAAG

ATTTCTAGGCCAGATTTAGA

ATTTTTAGGCCATCGATGAA

ATTTCTAGGCCATCAATATG

ATTTCTAGGCCATGTTTCAGA

ATTTCTAGACTATCAATAAAATTTTCTAAGCCATCGATAAGATTTCTGGACCATATTTAGA

ATTTCTAGGCCACCAATGAA

ATTTCTGGGCCAAATTTTCAATTTCTTTTTTTTTTTTA

ATTTCTAGGTCATATTCAAA

ACTTCTAGGCCCGCAATAAA

ATTTCTAGGCCAAATCTTTAAATTTCTAGGTCATATTTTGA

ATTTCTAGGCCACCAATGAGATTTCTAGAACAAAAAGCTTAAGTTCTAGGTCACATTTTGA

ATTTCTAGGCCACCAATAAAATTTCTAGATAATATTTTAAATGTCTAAAACACATTTAAAAATTTTCTAAGCCACTAAT
AAA

AGTTCTAGGCCACGGATAAG

Nr of selected repeats 13 Similarity 0.625153

Consensus:

ATTTCTAGGCCAtcnaTnAg

>Cele-UNSB01_1:1149569-1149724 Satlength=156 Nr of Repeats=10 RepeatLength=12
seed=CCTAAGCCTAAG

CCTAAGCCTAAG

CCTAAGCCTATGCCTAGCACAAG

CCTAAGCCTAAG

CCTCAGCCTAAACCTAAGCAAAAAG

CCTAAACCTAAG

CCTAAACCTAAGCAAAAAG

CCTAAGTCTAGG

CCTAAGCCTAAG

CCTAAACCTAAG

CCTAAGCCTAAGCCTAAG

Nr of selected repeats 6 Similarity 0.866667

Consensus:

CCTAAGCCTAAG

>Cele-UNSB01_1:1158888-1159076 Satlength=189 Nr of Repeats=5 RepeatLength=31
seed=ATTCCCGCCA

ATTCCCGCCAATTTTTTCTCAGGAAATGTGA

ATTCCCGCCAATTTTTTCTCAGAAATTTTGA

ATCCCGCCAATTTTTTCTAGCGAAATTTGA

ATTCCCGCCAAACTTTTTTCTCAGAAAGTTGAATTCGCGTCAAATTTGTTTCACAGGAAATTTGA

ATTCCCACCAAAATTTTTTCTCAGGAAATCTGC

Nr of selected repeats 3 Similarity 0.628472

Consensus:

ATtCCCGCCaAttTTTTTctcAGgAAaTtTGa

>Cele-UNSB01_1:1232170-1233535 Satlength=1366 Nr of Repeats=32 RepeatLength=43
seed=CCAGAAATTA

CCAGAAATTAGAATTTTCGGCAAATCGGCAAGCCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAACAAACTGACAAATTG
CCAGAAATTAATAATCTCCGGCAAATCGGCAAATTG
CCAGAAATTAATAATTTTCGGCAAATCAACAAACCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAGCAAACCTGACAAATTG
CCAGAAATTAATAATCTCCGGCAAATCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAGCAAACCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCGGCAAGCCGGCAAATTT
CCAGAAATTAATAATTTTCGGCAAATCGGCAAGCCGGCAAATTT
CCAGAAATTAGAATTTTCGGCAAATCAACAAACTGACAAATTG
CCAGAAATTAATAATCTCCGGCAAATCAGCAAATTG
CCAGAAATTAATAATCTCCGGCAAATCGGCAAGTTG
CCAGAAATTAATAATTTTCGGCAAACCGAAAAATTG
CCAGAAATTAATAATTTTCGGCAAATCAGCAAATTGCCAGATAGTAGAATTTTCGGCAAATCAGCAAACCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCGGCAAGCCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAGCAAACCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAGCAAACCGGCAAATTT
CCAGAAATTAGAATTTTCGGCAAATCGGCAAGCCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAACAAACTGACAAATTG
CCAGAAATTAATAATCTCCGGCAAATCAGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAGCAAACCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAGCAAACCTGACAAATTG
CCAGAAATTAATAATCTCCGGCAAATCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAGCAAACCGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCGGCAAGCCGGCAAATTT
CCAGAAATTAGAATTTTCGGCAAATCGGCAAACCTGACAAATTG
CCAGAAATTAATAATCTCCGGCAAATTTGGCAAATTG
CCAGAAATTAATAATTTTCGGCAAATCGGCAAACCGCCAGATTG
CCAGAAATCAAAATTTCTGCAAAATGCCAGAATTTTAATTTTCGGCAAATCGGCAAATTG
CGAGAAATTAGAATTTTCGGCAAATCAGCAAACCTGGCAAATTG
CCAGAAATTAGAATTTTCGGCAAATCAGCAAACCGGCGAATTG
Nr of selected repeats 22 Similarity 0.892211

Consensus:

CCAGAAATTAGAATTTTCGGCAAATCaGCAAAcCgGCAAATTg

>Cele-UNSB01_1:1234705-1235262 Satlength=558 Nr of Repeats=15 RepeatLength=35
seed=AAATCGGCAA

AAATCGGCAATATGCCTAAAAATGAAAATTTCCGGC
AAATCGGCAATTTGCCTAAAAATGAAAGGTTCCGG
AAATCGGCAATTTTCCCTAAAAATGAAAGGTTCCGGC
AAATCGGCAATTTTCCCTAAAAATGAAAGATTCCGGC
AAATCGGCAAGTTGTCAAAAAATGATAGATTCCGGC
AAATCGGCAAAAAGCCAGAAATTAATAATTTCTGCAAAATCCACAATTTGCCTAAAAATTAATAATTTCCGG
AAATCGGCAATTTGCCGAAAAATGAGAGATTCCGGC
AAATCGGCAATTTGTCAAAAAATGATAGATTCCGGC
AAATCGGCAAAAAGCCAGAAATTAATAATTTCCGGC
AAATCGGCAATTTGCCGAAAAATGATAGATTCCGGC
AAACCGGCAAAAAGCCAGAACTTAATAATTTCCGG
AAATCGGCAATTTGCCGAAAAATGAGAGATTCCGGC
AAATCGGCAATTTTCAAAAAATGATAGATTCCGGC
AAATCGGCAAAAAGCCAGAAATTAATAATTTCCGGC
AAATCGGCAATTTGCCTAAAAATGAAAATTTCCAGC

Nr of selected repeats 12 Similarity 0.802020

Consensus:

AAATCGGCAAttTgcCnAAAAATGAaAgaTTCCGGC

>Cele-UNSB01_1:1236946-1237103 Satlength=158 Nr of Repeats=7 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGG

GTACTGTAGGA

GTACGGTAGGATTACTGTAGTTTAGGGAAATTTGACTTTTTCTCTTTTGAATGGATATTGGTTTGGGGTTAGTGGGGGG

GATATGGTCGGG

GTACTGTAGTA

GTACTGTAGGG

GTACTGTAGGA

GTACTGTAGTA

Nr of selected repeats 6 Similarity 0.870707

Consensus:

GTACTGTAGga

>Cele-UNSB01_1:1302534-1303556 Satlength=1023 Nr of Repeats=33 RepeatLength=19
seed=TTCTAGGCCA

TTCTAGGCCACGCAGCAAAAAAAAAAAAAACAAAATCCAATTTTGAATACTATTTTTATGTCCGCAAAATAGATTAATTTTC
CTTGAAAATAGTAA

TCTAGGCCACCACTAGATTTGTAACTATGTGGGAAGAAAAGATGAACCTCGGCCACCTTGGGAAAACCTAGGCCGCGG

GTCAAAGCAAGGCCTCACTCCTAGACCACATTAAGCTTTAATTTATCGGATTGTCAAGGCCTGCTGATAAT

TTCTAGGCCATCTGATAAT

TTCTAGGCCATCTGAGGAT

TTCTAGGCCATCTGAGGAT

TTCTAGGCCATCTGAGGATTTCTAGGATATCTGAGGAT

TTCTAGGCCATCTGAGGAT

TTCTAGGCCACCTGGGGAA

TTCTAGGCCATCTGAGGAT

TTCAAGGCCATCTGAAAATTTCTGGGTTATCTGAGGAT

TTCTAGGCCATTTTCATGAT

TTCTAGGCCATTTGAGGAT

TTCTAGGCCATCTGAGGAT

TTCTAGGCCACCTGGGGAA

TTCTAGGCCATCTGAGGAT

TTCTAGGCCATCTGAGGAT

TTCTAGGCCATCTGGGGAAT

TTTAGGCCATCTGTGGAT

TTCTAGGCCATCTGAGGATTTCTAGGATATCTGAGGATTTCTAGTCCCCTGAAGAT

TTCTAGACCACCTGGGGAA

TTCTAGGCCAGCAATGGATT

TTTAGGCCATCTGTGGAT

TTCTAGGCCATCTGAGGATTTCTAGGATATCTGAGGAT

TTCTAGGCCACTGAAGAT

TTCTAGACCACCTGGGGAA

TTCTAGGCCAGCAATGGATTTTGTAGGCCCTTCAGAGGATTTGTAGGCCCTTTGAGGATTTCTAGGATATCTGAGGAT

TTCTAGGCCATTTGAGGATTTTGTGGCCATCTGAAAATTTCTGTGCTATCTGAGGAT

TTCTAGACCACCTGGGGAT

TTCTTGGCCACCTGGGTAA

TTCTAGGCCATTTGAGGAT

TTCTAGGCCAGCAATGGAT

TTCTAGGCCCTCCGAGGAT

TTCTATGCCAGCAATGGGT

Nr of selected repeats 21 Similarity 0.753383

>Cele-UNSB01_1:1346901-1347222 Satlength=322 Nr of Repeats=5 RepeatLength=42
seed=TTTGCCGGAA
TTTGCCGGAAATTTTCATTTTCAGGCAAATTGCCGGTTTGACG
TTTCCCGGAAGTTTTCATTTTCGACAAATTACCGATTTGTGCG
TTTGCCGAATATCAGA
TTTGCCGGAAATGTATAGATGGATTTTTTATAAGACAGAAACATTTAAACTGTGCCTTTTTGAATTTTTTCCCGTTTT
TTCTACATATTTTCATGGAATTTGCTTACTTTTCGAAAATTTTCGGCAAATTGCCGTTTTCTGACAAATTCGGCAAATC
GACAGTTTGCCAGTTTGCCGG
TTTGCCGGAAATTTAATTCCGGAAAATTGCCGATTTGCCAA
Nr of selected repeats 3 Similarity 0.705426
Consensus:
TTTgCCGGAAaTTTTcAtTTccGgcAAATTgCCGaTTTGNcG
>Cele-UNSB01_1:1386048-1386208 Satlength=161 Nr of Repeats=5 RepeatLength=32
seed=AAAATTTTGG
AAAATTTTGGCGGGAATTCAAAATTTTCTGAGA
AAAATTTTGGCGGGAATTCAAAATTTTCTGAGA
AAAATTTTGGCGGGAATTCAAAATTTTCTGAGA
AAAATTTTGGCGGGAATTCAAAATTTTCTGAGA
AAAATTTTGGCGGGAATTTAAATTTTCTGAGA
Nr of selected repeats 5 Similarity 0.983333
Consensus:
AAAATTTTGGCGGGAATTCAAAATTTTCTGAGA
>Cele-UNSB01_1:1435639-1436319 Satlength=681 Nr of Repeats=8 RepeatLength=71
seed=ATTTATGTGA
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGATGGAAATCTGAATATTTCCGCTTTTTCTGATGG
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAGGGAAATCTGATTTTTTTTCGATTTTCTGGCGA
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAGGGAAATCTGAATTTTTTCGGTTTTTCCGATGG
ATTTATGTGAAAATTTAAGGTTTTAGGGTATTTTTACGGGAAAATGGATTTTTAGCCGTTTTTGTGGAAAATCCGA
TTTTTTGCCGAATTTTAAGAAAATTTCCGATCAAAAAGACTTTTTCAGGCTTTTAGGAACATTTTTTAAGGAAATCT
GAATATTTCCGCTTTTTCTGATGG
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGATGGAAATCTGAATATTTCCGCTTTTTCTGATGG
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAGGGAAATCTGATTTTTTTTCGATTTTCTGGCGA
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAGGGAAATCTGAATTTTTCCGATTTTTCCAACCA
ATTTCTGTGAAAATGCAGGTTTTCGAGACACATTTTTGAAGGAAATCGTAAAATGTTCGGTTTTTCTGAAGG
Nr of selected repeats 6 Similarity 0.847840
Consensus:
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAgGAAATCTGAaTtTTTcCGatTTTTCTGacGa
>Cele-UNSB01_1:1456315-1457241 Satlength=927 Nr of Repeats=24 RepeatLength=35
seed=AAATTTGAAT
AAATTTGAATTTCCCGCCAAAATCTTTTTTCTCAGA
AAATCTGAATTTCCCGCCAAAATTTTTTTTCTCAGA
AAATTTGAATTTCCCGCCAAAATTTTTCAAAGA
AAATTTGAATTTCCCGCCAAAATTTCTTTTCTCATAAATTTGAAGTTCCCGCCCATATTTTTAAGGGTCTCACCACGAT
GGGTCTCGCCAGTTCCAGGTGGTACTTAAGCTAACAAAAGTTTCTTTGA
AAATTTGAATTTCCCGCCAAAATGTTTTTCACTGA
AAATTTGAAATTTCCCGCCAAAATGTTTTTCACTGA
AAATTTGAATTTCCCGCCAAAATTTTTTCACTGA
AAATTTGAACTTTCCCCCAAAATTTTTTCTCACAGA
AAATTTGAATTTCCCGCCAAAATTTTTTCACTGA
AAATTTGAAATTTCCCGCCAGAAAATTTTTTACTGA
AAATTTGAATTTCCCGCTAAAATTTTTTTCACTG
AAATTTGAATTTCCGCTAAAATTTTTTTCACTG
AAATTTGAATTTCCCGCCAAAATTTTTTCACTGA
AAATTTGAATTTCCCGCCAAAATTTTTTTCACTGA

AAATTTGAATTTCCCGCCAGAAATTTTTTTTACTGA
AAATTTGAATTTCCCGCTAAAAATTTTTTTTCACTG
AAATTTGAATTTCCCGCTAAAAATTTTTTTTCACTG
AAATTTGAATTTCCCGCCAAAAATTTTTTTTCACTGA
AAATTTGAATTTCCCGCCAAAAATTTTTTTTCACTGA
AAATTTGAATTTCCCGCCAAAAATTTTTTTTCACTGA
AAATTTGAATTTCCCGCTAAAAATTTTTTTTCACTG
AAATTTGAATTTCCCACCAAAAAATTTTTTTTCACTG
AAATTTGAATTTCCCGCCAAAAATTTTTTTTCACTGA
AAATTTGAATTTCCCGCCAAAAATTTTTTTTCACTGA
Nr of selected repeats 15 Similarity 0.827628
Consensus:

AAATTTGAATTTCCCGCCcAAAAATTTTTTTTCACTGa
>Cele-UNSB01_1:1457508-1457876 Satlength=369 Nr of Repeats=14 RepeatLength=11
seed=CTACAGTACT
CTACAGTACTA
CTACAGTACCCCGACCACATCCCATCACTAACCTCAAACCAATATCCCTTCAAAAGGCGAAAAGTCAATTTTTCTCAA
CTACAGTAATT
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCCGACCATATCCAACCACTAACCTCAAACCAATATCCCATCAAAGGCGAAAAGTCACATTTTCCCAA
CTACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCCGACCATATCCCACCACTAACCTCAAACCAATATCCCATCAAAGGCGAAAAGTCAATTTTTCCCAA
CTACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCCGACCATATCCCACCACTAACCTCAAACCAATATCCCATCAAAGGCGAAAAGTCAATTTTTCCCAA
CTACAGTAATC
CTACAGTACTCCTACAGTACCT

Nr of selected repeats 10 Similarity 0.753704
Consensus:

CTACAGTAcTn
>Cele-UNSB01_1:1530606-1531290 Satlength=685 Nr of Repeats=18 RepeatLength=31
seed=GGTTACTGTA
GGTTACTGTAGATCGATCCTGAAATCTAAAAAGTACTGTAGATCAATTTGGGGATACTTCA
GGTTACTGTAACTCAATTATAGGATTCCTCG
GGTTACTGTAGATAGATCCTAGGATTCGAAA
GTTACTGTAGATCGGTTCTAGGATACTTTG
GGTTACTGTAGATCGGGTCTAGGATACTTTG
GGTTATTGTAACCTCAATTATAGGATTCATCG
GGTTACTGTAGATCGGTTCTAGGATACTTTG
GGTTACTGTAGATCAGGTCTAGGATACTTTG
GGTTACTGTAACTCAATTATAGGATTCATCG
GGTTACTGTAGATCGATCCTAGGATTCATAAATTTACTGTAGATCGGTTCTAGGATACTTTT
GGTTACTGTAACTCAATTATAAAATACTTCG
GGTTACTGTAACTCAATTATAAGATTCATCG
GGTTACTGTAGATCGATCCTAGAATTCGAAAGTAACTGTAGATCGGTTCTAGGATTCCTCG
GGTTACTGTAGATCGGGTCTAGGATACTTTG
GGTTACTGTAACTCAATTATAAAATACTTTG
GGTTACTGTAACTCAATTATAAAATACTTTGGGTTCTGTGGCCCGATTCTAGGATTATTTCG
GGTTACTGTAGATCGGGTCTAGGATACTAAA
GGTTACTCTAGGATCAATCCTAGGATTCATAGG
Nr of selected repeats 11 Similarity 0.738025
Consensus:

GGTTACTGTAacTCaatTaTAgGATaCtTnG

>Cele-UNSB01_1:1591838-1592129 Satlength=292 Nr of Repeats=7 RepeatLength=35
seed=CGGCAAATCG

CGGCAAATCGGCAAATTGTCGGGAATTGAAAATTTTC
CGGCAAATCGGCAAATTGCCGGAATTGAAAATTTTC
CGGCAAATCGGCAAATTGCCGGAATTGAAAATTTTC
CGGCAAATCGACAAATTGCCGAAATTGAAAATTTTC
CGGCAAATCGGCAAATTGCCGGAATTGAAAATTTTC
CGGAAAATCGACAAATTGCCGAAATTGAAATCTTC
CGGCAAATCGGCAAATTGCCGGAAGACAATCCCTTCAGAAAAATCCGGTAAACTGCCGGAATTGAAAATTTCCGGCAAT
TT

Nr of selected repeats 6 Similarity 0.895873

Consensus:

CGGCAAATCGgCAAATTGCCGgAATTGAAAATTTTC

>Cele-UNSB01_1:1620106-1621181 Satlength=1076 Nr of Repeats=5 RepeatLength=189
seed=TTTTTTTTGA

TTTTTTTTGAGAAGTTTTTAAAAAGTTTCATTATGAAATTCGATGTTTTTCAGACAATTTTGAGTCTAATTAAGCAATAA
AAAAAATTCCTACTACACCCTTTAAATTTTGCCACGTCGCTAAATAAGCACTAGTTTTATCAATTTTAAAACCTGGAA
AAATCCAGAAAGAAAAATATGTTTTCTGGAAATTAATAATCAAATCCTTAATGATGTTTTGATTTTCCAGGTATCACCAT
CTCCAAATGAACGAATGCAGATGGGCCGAACCCACGTGGCTCAATGAGCCCATGTCTGTACACGGTGGAAAGTCAGCA
ACTATCCCACCTTATAGTTTTTTGACTATTCCTTTTCAATTTGTTACGTGTTACCAAGATTCACCTCTT
TCCGTTT

TTTTTTTTTAAATATCAATTGGTTTGCATTGTTTCAAGTGCCCCCTGATTTCTGCTCCTTAATTCACCTTATCTGTTTTCT
CACGGGTTTAGGATATTTTTTCTGTTA

TTTTTTTTGACTATGGAATTATAAAGAAAATCGAATTTCAAAAAGCATGTATTAGCCAATGTAAACGCGCTCCAATGA
TGATGTAGCCCACGTGGTATCAGAGTGTCTCTTTACGGCTTGATTTAAATACGTAGATCTACAAATTCACCTTATCTGTT
TTCTCACGGGTTTAGGATATTTTTTCTGTTA

TTTTTTTTGACTATGGAATTATAAAGAAAATCGAATTTCAAAAAGCATGTATTAGCCAATGTAAACGCGCTCCAATGA
TGATGTAGCCCACGTGGTATCAGAGTGTCTCTTTACGGCTTGATTTAAATACGTAGATCTACAAATTCACCTTATCTGTT
TTCTCACGGGTTTAGGATATTTTTTCTGTTA

TTTTTTTTGACTATGGAATTATAAAGAAAATCGAATTTCAAAAAGCATGTATTAGCCAATGTAAACGCGCTCCAATGA
TGATGTAGCCCACGTGGTATCAGAGTGTCTCTTTACGGCTTGATTTAAATACGTAGATCTACAAATTCACCTTATCTGTT
TTCTCACGGGTTTAGGATATTTTTTCTGTTA

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TTTTTTTTGACTATGGAATTATAAAGAAAATCGAATTTCAAAAAGCATGTATTAGCCAATGTAAACGCGCTCCAATGA
TGATGTAGCCCACGTGGTATCAGAGTGTCTCTTTACGGCTTGATTTAAATACGTAGATCTACAAATTCACCTTATCTGTT
TTCTCACGGGTTTAGGATATTTTTTCTGTTA

>Cele-UNSB01_1:1632570-1633118 Satlength=549 Nr of Repeats=6 RepeatLength=35
seed=AAATTTTCAA

AAATTTTCAAACATTTCCATATCGTGCGCCTTTAAAATAACGGAAATCGCGGCGAGACCCATTCCATGCACCTTTAAAG
TAGCACCACCAGCGTTGGATTTCTGCTTTAAAATCGGTTTTTTTACCATAATATCTAGTTTTTTTGGCTGAAAAATCGAT
TTTTTCGCAAATTTACGAAAAAAATCGCACAAAAATGTTTTTTTTGCTCATTTTTTTCCTCAAAAATCCGAATTTCCAG
GCAATTTCCATTA AAAACCCCGTTTTTTGCGCAAATTTCTTAATTTTTTCACTAAAAATCGTAAGCTTAAAATTTTTTA
AATTGAAATTCAAAATTTCCCGCAAAAATCGCTCCGGCAATTTGCTGATTTGCCGG

AAATTTTCAATTCCGGCATTGCGGATTTGCCGG

AAATTTTCAATTCCGGCATTGCGGATTTGCCGG

AAATTTTCAATTCCGGCATTGCGGATTTGCCGG

AAATTTTCAATTCCGGCATTGCGGATTTGCCGG

AAATTTTCAATTCCGGCAAATTTGCCGATTTGCCGA

Nr of selected repeats 5 Similarity 0.878095

Consensus:

AAATTTTcAATTCCGgCAatTTGCCGAtTtGCCGg

>Cele-UNSB01_1:1647038-1647577 Satlength=540 Nr of Repeats=9 RepeatLength=49
seed=CAATAATTTT
CAATAATTTTAAATTAGATTATCAATTTTTCTAAATTTTTCCGAAAAAT
CAATAATTTTAAATTAATTTATCAATTTTTCTAAATTATGCCGAAAAATCGATAATTTCAAATTTAATTATCGATTTTT
TTAAATTTTTTCGAAAAAT
CAATAATTTTAAATGTAATTATCGATTTTTCTAAATTTTGCCGAAAAAT
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CAATAATTTTAAATTAATGATCGATTTTTCTAAATTTTTCCGAAAAAT
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CAATAATTTTAAATTAATTTATCGATTTTTCTGAATTTTTCCGAAAAAT
CAATAATTTTAAATTAATTTGACTTTTTCTAAATTTTGCCGAAAAAT
Nr of selected repeats 7 Similarity 0.909297

Consensus:

CAATAATTTTAAATTaAATTATCGATTTTTCTAAATTTTTtCCGAAAAAT

>Cele-UNSB01_1:1679297-1679633 Satlength=337 Nr of Repeats=16 RepeatLength=21
seed=TCTCCTGGTA

TCTCCTGGTAAATTTAAAAAT
TCTCCTGGTAAATTTAAAAAT
TCTCCTGGTAAATTTAAAAAT
TCTCCTGGTAAATTTAAAAAT
TCTCCTGGTAAATTTAAAAAG
TCTCCTGGTAAATTTAAAAAT
TCTCCTGGTAAATTTAAAAAT

Nr of selected repeats 16 Similarity 0.963492

Consensus:

TCTCCTGGTAAATTTAAAAAT

>Cele-UNSB01_1:1680231-1680351 Satlength=121 Nr of Repeats=7 RepeatLength=12
seed=AGCCTAAACC

AGCCTAAACCTA
AGCCTAAACCTG
AGCCTGAACCAT
AGCCTAAACCTGAAACTGAACCATAGCCTAAGCAAT
AGCCTAAGCCTG
AGCTTAAACCTG
AGCCTGAACCATAGCCTAAGAAAT

Nr of selected repeats 5 Similarity 0.702564

Consensus:

AGCcTaAaCCTg

>Cele-UNSB01_1:1685357-1686631 Satlength=1275 Nr of Repeats=49 RepeatLength=26
seed=CAAACCGGC

CAAACCGGCAATTGCCGAAAACTTC
CAAACCGGCAATTGCCGAAAAATTC
CAAACCGGCAATCGCCGAAAAATTC

TCTGATCCTTTAGCTCCAAAGGATCACATGGGTACCTTCTGATGT

Nr of selected repeats 3 Similarity 0.743210

Consensus:

TCTGATCCTTcAGcTccgAAGGATCacAtGGGTaCCttcTGATGt

>Cele-UNSB01_1:1730783-1731662 Satlength=880 Nr of Repeats=24 RepeatLength=30
seed=AATTTGAATT

AATTTGAATTTTCTGGATTTTAAACGGA
AATTTGATTATTTCCGAATTTTATAGCGAA
AATTTGAATTTTCCCAGCTTTTAGTTGAAATTTAACTTTCCCAAAGTTTAAACGGA
AATTTGAATTTTCCCAGACTTTTAAACGAA
AATTTGAATTTTCCCAGACTTTTAAATCTA
AATTTGATTTTCTCGAATTTTAAAAGGA
AATCTGAATTTTCCCAGACTTTTAAAGCGAAA
AATTTGAATTTTCCGATTTTAAAGCGAA
AATTTAAATTTTCCGAAATTTTAAATCGAT
AATTTGAATTTTCCCAGACTTTTATAGTGAA
AACTTGAATTTTCTGGATTTTCAATCGAT
AATTTGAATTTTCTCGAAGTTTCAACGGA
AATCTGAATTTTCCCAGACTTTTAAACGAA
AATTTGAATTTTACCCGAGTTTAAAGCGAAAAGTTGAGTTTTTTTTCGAATTTTAAAGCGGA
AATTTGAATTTTCTCGAAGTTTCAACGGA
AATTTGAATTTTCTCGAAGTTTACCAAAGACTGAATTTTCCCAGACTTTTATAGTGAA
AATTTGAATTTTCTGGATTTTATAGTTGAA
AATTCGAATTTTCTCGAAGTTTCAACGGAATCTGCGTTTTCCCAGACTTTTATAGCAA
AATTTGACTTTTCCCAGACTTTTAAAGAA
AATTTGAATTTTCCCAGACTTTTATAGTGAA
AATTTGAGTTTTTCCGAGTTTTTATAGCAA
AATTTGAATTTTCCCAGACTTTTATAGTGAAAATTTTTCAGTTTTGCCGAATTTTGGAAATGAA
AATTTGAATTTCTTCAAAGTTTCCCAGACTTTTATAGTGCGAA
AATTTGAATTTTCCCAGACTTTTACTGGA

Nr of selected repeats 15 Similarity 0.732487

Consensus:

AATTTGAATTTTCCcGaAtTTTnAacGaA

>Cele-UNSB01_1:1781850-1784996 Satlength=3147 Nr of Repeats=154 RepeatLength=20
seed=CCACCAAAAA

CCACCAAAAAAGGTTTCTAGG
CCACCAAAAAAGATTTCTAGG
CCACCAAAAAATGTTTCTAGG
CCACCAAAAAATGTTTCTAGG
CCACCAAAAAATGTTTCTAGG
CCACCAAAAAATGTTTCTAGG
CCACCAAAAAATGTTTCTAGG
CCACCAAACAGGTTTCAATG
CCACCAAAAAATGTTTCTAGG
CCACCAAAAAATGTTTCTAGGC
CCACCAAAAAATTTTCTAGG
CCACCAAAAAAGGTTTCTAGG
CCACCAAAAAATGTTTCTAGG
CCACCAAAAAAGGTTTCTAGG
CCACCAAACAGGTTTCAATG
CCACCAAAAAAGGTTTCTAGGCCACCAACCAGGTTTCAATG
CCACCAAAAAATGTTTCTAGG
CCACCAAAAAAGGTTTCTAGG
CCACCAAAAAATGTTTCTAGG

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CCACCAAAAAGGTTTCTAGG
CCACCAAAAATGTTTCTAGA
CCACCAAAAAGGTTTCTAGG
CCACCAAAAATGTTTCTAGG
CCACCAAAAAGGTTTCTAGG
CCACCAAAAATGCTTCTAGG

Nr of selected repeats 145 Similarity 0.874815

Consensus:

CCACCAAAAAGGTTTCTAgG

>Cele-UNSB01_1:1787086-1788479 Satlength=1394 Nr of Repeats=64 RepeatLength=20
seed=TTCTAGGCCA

TTCTAGGCCACCAAAAAGGT
TTCTAGGCCACCAAGAAAGT
TTCTAGGCCACCAAAAGTAT
TTATAGGCCACCTAAGATGT
TTCTAGGCCACCTGAGATGT
TTCTAGGTCACCAAAAATGTTTCTCGGTCACCAAAAATGT
TTCAAGGCCACCGAAAAGGT
TTCTAGGCCACCTAAGTAT
TTCTAGGCCACCTAAGATGT
TTCTAGGCCACCTGAGATGT
TTCTAGGTCACCAAAAATGTTTCTAGGTTACCAAAAATGT
TTCAAGGCCATCGAAAAGGT
TTCTAGGCCACCAAAAGTAT
TTCTAGGCCACCTAAGATGT
TTCTAGGCCACCTGAGATGT
TTCTAGGTCACCAAAAATGT
TTCAAGGCCACCGAAAAGGT
TTCTAGGCCACCAAAAAGGT
TTCTAGGCCACCAAAAATAT
TTCTAGGCCACCTAAGATGT
TTCTAGGCCACCTGAGATGT
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TTCTAGGTCACCAAAAATGTTTCTCGGTCACCAAAAATGT
TTCAAGGCCACCGAAAAGGT
TTCTAGGCCACCTAAGTAT
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TTCTAGGTCACCAAAAATGTTTCTAGGTTACCAAAAATGT
TTCAAGGCCATCGAAAAGGT
TTCTAGGCCACCAAAAGTAT
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TTCTAGGCCACCAGATAT
TTCTAGGCCACCTAAGAGGT
TTCTGGGCCATCAAAAAGGTTTCAAGTCCATCAAAAAGGT
TTCTAGGCCACCAAAAAGGT
TTCTAGGCCACCGAAAAGGT
TTCTAGGCCACCAAAAAGGT
TTCTAGACCACCTAAGACAT
TTCTAGGCCAACAAAAGGT

Nr of selected repeats 51 Similarity 0.812235

Consensus:

TTCTAGGCCACCaaaAtGT

>Cele-UNSB01_1:1822719-1823169 Satlength=451 Nr of Repeats=9 RepeatLength=43

seed=AAATCGGCAA

AAATCGGCAAACCGGCAATTTGCCGAAATTGGAAATTTCTGGC
AAATCGGCAAACCCGCAATTTGCCAGAATTGAAAATTTCCGGA
AAATCGGCAAATCGGCAAACCGCAATTTGCCGGAATTTAAAATTTTCAGC
AAATCGGCAAACCGGCAATTTGCCGGAATTGAAAATTTCCGGA
AAATCGACAAACCGGCAGATTTGCCGGAATTTAAAATTTCCGGC
AAATCGGCAAACCGGTGAATAGCCGCAATTTGAAATTTCCGGC

AAATCGGCAAACTGGCAAATTGCCGTAATTTAAAATTTCTGGCAAATTACCAGAATTGAAAATTTACGGCAAATTAAC
GGAATTGAAAATTTCTGCC
AAATCGGCAAACCGGCAATTTACCGGAAATGAAAATTTCCGGC
AAATCGACAACCCGGCAAATTGCCGAAAATGACAATTTCCGGC
Nr of selected repeats 7 Similarity 0.793282
Consensus:
AAATCGgCAAaCCGGCAAtTTGCCGgAAAtTgaAAATTTCCGGc
>Cele-UNSB01_1:1824052-1824465 Satlength=414 Nr of Repeats=9 RepeatLength=43
seed=GCCGGAATTG
GCCGGAATTGAAAATTTCCGGCAAATCGGTAAGCCGGCCAATT
GCCGGAATTGAAAATTTCTGGCAAATCGGCAAACCGACACATA
GCCGGAATTGAAAATTTCTGGCAAATCAAAAACCGGCAAATTGCCGAAGTTTAAAATTTCTGGAAATCGGCAAATCGG
CAAAT
GCCGGAATTGAAAATTTCTGGCAAAT
GCCGGAATTGAAAATTTCTGGCAAGTCGGCTAACCGGCAAAT
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GCCGGAATTGAAAATGTCTGGCAAATCGGCAAACCGGCACATA
GCCGGAATTGAAAATGTCTGGCAAATCGGCAAACCGGCACATA
GCCGGAATTGAAAATGTCTGGCAAATCGGCAAACCGGCACATA
GCCGGAATTGAAAATGTCTGGCAAATCGGCAAACCGGCACATA
Nr of selected repeats 7 Similarity 0.864157
Consensus:
GCCGGAATTGAAAATtTCTGGCAAATCGGCAAACCGGCACaT
>Cele-UNSB01_1:1833668-1834030 Satlength=363 Nr of Repeats=11 RepeatLength=26
seed=TTGCCGGTTT
TTGCCGGTTTTACGAAATTTCCGGCAATTGTCTGTTTTGGGAATTATCGGCAA
TTGCTGGTTTTGGGAATTATCGGCAC
TTGCCGGTTTTCAAAATTTCCGGCAATTGTCTGTTTTGGAAATTTCCGGCAATTGTCTGTTTTGGGAATTATCGGCAA
TTGCTGGTTTTGGGAATTATCGGCAC
TTGCCGGTTTTCAAAATTTCCGGCAA
TTGCCGGTTTTGGGAATTTTGGCAA
TTGCCGGTTTTGGAAATTTTCCGGCTA
TTGCCGATTTTGGGAAATTTCCGGCAA
TTGCCGGTTTTGGGAATTTTGGCTA
TTGCCGGTTTTGGGAATTTTCCGGCTA
TTGCCGGTTTTGGGAATTTTAAAA
Nr of selected repeats 8 Similarity 0.798535
Consensus:
TTGCcGGTTTTGGgAATTTtTcGGCaa
>Cele-UNSB01_1:1840655-1841028 Satlength=374 Nr of Repeats=9 RepeatLength=35
seed=TTTCCGGAA
TTTCCGGAAATGTTTAAAGGAGGATTTTTTTTATACTTTGGAAGCACTTCAAACGTGCCTTTTTTAAAATTTTTTCCCG
TTTTTTGTTGCCAA
TTTCCGGAAATTTTCAAATCCGGCAATTTGCCGA
TTTCCGGAAATTTTAAATTTCTGGCAAATTACCGA
TTTCCGGAAATTTTCAATACCGGCAAGTTGCCAA
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TTTACCGGAAATGTTCAATACCGGCAAGTTGCCGA
TTTACCGGAAATTTTCAAATCCGGCAGTTTGCCGA
TTTCCGGAAATTTTAAATTTCTGGCAAATTACCGA
TTTCCGGAAATTTTAAATACCGGTAAGTTGACAT
Nr of selected repeats 8 Similarity 0.766700
Consensus:
TTTgCCGGAAAtTTTcAAAtCcGGCAAgTTgCCgA

>Cele-UNSB01_1:1841619-1842039 Satlength=421 Nr of Repeats=18 RepeatLength=19
seed=AAAATCAATA

AAAATCAATAAAATCCTAAG
AAAATCAATAAAATCCTAAG
AAAATCAATAAAATCCTAAG
AAAATCAATAAAATCCTAAG
AAAATCAATAAAATTCACAG
AAAATCAATAAAATCCAAT
AAAATCAATAAAATTCCTAAG
AAAATCAATAAAATTCGGATACAATCGATAATTTCCGAG
AAAATCAATAAAATTCATGAG
AAAATCAATAAAATTCGGAGAAAATTATTAAGTTCTGAGAAAATCGGTAAATTTCCAG
AAAATCAATAAAATTTAAAATA
AAAATCAATAAAATTCATGAG
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AAAATCAATAAAATTCCTAG
AAAATCAATAAAATTCCTAAG
AAAATCGATAAAATTCCTGAG
AAAATCAATAAAATTCGGAGAAAGTCGATAAAATTCCTGGG
AAAATCGATATGTTCCGAG

Nr of selected repeats 14 Similarity 0.796414

Consensus:

AAAATCAATAAAATtCtaAG

>Cele-UNSB01_1:1841619-1843394 Satlength=1776 Nr of Repeats=44 RepeatLength=19
seed=AAAATCAATA

AAAATCAATAAAATCCTAAG
AAAATCAATAAAATCCTAAG
AAAATCAATAAAATCCTAAG
AAAATCAATAAAATCCTAAG
AAAATCAATAAAATTCACAG
AAAATCAATAAAATCCAAT
AAAATCAATAAAATTCCTAAG
AAAATCAATAAAATTCGGATACAATCGATAATTTCCGAG
AAAATCAATAAAATTCATGAG
AAAATCAATAAAATTCGGAGAAAATTATTAAGTTCTGAGAAAATCGGTAAATTTCCAG
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AAAATCGATAAAATTCCTGAG
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GGCCACCGAAAAACTCACCACGTCATCGTGAATACTCTCATAAACAGCAAACCGCTTAGCTTTTGGCATTTCCTTCTT
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CGGTATTTGGTGGGATACCTGGATTACGAGGCGCGGTGGGTTTTTTCTTCAAAAAAATTTGTAAAAAATGTGCAAAAA
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AAAATCAATAAATTCTCAGAAAATCGTTAAACTGTAAAAAACTCGATACTATGGTCTCATTTTCCAGCTGCAACCTAAAA
CTATGCTCGAAATCCGACCAATTTCTTGTGACCTCCACCCGACACGTGGCACAAATCATATCGATTGCTGAACAATCGA
ACTCTTCGTGTAACGAATTATCAACAATTATTCTACGATACGAATTCGGGTACTACAATTAGAGGAGATTGACGGAGT
TACTACAATGACTAGCGGAGAGTATCAA
Nr of selected repeats 32 Similarity 0.769949
Consensus:
AAAATCaATAAAATtcnnAG
>Cele-UNSB01_1:1878726-1878810 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=CCTACTCTAG
CCTACTCTAGGCAGCCCCTAG
CCTACTCTAGGCAGCCCCTAG
CCTACTCTAGGCAGCCCCTAG
CCTACTCTAGGCAGCCCCTAG
Nr of selected repeats 4 Similarity 1.000000
Consensus:
CCTACTCTAGGCAGCCCCTAG
>Cele-UNSB01_1:1878816-1878916 Satlength=101 Nr of Repeats=5 RepeatLength=20
seed=CTAGGCAGAC
CTAGGCAGACTTAGCCTACC
CTAGGCAGACTTAGCCTACC
CTAGGCAGACTTAGCCTACC
CTAGGCAGACTTAGCCTACC
CTAGGCAGACTTAGCCTACC
Nr of selected repeats 5 Similarity 1.000000
Consensus:
CTAGGCAGACTTAGCCTACC
>Cele-UNSB01_1:1910732-1911187 Satlength=456 Nr of Repeats=11 RepeatLength=35
seed=AAATCGGCAA
AAATCGGCAAATTTGGCGGAATTGAAAATCTCCGGC
AAATCGGCAAATTTGCCGAAACTAAAAATTTCTGGT
AAATCGGCAAATTTGCCGAAACTGAAAATTTCTGGCAACACGGCAAATTTGCCGGAATTGAAAATTTCCGGC
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AAATCGGCAATACGCCGAAAATGAAAATTTCCAGC
AAATCGGCAATTTGCCGGAATGAAAATTTCCGAC
AAATCGGCAATTTGGCGAAAAATGAAAATTTCCGGCAAACCTGGC
AAATTGGCAAAAATGAAAAATTTCCGGCAAGTTGGCAATTTGCCGAAACTGGAAAATTCGGGT

Nr of selected repeats 8 Similarity 0.753742

Consensus:

AAATCGGCAAattGcCgaAATtgAAAATTTCCGgc

>Cele-UNSB01_1:1946077-1948348 Satlength=2272 Nr of Repeats=60 RepeatLength=35
seed=TTGCCGATTT

TTGCCGATTTGCCGATTTGCCGGAATTTTCTAATCCGGCAAT
TTGCCGATTTGCCGGAATTTTCATTTTTTCGCAA
TTGCCGATTTGCTGATTTGCCGGAATTTTTCATTTTTTCGCAATTTGCCCGT
TTGCCGATTTACCTGAAATTTTCATTTTTTCGAAAA
TGCCGATTTGCCGGAATTTTCTATTCCGGCAAT
TTGCCGATTTGCCGGAATTTTCATTTTTTCGCAAT
TTACCGATTTTCCGGAATTTTTCATTTTTTCGCAATTTGCCCGT
TTGCCGATTTTCCGGAATTTTCATTTTTTCGCAA
TTGCCGATTTGCCGGAATTTTTCATTTTTTCGCAA
TTGCCGATTTGCCGGAATTTTTCATTTTTTCGCAAT
TTGTTCGATTTGCCGGAATTTTTCATTTTTTCGCAATTTGCCCGT
TTGCCGATTTTCCGGAATTTTTCATTTTTTCGCAA
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Nr of selected repeats 44 Similarity 0.891070

Consensus :

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>Cele-UNSB01_1:1961569-1963172 Satlength=1604 Nr of Repeats=40 RepeatLength=35
seed=GAAATTTTCA

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Nr of selected repeats 33 Similarity 0.890620

Consensus:

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>Cele-UNSB01_1:1961569-1964216 Satlength=2648 Nr of Repeats=64 RepeatLength=35

seed=GAAATTTTCA

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Nr of selected repeats 47 Similarity 0.883388

Consensus:

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>Cele-UNSB01_1:1961569-1966139 Satlength=4571 Nr of Repeats=108 RepeatLength=35
seed=GAAATTTTCA

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Nr of selected repeats 73 Similarity 0.839524

Consensus:

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>Cele-UNSB01_1:1961569-1968269 Satlength=6701 Nr of Repeats=154 RepeatLength=35
seed=GAAATTTTCA

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GAAATTTTCAGTTTTCGGCAAATTGCCGATTTGCCGT
AAATTTTCAATTCCGGCAGTCTGCCGATTTGCCGTAAATTTTCGTTTTTGCAAATTTACCGATTTGCCG
GAAATGTTCAATCCCGCAATTTGCCAATTTGCCGTAAATTTTCGTTTTTGAAAAATTTACCGATTTGCCGTAAATTTTC
GTTTTTGCAAATTTACCGATTTGCCG
GAAATGTTCAATCCCGCAATTTGCCAATTTGCCGTAAATTTTCGTTTTTGAAAAATTTACCGATTTGCCG
GAAATTTTCAGTTTTCGGCAAATTTGCCAATTTGCCG
GAAATTTTCAATCCGGCAATTTGGTGATTTGCCG
GAAATGTTCAATCCGGCAATTTGCCAATTTGCCG
GAAATTTTCAGTTTCTGCAATTTGCAGATTTGACG
GAAATTTCAATTCCGGCAATTTCCCTGTTTGCCG
GAAATTTTCAGTTTTCGTCACTTTGCCAATTTACCG
GAAATTTTCAATCCGGCAATTTGCCTGTTTGCCGGAATTTTCGTTTTTCGGCAAATTTGCCGATTTGCC
GAAATTTTCAGTTTTCGGCAAATTGCCGATTTACTG
GAAATTTTCAATCCGGAAATTTGCCGATTTGCC
GAAATTTTCAGTTTTCGGCAAATTGCCGATTTGCC
GAAATTTTCAGTTTTCGGCAAATTGCCGATTTACTG
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GAAATTTTCAGTTTCGGCAAATTGCCGATTTGCC
GAAATTTTCAGTTTCGGCAAATTGCCGATTTGCCGT
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GTTTTTGGCAAATTACCGATTTGCCG
GAAATGTTCAATCCCGGCAATTTGCCAATTTGCCGTAAATTTTCGTTTTTGGAAAAATTACCGATTTGCCG
GAAATTTTCAGTTTCGGCAAATTGCCAATTCGCCG
GAAATTTTCAATTCCGGCAATTTGGTGATTTGCCG
GAAATGTTCAATCCCGGCAATTTGCCAATTTGCCG
GAAATTTTCAGTTTCTGCAATTTGCAGATTTGACG
GAAATTTTCAATTCCGGCAATTTCCCTGTTTGCCG
GAAATTTTCAGTTTCGTCACTTTGCCAATTTACCG
GAAATTTTCAATTCCGGCAATTTGCCGTGTTTGCCGGAATTTTCGTTTTTCGGCAAATTGCCGATTTGCC
GAAATTTTCAGTTTCGGCAAATTGCCGATTTACTG
GAAATTTTCAATCCGGAAATTTGCCGATTTGCC
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GAAATTTTCAATTCCGGCAATTTGGTGATTTGCCG
GAAATGTTCAATCCGGCAATTTGCCAATTTGCCG
GAAATTTTCAGTTTCTGCAATTTGCAGATTTGACG
GAAATTTTCAATTCCGGCAATTTCCCTGTTTGCCG
GAAATTTTCAGTTTCGTCACTTTGCCAATTTACCGAA
AAATTTTCAATTCCGGCAATTTGCCGTGTTTGCCGGAATTTTCGTTTTTCGGCAAATTGCCGATTTGCC
GAAATTTTCAGTTTCGGCGAATTTGTCGATTTACCG
GAAATTTTCAATCCGGCAATTTGCCAATTTGCCGTAAATTTTCGTTTTTGGAAAAATTGCCGTTTGCCGATTCGCCG
GAAATTTTCAGTTTCGGCAAATTGCCAATTTGCCG
GAAATTTTCAGTTTCGGCGAATTTGTCGATTTGCCG
GAAATTTTCAGTTTCGGCAAATTTGCCGGAATTTTCGTTTTTCGGCAAATTGTCGATTTGCCG
Nr of selected repeats 94 Similarity 0.828463

Consensus:

GAAATTTTCAGTTTCGGCAAaTTGCCgATTTgCCg

>Cele-UNSB01_1:1976543-1977056 Satlength=514 Nr of Repeats=5 RepeatLength=35

seed=TTTGCCGGAA

TTTGCCGGAAATTTTTTTTCGATTTTTCGGTAGAAAAAATCGAATTCAGTTTTTCACATACGGAATCTGAATAA
TATTTATGTAGGGGTGCGCGCGATTGCCGTTCCGGCAAATTGATTTGTGACAAATTCGGCAAATTCGGCAAATTGCCG
GTTTGCCGA

TTTGCCGGAAATTTTCATTTTTTGGCAAAGTGCCGA

TTTGCCGGAAATGTTAGAGGGATTTTTTGAAGACGGAAACACTTAAACTGTGCCTTTTTGTATTTTTTCCGTTTTT
TTCTACATATTTTCATAGAATTTGCTTACTTTTCAAATAGATGTAGGAACATTTATAGAATGCGTTAATTTTGCCAT
TTGAAATTGAAATTTGAAATTTCCAAAAATGTGCAAAACCACAATTTGGCGAAAAATTTTCGGCAAATTCGGCAAATTTG
CCG

TTTGCCGGAAATTTCAATTCGGGCAATTTACCTG

TTTGCCGGAAATTTCAATTCGGGCAATTTGCCGA

Nr of selected repeats 3 Similarity 0.759259

Consensus:

TTTGCCGGAAATTTCAaTTccGGCAAttTgCCGa

>Cele-UNSB01_1:1980049-1980327 Satlength=279 Nr of Repeats=8 RepeatLength=35

seed=TTGCCGGAAA

TTGCCGGAAATTTTAATTCTGACAAATTGCCGAT

TTGCCGGAAATTTCAATTCGGGCAATTTGCCGAT

TTGCCGGAAAGTATCAATTTCCGGCTGATTGCCGAT

TTGCCGGAAACGTTCAATTTCCGCACTTTGCCGAT
TTGCCGGAAATGTTCAATTTCCGGCGATTTGCCGCT
TTGCAGGAAATTTTCTTTTTCCGGCAGTTTGGCGAT
TTGCCGGAAATTTCCAATTTCCGGCAATTTGTTCGAT
TTGCCGGAAATGTTCAATTTCTGATAAATTGCCGAA

Nr of selected repeats 6 Similarity 0.654655

Consensus:

TTGCCGGAAAtgTTCAAtTTCgGCaaaTTGCCGAT

>Cele-UNSB01_1:2017348-2017684 Satlength=337 Nr of Repeats=5 RepeatLength=38

seed=AAAATCGATA

AAAATCGATAATTTTAGTATTGCTCTCAAAATTTTTTTGATTTTCCAGGAAATTATCAAAATTTTTAGTTTTTCAAAAAA
TTGTGCAAAATTTTCAATTTATTTTTTGAATAGAATTTGTTTTTTTTAAAAATTATTTCTAACTCTTGGCATTTCCTTTTT
TAAAAATAGAGG

AAAATCGATAAATTTCCAAGTGATTTTTTGCAATCCAAAAAAATTTCTTTCGAAA

AAAATCGATAAATTTTCAGTATGCAGTGAAATTTCTTGGGA

AAAATCGATAAATTTTCAGTATGCAGTGAAATTTCTTGGGA

AAAATCGATAAATTTTCAGTATGCAGTGAAATTTCTTGGGA

Nr of selected repeats 3 Similarity 1.000000

Consensus:

AAAATCGATAAATTTTCAGTATGCAGTGAAATTTCTTGGGA

>Cele-UNSB01_1:2044939-2045157 Satlength=219 Nr of Repeats=13 RepeatLength=11

seed=TTTTGCCGAA

TTTTGCCGAAG

TTTTGCCGATCTTTTGTGTAAC

TTTCGCCGAAC

TTTTGCCGAAC

TCTTGCCGAAG

TTTTGCCGAAG

TTTTGCCGAAG

TTTTGCCGAACCTTTCACCAACCTTTCGTCAAAATTCGCCAAACTTTCGTCAAAATTCGCCAAAC

TTTTGCCAAAT

TTTCGCCGAAC

TTTTGCCGAAC

TTTTGCCAAAC

TTTTGCCCAATTTTCGCCAAAC

Nr of selected repeats 10 Similarity 0.811448

Consensus:

TTTTGCCgAAc

>Cele-UNSB01_1:2141918-2142329 Satlength=412 Nr of Repeats=7 RepeatLength=35

seed=CAAACCGGCA

CAAACCGCAACCTGCCGAAAATCAATATTTTGAG

CAAACCGCATTTTGCCGGAAATTAACATTTAGAG

CAAATCGGCAAACCGGCAATTTGCCGAAAAGCAACATTTCCGGCAAATCAG

CAAACCGGCAAACCTACCGAAAATTAAGAATTTTCGG

CAAACCGGAATTTTGTGCGAAAATTTTACATTTCCGACAATTTGTTCAGTTTGCCGATTTTCTCTAAATGTTGATTTTTCG

GCAAATTTGCCAGTTTTCGCCGAAAATTTGAATTTCCAGAAATTTGCCGGTTTTCGGATTTGCTGGAAATTTTGATTTTGGG

CAAATGCGGGAAGTGAAAATTTCCCA

CAAACCGGCAATTTGCAGAAAAATAACATTTCCAG

CAAACCGGCAAATTTGCCGAAAAGCATCATTTAGAG

Nr of selected repeats 5 Similarity 0.675926

Consensus:

CAAACCGGCAantTgCcGaAAAttAacATTTngaG

>Cele-UNSB01_1:2169410-2169690 Satlength=281 Nr of Repeats=8 RepeatLength=35

seed=CGGCAAATTG

CGGCAAATTGATTTGTCCGAAAAATT
CGGCAAATTTTGCTGATTTGACGGAAATTTTCAATTC
CGGCAAATTGCCGATTTGCCGGAACTTTCAATTC
CGGCAAATTGCCGTTTGGCCGATTTGCCGGAAATCTTCGATTC
CGGCAAATTGTGCGATTTGCCGGATATTCTCAATTC
CAGCAAATTGCCGATTTGCCGGAAATTTTCAATTC
CGGCAAATTGCCCGTTTGGCCGAAATTTTCAATTC
CGGCAAATTGCCCGTTTGGCCGAAATTTTCAATTC
Nr of selected repeats 5 Similarity 0.878095
Consensus:

CgGCAAATTGcCgaTTTGGCCGAAAtTtTCAATTC
>Cele-UNSB01_1:2174082-2174248 Satlength=167 Nr of Repeats=10 RepeatLength=15
seed=AGATCTTGTT
AGATCTTGTTTTCGT
AGATCATGTTTTCCG
AGATCTTGTTGTGCGT
AGATCTTGTTTTCCGT
AGATCTCGTTTTTGTAGTTCTCCAAAATGT
AGATCTTGTTCTGGT
AGATCTTGTTTTCGT
AGGTCTTGTTTTCGT
AGGTCTTGTTTTCGT
AGATCTTTTTTTTTCGT
Nr of selected repeats 8 Similarity 0.831746
Consensus:

AGaTCTTGTTtTCGT
>Cele-UNSB01_1:2195476-2195914 Satlength=439 Nr of Repeats=10 RepeatLength=35
seed=TTTGCCGGAA
TTTGCCGGAAATATCCAATTCAGGCAATTTGGCCGTTTGCTGAA
TTTGCCGGAAATTTCCGAATTTGACAGTTTGCCGG
TTTGCCGAATCTGTCAACAATTTTCAATTCGGCAAATTACCGATTTGTCCGGAAATTCGGAATTCGACAA
TTTGCCGAATTCGCCGGAAATTTTCATTCGGCAAATTTACCGA
TTTGCTGGAAGTTGTCAATTTTCGGCAAATGGCCGATGTCTAGAAATTTTTATTTTTGGCAAATGGCCAA
TTTGCAGGAAATTTTTATTTTTGGCAAATGTTGA
TTTGCCTGAAATTTTGAATTCGACAATTTGCTAA
TTTGCCGGAAATTTTGAATTCGACAATTTGCCTA
TTTGCCGGAAATTTTGAATTCGACAATTTGCCGG
TTTGCCGGAAATTTTGAATTCGACAATTTGCTAA
Nr of selected repeats 6 Similarity 0.735873
Consensus:

TTTGCCGGAAATTTTGAATTCcGaCAATTTGCcga
>Cele-UNSB01_1:2263475-2263726 Satlength=252 Nr of Repeats=6 RepeatLength=43
seed=CAAATCGGCA
CAAATCGGCAACTCGACAAATTTCCGAAATTAATAATTTCCAG
CAAATCGGCAAACCGGCTGGAATTGAACATTTCCGG
CAAATCGGCAACTCGGCAAATTTCCGAAATTAATAATTTCCAG
CAAATTGGCAAACCGGAAATTTGCCGGAATTGAACATTTCCGG
CAAATCGGCAACTCGGCAAATTTCCGAAATTAATAATTTCCAG
CAAATTGGCAAACCGGAAATTTGCCGGAATTGAACATTTCCGG
Nr of selected repeats 5 Similarity 0.782946
Consensus:

CAAATcGGCAActCGgcAAATtCCGaAATTaAAaAtTtCaG
>Cele-UNSB01_1:2281114-2281247 Satlength=134 Nr of Repeats=4 RepeatLength=33
seed=TAAGAAAAGT

TAAGAAAAGTTAGGCCACCAAAC TTTGGTGAAC
TAAGAAAAGTTAGGCCACCAAACATTGGTGGAC
TAAGAAAAGTTAGGCCACCAAAC TTTGGCGAAT
TAAGAAAAGTTAAGTCACAAAAT TTTTGGTGGAC

Nr of selected repeats 3 Similarity 0.892256

Consensus:

TAAGAAAAGTTAGGCCACCAAACtTTGGtGaAc

>Cele-UNSB01_1:2284293-2285881 Satlength=1589 Nr of Repeats=82 RepeatLength=12

seed=CACGCAACGC

CACGCAACGCAG

CACGCAACGCTG

CACGCAGCGCAG

CACGCAACGCAG

CACGCAACGTGACACGCAATGAGG

CACGCACCGCAGCGGAAACGCAG

CACGCAACGCGA

CACGCAACGCAG

CACGCAACGCAG

CACGCAACGCAG

CACGCAACGCGAT

ACGCAACGCAG

CACGCGACGCAGT

ACGCAACGCGA

CACGCAACGCAACACAGTTCCTTTTTTCAGGAAGAACCAGCCTTGGGGAGAGACACCGTCAAATGCCACGTCAGCAAG

ACTCTCCACTTCGGTAACAATGTGTGAGGATGGAATGTGCAAGCTGACCCTTTTGGAGAAACATAATCACGAATTCGGA

ACAGAATCAAAAATCTCATCCGGTTCAGGGAATTTGAAAAAGAAGGTACGTTGTCCACGTGGAGTACACGATTTTGCCA

AATTTATTTTCAAAAAATTTGAATTTTCCGCGGAGCCAACAAGCGGAGTGTGCGTTGCAACAAATTTCTAAATTCAGG

TGTCACGAGTATCGTATGCCGGTGAGGAAATTTGTATACCCGGTTCGGATAGAGGATCTCGAGAATGACGTCATTTATAG

TATAGAAGAAGAACGTGAAGATTAATTGTCAATTTTGTATCCAAAAATTATTATTTGTGATCTTTTCTCTAATTGTAA

TCTACTAAATTAATTTTTTTGAACTATGAATAAATTCGGTAATTGTTAGTAAAAATCATTA AAAAAGGTTCGAATTTAGC

GCCAAAAATATTCAATTTAAAAATTGGAGTTTTGTCCGGCAG

CACGCAACGCAG

CACGCAACGCAA

CACGCAACGCAA

AATTTCCGGCAAATGGGCAAAGTCGGCAAATTGCCGAAATTAAA
AATTTCCAGCAAACCGGGCAAACCGACATGTTGCCGAAAAAGAA
AATTTCCGGCAAATCGGTAAACCGGCAATTTTCCGAAAATAAA
AATTTCCGGCAAATCGGCAAACCGGCAATTTGCCGAAAATAAG
AATTTCCGGCAAATCGGCAAAGTCGGCAAACCTGCCGGAATTAAA
AATTTCCGACAAATCGGCATGTCGGCAAATTGCCGGAATTGAA
AATTTCTGCAAATCGGCAAACCGGCAATTTTCCGAAAATAAA
Nr of selected repeats 11 Similarity 0.790839

Consensus:

AATTTCCGGCAAATCGGCAAacCGGCAAnTtGCCGAAaTaAA

>Cele-UNSB01_1:2301010-2301088 Satlength=79 Nr of Repeats=6 RepeatLength=12

seed=TAGGCTTAGG

TAGGCTTAGGCT

TAGGCTTAGGCT

TAGGCTTAGGCA

TAGGTTTAGGCTTAAGCT

TAGACTTAGGCT

TACGCTTAGGCA

Nr of selected repeats 5 Similarity 0.844444

Consensus:

TAggCTTAGGct

>Cele-UNSB01_1:2308046-2308235 Satlength=190 Nr of Repeats=5 RepeatLength=12

seed=AGGCTTAGGC

AGGCTTAGGCTCCTTAAGTTTGTAGTTTATGAAAAAAGTTGTGAAAAAACAATAGAATCTAAAAATAATTTCTCTT

CGAAATTTTAAAAATTTTCAAGATGTTCAAAGTTTTTCAAAGTCTTTAAT

AGGCTCAGGCTC

AGGTTTAGGCTT

AGGCTTAGGCCT

AGGCTCAGGCTTAGGCTTTGGT

Nr of selected repeats 3 Similarity 0.703704

Consensus:

AGGcTtAGGctt

>Cele-UNSB01_1:2365340-2366051 Satlength=712 Nr of Repeats=8 RepeatLength=20

seed=GGACTAGTTT

GGACTAGTTTTCTACCAAATTTCAAATTTTTCAGACATTTCTCGTCTCCGTTGCTGACGTCACCAGGAGGCACGAAATCG

GTGTGAAGCTCACCAAAATGTGATAATTGTGGATGTAAATTTACAGTTTTTCTTAAAATGTTTTTCTTAATTTTTTGAA

TTTTCAGAAACCAAATTTTTCAGCCAAGATGACGTGGAAATTTGATATGGACGAGGTTTTAAGACCATTATGGACCATTCAA

AATAGGCCATCTGACTTTGCAACGGTGTAGTTCTGGTGGTGGCCTAGAAATCCCATAGGTGGCCTAGAAGTTTCAAATGA

TGAATTTTACATTTTAAATTCGATTATTCTTTGAAGTGCACAAAACCTTCCACGGCCATATTCAAATTTCTAGGCC

ACCAACCTCAAAACTTAGACCATGTATTTTCAAGTGTTCGAATTTTTTCAATTTTCAATTTTCAATTTTCAATTTG

TACATCAAACCGAGAAATTTTCAAACAACTTTCAAACCGGAATTTCCACGTGGCAATTGCGGAACCTGTTTTCAATTTGC

GGCCTCGGTATGGCTGGAG

GGACTAGTTTTTGTAGTAGAG

GGACTAGTTTTTGTAGTAGAG

GGACTAGTTTTTGTAGTAGAA

GGACTAGTTTTTCCAGTTGGG

GGACTAGTTTTTCAAGTAGAG

GGACTAGTTTTTCCAGTAGAG

GGACTAGTTTTTCCAGTAGAG

Nr of selected repeats 6 Similarity 0.880000

Consensus:

GGACTAGtTTTTcGAGTAGAG

>Cele-UNSB01_1:2365340-2366212 Satlength=873 Nr of Repeats=11 RepeatLength=20

seed=GGACTAGTTT

GGACTAGTTTTCTACCAAATTTCAAATTTTCAGACATTTCTCGTCTCCGTTGCTGACGTCACCAGGAGGCACGAAATCG
GTGTGAAGCTCACCAAAAATGTGATAATTGTGGATGTAAATTTACAGTTTTTCTTAAAATGTTTTTCTAATTTTTGAA
TTTTCAGAAACCAAATTTTCAGCCAAGATGACGTGGAATTGATATGGACGAGGTTTTAAGACCATTATGGACCATTCAA
AATAGGCCATCTGACTTTGCAACGGTGAGTTCGGTGGTGGCCTAGAAATCCCATAGGTGGCCTAGAAGTTTCAAATGA
TGAATTTTCACATTTTAAATTCGATTATTCTTTGAAGTGCGCAAAAACCTTCCACGGCCATATTCAAATTTCTAGGCC
ACCAACCTCAAACTTAGACCATGTATTTTCAGTGCTTCAATTTTTTCAATGATGCAAACAACCTTGTGCGGAATT
TACATCAAACCGAGAAATTTCAAAAACCTTCAAAAACGGAATTCCACGTGGCAATTGCGGAACCTGTTTCAATTTGC
GGCCTCGGTATGGCTGGAG
GGACTAGTTTTTGGAGTAGAG
GGACTAGTTTTTGGAGTAGAG
GGACTAGTTTTTGGAGTAGAA
GGACTAGTTTCCAGTTGGG
GGACTAGTTTTCAAGTAGAG
GGACTAGTTTTCGAGTAGAG
GGACTAGTTTTCGAGTAGAG
GGACTAGTTTTCGAGTAGAGGGACTAACTTTCCAATTGGTGGACTAACTTTCCAATTGGTGGACTAACTTTCCAATTGG
CGGACTAACTTTCTAATTAGG
GGACTAATTTTGCCTTGGG
GGACTAGTTTTCCAAGTGGCCTAACTTTTTTCAAACAG

Nr of selected repeats 7 Similarity 0.745276

Consensus:

GGACTAGtTTTnGAGTAGAG

>Cele-UNSB01_1:2396315-2396849 Satlength=535 Nr of Repeats=20 RepeatLength=20

seed=TTATTGATTT

TTATTGATTTTTCTAAAAAA
TTATTAATTTTTCTAGGACA
TTATTGATTTGTCTAGGTCA
TTATTGATTTTTCTAGAACA
TTATTGATTTTTCTAGGACA
TTATTGATTTTTTAGGACA
TTATTGATTTTCTATAACAC
TATTGATTTTTCTAAAAAA
TTATTAATTTTTCTAGGACA
TTATTGATTTGTCTAGGTCA
TTATTGATTTTTCTACGACA
TTATTAATTTTTTTGGCCA
TTATTGATTTTTCTAGAACAA
TATTGATTTTTCTAGGTCA
TTATTGATTTGTCTAGGTCA
TTATTGATTTTTCTACGACA
TTATTGATTTTTCTAGAACAA
TATTGATTTTTCTAGAACA
TTATTGATTTTTCTAGGACT
TTATTGATTTTTCAGTGTAATCTGCTGTGATCGGGGACCTTATTGACATTTGGTACTGCAAAGAACCTCGGTTTGGGG
AAAGATGCAAAGATTTCAGCGAAGCCGATGCTCCTCGAGCAACTTTTGGAGGTATTTATTTGGCTTCCACTACACGAA

Nr of selected repeats 12 Similarity 0.816162

Consensus:

TTATTgATTTtTCTAgGaCA

>Cele-UNSB01_1:2402282-2402378 Satlength=97 Nr of Repeats=6 RepeatLength=12

seed=AAGCCTAAGC

AAGCCTAAGCAC
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT

AAGCCTAAGCCCTAGCATAAACCAAAGCCCTAGCCTA
AACCTAAGCCT

Nr of selected repeats 4 Similarity 0.839744

Consensus:

AAGCCTAAGCCT

>Cele-UNSB01_1:2461739-2462720 Satlength=982 Nr of Repeats=5 RepeatLength=175
seed=GATGCACCAT

GATGCACCATGAGGCTAAATTTAGTTTGACAGCCCATATCTCGGTGAATTCTGGTGCTATCAAAAACTTTTTGTATTTG
TATTTGTATTTATTACGATTGAAATCGTGATTAAAAATAAATAGTGAATAGACATGAATAAGTTTTTAACACTACAGAGCT
ATAGAAAATTATGCGCGCAATATTTTACCAGTTGACGGGTTTTTGACAACTGCAAAGAAAATCGAGATATGAGCTTCCA
AAGTTAGCTGGGCTACTAGTGATC

GATGCACCATGTCTTTGAAAGCCTATACTTCGGTTCATTTTCGTAGCTGTCAAAAACTTTTTAACAACACATCTATAGAA
ATCAACATGCTTAATATTTTCGTTCAGTTGACAGTTTTTTTGATAACTGCAATGAAATCCGAGATATGAGCTTTCAAAGTTG
AGAGACCTCACTCGGTT

GATGCACCATGTCTTTGACAGTCAATATCTCGGTTTTATTTTGTAGCTATCAAAAAATTTTCAACTACAAATCTATAGAA
AATTAATGTTCAACATTTTCTCAGTTGACAGTTTTTTTGATAACTGCAATGACATCCGAGATATGAGCTTTCAAAGTTG
AGAGACCTCACTCGGTT

GATGCACCATGTCTTTGACAGTCAATATCTCGGTTTTATTTTGTAGCTATCAAAAAATTTTCAACTACAAATCTATAGAA
AATTAATGTTCAACATTTTCTCAGTTGACAGTTTTTTTGATAACTGCAATGACATCCGAGATATAAGCTTTCAAAGTTG
AGTAAACCCATTTTGTA

GATGCACCATGAGGCTAAATCACTTTTGACCGCCCATATCTCGGTGAATTTTATAGCTATCAAAAACTTATAAATTACA
AACTATAGAAAATCATATGCGCAATATTTTAATATTTTGTAGTTGACGGGTTTTTGATAACTGCAAAGAAAATTGAG
AAATGAGCTTTCAAAGTTGAGTGTGCTACTTGTATC

Nr of selected repeats 3 Similarity 0.840552

Consensus:

GATGCACCATGTCTTTGAcAGtCaATAtcTCGGTtATTTtGTAGCTaTCAAAAAaTTTTcAAcTACAaATCTATAGaA
AATtAAATGtTcAAcATTTtTCAGTTGACAGTTTTTTGATAACTGCAATGAcATCCGAGATATgAGCTTTCAAAGTTG
AGAgACcTCAcTcgGtT

>Cele-UNSB01_1:2556234-2556523 Satlength=290 Nr of Repeats=10 RepeatLength=18
seed=GCCTAGGAAT

GCCTAGGAATACGAAAACCTTCCACCCATGCAAACCTGAGGGAGGTACCTCGTGACCTCCATTTTGGCATATATCCTAGCA
GCACGGAAACATCTTCAATCGCCTAGTACG

GACTAGGAATCCAATATG

GCCTAGGAATCCTATGTG

GCCTAGAAATCCAATATG

GCCTAGGAATGCTATGTGGCCTTGAACCCCATGTG

GCCTAGAAATCCAATATG

GCCTAGGAATCCCATGTG

GCCTAAGAATCCTATGTG

GCCTAGGAATCCCATGTG

GCCTAGAAATTCAATACA

Nr of selected repeats 8 Similarity 0.772487

Consensus:

GCCTAGgAATCCaATaTG

>Cele-UNSB01_1:2574462-2585290 Satlength=10829 Nr of Repeats=565
RepeatLength=19 seed=TACACGAAAA

TACACGAAAAATAGAATGT

TACACGAAAAATAGATTGT

TACACGAAAAATAGATTGT

TACACGAAAAATAGAATGT

TACACGAAAAATAGATTGT

TACACGAAAAAATAAGAAAAATAGATTGT

TACACGAAAAATAGAATGT

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TACACGAAAAATAGATTGT
TACACGAAAAATAGAATGT
TACACGAAAAATAGATTGT
TACACGAAAAATAGATTGT
TACACGAAAAATAGAATGT
TACACGAAAAATAGATTGT
TACACGAAAAATAGATTGT

Nr of selected repeats 539 Similarity 0.979754

Consensus:

TACACGAAAAATAGATTGT

>Cele-UNSB01_1:2599082-2599291 Satlength=210 Nr of Repeats=6 RepeatLength=35
seed=TTGCCGGAAT

TTGCCGGAATTAAAAATTTCTGGAAAATTGGCAAT
TTGCCGGAATGGAAAATTTTTTGGTAAATCGGCAAT
TTGCCGGAATTGAAAATTTTTTGGAAAATTGGCAA
TTGCCGGAATTAAAAATTTCTGGAAAATCGGCAAT
TTGCCGGAATTGAAAATTTTCTGGCAAATCGGTAAA
TTGCCGGAATTAAACATTTTTTGGTAAATCGGCCAT

Nr of selected repeats 5 Similarity 0.794286

Consensus:

TTGCCGGAATtgAAaaTTTtTGGnAAATcGGcaAt

>Cele-UNSB01_1:2691842-2691886 Satlength=45 Nr of Repeats=4 RepeatLength=11
seed=AAACTTGGGC

AAACTTGGGCC
AAACTTGGGTA
AAACTTGGGCT
AAACTTGGGCT

Nr of selected repeats 4 Similarity 0.770833

Consensus:

AAACTTGGGct

>Cele-UNSB01_1:2695367-2695539 Satlength=173 Nr of Repeats=4 RepeatLength=43
seed=TTGCCGATTT

TTGCCGATTTTCTGAATTGTTTCATTTCCGACAATATGACGAT
TTGCCGATTTGCCGAAATGTTTATTTCCGACAGTTGGCAGAT
TTGCCGATTTGCCGAAATATTTATTTCCGACAGTTGGCAGAT
TTGCCGATTTGCCGAAATGTTTGTTCGACAATTTGCCCAT

Nr of selected repeats 4 Similarity 0.798450

Consensus:

TTGCCGATTTgCCgGAAaTgTTtaTTTCCGACAaTtgGcagAT

>Cele-UNSB01_1:2780250-2780460 Satlength=211 Nr of Repeats=6 RepeatLength=35
seed=AATTTCAATT

AATTTCAATTCCGGCAATTTGCCGATTTGCCGGAA
AATTTCAATTTCCGGCAATTTGCCGATTTGCCGGAA
AATTTCAATTCTGGCAACTTTCCGATTTGCCGGAA

AATTTCAATTCCGGCAATTTGCGGATTTGCTGGAT
AATTTCAATTCCGGCAACTTTCCGATTTGCCGGAG
AATTTCAATTCTGGCAACTTTCCGATTTGCCGAAA
Nr of selected repeats 6 Similarity 0.860317
Consensus:
AATTTCAATTcGGCAAcTTgCCGATTTGCCGGAA
>Cele-UNSB01_1:2850958-2851167 Satlength=210 Nr of Repeats=5 RepeatLength=35
seed=GGAATTGAAA
GGAATTGAAAATTTCCGGCAAATTTGGCAAATTTGCCGTAATTGAACACTTCCGGCAAATTTGGCAACTTGTA
GGAATTGAAAATTTCCGGCAAATTCGGCAAATTTGCC
GGAATTGAAAATTTCCAGCGAATTCGGCAACTTGTA
GGAATTGAAAATTTCCGGCAAATTCGGCAAATTTGTC
GGAATTGAAAATTTCCGGCGAATTCGGCAAATTTGCC
Nr of selected repeats 3 Similarity 0.898413
Consensus:
GGAATTGAAAaTTtCCGGCaAATTCGGCAAATTTGcC
>Cele-UNSB01_1:2859395-2859671 Satlength=277 Nr of Repeats=5 RepeatLength=43
seed=TTGCCGATTT
TTGCCGATTTGCCAATTTGCCGGAAATTTACAATTTCCACTATT
TTGCCGGTTTCTCGATTTGCCGATATTTACAATTTCCACTATT
TTGCCGGTTTCCGATTTACCAGAAATTTACAATTTCCACTATT
TTGCCGGTTTCCGAT
TTGCCGATTTGTCCGAAGTTTTTAGACGAATTTTTACGACTGAAACTATTTGAAAAAAAAAAGTGCAGAACCACAACCTT
GCCGAAAATTTTCGGCAAGTTCGCCAACTTCGGCGATTTGCCATCTTGCCGAT
Nr of selected repeats 3 Similarity 0.834625
Consensus:
TTGCCGgTTTgCgATTTgCCgGAaATTTACAATtCCACTATT
>Cele-UNSB01_1:2881736-2881825 Satlength=90 Nr of Repeats=5 RepeatLength=12
seed=TAGGCTTAGG
TAGGCTTAGGCT
TAGGCTGAGGCG
TAGGCTTAGGCT
TAGGCCTAGGCT
TAGGCTTAGGCGTAAAGTCAGGCTTACGGTAGGCGCAGGGT
Nr of selected repeats 4 Similarity 0.833333
Consensus:
TAGGcttAGGct
>Cele-UNSB01_1:2886442-2886617 Satlength=176 Nr of Repeats=4 RepeatLength=35
seed=TTTGCCGATT
TTTGCCGATTTGCCAAAAAATTTTAATTTCCGGCAA
TTTGCCGACTTGTCAAAAAATTTTAATTTTAGCAC
TTTGCCGATTTGCCAAAAAATTTTAATTTCCGGCAATTTCCGACTTGTCAAAAAATTTTAATTTTCCAGCAA
TTTGCCGATTTGACGGAAAATTTTAATTTCCGGCAA
Nr of selected repeats 3 Similarity 0.733333
Consensus:
TTTGCCGAtTTGnCaAAAAAtTtTTAATTTccgCAa
>Cele-UNSB01_1:2899706-2899878 Satlength=173 Nr of Repeats=4 RepeatLength=43
seed=AAATCGGCAA
AAATCGGCAATCCGGCAAATTTGCGAAAAATGAAAATTTCCGGC
AAATCGGCAATCCGGCCAATTTGCAAAAAATGAAAATTTCCGGC
AAATCGGCAAACCGGCAAATTTGCGAAAAATGAAAATTTCCGGC
AAATCGGCAATTCGGCCAATTTGCAAAAAATGAAAATTTCCGGC
Nr of selected repeats 4 Similarity 0.906977
Consensus:

AAATCGGCAAtcCGGCaAATTGCaAAAAATGAAAATTcCCGGC
>Cele-UNSB01_1:3070958-3071149 Satlength=192 Nr of Repeats=5 RepeatLength=35
seed=TTGCCGGAAA

TTGCCGGAAATTTTCAATTCCGGCAATTTGCCATT
TTGCCGGAAATTTTCAATTCCGGCAAATTTGTTGTTTTTCCAAT
TTGCCGGAAATTTGTAATTCCGACATATTGCCGAT
TTGCCGGAAATTTGTAATTCCGACAAATTTGCCGAT
TTGCCGGAAATTTGTTATTCCGGCAATTTGTCGTTTTGCCAGT
Nr of selected repeats 3 Similarity 0.808642

Consensus:

TTGCCGGAAATTTgtAATTCCGaCAaATTGCCgAT

>Cele-UNSB01_1:3156606-3157000 Satlength=395 Nr of Repeats=8 RepeatLength=35
seed=CGATTTGCCG

CGATTTGCCGGAAGTTTCTGAAATTATTTTTAATAAGACGGAAACATTTAAAACGTGCCTTTTTGATTTTTTTTTTCA
TTTTCTTCAGATATTTTCATAAACTTACTTACTTTCAAGTCGGTTTTTTTTTGTCGGTTTTCCGGAAATTTTCATTTCC
GGCAAACGTG

CGATTTGCCGGAAATATTCATTTTCTGCAAATTGC
CGATTTTCCGGAAATTTTCATTTCCGGCAAACGTG
CGATTTGCCGGAAATATTCATTTTCTGCAAATTGC
CGATTTTCCGGAAATTTTCATTTCCGGCAAACGTG
CGATTTGCCGGAAATATTCATTTTCTGCAAATTGC
CGATTTTCCGGAAATTTTCATTTCCGGCAAACGTG
CGATTTGCCGATTTGC

Nr of selected repeats 6 Similarity 0.862857

Consensus:

CGATTTgCCGGAAATaTTCATTTcCgGCAAACtGc

>Cele-UNSB01_1:3158079-3158367 Satlength=289 Nr of Repeats=21 RepeatLength=12
seed=CTAAGCCTAA

CTAAGCCTAATTCTAAGG
CTATGCCTAAAC
CTAAGCCTAGAC
CTAAGCCTAACA
CTAAGCCTAAAC
CTAAGCCTAAGC
CTAAGCCTAAGC
CTAAGCCTAAGC
CTAAACCTAAACCTGAGT
CTAAGCCTAAGA
CTAAGCCTAAGCCTGAGC
CTAGGCCTAAGT
CTAAGCCTAAGC
CTCAGCCTAAGCCAAAGACTACGCG
TAAGCCTAAGC
CTAAGTCTAATC
CTAAGCCTAAGC
CTAAGCATAAGC
CTAAACCTAAGC
CTAAGCCTAAGT
CTGAGCCTAAGCCAAAGC
CAAAGCCTAAAC

Nr of selected repeats 15 Similarity 0.766138

Consensus:

CTAAGCCTAAgC

>Cele-UNSB01_1:3159205-3159335 Satlength=131 Nr of Repeats=4 RepeatLength=26
seed=GGCAGGCGTC

GGCAGGCGTCAAGCAGGCAGGTTTCA
GGCAGGCGTCAAGCAGGCAGGTTTTA
GGCAGGCGTCAAGCAGGCAGGTTTCT
GGCAGGCGTCCGGCAAGCAAAATTCAAGCAGGCGTAAGGCGGGTAGGTTTCA

Nr of selected repeats 3 Similarity 0.931624

Consensus:

GGCAGGCGTCAAGCAGGCAGGTTTca

>Cele-UNSB01_1:3213789-3217715 Satlength=3927 Nr of Repeats=151 RepeatLength=26
seed=CAGAGTCACT

CAGAGTCACTAAATTTGGTGAACGGT
CAGAGTCACTAAATTTGGTGAACGGC
CAGAGTCACTATTTTTGGGGAACGGC
CAGAGTCACTATTTTTGGGGAACGGC
CAGAGTCACTATTTTTGGTGAACGGC
CAGAGTCACTATTTTTGGGGAACGGC
CAGAGTCACTATTTTTGGGGAACGGC
CAGAGTCACTATTTTTGGTGAACGGT
CAGAGTCACTAAATTTGGTGAACGGC
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CAGAGTCACTAAATTTGGTGAACGGC
CAGAGTCACTATTTTTGGGGAACGGC
CAGAGTCACTATTTTTGGGGAACGGC
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CAGAGTCACTAAATTTGGTGAACGGC
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CAGAGTCACTATTTTTGGGGAACGGC

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CAGAGTCACTATTTTTGGGGAACGAC
CAGAGTCACTATTTTTGGTGAACGGC
CAGAGTCACTATTTTTGGGGAACGAC
CAGAGTCACTATTTTTGGTGAACGGC

Nr of selected repeats 151 Similarity 0.930474
Consensus:

CTAAGTCTAAGT
CTAAGTCTAATT

Nr of selected repeats 69 Similarity 0.908497

Consensus:

CTAAGtCTAAGt

>Cele-UNSB01_1:3325616-3325694 Satlength=79 Nr of Repeats=6 RepeatLength=12

seed=AGGCTTAGGC

AGGCTTAGGCTT

AGGCTTAGTCTTCAACCT

AGGCTTAGGCTT

AGGCTCAGGCTT

AGGCTCAGGCTT

AGGCTTAGGCTC

Nr of selected repeats 5 Similarity 0.888889

Consensus:

AGGCTtAGGCTt

>Cele-UNSB01_1:3430435-3430513 Satlength=79 Nr of Repeats=6 RepeatLength=12

seed=GGCTTAGGCT

GGCTTAGGCTCA

GGCTTAGGCTTC

GGCTTAGGCTTA

GGCTTAGGCTTAAGCTCA

GGCTTTGGCTTA

GGCTCAGGCTTT

Nr of selected repeats 5 Similarity 0.788889

Consensus:

GGCTtaGGCTta

>Cele-UNSB01_1:3435421-3440265 Satlength=4845 Nr of Repeats=323 RepeatLength=15

seed=CTCACCACGA

CTCACCACGATGGGT

CTCACCACGAAGGGTT

TCACCACGAAAGGT

CTCGCCACGATGGGT

CTCACCACGAAGTGT

CTCACCACGAAAGGT

CTCGCCACGAAAGGT

CTCGCCACGATGGGT
CTCACCACGAAAGGT
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CTCACCACGAAAGGC
CTCACCACGATCGGT

Nr of selected repeats 294 Similarity 0.881418

Consensus:

CTCACCACGAngGGT

>Cele-UNSB01_1:3453387-3453600 Satlength=214 Nr of Repeats=5 RepeatLength=32

seed=AATTCAAATT

AATTCAAATTTTCAAAAATAATATATGCGGGA

AATTCAAATTGTCAAGAATAATTTAGGTGGAA

AATTTAAATTTCTCTCAGAAAAAAGCTTTGGCAGGAAATTAGATTTTTTTTCAGAACTTTTTTCAGAAAAATATATGGC
GTGG

AATTCAAATTTTCTCTGTAAAAATTTTGGTTGA

AATTCAAATTATCTTTAACAATGTTTTGGCGGGA

Nr of selected repeats 3 Similarity 0.602694

Consensus:

AATTCAAATTTtTCaagaAtAATtTagGtgGaa

>Cele-UNSB01_1:3471234-3471484 Satlength=251 Nr of Repeats=6 RepeatLength=43

seed=TTGAAAATTT

TTGAAAATTTTCCGACAAAACCGGCAACTTGCCGGAA

TTGAAAATTTTCTAAAAATCGGCAAACCGGCAACTTGCCGGAA

TTGAAAATTTTTCGGCAAATCGACAATCCGGCAAATTGTCGGAA

TTGAAAATTTTCTAAAAATTTGGCAAACCTGGCAAATTGGCGGAA

TTGAAAATTTTCCGGCAAATCAGCAAATCGGCAAATTGGCGGAA

TTGAAAATTTTCCGGCAAATCGGCAAATCGGCAAATTGGCGGAA

Nr of selected repeats 5 Similarity 0.810853

Consensus:

TTGAAAATTTtCggcAAATcggCAAaccGGCAAaTTGgCGGAA

>Cele-UNSB01_1:3474380-3475480 Satlength=1101 Nr of Repeats=54 RepeatLength=20

seed=CTAGGCAGAC

CTAGGCAGACCTAGCCTACT

CTAGGCAGACCTAGCCTACT

CTAGGCAGACCTAGCCTACT

CTAGGCAGACCCAGTCCACC

CTAGGCAGACCCAGTCCACCCTAGGCAGGGCTAGCCTTCC

CTAGGCAGACCTAGCCTACC

CTAGGCAGACCTGGCCCACC

CTAGGCAGACCTAGCCTACT

CTAGGCAGACCTAGCCTGCT

CTAGGCAGACCTAGCCTGCC

CTAGGCAGACCCAGTCTACC

CTAGGCAGACCTAGCCTTCC

CTAGGCAGACCTAGCCTTCC

CTAGGCTGACCTGGCCTTTC

CTAGGCAGACCTAGCCTACC

CTAGGCAGACCTAGCCTACT

CTAGGCAGACCTAGTCTACC

CTAGGCAGACCTAGCCTACT

CTAGGCAGACCTAGCCTACT

CTAGGCAGACCTAGCCTACT

CTAGGCAGACCCAGTCCACC

CTAGGCAGGCTAGCCTTCC

CTAGGCAGACCTAGCCTACC

CTAGGCAGACCTGGCCCACC

CTAGACAGACCTAGCCTACT

CTAGGCAAACCTAGCCTACT

CTAGGAAGACCTAGTCCACC

CTAGGCAGACCTAGCATTCC

CTAGGCAGACCTAGCCTTCC

CTAGGCAGACCTGGCCTTTC

CTAGGCAGACCTAGCCTACC

CTAGGCAGACCTAGCCTACC

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CTAGGCAGACCTAGCATTCC
CTAGGCAGACCTAGCCTTCC
CTAGGCAGACCTGGCCTTTC
CTAGGCAGACCTAGCCTACC
CTAGGCAGACCTAGCCTACC
CTAGGCAGACCTAGCCTACC
CTAGGCAGACCTAGCCTACC
CTAGGCAGACCTGGCCTACC

Nr of selected repeats 53 Similarity 0.846734

Consensus:

CTAGGCAGACCTAGCCTaCc

>Cele-UNSB01_1:3474383-3476103 Satlength=1721 Nr of Repeats=83 RepeatLength=20
seed=GGCAGACCTA

GGCAGACCTAGCCTACTCTA
GGCAGACCTAGCCTACTCTA
GGCAGACCTAGCCTACTCTA
GGCAGACCCAGTCCACCCTA
GGCAGACCCAGTCCACCCTAGGCAGGGCTAGCCTTCCCTA
GGCAGACCTAGCCTACCCTA
GGCAGACCTGGCCCACCCTA
GGCAGACCTAGCCTACTCTA
GGCAGACCTAGCCTGCTCTA
GGCAGACCTAGCCTGCCCTA
GGCAGACCCAGTCTACCCTA
GGCAGACCTAGCCTTCCCTA
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GGCAGACCTAGCCTACTCTA
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GGCAGACCTAGCCTACTCTA
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GGCAGACCCAGTCCACCCTA
GGCAGGCCTAGCCTTCCCTA
GGCAGACCTAGCCTACCCTA
GGCAGACCTGGCCCACCCTA
GACAGACCTAGCCTACTCTA
GGCAAACCTAGCCTACTCTA
GGAAGACCTAGTCCACCCTA
GGCAGACCTAGCATTCCCTA
GGCAGACCTAGCCTTCCCTA
GGCAGACCTGGCCTTTCCTA

Nr of selected repeats 80 Similarity 0.844789

Consensus:

GGCAGACCTAGCCtACcCTa

>Cele-UNSB01_1:3489580-3490945 Satlength=1366 Nr of Repeats=56 RepeatLength=35
seed=TTTCGGCAAT

TTTCGGCAATTGCCGGTATCGTGAAT
TTTCGGCAATTTTCGGCAACTGCCGGTATCGTGAAT
TTTCGGCAATTTTCGGCAATTGCCGGTTTTGTGAAT
TTTCGGCAATTTTCGGCAACTGCCGGTATCGTGAAT
TTTCGGCAATTTTCGATAATTGCCAGTTCTGTAAAA
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TTCCGGCAATTTTCGGCAATTGCCGGTTTTGTGAAT
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TTGCGGCAATTTTCAGCAATTGCCGGTTTCATGATT
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TTTCGACAATTTTCGGCAATTGCCGGTTTTCTGAAT
TTCCGGCAATTTTCGGCAATTGCCGGTTTTGTGAAT
TTTCGGCAATTTTGGCAATTGCCGGTTTTTTGAAT
TTTCGGCAATTTTCGATAATTGCCAGTTCTGTAAAA
TTCCGGCAATTTTCGCAATTGCCGGTTTTCTAAATTTTCTGCAG

Nr of selected repeats 35 Similarity 0.808371

Consensus:

TTtCGGCAATTTcggCAATTGCCGGTTTTcnTGAaT

>Cele-UNSB01_1:3506179-3506592 Satlength=414 Nr of Repeats=8 RepeatLength=35
seed=TCCGGCAAAT

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TCCGGCAAATCGACAGA
CCGGCAAATTTGCCGAATTTGCCTGAAAAACGGCAAAAATGTTTCAGCAAATTATGGATTGCACTTTTTTTTTTTTTGGAA
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CTAAAACTTCTGTTTTTTTTTTTTTCAAAT

AAAAAATAGATTGACATACC
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Nr of selected repeats 115 Similarity 0.971320

Consensus:

AAAAAATAGATTGACATACC

>Cele-UNSB01_1:3600639-3600909 Satlength=271 Nr of Repeats=6 RepeatLength=45
seed=CTGAATCTTC

CTGAATCTTCATCTCCAAAGGATCACAAGGATCCTCCTTTATGAT
CTGAATCTTCAGCTCCAAAGGATCACAAGGATCCTCCTTTATGAT
CTGAATCTTCAGCTCCAAAGGATCACAAGGATCCTCCTTTATGAT
CTGAATCTTCAGCTCCAAAGGATCACAAGGATCCTCCTTTATGAT
CTGAATCTTCAGCTCCAAAGGATCACAAGGATCCTCCTTTATGAT
CTGAATCTTCAGCTCCAAAGGATCACAAGGATCCTCCTTTATGAT
CTGAATCTTCAGCTCCAAAGGATCACAAGGATCCTCCTTTATGAT

Nr of selected repeats 6 Similarity 0.990123

Consensus:

CTGAATCTTCAGCTCCAAAGGATCACAAGGATCCTCCTTTATGAT

>Cele-UNSB01_1:3650776-3650949 Satlength=174 Nr of Repeats=5 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATGTTCAATTCCGACAATTTGCCGG
TTTGCCGGAAAATTTAATTCCAGCAATTTGCCGA
TTTGCCGGAAATTTCAAATCCGGCAATTTGCCGA
TTTGCCGGAAATGTTCAATTCCGACAATTTGCCGG
TTTGCCGGAAAATTTCAAATCCGGCAATTTACCGA

Nr of selected repeats 3 Similarity 0.822222

Consensus:

TTTGCCGGAAAtgTTcAATTCcgaCAATTTgCCGg

>Cele-UNSB01_1:3711978-3718275 Satlength=6298 Nr of Repeats=242 RepeatLength=26
seed=ATGGTTAGAG

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Nr of selected repeats 238 Similarity 0.970067

Consensus:

ATGGTTAGAGTCATATTTTTAGGTGA

>Cele-UNSB01_1:3764869-3765030 Satlength=162 Nr of Repeats=5 RepeatLength=14

seed=TTTTTGTAGA

TTTTTGTAGATCCCATTTTCATAGATTCCCCA

TTTTGTAGAACGTC

TTTTCGTAGATCTACTTTTCGTGGAACCTCTTTTCATTTAACCTCTTTTCGTAGAACCTTTTTCGTAAGTCCCCTTCAT
AGATCATC

TTTTTGTAGATACT

TTTTTGTAGATCAC

Nr of selected repeats 3 Similarity 0.588235

Consensus:

tTTTTGTAGAtACn

>Cele-UNSB01_1:3798271-3798674 Satlength=404 Nr of Repeats=9 RepeatLength=45

seed=TCTGATCCTT

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TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG

TCTGATACTTCAGCTCCAAAGGATCACGAGGCTCTTCCTGATGT

TCTGATCCTTCAGCTCCGAAGGATCACATGGGCATCTTCTGATGA

TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCACCTGATGG

TCTGATACTTCAGCTCCAAAGGATCACGAGGCTCTTCCTGATGT

TCTGATCCTTCAGCTCCGAAGGATCACATGGGCACCTTCTGATGT

TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGT

TCTGATCCTTCAGCTCCGAAGGATCACATGGGCACCTTCTGATGA

Nr of selected repeats 7 Similarity 0.825044

Consensus:

TCTGATCCTTCAGcTccGAAGGATCacAtGGGtACCTtCTGATGn

>Cele-UNSB01_1:3799094-3799407 Satlength=314 Nr of Repeats=7 RepeatLength=45

seed=CTGAAGGATC

CTGAAGGATCAGAACATCAGAAGGTGCCCATGTGATCCTTCGGAG

CTGAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAG

CTGAAGTATCAGACCATCAGGTGGTACCCTTACGATCCTTCTTAT

CTGAAGGATCAGATCATCAGAAGATGCCCATGTGATCCTTCGGAG

CTGAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAG

CTGAAGTATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTAT

CTGAAGGATCAGAACATCAGAAGGTACCCATGTGATCCTTCGGAG

Nr of selected repeats 5 Similarity 0.792593

Consensus:

CTGAAGgATCAGAnCATCAGaaGgTaCCCaTgtGATCCTTCggAg
>Cele-UNSB01_1:3815334-3818659 Satlength=3326 Nr of Repeats=133 RepeatLength=25
seed=TTTACTCTCT
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TTTACTCTCTGGCTTCACCAAATAT
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TTTACTCTCTGGCTTCACCAAATAA
TTTACTCTCTCGCTTCACAGTATAT
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Nr of selected repeats 133 Similarity 0.898680

Consensus:

TTTACTCTCTGGCTTCACcaaATAt

>Cele-UNSB01_1:3888641-3889727 Satlength=1087 Nr of Repeats=26 RepeatLength=34
seed=TGCCGGAATT

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TGTCGGAATTGAAATTTCCAGCAAATCGGCAAAT
TGTCGGAATTGAAATTTCCGGCAAATCGACAAAT
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TGCCGGAATTGAAATTTTCATGCAAATCGGCAAATTGTGGGAATTTAAATTTCCAGCAATTGGGCAAAT
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TGCCGGAATTGAAATTTCTGACAAATCGGCAAAC
TGCCGGAATTGAGATTTTGGCAAATCGGCAAAT

Nr of selected repeats 16 Similarity 0.878105

Consensus:

TGCCGGAATTgAAATTTCCaGcAAATCGGCAAAT

>Cele-UNSB01_1:4033028-4033133 Satlength=106 Nr of Repeats=7 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

Nr of selected repeats 7 Similarity 0.949206

Consensus:

TCGTGGTGAGACCCT

>Cele-UNSB01_1:4033525-4033725 Satlength=201 Nr of Repeats=6 RepeatLength=40

seed=TTTCTAGAAA

TTTCTAGAAAATTCGAGAAAATTCGGGAATGGTCCAGAAT

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TTCTAGAAAGTTCTGGAATGGTCCAGAAT

TTTCTAGAAAATTCGGGAAAATCTGGAATATTCAGAAC

TTTCTAGAAAATTCGAGAAAATGTCTGCAATGTTCCAGAAG

TTTCTAGAAAATTCGAGAAAATTCGGGAATGGTCCAGAAT

Nr of selected repeats 4 Similarity 0.816667

Consensus:

TTTCTAGAAAATTCGaGAAAATTCcGgAATggTCCAGAAT

>Cele-UNSB01_1:4042754-4055380 Satlength=12627 Nr of Repeats=214

RepeatLength=59 seed=AAAACCCAGTG

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AAAACCAGTGAAGTCTTGAAATTTCCATATTTCCATAATTTCAGTTTTAAAAAATTTG
Nr of selected repeats 214 Similarity 0.852508

Consensus :

AAAACCAGTGCACATTTgAAATTTtataTTCTCCAtAaTTcTCgGTTTTAAAAtATTTTg

>Cele-UNSB01_1:4183555-4184714 Satlength=1160 Nr of Repeats=5 RepeatLength=223
seed=TTTCAGAATT

TTTCAGAATTTTAAATCGGCAAATTTGTACGCATCCTATGAATGTTCTACATCTATTTTAAAAATAAGCAAGT
TTTATGAAAATATCTAAAGAATACGGGAAGCGGCAAACCGGCATCTTGCCAAAAATGAAAATTTCCGGCAAACCGGCAA
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ATATCTGGCTTCAAACTAACTTTTTTAAAAATCCCCGTAGCCATTTTGTGCAAATTTTGTGCTC

TTTCAGAATTTAAAAACGGCATTCCAAAAACTTTTCAACCGCCAAGTTCAAGCAAAAAAGTAAACTTCAGTCATAACC
TTTCAGAGCAAACCTTTGAAATGAATGAAATAGACCATTTATTTGCAAAATTAGTAGATTTTCCAATTTTAAAAATTA
ATATCTGGCTTCTAAATAACTTTTTTAAAAATCCCCGTAGCCATTTTGTGCAAATTTTGTGCTC

Nr of selected repeats 4 Similarity 0.971101

Consensus :

TTTCAGAATTTAAAAACGgCATTCCAAAACTtTCAcAACCGCCAAGtTCAAGCAAAAAAGTAAACTTCAGTCATACC
TTTCAGAGCAAACCTTTGAAATTGAATGAAATAgAcATTTATTTGCAAAATTAGTAGATTTTCCAATTTTTAAAAATTA
ATATCTGGCTTCaAAaTAACTTTTTGAAAATCCCCGTAGCCATTTTGTGCAAAATTTGTGCTC

>Cele-UNSB01_1:4232491-4233003 Satlength=513 Nr of Repeats=13 RepeatLength=39
seed=TATTTTAAAT

TATTTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACC
TATTTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACT
TATTTTAAATTTGACCTACTTAAAAAGTAGGTCATGACC
TATTTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACC
TATTTTAAATTTAACCTACTTAAAAAGTAGGTCACGACC
TATTTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACT
TATTTTAAATTTGACCTACTTAAAAAGTAGGTCATGACC
TATTTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACC
TATTTTAAATTTAACCTACTTAAAAAGTAGGTCACGACC
TATTTTAAATTTGACCTACTTAAAAACTAGGTCATGGCC
TATTTTAAATTTGACCTACTTAAAAAGTAGGTCATGACC
TATTTTAAATTTGACCTACTTAAAAACTAGGTCATGACC
TATTTTAAATTTGACCTACCTAAAAAGTAGGTCATGACT

Nr of selected repeats 8 Similarity 0.954823

Consensus:

TATTTTAAATTTGgCCTACTTAAAAAGTAGGTCATGACc

>Cele-UNSB01_1:4250268-4250328 Satlength=61 Nr of Repeats=4 RepeatLength=15

seed=TTTCCGGATC

TTTCCGGATCTACCA
TTTCCGGATCTACGT
TTTCCGGATCTACGT
TTTCCGGATCTACGT

Nr of selected repeats 4 Similarity 0.911111

Consensus:

TTTCCGGATCTACgt

>Cele-UNSB01_1:4250510-4250645 Satlength=136 Nr of Repeats=9 RepeatLength=15

seed=AGATCCGGAA

AGATCCGGAAAACGT
AGATCCGGAAAACGT
AGATCCGGAAAACGT
AGATCCGGAAAACGT
AGATCCGGAAAACGT
AGATCCGGAAAACGT
AGATCCGGAAAACGT
AGATCCGGAAAACGT
AGATCCGGAAAACGT

Nr of selected repeats 9 Similarity 1.000000

Consensus:

AGATCCGGAAAACGT

>Cele-UNSB01_1:4344690-4345849 Satlength=1160 Nr of Repeats=6 RepeatLength=226

seed=ACAAGAAGCT

ACAAGAAGCTTTACAATATTCAGTAGGT

ACAAGAAGCTTCACGTAGTTACAGAAATAGTAGATTTTTAGCCCTACCTTTTAGAGCGTATTTTATTATTTAATGAAAA
CTACCACTTATAGGCAAAAATAGAGGATTTTCGTAATTTTGAAAATTCATAAATCTCTCAAAGTAATTTTTTTGCGAA
ATGTCTTTTCAGAACTTTGTAGTAAATTTTAAGCTCTTTTAGAATATATTAACAATATTCAGTAGGT
ACAAGAAGCTTCACGTAGTTACAGAAATAGTACATTTTTAGCCCTACCTTTTAGCGCGTATTTTATTATTTAATGAAAA
CTACCACTTATAGGCAAAAATAAATGGATTTTCCAACTTTGAAAATTCATAAATCTCTCAAAGTAACCTTTTTTTGAA
ATGTCTTTTAGAACTTTGTAGTAAATTTTATGCTCTTTTAGAATATATTAACATTTATTCAGTAGGT

ACAAGAAGCTTCACGTAGTTACAGAAATTGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTAATTAATGAAAA
CTACCACTTATAGGCAAAATAGAGGGATTTTCGTAATTTTGAAAATTCATAAATCTCTTCAAAGTAATTTTTTTGCGAA
ATGTCTTTTCAGAACTTTGTAGTAAATTTTAAGCTCTTTTAGAATATATTAACAATATTCAGTAGGT
ACAAGAAGCTTCACGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTAATTAATGAAAA
CTACCACTTATAGGCAAAATAGAGGGATTTTCGTAATTTTGAAAATTCATAAATCTCTTCAAAGTAATTTTTTTGCGAA
ATGTCTTTTCAGAACTTTGTAGTAAATTTTAAGCTCTTTTAGAATATATTAACAATATTCAGTAGGT
ACAAGAAGCTTCACGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTAATTAATGAAAA
CTACCACTTATAGGCAAAATAGATGGATTTTCCAAAATTTGAAAATTCATAAATCTCTTCACAGTAACTTTTTTGAA
ATGTCTTTTCAGAAACCATGGAGTAAATTTTAAGCTCTTTCAGAATATATTAACAATATTCAGTAGGT

Nr of selected repeats 5 Similarity 0.915789

Consensus:

ACAAGAAGCTTCACGTAGTTACAGAAATaGTAcATTTTcAGCCCTACCTTTTAGTgGCgTATTTTATTAtTTAATGAAAA
CTACCAcTTATAGGCAAAATAgAgGGATTTTcGtAAtTTTGAAAATTCATAAATCTCTTCAaAGTAATTTTTTTGcgAA
ATGTCTTTcAGAAActtTgTAgTAAATTTTAaGCTCTTTtAGAATATATTAACAaTATTCcAGTAGGT

>Cele-UNSB01_1:4346155-4359862 Satlength=13708 Nr of Repeats=146

RepeatLength=94 seed=TCAAAATCTT

TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCAATGCTCTTTGTAGACAAAATCAATGGGAAAATGATCAATTTTC
TGGAGGCAGTAAATC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCTCTTTGTAGACAAAATCAATGGGAAAATTTGTCAATTTTC
TGAAGGCAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGAAAAATCAATGGGAAAATCATCAATTTTC
TGAAGGCAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCTCTTTGTAGACAAAATCAATGGGAAAATCATCAATTTTC
TGAAGGCAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCTCTTTGTAGACAAAATCAATGGGAAAATCATAAATTTTC
TGAAGGCAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCTCTTTGTAGACAAAATCAATGGGAAAATCATAAATTTTC
TGAAGGCAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAAATCAATGGGAAAATCATCAATTTTC
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TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAAATCAATGGGAAAATCATCAATTTTC
TGAAGGAAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCTCTTTGTAGACAAAATCAATGGGAAAATCATAAATTTTC
TGAAGGCAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAAATCAATGGGAAAATCATCAATTTTC
TGAAGGAAGTAATTC
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TGAAGGCAGTAATTC
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TGAAGGAAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCTCTTTGTAGACAAAATCAATGGGAAAATCATAAATTTTC
TGAAGGCAGTAATTC
TCAAAATCTTCTGTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAAATCAATGGGAAAATCATCAATTTTC
TGAAGGAAGTAATTC

CTTCAAGAGCTCAGTGTTATTTATGACATGCCAACTTCTACAATTGACCTGAAACATGCTCCAAGGAATCGAAGACAACT
TGAACAGCCTTCCAGCTGAAGAATCTGATAAGATCCGAGAGAAGATTAACGATCTGAGAAGAAGGAAACAAGAAAGCGA
TCAAGCTGAAGCTCTT

Nr of selected repeats 4 Similarity 0.868455

Consensus:

CTTCAAGAGCTCAGTGTTATTTaTGACATGCCAAccTCgACaaTtGACcTGAACATGcTcCAAGGAaTcGAAGACAACT
TgAACAGcCTtCCAgCTGAAGAAAtCTGATaAGATCCGaGAGAAGaTtAAcGAtCTGAGAAGAAGgAAaCAAGAAAGcGA
tCaaGCTGAAGCTCTt

>Cele-UNSB01_1:4530676-4530829 Satlength=154 Nr of Repeats=8 RepeatLength=19

seed=TTTTTCGTGT

TTTTTCGTGTAAACAATCTA

TTTTTCGTGTAAACAATCTA

TTTTTCGTGTAAACAATCTA

TTTTTCGTGTAAACAATTAA

TTTTTCGTGTAAACAATCAA

TTTTTCGTGTAAACAATCTA

TTTTTCGTGTAAACAATCTA

TTTTTCGTGTAAACAATCTAT

Nr of selected repeats 7 Similarity 0.900000

Consensus:

TTTTTCGTGTAAACAATCTA

>Cele-UNSB01_1:4605678-4635032 Satlength=29355 Nr of Repeats=1129

RepeatLength=26 seed=TTTTCTAAAA

TTTTCTAAAATCCGCCGAGTGCCAT

TTTTCTAAAATCCGCCGCAATGCCAT

TTTTTTTTTTA
TTTTTATTTTTA
TTTTTATTTTTG
TTTTTATTTTTA
TTTTTATTTGTG
TTTTTATTTTTA
TTTTTATTTTTTATTCTCA
TTTTTATTTTTTATTTTTA

Nr of selected repeats 26 Similarity 0.967179

Consensus:

TTTTTATTTTTA

>Cele-UNSB01_1:4669638-4670196 Satlength=559 Nr of Repeats=41 RepeatLength=12

seed=TTTTTATTTTT

TTTTTATTTTTA
TTTTTATTTTTT
TTTTTATTTTTATT
TTTTTTTTTTA
TTTTTATTTTTA
TTTTTATTTTTTTTT
TTTTTTTTTTTATTTTTTTTTTT
TTTTTTTTTTA
TTTTTATTTTTA
TTTTTATTTTTG
TTTTTATTTTTA
TTTTTATTTGTG
TTTTTATTTTTA

TTTTTATTTTTATTCTCA
TTTTTATTTTTA
TTTTTATTTTTATTTTTATTATTATTATTATTATT
TATTATTTTTTAA
TTTTAATTTTAATTTCAA
TTTTAATTTTAATTTCAA
TTTTAATTTTAATTTCAA
TTTTTATTTTTA
TTTTTATTTTTAT
TTTTTATTTTATTTTTA

Nr of selected repeats 27 Similarity 0.968344

Consensus:

TTTTTATTTTTA

>Cele-UNSB01_1:4669638-4670946 Satlength=1309 Nr of Repeats=43 RepeatLength=12
seed=TTTTTATTTTT

TTTTTATTTTTA
TTTTTATTTTTATT
TTTTTTTTTTA
TTTTTATTTTTA
TTTTTATTTTTTTTT
TTTTTTTTTTATTTTTTTTTTT
TTTTTTTTTTA
TTTTTATTTTTA
TTTTTATTTTTG
TTTTTATTTTTA
TTTTTATTTGTG
TTTTTATTTTTA
TTTTTATTTTTATTCTCA
TTTTTATTTTTA
TTTTTATTTTTATTTTTATTATTATTATTATTATT
TATTATTTTTTAA
TTTTAATTTTAATTTCAA
TTTTAATTTTAATTTCAA
TTTTAATTTTAATTTCAA
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TTTTTATTTTTAT
TTTTTATTTAT
TTTTTATTTTTAT

TTTTTATTCTCATTTCCTACCAGAATATATTCAGAAATATATTCAGAAATATATTCAGAAATATACTC
CAAAATATATTCAGAGTATATTCAGAAATATATTCAGAAATTTATTCAGAAATATATTCAGAAATATATTCAGAAATA
TATTCAGAAATATATTCAGAAATATATTCAGAAATTTATTTTTCAGAAATATATTCAGAAATATATTCAGAAATATATTCAGAAATATA
GAATATATTCAGAAATATATTCAGAAATATATTCAGAAATATATTCAGAAATATATTCAGAAATATATTCAGAAATATA
TTCCCTTATTGATCTTACGAAAACCTGAAACATGAAACTAGATTAGAAATGACCTATCTAACTGTTATACGGCTACAGTC
CATTTTTTAGCAGGCTTGGTTTCAGGGACCTGTCGTCCTCACACGAAGCTGGTTTTTGGCGCCTATATGGAAGCCCTGTC
TGCCTCATGCCTTTACCAATTTTCTATGAAATCTCCGGAGTTCGGTGTTCGACTGTTAATTATAAGTTTTATCATTTC
ATTAATTTTTTTGAAAATCAATTCATAAAACTTCAAGGTTTCAGGTCATTCTGGCAATAGGCACACCATTTTTTTTTATT
GGATAAAATAGAAAATAGTGTCTATGAGGTAATTTGAAATTTTAGAATCTGAAATTTTCAGACTCGATTCTTAAAATC
AATGAAATGACGGATCTTGTCAAGTTCGTCC

Nr of selected repeats 27 Similarity 0.968344

Consensus:

TTTTTATTTTTA

>Cele-UNSB01_1:4694849-4695647 Satlength=799 Nr of Repeats=20 RepeatLength=40
seed=CATTCCAGAA

CATTCCAGAAATTTTCTCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCTCGATTTTTCTAGAAAGTTCCTGGAG
CATTCCAGAAATTTTCTCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCCCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCTCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCCCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCTCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCCCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCCCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCTCGATTTTTCTAGAAAGTTCCTGGAA
CATTCCAGAAATTTTCCCGATTTTTCTAGAAAGTTCCTGGAA

Nr of selected repeats 18 Similarity 0.964052

Consensus:

CATTCCAGAAATTTTCTCGATTTTTCTAGAAAGTTCCTGGAA

>Cele-UNSB01_1:4695896-4696451 Satlength=556 Nr of Repeats=34 RepeatLength=15
seed=GGGTCTCACC

GGGTCTCACCACGAC
GGGTCTCACCACGGT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGATGGGTTTCGCCACGAT
GGGTCTCGCCACGACGGGTCTTATCACGGT
GGGTCTCGCCACGAT
GGGTCTCACCACGAT
GGGTCTTACCACGAT
GGGTCTCACCACGAC
GGGTCTCACCACGGT

GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCGCCACGACGGGTCTTATCACGGT
GGGTCTCACCACGGT
GGGTCTCACCACGGT
GGGTCTCGCCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGGT
GGGTGTACACCACGAT
GGGTCTCACCACGGT
GGGTCTCACCACGAT
GGGTATCACCACGAC
GGGTCTCACCACGAT
GGGTCTCACCACGAC
GGGTCTCACCACGGT
GGGTCTCGCCACGAC
GGGTCTCACCACGAT
GGGTCTCACCACGGT
GGGTCTCGCCACGAT
GGGTCTCACCACGAT
GGGCCTCACCACGAT
GGGTCTCACCACGAT

Nr of selected repeats 31 Similarity 0.896583

Consensus:

GGGTCTCACCACGaT

>Cele-UNSB01_1:5080040-5080117 Satlength=78 Nr of Repeats=5 RepeatLength=15

seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA

CGAAAAGGGGATCTG

CGAAAAGGGGAGATA

CGAAAAGGGGAGATA

CGAAAAGGGGAGCAA

Nr of selected repeats 4 Similarity 0.807407

Consensus:

CGAAAAGGGGAgata

>Cele-UNSB01_1:5080289-5080381 Satlength=93 Nr of Repeats=5 RepeatLength=15

seed=CTCCCCTTTT

CTCCCCTTTTTCGTTG

CTCCCCTTTTTCGTAT

CTCCCCTTTTTCGTAT

CTCCCCTTTTTCGCAGA

TCCCCTTTTTCGAGATCGCCTTTTTCGTTCTG

Nr of selected repeats 3 Similarity 0.847222

Consensus:

CTCCCCTTTTTCGTaT

>Cele-UNSB01_1:5082880-5082987 Satlength=108 Nr of Repeats=6 RepeatLength=15

seed=CTCCCCTTTT

CTCCCCTTTTTCGTTG

CTCCCCTTTTTCGTAT

CTCCCCTTTTTCGTAT

CTCCCCTTTTTCGTAT

CTCCCCTTTTTCGCAGA

TCCCCTTTTTCGAGATCGCCTTTTTCGTTCTG

Nr of selected repeats 4 Similarity 0.869792

Consensus:

CTCCCCTTTTCGTaT

>Cele-UNSB01_1:5266039-5266863 Satlength=825 Nr of Repeats=51 RepeatLength=15

seed=CGTGGTGAGA

CGTGGTGAGACCCAT

CGTGGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGGTGAGACCCAT

CGTGGTGAGACCTTT

CGTGTTGAGACCCAT

CGGGGTGAGACCTTT

CGTGGTGAGACCTTTTCGTGTTGAAACCTTT

CGTGGTGAGACCTTTTCGTGTTGAGGCCTTT

CGTGGTGAGACCCAT

CGTGGTGAGACCTTC

CGTGGTCAGAACTTT

CGTGTTGAGATCCAT

CGTGGTGAGACCTTC

CGTTGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGTTGAGACCCAT

CGGGGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGGTGAGACCCAT

CGTGGTGAGACCCAT

CGTGGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGGTGAGACCTTTTCGTGTTGAGGCCTTT

CGTGGTGAGACCCAT

CGTGGTGAGACCTTC

CGTGGTGAGAACTTT

CGTGTTGAGACCCAT

CGTGGTCAGACCCTCCGTTGTGAAACCTTT

CGTGGTGAGACCTTT

CGTGTTGAGACCCAT

CGGGGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGGTGAGACCTTC

CGTGGTGAGACCTTT

CGTGTTGAGACCCAT

CGTGGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGGTGAGACCCAC

CGTGGTGAGACCTTC

CGTGGTGAGACCTTT

CGTGTTGAGACCCAT

CGTGGTGAGACCTTC

CGTTGTGAGACCTTT

CGTGGTGAGACCTTT

CGTGGTGAGACCTTC

CGTGGTGAGACCTTT

CGTGTTGAGACCCAT

CGGGGTGAGACCTTT

Nr of selected repeats 47 Similarity 0.827485

Consensus:

CGTGTTGAGACCtT

>Cele-UNSB01_1:5273525-5290948 Satlength=17424 Nr of Repeats=599

RepeatLength=29 seed=TTGTAAGGAT

TTGTAAGGATTTCCCATTATGTCAATACA

TTGTAAGGATTTCCCAC TTTATCAATACA
TTGTAAGGATTTCCCAC TATGTCAATACA
TTGTAAGGATTTCCCAC TATGTCAATACA
TTGTAAGGATTTCCCAC TTTGTCAATACA
TTGTAAGGATTTCCCAC TTATGTCAATACA
TTGTAAGGATTTCCCAC TATGTCAATACA
TTGTAAGGATTTCCCAC TTATGTCAATACA
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TTGTAAGGATTTCCCAC TTTGTCAATACA
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TTGTAAGGATTTCCCAC ATATGTCAATACA
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TTGTAAGGATTTCCCT TATGTCAATACA
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TTGTAAGGATTTCCCACTTTGTCAATACA
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TTGTAAGGATTTCCCACTATGTCAATACA
TTGTAAGGATTTCCCACTTTGGTCAATACA

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TTGTAAGGATTTCCCATTGTCAATACA
TTGTAAGGATTTCCCATTATGTCAATACA
TTGTAAGGATTTCCCATTGTCAATACA
TTGTAAGGATTTCCCATTATGTCAATACA
TTGTAAGGATTTCCCATTGTCAATACA
TTGTAAGGATTTCCCATTATGTCAATACA
TTGTAAGGATTTCCCATTGTCAATACA

Nr of selected repeats 565 Similarity 0.955515

Consensus:

TTGTAAGGATTTCCCACaTaGTCAATACA

>Cele-UNSB01_1:5313372-5313447 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTTCGAGA

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTTCGtagc

>Cele-UNSB01_1:5700313-5700505 Satlength=193 Nr of Repeats=16 RepeatLength=12

seed=GAAATTTTTTT

GAAATTTTTTCC

GAAATTTTTTCT

GAAATTTTTTCC

GAAATTTTTTCC

Nr of selected repeats 16 Similarity 0.949074

Consensus:

GAAATTTTTTCC

>Cele-UNSB01_1:5758991-5759083 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTTCGAGA

TCCCCTTTTTCGAGA

TCCCCTTTTCGTTCTGC

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTcGcaga

>Cele-UNSB01_1:5777645-5778359 Satlength=715 Nr of Repeats=6 RepeatLength=119
seed=GCCACCTTTA

GCCACCTTTAACCTAATCCAAGCAGAGCAGGCCGTAGGCCTGCTAGGCGGTAGCGACACGCTCAAGCCCAACAGTCCG
GGATGAGGGTTCGAGGCCCTCTTACTCTTAGAACTTTAG
GCCACCTTTAACCTAATCCAAGCAGAGCAGGCCTGTAGGCCTGCTATGCGGTAGCGACACGCTCAGGCCCAATAGTCCG
GGATGAGGGCCGAGGCCCTCTTACTCTTAGAACTTTAG
GCCACCTTTAACCTAATCCAAGCAGAGCAGGCCTGTAGGCCTGCTATGCGGTAGCGACACGCTCAGGCCCAATAGTCCG
GGATGAGGGCCGAGGCCCTCTTACTCTTAGAACTTTAG
GCCACCTTTAACCTAATCCAAGCAGAGCAGGCCGTAGGCCTGCTATGCCGTAGCGACACGCTCAGGCCCAATAGTCCG
GGATGAGGGCCGAGGCCCTCTTACTCTTAGAACTTTAG
GCCACCTTTAACCTAATCCAAGCAGAGCAGGCCGTAGGCCTGCTATGCGGTAGCGACACGCTTAGGCCCAATAGTCCG
GGATGAGGGCCGAGGCCCTCTTACTCTTAGAACTTTAG

Nr of selected repeats 6 Similarity 0.967880

Consensus:

GCCACCTTTAACCTAATCCAAGCAGAGCAGGCcGTAGGCCTGCTATGCgGTAGCGACACGCTCAGGCCCAATAGTCCG
GGATGAGGGCCGAGGCCCTCTTACTCTTAGAACTTTAG

>Cele-UNSB01_1:6112428-6113232 Satlength=805 Nr of Repeats=18 RepeatLength=45
seed=TCTGATCCTT

TCTGATCCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT
TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTTCTGATGG
TCTGATCCTTTAGCTCCAAAGGATCACGAGGCTCTTCCTGATGT
TCTGTTCCCTTCAGCTCCGAAGGATCACAAGGGTACCTTCTGATGT
TCTGATCCTTCAGCTCCAAAGGATCACGACGCTCTTCCTGATGT
TCTGAACCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT
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TCTGAACCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT
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TCTGATCCTTCCGATCCGAAGGATCACATGGGTACCTTCTGATGA
TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG
TCTGATCCTTCAGCTCCAAAAGAACATGAGGCTCTGCCTGATGA
TCTGATCTTTCAGAGCCGAATGATCACATGGGTACCTCCTGATGT

Nr of selected repeats 12 Similarity 0.835690

Consensus:

TCTGATcCTTCAGaTccGAAGGATCacAaGGGTACCTtCTGATGt

>Cele-UNSB01_1:6114632-6114855 Satlength=224 Nr of Repeats=5 RepeatLength=45
seed=AAGGATCAGA

AAGGATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTATCTG
AAGGATCAGATCATCAGAAGGTACCCTATGTGATCCTTCGGAGCTG
AAGGTTTCAAGACATCAGGCAGAGCCTCATGTTCTTTTAGAGCTG
AAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCTA
AAGGATCAGACCATCAGAAGGTACCCTTACGATCCTTCTTATCTG

Nr of selected repeats 3 Similarity 0.841975

Consensus:

AAGGATCAGAcCATCAGaAGGTACCCTTacGATCCTTcttAtCTG

>Cele-UNSB01_1:6226496-6226583 Satlength=88 Nr of Repeats=5 RepeatLength=17
 seed=AGGTAGTCAA
 AGGTAGTCAAAGAGCATTTGA
 AGGTAGTCAATGAGCAA
 AGGTAGTCAATGAGCAA
 AGGTAGTCAATGAGCAA
 AGGTAGTCAATGAGA
 Nr of selected repeats 3 Similarity 1.000000
 Consensus:
 AGGTAGTCAATGAGCAA

>Cele-UNSB01_1:6651710-6652545 Satlength=836 Nr of Repeats=13 RepeatLength=30
 seed=TGGTGGAAGT
 TGGTGGAAGTGGATTTCGGCAGTGGAAATGC
 TGGTGGAAGTGGATTTCGGCAGTGGAAATGC
 TGGTGGAAGTGGATTTCGGCAGTGGAAATGC
 TGGTGGAAGTGGGTTTCGGCAGCGGAAATGC
 TGGTGGAAGTGGATTTCGGCGGTGGAAATGC
 TGGTGGAAGTGGATTTCGGCAGTGGAAATGC
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 TTTTATTTTATAGTGTGTACAATTGCCAGCAGCCTGGTCACTCTCGCGATTGTCCAGAAGAGCGGAAACCGCGTGA
 AGGCCGAAATGGATTCAACCGTGGGAAAGCTCTGGTTTCGGAGGAGGAAATGG
 Nr of selected repeats 11 Similarity 0.953131
 Consensus:
 TGGTGGAAGTGGATTTCGGCAGTGGAAATGC

>Cele-UNSB01_1:6785229-6785394 Satlength=166 Nr of Repeats=11 RepeatLength=15
 seed=GAGACCCATC
 GAGACCCATCGTGGC
 GAGACCCACCGTGGT
 GAGACCCATCGTGGC
 GAGACCCATCGTGGC
 GAGACCCATCGTGGC
 GAGACCCGTCGTGGC
 GAGACCCATCGTGGT
 GAGACCCATCGTGGC
 GAGACCCACCGTGGT
 GAGACCCGTCGTGGT
 GAGACCCGTCGTGGT
 Nr of selected repeats 11 Similarity 0.883636
 Consensus:
 GAGACCCaTCGTGGC

>Cele-UNSB01_1:6785543-6785983 Satlength=441 Nr of Repeats=11 RepeatLength=40
 seed=TTCTGGAATG
 TTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAA
 TTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAA
 TTCTGGAATGTTCCAGAACTTTCTAAAAAATCGAGAAAA

GAAGCCAGAGAGTAAATTATTATGT
GAAGCCAGAGAGTAAAATATACTGT
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GAAGCCAGAGAGTAAAAATATACTGT

Consensus :

CgAAAAGGGGAtCag

>Cele-UNSB01_1:7886332-7886407 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTAAGACCCA

TCGTGGTGAGACCCT

Nr of selected repeats 5 Similarity 0.911111

Consensus :

TCGTGGTgAGACCct

>Cele-UNSB01_1:7886430-7887346 Satlength=917 Nr of Repeats=26 RepeatLength=35

seed=GCGGGAAATT

GCGGGAAATTCAAATTTTCAGTAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTAAGGGAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTAAGTGAAAAAAAAATTTTGA

GCGGGAAATTCAAATTTTAAGTGAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTCAGTAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTAAGTGAAAAAAAAATTTTGG

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GCGGGAAATTCAAATTTTCAGTAAAAAAAAATTTTGG

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GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTAAGGGAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTTGG

GCGGGAAATTCAAATTTTCAGTGAAAACAATTTTGG

GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTTA

Nr of selected repeats 17 Similarity 0.870370

Consensus :

GCGGGAAATTCAAATTTTcAGtGAAAAAAaTTTTG

>Cele-UNSB01_1:7887436-7887916 Satlength=481 Nr of Repeats=13 RepeatLength=40

seed=TTTCTAGAAA

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TTTCTAGAAAATTCGAGAAATGTCTGCAATGTTCCAGAAG

TTTCTAGAAAATTCGAGAAATTCGGGAATGGACCAGAAT

TTTCTAGAAA

TTCTAGAAAGTTCTGGAATGGTCCAGAAT

TTTCTAGAAAATTCGGGAAAACCTCTGGAATATTCCAGAAC

TTTCTAGAAAATTCGAGAAATTCGGGAATGGTCCAGAAT

TTTCTAGAAAATTCGGGAAAACCTCTGGAATATTCCAGAAC

TTTCTAGAAAATTCGGGAAAAGTTCGGCAATGTTCTTGAAC

TTTCTAGAAAATTCGAGAAAATTCGGAAATGGTCCAGAAT
TTTCTAGAAAATTCGGGAAAACCTCTGGAATATTCCAGAAG
TTTCTAGAAAATTCGAGAAAAGTTCTGGAATGGTCCAGAAT
TTTCTAGAAAATTCGGAAAAATTCGGAATATTCCAGAAC
Nr of selected repeats 11 Similarity 0.818182

Consensus:

TTTCTAGAAAATTCGgGAAAAnTcTgGAATgtTCCAGAAAn

>Cele-UNSB01_1:7925712-7926382 Satlength=671 Nr of Repeats=39 RepeatLength=16

seed=AATTTTTCCG

AATTTTTCCGCCACGA

AATTTTTGCCGCGTCGA

AATTTTTCCGCGGCGA

AATTTTTCAGCAGCAA

ATTTTTCCGCGTCGA

AATTTTTCCGCAGCAA

AATTTTTCCGCCACG

AATTTTTGCCGCGTCGA

AATTTTTCCGCGGCGA

AATTTTTCAGCAGCAACATTTTTCCGCGGCGA

AATTTTTCCGCAGCAA

AATTTTTCCGCGTCGA

AATTTTTCCGCAGCAA

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AATTTTTCAGCAGCAA

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AATTTTTCAGCAGCAA

AATTTTTCCGCGGCGA

AATTTTTCCGCGACG

AATTTTTCCGCAGCAATTTTTCAGCAGCAA

AATTTTTCCGCGTCGA

AATTTTTCCGCGGCGA

AATTTTTCAGCAGCAA

AATTTTTCCGCGGCGA

AATTTTTCCGCAGCAA

AATTTTTCCGCGTCGA

AATTTTTCAGCAGCAA

AATTTTTCCGCGACGA

AATTTTTCAGCAGCAA

AATTTTTCCGTGTCGA

Nr of selected repeats 31 Similarity 0.813978

Consensus:

AATTTTTCCgCngCgA

>Cele-UNSB01_1:8014213-8014468 Satlength=256 Nr of Repeats=17 RepeatLength=15

seed=ACCCATCGTG

ACCCATCGTGGCGAG

ACCCATCGTGGCGAA
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAT
ACCCATCGTGGCCAG
ACCCATCGTGGTGAG
ACCCGTCGTGGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCACCGTGGTGAG
ACCCGTCGTGGTGAG
ACCCATCGTGGTAAG
ACCCATCGTGGTGAA
ACCCATCGTGGCGAG
ACCCACCGTGATGAG
ACCCGTCGTGGCGAG

Nr of selected repeats 17 Similarity 0.847712

Consensus:

ACCCATCGTGGtGAG

>Cele-UNSB01_1:8014573-8014958 Satlength=386 Nr of Repeats=11 RepeatLength=35
seed=GGGAAATTTA

GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGC
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGC
GGGAAATTTAAATTTTCTGAGAAAAATATTTTGGG
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGC
GGGAAATTTAAATTTTCTGAGAAAAATTTTTTGGC
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GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGC
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GGGAAATTTAAATTTTCTGAGAAAAATATTTTGGG
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGC
GGGAAATTTAAATTTTCTGAGAAAAATTTTTTGGC

Nr of selected repeats 11 Similarity 0.944589

Consensus:

GGGAAATTTAAATTTTCTGtGAAAAATATTTTGGC

>Cele-UNSB01_1:8015067-8016984 Satlength=1918 Nr of Repeats=48 RepeatLength=40
seed=GAATGTTCCA

GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTCCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAGTTCTG
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GAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAGTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAGTTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAGTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAGTCTG
GAATGTTCCAGAACTCCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAGTTCTG

AACAGAATTTTAAAAAATTTTCGAAAATGCCAAGTTCAAGCATTAAAAAGTGAATTTTCAGTCATACCTTGTAGACCACAA
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TTGCCATTTTGTAGCAAATTTTATGTTCTTTCAGAATTTGAA
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AACAGAATTTTAAAAAATTTTCGAAACCGCCAAGTTCAAGCAGAAAAAGTGAATTTTCAGTCATACCTTGTAGACCACAA
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TAGCCATTTTGTAGCAAATTTTATGTTCTTTCAGAATTTGAA

Nr of selected repeats 13 Similarity 0.975385

Consensus :

AACAGAATTTTAAAAAATTTTCGAAACCGCCAAGTTCAAGCAGaAAAAAGTGAATTTTCAGTCATACCTTGTAGACCACAA
TTTATATaCAAAATTAATAGATTTTCCAAACTTTGAAAATTAATTTCTGGCTTCAAACCTAACTTTTTTAGAAATTCCTCG
TtGCCATTTTGTAGCAAATTTTATGTTCTTTCAGAATTTGAA

>Cele-UNSB01_1:9977112-9977772 Satlength=661 Nr of Repeats=41 RepeatLength=15

seed=CACGATGGGT

CACGATGGGTCTCAC

CACGAAGGGTATCAC

CACGATGGGTCTCAC

CACGAAGGGTATCAC

CACGATGGGTCTCAC

CACGATGGGTCTCAC

CACGATGGGTCTCGT

CACGATGGGTCTCAC

CACGATGGGTCTCAC

CACGATGGGTCTCAG

CACGACGGGTCTCAC

CACGATGGGTCTCAC

CACAATGGGTCTCGT

CACGATGGGTCTCAC

CACGATGGGTCTCGT

CACGATAGGTCTCAC

CACGATGGGTCTAAC

CACGATGGGTCTCAC

CACGATGGGTCTCACCACGATGAGACTCAC

CACGACGGGTCTTAC

CACGATGGGTCTCAGCACAAACGGGTCTCAC
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CACAAATGGGTCTCGT
CACGATGGGTCTCAC
CACGATGGGTCTCGT
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CACGATGGGTCTCGT
CACGATAGGTCTCAC
CACGATGGGTCTAAC
CACGATGGGTCTCAC
CACGATGGGTCTCGTCACAATGGCTCTCAC
CACGACGGGTCTTAC

Nr of selected repeats 38 Similarity 0.852821

Consensus:

CACGATGGGTCTCac

>Cele-UNSB01_1:10089590-10089728 Satlength=139 Nr of Repeats=5 RepeatLength=37

seed=ATAATTTTTTC

ATAATTTTTTCAC

ATACTTTTTTCATAAT

ATAATTTTTTCTTGAGTAATGAGAGACTTTTTTCATAAT

ATAATTTTTTCTTGAGTAATGAGAGACTTTTTTCATAAT

ATAATTTTTTCTTGAGTAATGAGAGACTTTTTTCATAAT

Nr of selected repeats 3 Similarity 1.000000

Consensus:

ATAATTTTTTCTTGAGTAATGAGAGACTTTTTTCATAAT

>Cele-UNSB01_1:10295164-10303189 Satlength=8026 Nr of Repeats=319

RepeatLength=25 seed=TTACTCTAAT

TTACTCTAATGTTCTGCCAATTTAT

TTACTCTAATTTTTCTGCCAATTTAT

TTACTCTAATGTTCTGCCAATTTAT

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AAAACCATTGTCAACTGAATAGGTTGATTTGTGTTTTCTTTCTGAAATTCTAAGAATTTTGGTAAAAG
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Nr of selected repeats 123 Similarity 0.979909

Consensus :

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Nr of selected repeats 92 Similarity 0.829532

Consensus:

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>Cele-UNSB01_1:10475895-10475986 Satlength=92 Nr of Repeats=6 RepeatLength=14
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GCTATACGCTATAC

GCTATACGCTATAC

GCTATACGCTATAC

GCTATACGCTATAC

GCTATACGCTATACGCTATAC

Nr of selected repeats 5 Similarity 1.000000

Consensus:

GCTATACGCTATAC

>Cele-UNSB01_1:10588945-10589028 Satlength=84 Nr of Repeats=6 RepeatLength=12

seed=TAGGCTTAGG

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TAGGCTTAGGCA
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Nr of selected repeats 4 Similarity 0.777778

Consensus:

TAGGCTTAGgct

>Cele-UNSB01_1:10648848-10654019 Satlength=5172 Nr of Repeats=115

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Nr of selected repeats 24 Similarity 0.936516

Consensus:

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>Cele-UNSB01_1:11104747-11105884 Satlength=1138 Nr of Repeats=5 RepeatLength=94
seed=TGTAGACAAA

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Nr of selected repeats 4 Similarity 0.971631

Consensus:

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>Cele-UNSB01_1:11137320-11159590 Satlength=22271 Nr of Repeats=783

RepeatLength=32 seed=GCACCAAATA

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Nr of selected repeats 516 Similarity 0.905773

Consensus:

GCACCAAATAGCACCAATTTAGCACCGAtgGA

>Cele-UNSB01_1:11159617-11160082 Satlength=466 Nr of Repeats=4 RepeatLength=26
seed=TTTTTGAAAA

TTTTTGAAAAATGGCATTGCGGCGGA

TTTTTGAAAAATGGCATTGCGGCGGA

TTTTTGAAAAATGGCATTGCGGCACA

TTTTTCAAAAATCCGCCCAATGCCATTTTTCTAAAATCCACCTGTGCCATACGTGTTTACATATCGAAAGAACACCCT
GAAATTCACAGTTTTCCATATTACTAACCATCTAGTTGTCTTACATATACTGTTACGTCGGGACAAGTCATTCCGACT
GGAGGTCCACAAAACAAGTTTTGCTCTATGCAATCTTCTCCTGTTGGTGTGTTGGTCTGAAATGATCAAAACAATTTT
GGAGCATTAAGATGTATTTAGAGTATTTAGTATAGTTTGTTTAAAGGTGGACTACGCTCGGTGGGGAAATTTCTTTGAA
CGGCATATGGGGTCACAAATGACCGAATATCATAATAAAAAAATTTCAAAAAAATTTTCTAAATTTTATGAT

Nr of selected repeats 3 Similarity 0.931624

Consensus:

TTTTTGAAAAATGGCATTGCGGCgA

>Cele-UNSB01_1:11183622-11184094 Satlength=473 Nr of Repeats=10 RepeatLength=35
seed=TTGCCGATTT

TTGCCGATTTGATGGAATTTTTTCAGTACCGGCAAT

TTACCGATTTGCCGGAATTTTTCAATTCCGGCAAT

TTGCCGACTTGCCGGAAGTTTTTCGTTCCGGCAAATTTATCGGT

TTGCCGATTTGCCGGAATTTTTCAATTTCCGGCAA

TTGCCGATTTATCGAAAAATTATTAATCCGGCAAT

TTGCCGATTTGCCGAAAATTTTTCAATTTCCGAAAGCTGTCCGTTTTCCAAAAATTTTCAATTCTGGCAA

TTGCCGGTTTTGCCGGAAGTTTCAATTCCTGCAA

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TTGCCGGTTTTGTGATTTGCCAAAAATTTTCTATTCCGCCAATTTACCGTTTTGCCGAAAATTTTTAAATTTTGGCAAT

TTGCCGGAAGTTTCAATTCCTGCAA

TTGCCGATTTGCCGGAATTTTTCAATTCGCAAT

Nr of selected repeats 6 Similarity 0.702469

Consensus:

TTGCCGATTTGCCGGAAtTTTCAATtCCGGCAAt

>Cele-UNSB01_1:11199905-11200227 Satlength=323 Nr of Repeats=8 RepeatLength=35
seed=GCCGGAATTG

GCCGGAATTGAAATTTTCCGGCAAATTGGTAAATT
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GTCGGAATTGAAATTTTCCGACAAATCGGCAGATT
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GCCGGAATTGAAAATTTCCGGCAAATCAGCAAATT

Nr of selected repeats 7 Similarity 0.829478

Consensus:

GCCGGAATTGAAAtTTTCCGgCAAATCgGCAaAtT

>Cele-UNSB01_1:11239237-11239369 Satlength=133 Nr of Repeats=12 RepeatLength=11
seed=TATGCCTAGC

TATGCCTAGCC
TATGCCTAGCC

Nr of selected repeats 12 Similarity 1.000000

Consensus:

TATGCCTAGCC

>Cele-UNSB01_1:11267568-11267793 Satlength=226 Nr of Repeats=15 RepeatLength=15
seed=CGATGCTCCA

CGATGCTCCACTCGA
CGATGCTCCACCCGG
CGATGCTCCACCCGA
CGATGCTCCACCCGG
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CGATGCTCCACCCGG
CGATGCTCTACCCGG
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CGATGCTCCACCCGA

Nr of selected repeats 15 Similarity 0.900106

Consensus:

CGATGCTCCACcCGa

>Cele-UNSB01_1:11268535-11268966 Satlength=432 Nr of Repeats=11 RepeatLength=34
seed=TTCCGGCAAAA

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TTCCGGCAAATCGGAAAATTGCTGGAAACTAAAA

TTCCTGCAAATCGGCAAATGCGCGAATTTAAAT
TTCCGGCAAATCGGCAAATCGGCAAATAGCCGGAATTTAAATTTCCAGCGAATCGGTAGATTGCCGGAATTTAAAT
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TTCCGGCAAATCGGCAAATAGCCGGAATTTAAAT
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Nr of selected repeats 9 Similarity 0.844227

Consensus:

TTCCGGCAAATCGGAAAttGcCGAAAtTTAAAt

>Cele-UNSB01_1:11276130-11276202 Satlength=73 Nr of Repeats=6 RepeatLength=12

seed=CGATCTCCAC

CGATCTCCACCT

CGATCTCCACCA

CGATCTCCACCT

CGATCTCCACCA

CGATCTCCACCT

CGATCTCCACCA

Nr of selected repeats 6 Similarity 0.933333

Consensus:

CGATCTCCACCa

>Cele-UNSB01_1:11291527-11291639 Satlength=113 Nr of Repeats=7 RepeatLength=14

seed=AGCTTGAAGC

AGCTTGAAGCTTGG

AGCTTGAAGCTGGA

AGCTTGGAGCTTGA

AGCTGGAAGCTTGG

AGCTTGAAGCTAGG

AGCTTGGAGCTTAAAGCGTGG

AGCTTGAAGCTTGGAGTTTTTC

Nr of selected repeats 5 Similarity 0.800000

Consensus:

AGCTtGaAGCTtGg

>Cele-UNSB01_1:11320046-11320214 Satlength=169 Nr of Repeats=4 RepeatLength=42

seed=TGCCGGAAT

TGCCGGAATTTCAAACCCGGTAGTTTGCCCATTTGCCGAGC

TGCCGGAATTTCAAACCCGTCAATTTGTTGATTTGCCGATT

TGCCGGAATTTGAAAGCCGGTAGTTTGCCCATTTGCCGAGC

TGCCGGAATTTCAAACCCGGCAATTTGTTGATTTGTGCGATT

Nr of selected repeats 4 Similarity 0.788360

Consensus:

TGCCGGAATTTcAAAcCCGgcAaTTTGcccATTTGcCGAgc

>Cele-UNSB01_1:11351419-11351614 Satlength=196 Nr of Repeats=13 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGACCCA

TCGTAGTGAGACCCA

TCGTAGTGAGACCCA

TCGTAGTGAGACCCT

TCGTGGTGAGGCCAA

TCGTGGTGAGACCCT

TCGTGGTGAGATCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACCCA
TCGTAGTGAGACCT
TCGTGGTGAGGCCAA
TCGTGGTGAGACCT
TCGTGGTGAGATCCA

Nr of selected repeats 13 Similarity 0.842735

Consensus:

TCGTgGTGAGACCCa

>Cele-UNSB01_1:11352081-11352141 Satlength=61 Nr of Repeats=5 RepeatLength=12

seed=TATACATATA

TATACATATA

TATACATATA

TATACATATA

TATACATATA

TATACATATA

Nr of selected repeats 5 Similarity 1.000000

Consensus:

TATACATATA

>Cele-UNSB01_1:11361560-11361658 Satlength=99 Nr of Repeats=7 RepeatLength=14

seed=AACTACTAAC

AACTACTAACTACT

AACTACAAACTACA

AACTACAAACTATC

AACTACTAACTACT

AACTACTAACGACT

AACTACTAACTACT

AACTACTAACTACT

Nr of selected repeats 7 Similarity 0.803175

Consensus:

AACTACTAACTACT

>Cele-UNSB01_1:11393763-11394894 Satlength=1132 Nr of Repeats=15

RepeatLength=35 seed=TTCCGGCAAA

TTCCGGCAAAATCGGCAAAATGTCTGAACTGAAAGCTTCTGACAAACTGGCGAATTGCCGGAATTGAAAAG

TTCCGGCAAAATCGGCAAAATGCCGGGACTGAAAAT

TTCCGACAAATGGGCAAAATGCCGGAATTGAAAAT

TTCCGGCAAAACCGGCAAAACGGCCAGAACTGAACAT

TTCCGGCAAAATCGGCAAAATGTCTGAACTGAAAATATCTGGCAAAATGACAAATGCCGGAATTGAAAAT

TTCCGGCAAAATTAACCAAGTTGTCTGAACTGAAAATATCTGGCAAAATAGGCAAAATGCCGAACTAAGTAT

TTCCGGCAAAATCAGCAAAATGCTGAACTTAAAAT

TTCCGGCAAAATCGGCAAAATGCTGGAATTGTGAAT

TTCCGGCAAAATCAGCAAAATGCTAGAACTGAAAGT

TTACGGCAAAATCGGCAAAATGCCGAACTGGGAAT

TTCCGGCAAAATGACAAAACGCAAGAACTGAAAAT

TTCCGGCAAAACCGCAAAATGCCGAACTGAAAAT

TTCCGGCAAAATCGGCAAAATGCCGAAAATAAAAATATCTGACAAGTCCGGCAAGCGTCGCTCTACATGACGAGTATTTAA

CTTTTTAACTCAAATCAAAGCAAATTCACAGTTTAATTGAACTATAACCAAAAAGTCTCCATTTCCCATCAAATTCAC

CCAAAAAAGTTCCAAAAAGCACTCTAAATCCCCGATCCAGCCTGGAAAAACCTCTAAAATTTCCGAAAAAAGATGC

TAAAATTTCAAGATGGGTGAGCGGAGATAGTGAGAGGCGGCTGGATGAGGCTGGGAAGGACGAGTGAATTTCAAGTC

ATCTTTCTTTTTTTTTTGTCTGCTTTTCTTCTTTTTTCCCAATTTTCTTCGACTTTTCGGACATTTCAAAGGTTCGGTG

AGACGCAGAGAACTGCAGTGTAAATCGGACGTTAAATGTTGTCTTGAATTTGTATGTTGAAATTTTCGTAAGACGAAGAC

TACAACTACAAATTTGCGGTTTGTCTGAATTTTCTAAAACAAACAAACAAAGACAACTGT

TTCCGGCAAAATGGCAAAATGCCGGAATTGTAATTTACGGCAA

TTCCGGCAAAATGCCGGAATTGTAAGT

Nr of selected repeats 9 Similarity 0.743915

Consensus :

TTCCGGCAAAtcggCAAAttGCcnGAAcTGaaAAT

>Cele-UNSB01_1:11398081-11398840 Satlength=760 Nr of Repeats=4 RepeatLength=35
seed=TCGGCAAATT

TCGGCAAATTACGGAAAATGAAAATTTCCGGCAA

TCGGCAAATTACGGAAAATGAAAATTTCCGGCAA

TCGGCAAATTACGGAAAATGAAAATTTCCGGCAA

TCGGCAAATTGTGGAATTGAAGGCGGAAGTCGGCGCGGCTGCCGTTTTGGCGCCTGCATGGAAGCCCCACAGCCTCAA

TCAAAAATCGCTACTCCCTTTCTTTAACCTCCGGCTCTTTTTTTGTGCTAAAACCTGCTCTCTGAATAGAAAATCAAA

TCTTTTCAGAAGTTTCTTGAAGGGGGCCCTGACCTCTTGAACCTTTCCACAACCTCCGCCGCTTTCTTCTTCTTATT

CCCTTTTGACTCTCTCCGCAATTTTATGAATTTCTGAATAGAGGGAAACTGCCGCTCCGTGAGCACAAAGGTACTTTTTT

GATGGTGCCTGAGACCTGCTGAAACGGGAAGGAATCGTAGGAGTTTTCGTCCAAATCCACAATTTTCTCTTACTTT

ACACTCTGGGGCTCCATCACCAAGTGACACTTACCCACAATGCCCTGGAAATGCACCTTACTCTGTGAGGATTTTTTT

GTTGTTGAAAATCTGGATTTCTAGGTGAAACTCTCTTGAATGTGGAATTTTGGACGGTTCTTTTTTTTTGCTCTT

TTCTGAAATTTTTAGCTGTCAAATTTGACAATTTTCACTTAAGTTTACTGGAATTTTCGCCTGAAAATTA

AAGATTGCGGTGTGAAGCAGGT

Nr of selected repeats 3 Similarity 1.000000

Consensus :

TCGGCAAATTACGGAAAATGAAAATTTCCGGCAA

>Cele-UNSB01_1:11408393-11409029 Satlength=637 Nr of Repeats=9 RepeatLength=35
seed=AATTGCCGAA

AATTGCCGAATTTCTCGTTTTGCAATTTACCAA

CGTTGCATGTTCG
CGTTGCGTGTTCG
CGTTGTGTGTTCG
CGTTGCGTGTTCG
CGTTGCGTGTTCG
CGTTGCGTGTGG
CGTTGCGTGTTCG
CGTTGCGTGTCCG
CGTTGCGTGTGG
CGTTGCGTGTTCG
CGTTGCATGTTCG
CGTTGCGTGTAG
CGTTGCGTGTGG
CGTTGCGTGTTCG
CGTTGCGTGTTCG
CGTTGCGTGTCCG
CGTTGCGTGTTCG
CGTTGCGTGTGG
CGTTGCGTGTTCG
CGTTGCGTGTTCGCGATGCATGTTCG
CGTTGCGTGTGG
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CGTTGCGTGTGG
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CGTTGCATGTTCG
CGTTGCGTGTTCG
CGTTGCGTGTGG
CGTTGCGTGTTCG
CGTTGCGTGTGG
CGTTGCGTGTTCG
CGTTGCATGTTCG
CGTTGCGTGTTCG
CGTTGCATGTTCG
CGTTGCGTGTCA
CGTTGCGTGTGG
CGTTGCGTGTTCG
CGTTGCGTGTTCG
CGTTGCGTGTTCG
CGTTGCGTGTCA
CGTTGCGTGTGG

Nr of selected repeats 58 Similarity 0.901727

Consensus:

CGTTGCGTGTcG

>Cele-UNSB01_1:11481110-11481222 Satlength=113 Nr of Repeats=7 RepeatLength=16

seed=CTACATGCCT

CTACATGCCTAAATTT

CTACATGCCTATATGC

CTACATGCCTACATGC

CTACATTcCTACATGC

CTACATGGCTACATTT
CTACATGCCTACATGC
CTACACGCCTACATGC

Nr of selected repeats 7 Similarity 0.805556

Consensus:

CTACATGCCTAcATgc

>Cele-UNSB01_1:11481110-11482230 Satlength=1121 Nr of Repeats=68

RepeatLength=16 seed=CTACATGCCT

CTACATGCCTAAATTT
CTACATGCCTATATGC
CTACATGCCTACATGC
CTACATTCCTACATGC
CTACATGGCTACATTT
CTACATGCCTACATGC
CTACACGCCTACATGC
CTACATGCCTACATTC
CTACATGCCGACATGG
CTACATGGCTACATGG
CTACATGGCTACATGC
CTACATGTCTACATGCCTACATTT
CTACATGCCTAAATGC
CTACATGCCTACATGC
CTACATGCCTACATGC
CTACATGCCTACATGC
CTACATGCCTACATGC
CTACATGCCTACATGC
CTACATGTCTACATGC
CTACATGCCTACATGC
CTACATTCCTACATGC
CTATATGCCTACATGC
CTACATGCCTACATTC
CTACAGGCCTACATGGCTACATTT
CTACATGCCTACATGC
CTACATTCCTACATGCCGACATGG
CTACATGGCTACATGG
CTACATGCCTACATGT
CTACATGCCTACATTT
CTACATGCCTAAATGC
CTACATGCCTACATGC
CTACATGCCTACATGC
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CTACATGCCTACATGC
CTACATTCCTACATGC
CTACATGGCTACATTT
CTACATGCCTACATGC
CTACACGCCTACATGC
CTACATGCCTACATTC
CTACATGCCGACATGG
CTACATGGCTACATGG
CTACATGCCTACATGT
CTACATGCCTACATTT
CTACATGCCTAAATGC
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CTACATGCCTACATGC
CTACACGCCTACATGC
CTACATTCCCTACATGCCGACATGG
CTACATGGCTACATGG
CTACATGCCTACATGT
CTACATGCCTACATTT
CTACATGCCTACATTT
CTACATGCCTACATGC
CTACATGCCTATATGC
CTACATTCCCTACATGC
CTACATGCCTACATGC
CTACATTCCCTACATGC
CTATATGCCTACATGC
CTACATGCCTACATTC
CTACATGCCTACATGG
CTACATGGCTACATGC
CTACATGTCTACATGC
CTACATGCCTACATGC

Nr of selected repeats 64 Similarity 0.868304

Consensus:

CTACATGCCTACATGc

>Cele-UNSB01_1:11519985-11520529 Satlength=545 Nr of Repeats=18 RepeatLength=26
seed=ACCTACAGTA

ACCTACAGTAACCCAGGCATATAGTAGGATAAAGTACTTATAAGCTATAGTA
ATCTACAGTACCCCTATTCTAGAGTG
ACCTACAGTAACCTACAGAGAATCGAAGGATTCCAATCGAGCTATAGTAACCCACCGTAACCCGTAGCCGCTAGCTACA
GAACCCATATGCTACAGTA
ACCTACAGTATCCTCGACATTCGGCTAA
AGCTACAGTACCCCTGCTCTAGAATG
ACCTACAGTACCCCTTGTCCTAGAGTG
ACCTACAGTACCCCTGTCTAGAAATG
ACCTACAGTATGCCTGTG
ACCTACAGTACCCCTGCCCTAGAATG
ACCTACAGTACCCCTTGTCCTAGAGTG
ACCTACAGTACCCCTGTCTAGAAATG
ACCTACAGTATGCCTGTG
ACCTACAGTACCCCTGCCCTAGAATG
ACCTACAGTACCCCTTGTCCTAGAGTG
ACCTACAGTACCCCTGTCTAGAAATG
ACCTACAGTATGCCTGTG
ACCTACAGTACCCCTGCCCTAGAGTG
ACCTACAGTACCCCTTGTCCTAGAGTG

Nr of selected repeats 12 Similarity 0.881896

Consensus:

ACCTACAGTACCCcTGtCCTAGAaTG

>Cele-UNSB01_1:11521003-11522550 Satlength=1548 Nr of Repeats=48
RepeatLength=32 seed=GCAATTTTTTA

GCAATTTTTTAAGCTAAAAATCACGAAAAAACC
GCAATTTTTTAGGCTAAAAATCACTAAAAAACT
GCAATTTTTTAGGATAAAAAATCACTAAAAAACT

GCAATTTTTAGGCTAAAAATCACTTAAAAAACT
GCAATTTTTAGTCTAAAAATCACTAAACAAC
GCAATTTTTAGGCTAAAAATCACTAAACAAC
GCAATTTTTAGGCTAAAAATCACTAAAAAACT
GCAATTTTTAGGATAAAAAATCACTAAAAAACT
GCAATCTTTAGGCTAAAAATCACTAAAAAACT
GCAATTTTTAGGATAAAAAATCACTAAACAACC
GCAATTTTTAGGATAAAAAATCACTAAACAACC
GCAATTTTTAGGATAAAAAATCACTAAACAACC
GCAATTTTTAGGCTAAAAATCACTAAAAAACT
GCAATTTTTAGGCTAAAAATCACTTAAAAAACT
GCAATTTTTAGTCTAAAAATCACTAAACAAC
GCAATTTTTAGGCTAAAAATCACTAAACAAC
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GCAATTTTTAGTCTAAAAATCACTAAACAAC
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GCAATTTTTAGGATAAAAAATCACTAAAAAACT
GCAATTTTTAGGCTAAAAATCACTTAAAAAACT
GCAATTTTTAGGCTAAAAATCACGAAAAAATT
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GCAATTTTTAAGCTAAAAATCACGAAAAAACC
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GCAATTTTTAAGCTGAAAAATCACAAAAAAACT
GCAATTTTTAGGATAAAAAATCAGTAAAAAACT
GCAATTTTTAGGCTAAAAATCACTTAAAAAACT
GCAATTTTTAGGCTAAAAATCACGAAAAAATT
GTAATTTTTAAGCAAAAAATCACGAAAAAACC
GCAATTTTTAGGATAAAAAATCACTAAACAACC
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GCAATTTTTAGGCTAAAAATCACTTAAAAAACT
GCAATTTTTAGTCTAAAAATCACGAAAAAACC
GCAATTTTTAAGCTAAAAATCACGAAAAAACA
GCAATTTTTAAGCTGAAAAATCACAAAAAAACT
GCAATTTTTAAGCTAAAAATCACTAAAAAACT
GCATTTTTTAAGCTAAAAATCACTAAAAAACT
GCAATTTTTAGGATAAAAAATCACTAAAAAACT
GCAATTTTTAAGCTGAAAAATCACAAAAAAACT
GCAATTTTTAAGCTAAAAATCACTAAAAAACT
GCATTTTTTAAGCTAAAAATCACTAAAAAACT
GCATTTTTTAAGCTAAAAATCACTAAAAAACT

Nr of selected repeats 37 Similarity 0.890140

Consensus :

GCAATTTTTAGGcTAAAAATCACTAAAaAACT

>Cele-UNSB01_1:11550058-11550130 Satlength=73 Nr of Repeats=6 RepeatLength=12
seed=TATATGTATA
TATATGTATATG
TATATGTATATG
TATATGTATATG
TATATGTATATG

TATATGTATATG

TATATGTATATG

Nr of selected repeats 6 Similarity 1.000000

Consensus:

TATATGTATATG

>Cele-UNSB01_1:11556393-11558176 Satlength=1784 Nr of Repeats=47

RepeatLength=35 seed=GGCAAATCAG

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAGTTACCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAGTTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAGTTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAGATGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGTCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTCGCCGGAATTGAAAATTTCC

GGCAAATCAACAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAATTTCC

GGCAAATCAGCAAATTGCCGAGTTGAAAATTTT

GGCAAATCAGCAAATTGCCGAGTTGAAAATTTT

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCTACTAATAAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCTAATTACCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTAAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

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GGCAAATCAGCAAATTGTCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGACGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGAGTTGAAAATTTT

GGCAAATCAGCAAATTGCCGAGTTGAAAATTTT

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCTACTAATAAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCTAATTACCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTAAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAGTTTCC

GGCAAATCAGCAAATTGTCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGACGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCTAGTAATAAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCTAATTACCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTAAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCC

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTCCGTGCAAATAGGCAAATTACCGGTTTTGAAAATTTCC

GGCAAATCGGCAAATTCGGAAATTGAACATTTCT

GGCAAATCGGCAAATTCGCCGGAATTGATAATTTCC

Nr of selected repeats 42 Similarity 0.911023

Consensus:

GGCAAATCAGCAAATTGCCGGAATTGAAAATTTTCc

>Cele-UNSB01_1:11564527-11564628 Satlength=102 Nr of Repeats=5 RepeatLength=20
seed=TGTAACAATC

TGTAACAATCTATTTTTTTTG

TGTAACAATCTATTTTTTTTCG

TGTAACAATCTATTTTTTTTCG

TGTAACAATCTATTTTTTTTCAT

TGTAACAATCTATTCTTTTCG

Nr of selected repeats 4 Similarity 0.933333

Consensus:

TGTAACAATCTATTTtTTTcG

>Cele-UNSB01_1:11591612-11591946 Satlength=335 Nr of Repeats=14 RepeatLength=20
seed=AAAAATCAAT

AAAAATCAATAATTTTCATCG

AAAAATCAATAATTTTCATCG

AAAAATCAATAATTTTCATCG

AAAAATCAATAATTTTCATCG

AAAAATCAATAATTTTCATCG

AAAAATCAATTATTTTAAC

AAAAATCAATAATTTCCACA

AAAAATCGATAACTTCATCA

AAAAATCGATAATTTTCATCA

AAAAATCAATAATTTTCATCA

AAAAATCAATAATTTTCATCAAAAAGTCGATAATTTCAACA

AAAAATCAATATTTTCATCG

AAAAATCAATAATTTCAACA

AAAAATCAATAATTTTCATCAAAAAGTCGATAATTTTACCGAATTTTCCACAACAA

Nr of selected repeats 11 Similarity 0.883636

Consensus:

AAAAATCAATAATTTTCATCg

>Cele-UNSB01_1:11592271-11597890 Satlength=5620 Nr of Repeats=277
RepeatLength=20 seed=ATTGATTTTT

ATTGATTTTTTTGAGAAAATT

ATTGATTTTTTTGAGAAAATT
ATTGATTTTTTTGAGAAAATT
ATTGATTTTTTTGAGAAAATT
ATTGATTTTTTTGAGAAAATT
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ATTGATTTTTTGATGAAATT
ATCGATTTTTTATGAAGTT
ATTGATTTTTTGAGGAAATT
ATTGATTTTTTGGTGAAATT
ATTGATTTTTTGATGAAATT
ATCGATTTTTTGATGAAGCT
ATTGATTTTTTGAGGAAATT

Nr of selected repeats 273 Similarity 0.884518

Consensus:

ATTGATTTTTTGAggAAATT

>Cele-UNSB01_1:11615647-11616001 Satlength=355 Nr of Repeats=10 RepeatLength=30
seed=CCTTGGGCTC

CCTTGGGCTCCGACTTCAGCTCCAGGGGGTC

CCTGGGCTCCGTTTTGATATCCATGTGCTCCTGGAGCAGGTCCATAGGAAGCTTGAGGTGGTGTGGGGGCTCCATAGCT
TGCCGGTGGTGA

CCTTGGGCTCCCTGAGCTCCAAATTGTGT

CCTTGGGCTCCTTGTGCTCCAAAATGTGCT

CCTTGGGCTCCTTGTGCTCCAAAATGTGCT

CCTTGGGCTCCCTGAGCTCCAAATTGTTCT

CCTTGGGCTCCCTGAGCTCCGAATTGTGCT

CCTTGGGCTCCTTGTGCTCCAAAATGTGCT
CCTTGGGCTCCCTGAGCTCCAAATTGTACT
CCTTGTGCTCCAAAATGTGCT
Nr of selected repeats 7 Similarity 0.875132
Consensus:
CCTTGGGCTCCcTGaGCTCCAAAAtTGTgCT
>Cele-UNSB01_1:11631541-11632264 Satlength=724 Nr of Repeats=15 RepeatLength=11
seed=GTACTGTAGG
GTACTGTAGGG
GTACTGTAGGTATACGGTAGGATTACTGTAGTTTGGAGAAAATTTGAATTTTTCAGCTTTTGAACAGGTATTGGGTTGGGA
GTTGGTGGGGGATAATGTCAAG
GTACTGTAGTG
GTACTGTAGGG
GTACTGTAAGTATACGGTAGGGTTACTGTAGTTTGGGAAAATTTGAATTTTTCAGCTTTTGAACAGATATTGGGTCGGGAG
TTGATGTGGGATAATATCAAGGTATTGTGGTG
GTACTGTAGGC
GTACTGTAGGTATACGGTAGGATTACTGTAGTTTGGAGAAAATTTGAATCTTTTCAGCTTTTGAAGAGATAGTGGGTTGGGA
GTTGGTGGGGGATAATGTCAAG
GTACTGTAGGT
GCACTGTAGGG
GTACTGTAGGTATACGGTAGGATTACTGTAGTTGGAGAAAATTTGAATTTTTCAGCTTTTGAACAGGTATTGGGTTGGGAG
TTGGTGGGGATGATGTCAAG
GTACTGTAGTA
GTACTGTAGGG
GTACTGTAGGTATACGGTAGGATTACTGTAGTTTGGAGAAAATTTGAATTTTTCAGCTTTTGAACAGATATTGGGTCGGGAG
TTGATGTGGGATAATATCAAGGTATTGTGGTG
GTACTGTAGGC
GTACTGTAGGTATACGGTAGGATTACTGTAGTTTAGGAAAGTTTGAATCTTTTCAGCTTTTGAAGAGATAGTGGGTTGGGA
GTTGGTGGGGGATAATGTCAAG
Nr of selected repeats 9 Similarity 0.841751
Consensus:
GTACTGTAGgg
>Cele-UNSB01_1:11636321-11636670 Satlength=350 Nr of Repeats=9 RepeatLength=35
seed=ATTCCGGCAA
ATTCCGGCAATTTGCCGGTCTGCCGATTTGCCGAAATTTTCA
ATTCCGGCAATTTGCTAAATGTTTCA
ATTCCGGCAATTTGTGCGATTAAACGAAAATTTACATTTCCGGAAATTTGCCATTTTCCAGAAATTTTCA
ATTCCGGCAATTTGCCGATTTTCCAGAAAATTTTCA
ATTCCGGCAATTTGCTGATTTTCCAAAAATTTACA
ATTCCGGCAATTTGCCGATTTTCCAGAAAATTTTCA
ATTCCGGCAATTTGCTGATTTTCCAAAAATTTACA
ATTCCGGCAATTTGCCGATTTTCCAGAAAATTTTCA
ATTCCGGCAATTTGCCGATTTTCCAGAAAATTTTCA
ATTCCGGCCATTTGCCGATTTGCCGAAATTTTCC
Nr of selected repeats 6 Similarity 0.888254
Consensus:
ATTCCGGCAATTTGCcGATTTTCCAgAAATTTtCA
>Cele-UNSB01_1:11643779-11644036 Satlength=258 Nr of Repeats=6 RepeatLength=34
seed=ATGCACCATG
ATGCACCATGTTTGGCTCACTCTCAATAGTTTTAAAATGGTTTGATAAATTTAGGAGGAACCAATGTATAAGATGTTAA
AATTATTCGGGGTCATATCA
ATGCACCATGCCAAAAAATATATCCAAAACCCCG
ATGCACCGTGTCCAAAAGTATATATAAAAGTGCG
ATGCACCATGTTCAAAAATATATTCAAAATATG
ATGCTCCATGTTCAAAAATACG

ATGCACCATGTCAAAAAGTATATCTTGAAGTATG

Nr of selected repeats 4 Similarity 0.679739

Consensus:

ATGCACCaTgtcaAAAAaTATATccaaAAgtacG

>Cele-UNSB01_1:11661653-11661731 Satlength=79 Nr of Repeats=6 RepeatLength=12

seed=AAGCCTAAGC

AAGCCTAAGCCT

AAGCCTAAGCCT

AAGCCTAAGCCT

AAGCCTAAGCCT

AAGCCTAAGCCT

AAGCCTAAGCCTAAGCCA

Nr of selected repeats 5 Similarity 1.000000

Consensus:

AAGCCTAAGCCT

>Cele-UNSB01_1:11662428-11662542 Satlength=115 Nr of Repeats=9 RepeatLength=12

seed=GCTTAGGCTT

GCTTAGGCTTTG

GCTTGGGCTTAG

GCTTACGCTTAG

GCTTAGGCTTAG

GTTTAGGCTTAGGCACAT

GCTTAGGTTTAG

GCTTAGGCTTAG

GCTTTGGCTTGG

GTTTAGGCTTAG

Nr of selected repeats 8 Similarity 0.813492

Consensus:

GCTTaGGCTTaG

>Cele-UNSB01_1:11667166-11667423 Satlength=258 Nr of Repeats=6 RepeatLength=34

seed=ATGCACCATG

ATGCACCATGTTTGGCTCACTCTCAATAGTTTTAAAATGGTTTGATAAATTTAGGAGGAACCAATGTATAAGATGTTAA

AATTATTCGGGGTCATATCA

ATGCACCATGCCAAAAAATATATCCAAAACCCCG

ATGCACCGTGTCCAAAAGTATATATAAAAAGTGCG

ATGCACCATGTTCAAAAATATATTCAAAAATATG

ATGCTCCATGTTCAAAAATACG

ATGCACCATGTCAAAAAGTATATCTTGAAGTATG

Nr of selected repeats 4 Similarity 0.679739

Consensus:

ATGCACCaTgtcaAAAAaTATATccaaAAgtacG

>Cele-UNSB01_1:11682141-11682225 Satlength=85 Nr of Repeats=7 RepeatLength=12

seed=GGCTTAGGCT

GGCTTAGGCTTT

GGCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGGCTTA

Nr of selected repeats 7 Similarity 0.968254

Consensus:

GGCTTAGGCTTA

>Cele-UNSB01_1:11685636-11685851 Satlength=216 Nr of Repeats=5 RepeatLength=43
seed=CGGCAAATCG

CGGCAAATCGGCAAATCGGCAACTTGCCGGAATTGAAAATTTTC
CGGCAAATCGGCAAACCAGCAAGTTGCCAAAAATCAAATTTTC
CGGCAAATCGGCAAAGTAGCAAATTTCTGGAATTGAAAATTTTC
CGGCAAATCGGCAAACCGCCAATTTGCTGAAAATGAAACTTTTC
CGGCAAATCGGCAAACCGGCAATTTGCCGAAAATGAAAATTTTC

Nr of selected repeats 5 Similarity 0.801550

Consensus:

CGGCAAATCGGCAAACcggCAAnTTgCcgaAAaTgAAAaTTTC

>Cele-UNSB01_1:11691383-11691503 Satlength=121 Nr of Repeats=8 RepeatLength=15
seed=TCGTGGTGAG

TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGTGGTGAGATCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA

Nr of selected repeats 8 Similarity 0.930159

Consensus:

TCGTGGTGAGACCCa

>Cele-UNSB01_1:11691539-11692754 Satlength=1216 Nr of Repeats=24
RepeatLength=35 seed=TGGCGGGAAA

TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTTG
GGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TAGCGGGAAATCAAGTTTTCAGTAAAAAATTTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTTG
GGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TAGCGGGAAATCAAGTTTTCAGTAAAAAATTTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCAGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TAGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCAGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TAGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TAGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCAGGAAATTCAAATTTTCAGTGAAAAAATTT
TGGCGGAAAATTCAAATTTTCAGTAAAAAATTT
TCCGGAATGGTCCAGAATTTTCTAGAAAATTCAGAAAGTTCTGGAATGGTCCAGAAGTTTCTAGAAAATTCGAGAAA
TTCCGGAATGGTCCAGAATTTTCTAGAAAATTCAGAAAGTTCTGGAATGGTCCAGAATTTTCTAGAAAATTCGGGAAA
ATTCTGGAATATTCCAGAATTTTCTAGAAAATTCGGGAAAAGTCTGCAATGTTCCAGAACTAAAAAATTCGATAAAACT
CTGAAATGTTCAATTTTCGTGAAAAATTCAGAAACTTCTGCAAGTTCTACACGGGTTCTGGCTCGATCCCGCGCTC
CATTGGACACTGAAA

Nr of selected repeats 17 Similarity 0.860771

Consensus:

TgGCGGGAAAtTCAAaTTTTTCAGTgAAAAAAATTT

>Cele-UNSB01_1:11696177-11696255 Satlength=79 Nr of Repeats=6 RepeatLength=12
seed=TAGGTCTAGG

TAGGTCTAGGTC

TAGGTCTAGGTC

TAGGTCTAGGTC

TAGGTCTAGGTC

TAGGTCTAGGTC

TAGGTCTAGGTC

Nr of selected repeats 5 Similarity 1.000000

Consensus:

TAGGTCTAGGTC

>Cele-UNSB01_1:11696998-11697105 Satlength=108 Nr of Repeats=5 RepeatLength=19
seed=TCAAAAATCA

TCAAAAATCAAAAATTTTCATCAAAAATTTCA

TCAAAAATCAATAATTTCA

TCAAAAATCAATAATTTCA

TCAAAAATCAATAATTTGC

TCAAAAATCAATAATTTCT

Nr of selected repeats 4 Similarity 0.873611

Consensus:

TCAAAAATCAATAATTTCa

>Cele-UNSB01_1:11697315-11697448 Satlength=134 Nr of Repeats=7 RepeatLength=19
seed=TTATCGATTT

TTATCGATTTTCCGAGAAAT

TTTCGATTTTTTATGAAA

TTATCGATTTTCCGAAA

TTATCGATTTTCAAGAAT

TTATCGATTTTCAAGAAA

TTATCGATTTTCCAGAAA

TTATCGATTTTCTGAAA

Nr of selected repeats 5 Similarity 0.873684

Consensus:

TTATCGATTTTTCnaGAAa

>Cele-UNSB01_1:11696961-11698223 Satlength=1263 Nr of Repeats=20

RepeatLength=19 seed=AAAAATCGAT

AAAAATCGATAATTTTCATCA

AAAAATCGATAATTTGCTCAAAAATCAAAAATTTTCATCAAAAATTTTCATC

AAAAATCAATAATTTTCATC

AAAAATCAATAATTTTCATC

AAAAATCAATAATTTGCTC

AAAAATCAATAATTTCTTC

AAAAATCAATAAAATACTC

AAAAATCGATATATCCGCTA

AAAAATCAATATTTTCCACTTACATAACGCCAATCATTGCGTATTTATAACTATCCCTGTTGCCTGTACGCAAATTGT

CCACCAAAATCATAGTGTGTGGAAATCACCTTCGGCCGCCGGAACAACCATCTG

AAAAATGGATTTTTATGAGAAATTTCTCAATTAATTTATCGATTTTCCGAGAAATTTTCGATTTTTTATGAAATTATCG

ATTTTTCCGAAATTATCGATTTTCAAGAATTTATCGATTTTCAAGAAATTTATCGATTTTCCAGAAATTATCGATT

TTTCTGGAAATTATCGATTTTCCGAGAAATTTCAATATTTTCTCAATGGAGCGCACTTACTCACCGTTTTTTCAATT

CGAAGCCCCTTGGTACATCGGGTTGCTGTGCTTTGGCTTCTGGGTCGCCGAGTCTGCTGCCAACGAGAATTGCACAAG

TTGGAGCATCAAAAAGACTGCGAGAAATGATGACGTCATCGTGTGAGGCGGCGAGTTTCGGTTGGTTGGTTATCCAA

TTCACACCGATGAAAATCCGATGAATGAAAATCGAATACTGATATCGATTATTGATTGATTTCGATCGGATTGAACTGAT
ATCGATGATTTGGAAGAAAATGACGTGGCTTAATTGTACCGGGGTTTGGCCGAAAATTTGGAATTTTTCCAG
AAAAATCGATAATTTCTTC
AAAAATCGATAATTTTCATC
AAAAATCGATAATTTCCAG
AAAAATCGATAATTTCCAG
AAAAATCAATAAATTTCTTC
AAAAGTCGATAATTTTCATC
AAAAATCAATAATTTTCATCAGAATTCGATAATTTCCAG
AAAAATCGATAATTTCTTC
AAAAATCGATAATTTTCATC
AAAAGTCGATAATTTCTTCCAAAGTCGATAATTTTTGAAAACCTGTAGATAATATTAGAAAATTAATTTTTCTTCTTTT
TTAAATCAATAAATTTGAGCTCCCGTCAATCAATCAATACTTTATTTCAGACCCAAGTCAACCCAAAATTTGCAATAAATA
GTTCTATTTATTTCGTGTAGAAATGGCTTCTTGCAGAACACTTCAGCCTGA

Nr of selected repeats 12 Similarity 0.725830

Consensus:

AAAAATCgATAATTTcNtC

>Cele-UNSB01_1:11744458-11744933 Satlength=476 Nr of Repeats=17 RepeatLength=19
seed=TTTCACAAA

TTTCACAAAATCGATAATTTTGATGAAAACCAATAAT
TTTCACAAAATCGATAAT
TTTCACAAAATCAATAAT
TTTCACAAAATCAATAAT
TTTCACAAAATCGATAAT
TTTCACAAAATCAATAAT
TTTCACAAAATCCATCATTTTGACGAAAATCAATAAT
TTTCACAAAATCAATAAT
TTTCACAAAATCCATCATTTTGACGAAAATCAATAATTTTGACGAAAATCAATAAT
TTTCACAAAATCGATAAT
TTTCACAAAATCAATAAT
TTTCACAAAATCCATCATTTTGACGAAAATCAATAATTTTGACGAAAATCCATCATTTTGACGCAAATCAATAAT
TTTCACAAAATCGATAAT
TTTCACAAAATCAATAAT
TTTCACAAAATCAATAAT
TTTCACAAAAGTCAATAAT
TTTCACAAAATCGATAATTTTGATGAAATCCAATAAT

Nr of selected repeats 12 Similarity 0.943647

Consensus:

TTTCACAAAATCaATAAT

>Cele-UNSB01_1:11743735-11745857 Satlength=2123 Nr of Repeats=45

RepeatLength=19 seed=AAAATCGATA

AAAATCGATATTTCTCAGCGATAAGGCTTACCGCATGCTTTGTGCTTTTCGGAGATGACTAATCGATGCATGACAGCTAG
CCAGACTATTGATTGAGGTTCTTGAAAAACAAAATTTGAAAGGAAAACTTTTGAAAAATCACCTTCTTGACCCAAT
CGATAAAAGCGCCTTCCGATATTGTTGGCGCCAATCGTACAGTTTCGAAGCACGATCGGACCGATGGCTCCACATTGGT
ACCTCCAAATGCGGCGGATTCACCGACCAAACGAGGAATCTGAGAGTCAAA
AAAATCGATAATTCACCA
AAAATCGATTTTTTTTTAAAAACAAAATGAATTGTTACCTAAAAATAAATCAATAAAACACTTACGTGGATAAGATCAT
ATAAAAGCAATGCAATTTGTTTTTGGGTCGCATGACCGTCTGGGAAACTAATTTGAAAAGATCTGGAAATTA AAAACC
GATTTCAAGGTACAGGGAGTCAGAAAAAAGCGTACATCTATATTTTCTCTAATGGAATGTTTCGAGAATACGATCAT
GGCAATTTTAAAGGAGAGAACACGCATTATCCGTGCGGGATCTGCAAAAATATGTTAGTTAGTTTTAAAAA
AAAATCGATAATTTTGTGAAAGGCGGAATTTTTATCGGAAATCCATAAATTTGCCGAAATATATGATTTTCTGG
AAAATCGATAATTTCTCAT
AAAGTCGATAAATTTTCA
AAAATCGATAATTTTGATGAAAACCAATAATTTTCA

AAAATCGATAATTTTCACA
AAAATCAATAATTTTCACA
AAAATCAATAATTTTCACA
AAAATCGATAATTTTCACA
AAAATCAATAATTTTCACAAAAATCCATCATTTTGACG
AAAATCAATAATTTTCACA
AAAATCAATAATTTTCACAAAAATCCATCATTTTGACG
AAAATCAATAATTTTGACG
AAAATCAATAATTTTCACA
AAACTCGATAATTTTCACA
AAAATCAATAATTTTCACAAAAATCCATCATTTTGACG
AAAATCAATAATTTTGACGAAAAATCCATCATTTTGACGCAAATCAATAATTTTCACA
AAAATCGATAATTTTCACA
AAAATCAATAATTTTCACA
AAAATCAATAATTTTCACAAAAAGTCAATAATTTTCACA
AAAATCGATAATATTTGATGAAATCCAATAATTTTCACA
AAAATCGATAATTTTGACG
AAAATCGATAATTTTCCGAATTTTTTTTTAATCTATAAATTTCAAGAAAAATCTATCATAATTTTTTTTAAAATTTTTTCC
TTCAGTTCAAAAAATTATCAAATTTGTA
AAAATCGATAACTCACTGATCAAAAAAGGTTCAACAAGAAATTAATGCAAATATCGACAGCCAACGAGACACTTTGCACT
TGATTTGGATATTTTGCATGAAGAGCTTCATACATCGGCAGCAGAGCACAAACCATACCCCTCCAGTCCCGGACATTCTT
CAGCTGAAAGTCTTTTCAGTCGAACAAACGCCTTTTCCAAAAGTGTTAGGTCGACTAGATCGAGACAGAGCCGTTTTTG
AAGGGCTCGGAGCTTTCATGGCGGTACGGTAGGCGAGGAATTTGACGCGGTTGAATTTGTGAGAGCTCTTTTACGATTTCC
ACCCATACTGGATGCTCCCATTTGTGTTTTTTTCACTGGTTTTGCTGGAATTTGTTACATTCGGTTATTTTTTCCAAAAA
TAAATTTCTGG
AAAATCGATAATTTCCCGA
AAAACCGATAATTTTCCGA
AAAATCGATAATTTCCGGAAAA
AAAGTCGATAATTTCCCGA
AAAATCGATAATTTCCAAA
AAAATCGATACTTCTCCGA
AAAATCGATAATTTCCCGA
AAAATCGATAATTTCTCGA
AAAATCGATAATTTCCAAA
AAAATCGATACTTCTCCGA
AAAATCGATAATTTCCCGA
AAAATCGATAATTTCCCGA
AAAATCGATAATTTCCCGA
AAAATCGATAATTTCCCGA
AAAATCGATAATTTCCCGA
AAAATCGATAATTTCCGAAAAATCATTAATTTTCAGA
AAAATCAATAATTTTCCGA
AAAATCGAAACTTTTCCGA
AAAATCGATATTTTCCCGA
AAAATCGATAATTTCCGGAAAA
AAAGTCGATAATTTCCCGA
AAAATCGATAATTTCCAGA
Nr of selected repeats 29 Similarity 0.730706
Consensus :
AAAATCgATAATTTtCanA
>Cele-UNSB01_1:11752079-11752337 Satlength=259 Nr of Repeats=16 RepeatLength=12
seed=AAGCCAAAGC
AAGCCAAAGCCA
AAGCCAAAGAAT
AAGCCGAAGCCTCAGCCTAAGAAC
AAGCCTAAGCCTCAGCCTAAGCCTAAGAGTGAGCCTAAGTCT
AAGCCTAAGCCA

GCATGTGGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCTTGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAA
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATCTAGGCATGTGG
GCATGTAGGCATGTGG
GCATGTAGGTATGTAGGCATGCCG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GCATGTAGGCATGTAG
GTATGTAGGCATGTAGGCATGTAG

Nr of selected repeats 50 Similarity 0.957891

Consensus:

GCATGTAGGCATGTAG

>Cele-UNSB01_1:11907174-11907313 Satlength=140 Nr of Repeats=13 RepeatLength=11

seed=TTTTGCACAT

TTTTGCACATT

TTTTGCACAT

TTTTCCACATT

TTTTGCACTTT

TTTTGGACATT

TTTTGCACATT

TTTTGCACAC

TTTTGCACATA

TTTTGCACAT

TTTTGCACATT

TCTTGCACATT

TTTTGCAAAT

TTATGCACATT

Nr of selected repeats 9 Similarity 0.838384

Consensus:

TTTTGCACATT

>Cele-UNSB01_1:11925845-11930260 Satlength=4416 Nr of Repeats=27

RepeatLength=164 seed=ATACCAGAAA

ATACCAGAAAATGCCAATCAAAGTATATTAGCTTGTACGGAAGTAATTTTTTTTTTAATTGATAAAAAATATATAAAAAGCT

GATTTTTTTCAAAATTCAAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTTATCCATAAAACTGTTTCAGCATAGT

CAAAA

ATACCAGAAAATACCAAATAAGTAGGCTAGCTTGTACGGAAGTAATTTTTTTTTTAAATTGATAAAAATATATAAAAGC
TGATTTTTTCAAAAATTCAAAAGTATGGGAAAATCAATGGAGTCATTCTTTTTTATTCTATAAAACTGTTTACCATAG
TCAAAA
ATACCAGAAAATGCCGATCAAAGTATATTAGCTTGTACGGAAGTAATTTTTTTTTTAAATTGATAAAAATATATAAAAGC
TGATTTTTTCAAAAATTCAAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTATTCTATAAAACTGTTTACCATAG
TCAAAA
ATACCAGAAAATGCCAATCAAAGTATATTAGCTTGTACGGAAGTAATTTTTTTTTTAAATTGATAAAAATATATAAAAGC
TGATTTTTTCAAAAATTCAAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTATTCTATAAAACTGTTTACCATAG
TCAAAA
ATACCAGAAAATGCCAATCAAAGTATATTAGCTTGTACGGAAGTAATTTTTTTTTTAAATTGATAAAAATATATAAAAGC
TGATTTTTTCAAAAATTCAAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTATTCTATAAAACTGTTTACCATAG
TCAAAA
ATACCAGAAAATGCCAATAAAGAATATCAGCTTGTACGGAAGTATTTTTTTTTTAAATTGATAAAAATATATAAAAGCTG
ATTTTTTCAAAAATTCAAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTATTCTATAAAACTGTTTACCATAGTC
AAAA
ATACCAGAAAATGCCAATAAAGTATATCAGCTTGTACGGAAGTATTTTTTTTTTAAATTGATAAAAATATATAAAAGCTG
ATTTTTTGAAACTTCGAAAAGTACGATAAAATCATATGAAGTGCTTTTTTTTTCTTTCATAAAACTGTTAAGTATTGCC
GAAT
ATACCAGAAAATACCAAATAAGTAGGCTAGCTTGTACGGAAGTAATTTTTTTTTTAAATTGATAAAAATATATAAAAGC
TGATTTTTTCAAAAATTCAAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTATTCTATAAAACTGTTTACCATAG
TCAAAA
ATACCAGAAAATGCCGATCAAAGTATATTAGCTTGTACGGAAGTAATTTTTTTTTTAAATTGATAAAAATATATAAAAGCTG
ATTTTTTGAAACTTCGAAAAGTACGATAAAATCATATGAAGTGCTTTTTTTTTCTTTCATAAAACTGTTAAGTATTGCC
AAT

Nr of selected repeats 20 Similarity 0.942191

Consensus:

ATACCAGAAAATGCCaATCAAAGTATATTAGCTTGTACGGAAGTAATTTTTTTtAaATTGATAAAAATATATAAAAGC
TGATTTTTTCAAAAATTCAAAAGTATGGGAAAaTCAaATGGAGTCATTCTTTTTTATTcCATAAAAcTgTTcAgCATAG
TCAAAA

>Cele-UNSB01_1:11979429-11979575 Satlength=147 Nr of Repeats=6 RepeatLength=11
seed=AGTACTGTAG

AGTACTGTAGT

AGTACTGTAGG

AGTACTGTAGGATTACTGTATTTTTGAAAAAATTGGCTTTTCGTCTTTTGAAGTGATATTGGTTTGGAGTTAGTGGTG
GGATATGGTTGGG

GTACTGTAGTT

GTACTGTAGAG

GTACTGTAGG

Nr of selected repeats 4 Similarity 0.731481

Consensus:

aGTACTGTAGtn

>Cele-UNSB01_1:12045808-12046235 Satlength=428 Nr of Repeats=5 RepeatLength=42
seed=TCGGCAAATC

TCGGCAAATCGGCTATTCTGGTTTTTCAAAATTTGCCGAGC

TCGGCAAATTCGGCAAATCTCTTTTTTCAATATTTGCCGAGCAGGGCAAAT

TCGGCAAATTTGCCGTGCTTAACAACTCGGAAAATTTGATTTTTTTAAATGTTTTTTGGAGCACCAAACTACTGAA
TTCTTAACATCTGGTTTCTGAATAAGTCCGCGTAGTATGTCTGTTAAGCATCAAAATAGCTCAATTTTGTGTCATTT
TACTAAATTTTTGGCTAAAAAATCAATAGTTTTAGTCAAATTTGACTGTCAAATTTTTGACGTGTGCGGCAAATTTGC
AAATTTGCCGAGC

TCGGCAAATTCGGCAAATCTACTTTTTTGAATTTGCCGAGC

TCGGCAAATTCGGCAAATGCTGGTTTTTTTTAAATTTGCCGAAT

Nr of selected repeats 3 Similarity 0.723514

Consensus:

TCGGCAAATCGGCaAtTnCTggTTTTTtnAAAtTTGCCGAgc

>Cele-UNSB01_1:12056400-12056477 Satlength=78 Nr of Repeats=7 RepeatLength=11
seed=CAAAAAATGT

CAAAAAATGTC
CAAAAAATGTC
CAAAAAATGTC
CAAAAAATGTC
CAAAAAATGTC
CAAAAAATGTG
CAAAAAATGTG

Nr of selected repeats 7 Similarity 0.942280

Consensus:

CAAAAAATGTc

>Cele-UNSB01_1:12149612-12149804 Satlength=193 Nr of Repeats=15 RepeatLength=12
seed=TTAGGCTTAG

TTAGGCTTAGACTTAGGA
TTACGCTTAGGC
TTAGGCTTAGGC
TTAGGCTTAGACTATGGC
TTAGGCTTAGGC
TTAGGCTAAGGC
TAAGGCTTAGGCA
TAGGCTTAGTC
TTAAGCTTAGCT
TTAGGCTTAGGC
TTAGGCTTAGGC
TTAGGCTTAGGC
TTAGGCTTAGGC
TTAGGCTTAGGC
TTAGGCTTAGGC

Nr of selected repeats 11 Similarity 0.838695

Consensus:

TTAGGCTTAGGC

>Cele-UNSB01_1:12200484-12200598 Satlength=115 Nr of Repeats=7 RepeatLength=12
seed=CTAAGCCTAA

CTAAGCCTAAGCCTTTGTCTAAGT
CGAAGCCTAAGC
CTAAGCCTAAAC
CTAAGACTAAGC
CTAAACCTAAAC
CAAAGCCTAAAC
CTAAGCCTAAGACAAAGCCTAGACTTAAGC

Nr of selected repeats 5 Similarity 0.766667

Consensus:

CtAAgcCTAAaC

>Cele-UNSB01_1:12310642-12315079 Satlength=4438 Nr of Repeats=373
RepeatLength=11 seed=CACATTTTTT

CACATTTTTTA
CACATTTTTTG
CACAATTTTTTA
CACAATTTTTTA
CACATTTTTTG
CACATTTTTTG
CACATTTTTTA
CACATTTTTTGAACATTTTTTCG

CACATTTTTTA
CACATTTTTTG
CACATTTTTCG
CACATTTTTTTG
CACATTTTTTG
CACATTTTTTG
CACATTTTTTG
CACAATTTTTG
CACATTTTTTA
CACATTTTTCG
CACATTTTTTTG
CACATTTTTTTG
CACCTTTTTTG
CACATTTTTTG
CACATTTTTTA
CACAATTTTTA
CACATTTTTTA
CACAATTTTTA
CACATTTTTTG
CACATTTTTCG
CACATTTTTTTG
CACATTTTTCG
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CACATTTTTCG
CACATTTTTTTG
CACATTTTTCG
CACATTTTTTTG
CACATTTTTTA
CACAATTTTTA
CACATTTTTTA
CACAATTTTTA
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CACATTTTTTG
CACATTTTTCG
CACATTTTTTTG
CACATTTTTTG
CACCTTTTTTG
CACAATTTTTG
CACATTTTTA
CACAATTTTTA
CAAATTTTTTA
CACAATTTTTA
CACATTTTTTA
CACAATTTTTA
CACATTTTTTG
CACATTTTTTG
CACATTTTTTA
CACATTTTTTTGAACATTTTTCG
CACATTTTTTTG
CACATTTTTTG
CACAATTTTTG
CACATTTTTTA
CACATTTTTTG
CACATTTTTCG

CACATTTTTTTG
CACATTTTTTTG
CACATGTTTTG
CACAATTTTTG
CACATTTTTTA
CACAATTTTTG
CACATTTTTTA
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CACTTTTTTTG
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CACATTTTTTA
CACAATTTTTA
CACATTTTTTTG
CACATTTTTTTG
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CACATTTTTTTG
CACATTTTTTAA
CACTTTTTTTGA
ACATTTTTTTG
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CACATTTTTTA
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CACTTTTTTTG
CACAATTTTTG
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CACATTTTTTTG
CACAATTTTTG
CACATTTTTTA
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CACATTTTTCG
CACATTTTTTTG
CACATTTTTTA
CACAATTTTTA
CACTTTTTTTG
CACATTTTTTACAAATTTTTCG
CACATTTTTTTG
CACATTTTTTA
CACAATTTTTA
CACATTTTTTTG
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CACATTTTTTA
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CACTTTTTTTG
CACAATTTTTG
CACTTTTTTTA
CACATTTTTTTGAACATTTTTTCG
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CACATTTTTTA
CACAATTTTTG
CACTTTTTTTGA
ACATTTTTTTG
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CACATTTTTTTG
CACATTTTTTA
CACTTTTTTTGAACATTTTTTCG
CACTTTTTTTG
CACAATTTTTG
CACTTTTTTTA
CACATTTTTCG
CACATTTTTTTG
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CACAATTTTTG

CACATTTTTTA
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CACATTTTTTTA
CACAATTTTTTG
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CACAATTTTTTA
CACTTTTTTTG
CACATTTTTTTA CAAATTTTTTCG
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CACATTTTTTTG
CACCTTTTTTTG
CACAATTTTTTG
CACATTTTTTA
CACAATTTTTTA
CAAATTTTTTTA
CACAATTTTTTA
CACATTTTTTTA
CACAATTTTTTA
CACATTTTTTTG
CACATTTTTTTG
CACATTTTTTTA
CACATTTTTTTG AACATTTTTTCG
CACATTTTTTTG
CACATTTTTTTG
CACAATTTTTTG
CACATTTTTTTA

CACATTTTTTG
CACATTTTTCG
CACATTTTTTTG
CACATTTTTTG
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CACATTTTTTA
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CACATTTTTTA
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CACATTTTTTG
CACATTTTTAA
CACTTTTTTTGA
ACATTTTTTG
CACATTTTTTACAAATTTTTTCG
CACATTTTTTG
CACATTTTTTA
CACTTTTTTTGAACATTTTTTCG
CACTTTTTTTG
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CACATTTTTCG
CACATTTTTTTG
CACAATTTTTTCGCA
CACTTTTTTG
CACATTTTTTG
CACATTTTTTG
CACAATTTTTGCAGAATTTTAGCACAATCTTAG

Nr of selected repeats 292 Similarity 0.843776

Consensus:

CACAtTTTTTg

>Cele-UNSB01_1:12330775-12330985 Satlength=211 Nr of Repeats=7 RepeatLength=30

seed=GTCATTATCA

GTCATTATCAGCTTCTAGTGTCTTAGAAGA

GTCATTATCAGCTTCTGGTGTCTTAGAAGA

GTCATTATCAGCTTCTGGTGTCTTAGAAGA

GTCATTATCAGCTTCTGGTGTCTTAGAAGA

GTCATTATCAGCTTCTGGTGTCTTAGAAGA

GTCATTATCAGCTTCTGGTGTCTTAGAAGA

GTCATTATCAGCTTCTGGTGTCTTCGAAGA

Nr of selected repeats 7 Similarity 0.974603

Consensus :

GTCATTATCAGCTTCTGGTGTCTTAGAAGA

>Cele-UNSB01_1:12340678-12340816 Satlength=139 Nr of Repeats=10 RepeatLength=12

seed=TAAGCCTAAG

TAAGCCTAAGCG

TAAGACTAAGCCTGTGCC

TAAGCCTAAGCT

TAAGCCTAAGCCTAAGCCA

TAGCCTAAGCC

TAAGCCTAAGCC

TAAGACTAAGCC

TAAGCCTAAGCC

TAAGCCTAAGAC

TAAGCCTAAGCCTAAGCC

Nr of selected repeats 6 Similarity 0.859259

Consensus :

TAAGCCTAAGCc

>Cele-UNSB01_1:12350087-12350549 Satlength=463 Nr of Repeats=41 RepeatLength=11

seed=TTGCACATTTT

TTGCACATTTT

TTGCACATTTTC

TTGCACATTTTTT

TTCACATTTTTTGCACATTTTC

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTTTT

TTCACATTTTTTGCACATTTTC

TTGCACATTTT

TTGCACATTTT

TTGCCCATTTTTTAGCCCATTTTTT

TTGCACATTTT

TTGCACATTTT

TCGCACATTTG

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCCCATTTT

TTGCCCATTTTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTT

TTGCACATTTT

TTGCACATTTT

TTGCACATTTT

TTGCCCATTTT

TTGCCCATTTTTT

TTGCACATTTT
TTGCACATTTT
TTGCACATTTT
TTGCACATTTT

Nr of selected repeats 31 Similarity 0.961681

Consensus:

TTGCACATTTT

>Cele-UNSB01_1:12396670-12396802 Satlength=133 Nr of Repeats=9 RepeatLength=12

seed=GCCTAAGCCT

GCCTAAGCCTAA

GCCTAAGCCTAT

GCCTATGCCTTAGACCAATCCCAA

GCCTAAGCCTAT

GCCTAAGCCTGG

GCCTAAGACTGG

GTCTAAGCCTAA

GCATAAGCCTAA

GCCTAATCCTAAGCTTAAGCATAA

Nr of selected repeats 7 Similarity 0.767196

Consensus:

GCCTAAGCCTan

>Cele-UNSB01_1:12413207-12413533 Satlength=327 Nr of Repeats=4 RepeatLength=73

seed=AATAAAATAT

AATAAAATATATGAAACCCCTCTTAAAAAGTTACAAGAAGGTTTTTTCCTTGCGCTTTGAGCGCAAAGAAAAGAAAAGA

GCTATTTAGACTTAGGGTGCCCAACTGG

AATAAAATATAGAAAATCCTTATGACACACTTAAGCCTAAAGGCCCGAAAAACATACTAGGATGCCCAACTGG

AATAAAATATTGGAAATCCCTATGACACACTTAAGCCTAAAGGCCCGAAAAACATACTAGGATGCCCAACTGG

AATAAAATATTGGAAATCCCTATGACACACTTAAGCCTAAAGGCCCGAAAAACATACTAGGATGCCCAACTGG

Nr of selected repeats 3 Similarity 0.963470

Consensus:

AATAAAATATtGgAAATCCcTATGACACACTTAAGCCTAAAGGCCCGAAAAACATACTAGGATGCCCAACTGG

>Cele-UNSB01_1:12444291-12444339 Satlength=49 Nr of Repeats=4 RepeatLength=12

seed=GCCTAAGCCT

GCCTAAGCCTAA

GCCTAAGCCTAG

GCCTAAGCCTGA

GCCTAGGCCTAT

Nr of selected repeats 4 Similarity 0.796296

Consensus:

GCCTAaGCCTaa

>Cele-UNSB01_1:12478910-12479068 Satlength=159 Nr of Repeats=5 RepeatLength=34

seed=ATGCACCATG

ATGCACCATGCCAAAAAATATATCCAAAACTCCG

ATGCACCGTGTCCAAAAGTATATATAAAATTGCG

ATGCACCATGTTAAAAAATATATCCAAAAATATG

ATGCTCCATGTTTTAAAAATACG

ATGCACCATGTCAAAAAGTATATCTTGAAGTATG

Nr of selected repeats 4 Similarity 0.712418

Consensus:

ATGCACCAtGtcaAAAAaTATATccaaAAntacG

>Cele-UNSB01_1:12487096-12487168 Satlength=73 Nr of Repeats=5 RepeatLength=12

seed=GGCTTAGGCT

GGCTTAGGCTTA

GGCTTCGGCTTA

GGCTTCGGCTTC
GGTTTAGGCTTA
GGCTTAGGTTTTGGTTGTGGCTTT
Nr of selected repeats 4 Similarity 0.814815
Consensus:
GGcTTaGGCTTa
>Cele-UNSB01_1:12700590-12700802 Satlength=213 Nr of Repeats=16 RepeatLength=12
seed=GAAATTTTTTT
GAAATTTTTTCC
GAAATTTTTTCC
GAACTTTTTTCC
GAAATTTTTTCA
GAAATTTTTTCT
GAAATTTTTTTTAAATTTTTTCC
GAAATTTTTTCC
GAAATTTTTTCT
GAAATTTTTTCC
GAAATTTTTTCT
GAAATTTTTTCC
GAAATTTTTTCT
GAAATTTTTTTTAAATTTTTTCCGA
AAATTTTTTCC
GAAATTTTTTCC
GAAATTTTTTCA
Nr of selected repeats 12 Similarity 0.915825
Consensus:
GAAATTTTTTCC
>Cele-UNSB01_1:12700867-12701490 Satlength=624 Nr of Repeats=50 RepeatLength=12
seed=AAAAAATTTTC
AAAAAATTTTCGGAA
AAAAAATTTTCGGAAAAATTA
AAAAAATTTTCGG
AAAAAATTTTCAG
AAGAAATTTTCGGAA
AAAAAATTTTCGGAAAAATTTTC
AAAAAATTTCCG
AAAAAATTTTCGGT
AAAAAATTTTCAG
AAAAAATTTTCGG
AAAAAATTTTCAG
AAAAAATTTTCGGT
AAAAAATTTTCAG
AAAAAATTTTCGA
AAAAAATTTTCAG
AAAAAATTTTCGG
AAAAAATTTACAG
AAAAAATTTTCGG
AAAAAATTTTCGG
AAAAAATTTTCAG
AAAAAATTTTCGG
AAAAAATTTTCAG
AAAAAATTTTCGA
AAAAAATTTTCAG

AAAAAATTTTCGG
AAAAAATTTTCAG
AAAAAATTTTCGG
AAAAAATTACAG
AAAAAATTTTCGG
AAAAAATTTTCGG
AAAAAATTTTCAG
AAAAAATTTTCGG
AAAAAATTTTCGG
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AAAAAATTTTCGGA
AAAAAATTTTCAG
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AAAAAATTTTCAG
AAAAAATTTTCGGT
AAAAATTTTCAG
AAAAAATTTTCGG
AAAAAATTTTCAG
AAAAAATTTTCGG
AAAAATTTTCAG
AAAAAATTTTCGA
AAAAAATTTTCGA

Nr of selected repeats 37 Similarity 0.905572

Consensus:

AAAAAATTTTCgG

>Cele-UNSB01_1:12702448-12702698 Satlength=251 Nr of Repeats=5 RepeatLength=50
seed=ACACATGCTA

ACACATGCTATAACATTGTCTCCTTCCCCTAGTGCACGAGAGCGGCCGTT
ACACATGCTATAACATTGTCTCCTTCCCTCTAGTGCACGAGAGCGGCCGCC
ACACATGCTATAACATTGTCTCCTTCCCCTAGTGCACGAGAGCGGCCGTT
ACACATGCTATAACATTGTCTCCTTCCCTCTAGTGCACGAGAGCGGCCGCC
ACACATGCTATAACATTGTCTCCTTCCCCTAGTGCACGAGAGCGGCCGTT

Nr of selected repeats 5 Similarity 0.952000

Consensus:

ACACATGCTATAACATTGTCTCCTTCCCCTAGTGCACGAGAGCGGCCGtt

>Cele-UNSB01_1:12783664-12784000 Satlength=337 Nr of Repeats=20 RepeatLength=16
seed=TGATCTGATG

TGATCTGATGATCTGA
TGATCTGATGATCTCA
TGATCTGATGGTCTGA
TGATCTGTTGATCTGA
TGGTCTGATGGTCTGA
TGATCTCATGATCTGA
TGATCTGTTGATCTGT
TGATCTGATGATCTGA
TGATCTGATGATCTGATGACCTGA
TCATCTGATGGTCTGA
TGATCTGTTGATCTGA
TGGTCTGATGGTCTGA
TAATCTGATGATCTGA
TGATCTGTTGATCTGT

TGATCTGATGATCTGA
TGATCTGTTGATCTGT
TGATCTGATGATTTGA
TGATCTGTTGATCTGT
TGATCTGATGATCTGT
TGATCTGATGATCTGATGACCTGA

Nr of selected repeats 18 Similarity 0.831699

Consensus:

TGATCTGaTGaTCTGa

>Cele-UNSB01_1:12807224-12807329 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=ACCACCCCTA

ACCACCCCTACAACCTACCACC
ACCACTCCTACAACAACCACT
ACCACCCCAACAACCACCACG
ACCACCCCTACAACCACGACC
ACCACCCCTACAACCTACGACC

Nr of selected repeats 5 Similarity 0.815873

Consensus:

ACCACcCctACAACnACcACc

>Cele-UNSB01_1:12834373-12834766 Satlength=394 Nr of Repeats=5 RepeatLength=32
seed=GCTGATTGGT

GCTGATTGGTTCAAAAGTGGGCGTGGCCAATC
GCTGATTGGTTTCAAGTTTGTGAAGGGTTTTTTGTGTTTCATGTTGAATTTTTGAAATACTGGAATGACACAAAAACAA
GAAACTTTCCAATAAACAGCGTATCTTTTGGGCTTAACCGTTTTGCAGATAGTACGCC
GCTGATTGGTTCAAAAGTGGGCTTGGCTTATG
GCTGATTGGTCTACGTTTTATGGACGTTTTTCATGAAGCTAATATCGATTTTTTTTTTTTTTAAAGAACTTCAAATTATT
ACCCGAATCGCTAGATCACCAGAAAAAGTGAGATTTTTCAACAGTAGCTCATCTTTTGAATCTCCTGGCAGATGGGACG
CC

GCTGATTGGTTCAAAAGTGGGCGTGGCTATTC

Nr of selected repeats 3 Similarity 0.861111

Consensus:

GCTGATTGGTTCAAAAGTGGGCGTGGCtaaTc

>Cele-UNSB01_1:12842011-12842077 Satlength=67 Nr of Repeats=5 RepeatLength=12
seed=TACCTATAACC

TACCTATAACCTA
TACCTATAACCTT
TACCTATAACCTA
TACCTATAACCTA
TACCTATAACCTATAACCTA

Nr of selected repeats 4 Similarity 0.944444

Consensus:

TACCTATAACCTa

>Cele-UNSB01_1:12905958-12906024 Satlength=67 Nr of Repeats=5 RepeatLength=11
seed=TTTGGAGCGG

TTTGGAGCGGA
TTTGGAGCGGTTTCAGAGCGAT
TTCGGAGCGGT
TTTGGAGCGCA
TTTGGAGCGGG

Nr of selected repeats 4 Similarity 0.777778

Consensus:

TTtGGAGCGga

>Cele-UNSB01_1:13114799-13114994 Satlength=196 Nr of Repeats=5 RepeatLength=39
seed=TATTTTTAAT

TATTTTTAATTTAACCTACTTAAAAAGTAGGTCATGACC
TATTTTTAATTTAACCTACTTAAAAAGTAGGTCATGACC
TATTTTTAATTTGACCTACTTAAAAAGTAGGTCATGACC
TATTTTTAATTTGACCTACTTAAAAAGTAGGTCATGACC
TATTTTTAATTTAACCTACCTAAAAAGTAGGTCATGACC

Nr of selected repeats 5 Similarity 0.965812

Consensus:

TATTTTTAATTTaACCTACTTAAAAAGTAGGTCATGACC

>Cele-UNSB01_1:13115312-13116088 Satlength=777 Nr of Repeats=11 RepeatLength=23
seed=ACTACAAACT

ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA
ACTACAAACTACAAACTATGAAA

ACTACAAACTTGCAGGTAATCCACGAGAACGCTACTCCAACACCATCATCAACATCAATGGTTGGTCATGCAATGTCAG
TTATTTCCCGGATCAAAAAGTAGCGACAGAAGTATTTCTCCAATTGGGAAAAGTATTTCTCAATGAGTGGAGACTCTGGCGG
TGTCATATCAAAAACGACAGTTCCCGACAACATGGAAATGGATGGCGTCAAGCACAATCAGACATGCTCTCATCACTT
CCACACTCTCTTGCCACTATTTGTAATGTATGGACTGTTGTCCGAGGGCTCAGCCACCGATTGTACCAATTGGAACGA
ATAGTCAGTTGAGACGGCTTGTGCTCCATCTCCTATCACCTATTGCTCAATATCATAAGCACGCATTCCTAACGTCTCT
TGCGTTGGTTTTGGCTCACGCGGAGCACTGCGAAACCTACAGTAACCCCTTCGGAAACAGGATCCAGATCGAGCGACGTTT
GAGTATTCATCTGCACAATTGGATATTACTAATCTTTTGTATCACTTCAAGTTATTCATTTGAGGTAGAC

Nr of selected repeats 10 Similarity 1.000000

Consensus:

ACTACAAACTACAAACTATGAAA

>Cele-UNSB01_1:13121380-13121635 Satlength=256 Nr of Repeats=17 RepeatLength=15
seed=AAAAGGGGAT

AAAAGGGGATCTGCA
AAAAGGGGATCTGCG
AAAAGGGGATCGGCA
AAAAGGGGATCTGCG
AAAAGGGGATCGGCA
AAAAGGGGATCTGCA
AAAAGGGGATCTGCA
AAAAGGGGATCTGCG
AAAAGGGATCTGCA
AAAAGGGGATCTGCA
AAAAGGGGATCTGCA
AAAAGGGGATCTGCG
AAAAGGGGATCTGCA
AAAAGGGGATCTGCGA
AAAAGGGGATCTGCA
AAAAGGGGATCTGCG
AAAAGGGGATCTGCA

Nr of selected repeats 15 Similarity 0.935661

Consensus:

AAAAGGGGATCTGCa

>Cele-UNSB01_1:13132164-13132288 Satlength=125 Nr of Repeats=6 RepeatLength=21
seed=AATCCAATAT

AATCCAATATGGATTTTCT
AATCAAATATGGTTGAAATCT
AATCCAATATGGCCGAAATCT
AATCCAATATGGAACAATTCA
AATCCAATATGGACGAAATCT
AATCCAATATGGAACAAATCT

Nr of selected repeats 5 Similarity 0.790476

Consensus:

AATCcAATATGGAngAAaTcT

>Cele-UNSB01_1:13177981-13178228 Satlength=248 Nr of Repeats=13 RepeatLength=19
seed=CAAGGCACTA

CAAGGCACTAGAAAAGCGC
CAAGGTACTAGAAATGCGC
CAATGCACTAGAAATGCGT
CAAGGCACTAGGAATGCGC
CAAGGCAATAAAAAATGCGT
CAAGGCACTAGGAATGCGC
CAAGGCAATAAAAAATGCGT
CAAGGCACTAGGAATGCGC
CAAGGCAATAAAAAATGCGT
CAAGGCACTAGGAATGCGC
CAAGGCAATAAAGATGCGC
CAAGGCACTAGAAATGCGT
CAAGGCAATAAAAAATGCGC

Nr of selected repeats 13 Similarity 0.816464

Consensus:

CAAGGCActAgaAATGCGc

>Cele-UNSB01_1:13199796-13200258 Satlength=463 Nr of Repeats=10 RepeatLength=35
seed=GCCGGAAAT

GCCGGAAATTTTAATTTTCGGAAAATTAACGAAATGCCGATTTGCCGAAAATGTTTGATTCCGGCAAATT
GCCGGAAATTTTCAATTCTGGCAGTTTACCAATTT
GCCGGAAATTTTCAATTCTGGCAGTTTACCAATTT
GCCGGAAATTTTCATTTTCGGAAAATTAACGGTATGCCGATTT
GCTGGAAATTGTTAATTCCGGCAATTTGCCGATTT
GCAGGAAATTATCAATTCCGGCAAATTTACCGGTTT
GCCGGAACTTTTGAATTCAGCAATTTGCCGATTC
GCCGGAAATTTCTAAATTCAGCAATTTGCCGATTT
GCCGGAAATTTCTGAATTCGGCAATTTGCCAATTT
GCCGGAAATTTTCAATTCCGCAATTTGCCGTTCTCTGGAAATTTTCATTTTCGGCAAATCGGCAAAGTGCCGGAAAAA
TCAATTCCGGCGAATTACCGAGTT

Nr of selected repeats 7 Similarity 0.776871

Consensus:

GCcGGAAATtnTnAATTCcgGCAaTTTgCCgATTT

>Cele-UNSB01_1:13236201-13236854 Satlength=654 Nr of Repeats=16 RepeatLength=35
seed=ATTGCCGGAA

ATTGCCGGAAATTAATAATTTTCGGAAAATAGGCAT
ATTGCCGGAAATTGAAAAATGCAGGCAAATCGGCAT
ATTGCCGGAAATTGAAAAATGCAGGCAAATCGGCAA
ATTGCCGGAAATTGAAAAATTTTCGGCAAATCGGCAAACCGGTAA
ATTGCCGGAAATTGAAAAATTAGCTGCAAATTGCCAA
ATTGCCGGAAATTGAAAAATTTTCGGCAAATCGGCAAACCGGTAA
ATTGCCGGAAATTAATAATTTTCGGCAAATAGGTAA
ATTGCCGAAATTGAAAAATTTTCGGCAAATCGGCAAATGACAATTTACTGAAAACAAAAAATTCGGCAAATCGGCAAAC
CGGCAATTATTAATAATTTTCGGAAAATAGGCAA

ATTGCCGGAATTA AAAAATTTTGGGCAAATCGGAAA
ATTGCCGGACATGAGAATTTCCGGCAAATCGGCAT
ATTGCCGGAATTGAAAATTTTCGGCAAATCGGCAAACCGGTAA
ATTGCCGGAATTGAAAATTAGCTGCAA
ATTGCCGGAATTGAACATTTCCGACAAATCGGTAA
ATTGCCGGAATTGAAAATTTTCGGCAAACCGGTAA
ATTGCCGGAATTGAAAATTTCCGGCAAATCGGAAA
ATTGCCGGAATTA AAAATTTTCGGCAAATCGGTAA

Nr of selected repeats 10 Similarity 0.780741

Consensus:

ATTGCCGGAATTgAAAatTtccGGCAAATcGGnAa

>Cele-UNSB01_1:13241763-13242154 Satlength=392 Nr of Repeats=8 RepeatLength=14

seed=AGTTTGTAGT

AGTTTGTAGTCTGT

AGTCTGTAGTTTGT

AGTTTGTAGTTTGTAGTTTGTAGTTTGTATTCTCCAAAACCTACACGATTTTCAAAAATGCAATTTTGTAGTAATATCCGAAAAATCT

AAATTTTCCACCAAATTTTGTATTTTAAAAAGTTTGTATCTCCACCTAAATGACAATGAAACTTCAA

AGTTTGTAGTTTGT

AGTTTGTAGTTTGT

AGTCTGTAGTCTGT

AGTCTGTAGTCTGTAGTTTATAGCTGAATTTCCAAAACCTACACGATTTCCAAAAAGAAAATTTCTTATGTCAAATCTCA

AAAATCTGAATATTTCACTTAAATTTTACAATCACTGAAAGGCTTTTTGCACCTAAATAAAGACTGAAACTTCAA

AGTTTGTAGTTTGTAGTTTGT

Nr of selected repeats 5 Similarity 0.885714

Consensus:

AGTtTGTAGTtTGT

>Cele-UNSB01_1:13307625-13307715 Satlength=91 Nr of Repeats=4 RepeatLength=22

seed=TCGAGAAAAA

TCGAGAAAAAATCTGAAAAAAT

TCGAGAAAAAATGGAAAAATTC

TCGAGAAAAAATCTGAAAAAAT

TCGAGAAAAAATCTGAAAAAAT

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TCGAGAAAAAATCTGAAAAAAT

>Cele-UNSB01_1:13315136-13315216 Satlength=81 Nr of Repeats=5 RepeatLength=16

seed=AATACGGGAA

AATACGGGAATACGGG

AATACGGGAATACGGG

AATACGGGAATACGGG

AATACGGGAATACGGG

AATACGGGAATACGGG

Nr of selected repeats 5 Similarity 1.000000

Consensus:

AATACGGGAATACGGG

>Cele-UNSB01_1:13324034-13324147 Satlength=114 Nr of Repeats=5 RepeatLength=22

seed=TTTTTCTCG

TTTTTCTCGAATTTTTTCAGA

TTTTTCTCGAATTTTTTCAGA

TTTTTCTCGAATTTTTTCAGA

TTTTTCTCGAGAATTTTTCCATT

TTTTTCTCGAATTTTTTCAGA

Nr of selected repeats 4 Similarity 1.000000

Consensus:

TTTTTCTCGAATTTTTCAGA

>Cele-UNSB01_1:13379937-13380822 Satlength=886 Nr of Repeats=18 RepeatLength=39
seed=TTAAAAAGTA

TTAAAAAGTAGGTCATGACCTAATTTTAAATTTGACCTAC
TTAAAAAGTAGGTCATGACCTAATTTTAAATATGACCTAC
TTAAAAAGTAGGTCATGACCTACTTTTTTAAACGTGACCCACT
TTAAAAAGTAGGCCATGACCTACTTTTTTAACTTGACCTAC
TTAAAAAGTAGGTCATGACCTAATTTTAAATTTAGGTCAC
TTAAAAAGTAGGTCATGACCTAGATTTAATTTGACCTAC
TTAAAAAGTAGGTCATGACCTAAATTTAATTTGGGCATAC
TTAAAAAGTAGGTCATCACCTAATTTTAAATTTAGGTCAA
TTAAAAAGTAGGTCATGACCTAAATTTAATTTGGCCTAC
TTAAAAAGTAGGTCATGACCTAATTTTAAATTTAGGTCAC
TTAAAAAGTAGGTCATGACCTAAATTTAATTTGGCCTAC
TTAAAAAGTAGGTCATGACCTAATTTTAAATTTAGGTCAC
TTAAAAAGTAGGTCATGACCTAATTTTAAATTTGGCCTAC
TTAAAAAGTAGGTCATGACCTAATTTTAAATTTAGGTCAC
TTAAAAAGTAGGTCATGACCTAATTTTAAATTTGACCTAC
TTAAAAAGTAGGTCATGACTTAAATTTTAAATTTGACCTAC
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ATCCCGGCATTGGTCTCGCCACGCGCTCAACAAATCAATGGGATGTGCGTGGCGAGACCATTGCGCGAAAATGCGCGCG
CCTTTAAAGTCGTAGAAGTTGGAAAAAATGCACCTGTAATTTTAAATTTAGGTCAC
TTAAAAAGTAGGTCATGACCTACTTTTCAACTTGACCTAC

Nr of selected repeats 13 Similarity 0.822863

Consensus:

TTAAAAAGTAGGTCATGACCTAatTTTAAATTTGgcCtAC

>Cele-UNSB01_1:13456302-13456675 Satlength=374 Nr of Repeats=12 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGA
GTACTGTAGGA
GTACGGTAGGATTACTGTAGTTTAGGAAAAATTGAGTTTTGTCTTTTGAAGAGATATAGGTTTGGGGTTATTAGTGGGA
TATGGTCGGG
GTACTGTAGTA
GTACTGTAGGA
GTACTGTAGGA
GTACGGTAGGATTACTGTAGTTAATGAATAATTGTGTTTTTGTCTTTTGAAGAGATATAGGTTTGGGGTTATTAGTGGG
ATATGGTCGGG
GTACTGTAGTA
GTACTGTAGGA
GTACTGTAGGA
GTACGGTAGGATTACTGTAGTTAATGAATAATTGTGTTTTTGTCTTTTGAAGAGATATAGGTTTGGGGTTAGTAGTGGG
ATATGGTCGGGGTACT
GTACTGTAGGA

Nr of selected repeats 9 Similarity 0.952862

Consensus:

GTACTGTAGgA

>Cele-UNSB01_1:13456767-13461871 Satlength=5105 Nr of Repeats=124
RepeatLength=40 seed=AATGTTCCAG

AATGTTCCAGAActTTCTAGAAAAATCGAGAAAATTCTGA
AATGTTCCAGAActTTCTAGAAAAATCGAGAAAATTCTGA
AATGTTCCAGAActTTCTAGAAAAATCGAGAAAATTCTGA
AATGTTCCAGAActTTCTAGAAAAATCGAGAAAATTCTGA
AATGTTCCAGAActTTCTAGAAAAATCGAGAAAATTCTGG
AATGTTCCAGAActTTCTAGAAAAATAGAGAAAATTCTGGAAGTGTATGTGTGCCAAATTCTGA

AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGG
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGG
AATGTTCCAGAACTTTCTAGAAAAATGAGAAAATTCTGA
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGA
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGA
AATGTTCCAGAACTTTCTAGAAAAATGAGAAAATTCTGA
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGG
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGG
AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATTCTGA
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGG
Nr of selected repeats 118 Similarity 0.974311
Consensus:

AATGTTCCAGAACTTTCTAGAAAAATcGAGAAAATTCTGA
>Cele-UNSB01_1:13507191-13507550 Satlength=360 Nr of Repeats=18 RepeatLength=20
seed=AAAATAGATT

AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
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AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTTCACGA

Nr of selected repeats 17 Similarity 0.992157
Consensus:

AAAATAGATTGTTACACGAA
>Cele-UNSB01_1:13507576-13507758 Satlength=183 Nr of Repeats=7 RepeatLength=26
seed=CTCTGGCAGT

CTCTGGCAGTTCACTAAAATAAGTGG
CTCTGGCAGTTCACTAAAATAAGTGA
CTCTGGCAGTTCACTAAAATAAGTGG
CTCTGGCAGTTCACTAAAATAAGTGG
CTCTGGCAGTTCACTAAAATAAGTGG
CTCTGGCAGTTCACTAAAATAAGTGA
CTCTGGCAGTTCACTAAAATAAGTGA
CTCTGGCAGTTCACTAAAATAAGTGA

Nr of selected repeats 7 Similarity 0.941392
Consensus:

CTCTGGCAGTTCACTAAAATAAGTGg
>Cele-UNSB01_1:13634561-13638668 Satlength=4108 Nr of Repeats=158
RepeatLength=26 seed=TTTTAGGTGA
TTTTAGGTGAATGGTTAGAGTCATAA
TTTTAGGTGAATGGTTAGAGTCATAA
TTTTAGGTGAATGGTTAGAGTCATAA
TTTTAGGTGAATGGTTAAAGTCATAT

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TTTTAGGTGAATGGTTAGAGTCATAA
TTTTAGGTGAATGGTTAGAGTCATAA
TTTTAGGTGAATGGTTAGAGTCATAA
TTTTAGGTGAATGGTTAGAGTCATAC

Nr of selected repeats 157 Similarity 0.972948

Consensus:

TTTTAGGTGAATGGTTAGAGTCATAA

>Cele-UNSB01_1:13683275-13683450 Satlength=176 Nr of Repeats=5 RepeatLength=35
seed=TGAAAATTTTC

TGAAAATTTCCGGCAAATCCGGCAAATTTGTCGGAAT
TGAAAATTTCCGGCAAAACGGCAAATTTTCGAAAA
TGAAAATTTCCGGCAAATCCGGCAAATTTGTCGGAAT

TGAAAATTTCCGGCAAAACGGCAAATTTTCGAAAA
TGAAAATTTCCGGCAAATCGGCAAATGCGCGGAAT
Nr of selected repeats 5 Similarity 0.878095
Consensus:
TGAAAATTTCCGGCAAAtCGGCAAAtTgtCGgAAt
>Cele-UNSB01_1:13729567-13730578 Satlength=1012 Nr of Repeats=11
RepeatLength=14 seed=TAGTTTGTAG
TAGTTTGTAGTCACTGAGCCTCAATTAATATGCTATTGACAACCTTATGAATTAGGTGTTGGTATTAATTTAATTTAA
GAAAAGTTTCAAATTTGGTTGAGGCTAAAAGTTTTG
TAGTTTGTAGGAGTTTAGAGACTACAAACTACACAATAATTCCCCACCACCATAATTCATAAGAAACAAAGGAGATA
GGTGTAAATTTATGACAGGGGGGGGGGGGTCACATGGACATCTGGTGAAGGGAGGTATCCGTGTAATAAGATAC
CTCCAGTTGAAGACCAAAAAAAAAACTTTTTGATGGTTGAGGCTATCGGAGACTACAACTACAAAGCTGCAAAGCCTT
AACCAATTGTCCTTTTTAAGGCTATTTACACTATTTATATACAACCTTACATTTGACAAACGGTTAGTCACCACAAAA
TGACTAAGATATTAACCTTGATTTGTGAGAACTGGTTGAGGCTAACACTACAACTACAATATCGGCTTAGCCTCACC
AATTTTTTTTTTCAAATTTTATCAAGTTCATTGCTCCGTAGAATATTTGAGCATACAGTATTGTGTTTTCAAATTTAT
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AAACTCGTTGTGTTGCACATTATTAACCTATTGAATAACTATTAACCGTATTACAATACCTTAAAAATTTATG
Nr of selected repeats 7 Similarity 0.845805
Consensus:
TAGTTTGTAGTTTg
>Cele-UNSB01_1:13730896-13731271 Satlength=376 Nr of Repeats=11 RepeatLength=14
seed=TACAAACTAC
TACAAACTACAACTATAAAC
TATAAACTACAAAC
TACAACTACAAAC
TACAAGCTACAAAC
TACAAACTACAACTACAAGTAATTATTTACATAGTTAAGTCTATCTCATATGGTTTTAAAATTAATGTATGTTGAG
TTAACACAATGTGGCAATTGTTTATCGTTCTATGAAATGATGGAC
TACAAACTACAAAT
TACAAACTACAAAC
TACAAACTACAAAC
TACAAACTACAAAC
TACAAATCTACAATTTTACATATTAAGTTTATAGAAGTTTTAAAACAATCTCGAATGTTTTTAAAATTCATGTATGTT
GAGTTAACACAATTATTTATCGTTTTACAAGATGATAGAC
TACAAACTACAAAC
Nr of selected repeats 7 Similarity 0.918367
Consensus:
TACAAACTACAAAC
>Cele-UNSB01_1:13831060-13832042 Satlength=983 Nr of Repeats=52 RepeatLength=14
seed=TGTAGTATGT
TGTAGTATGTAGTT
TGTAGTATGTAGTT
TGTAGTATGTAGTT
TGTAGTATGTAGTA

TGAATTCCCGCCAAAACTTTTACAGAAAATT
TGAATTCCCGCCAAAATTTTTACAGAAAATT
TGAATTCCCGCCAAAACTTTTACAGAAAATT
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GAATTCCTCCGCTAAAAATTTTTCACAGAAATTT
TGAATTCCTCCGCCCCAAAATTTTTCACAGAAATTT

ATAGGTATAGGT
ATAGGTATAGGT
ATAGGTATAGGTATAGGT

Nr of selected repeats 10 Similarity 0.955556

Consensus:

ATAGGTATAGGT

>Cele-UNSB01_1:14006347-14006515 Satlength=169 Nr of Repeats=7 RepeatLength=21

seed=CAAAATTCGT

CAAAATTCGTCCGAAAATGCT
CAAAATTCGTCCGAAAATGGCCAAAATACGACCAAAAAAGGC
CAAAATTCGCCCAAAAATGCT
CAAAATTCGTCCGAAAATGCT
CAAAATTCGTCCAAAATGGC
CAAAATTCGTCCGAAAATGAC
CAAAATTCGTCCGAAAATAGC

Nr of selected repeats 6 Similarity 0.814646

Consensus:

CAAAATTCGTCCgAAAATnGct

>Cele-UNSB01_1:14038349-14038662 Satlength=314 Nr of Repeats=9 RepeatLength=35

seed=AATTCGGCA

AATTCGGCAATTTGCCAATTTACCGGACAATTTA
AATTCGGCAATTTGCCGATTTGCCGAAAATTTA
AATTCGGCAATTTGCCCATTTGCCGAAAATTTA
AATTCGGCAATTTGCCCATTTGCCGAAAATTTA
AATTCGGCAATATTCCAATTTGCCGAAACTTTC
AATTCGGCAATTTGCCGGTTGCCGAAAATTTT
AATTCGGCAATTTGCAAGCTAGACGGAAATGTTT
AATTCGGCAATTTGCCGATCTGGCGAAAATTTT
AATTCGGCAATTTGCCGGTTGCCGAAAATTTT

Nr of selected repeats 7 Similarity 0.756173

Consensus:

AATTCGGgCAATTTGCCnATtTGcCGGAAAaTTTa

>Cele-UNSB01_1:14122632-14123925 Satlength=1294 Nr of Repeats=19

RepeatLength=68 seed=TTGGTTGAGG

TTGGTTGAGGCTAGAAAATGTTGTAGTTTGTAGTGTGTTAGCCTCAACCAAAATTAATTTTTTTTTTAA
TTGGTTGAGGCTAGAAAATGTTGTAGTTTGTAGTGTGTTAGCCTCAACCAAAATTAATTTTTTTTTTAA

Nr of selected repeats 14 Similarity 0.987503

Consensus :

TTGGTTGAGGCTAGAAAATGTTGTAGTTTGTAGTGTGtTAGCCTCAACCAAAATTAATTTTTTTTTTAA
>Cele-UNSB01_1:14164675-14164835 Satlength=161 Nr of Repeats=8 RepeatLength=20
seed=AAAAAATAGA
AAAAAATAGATTGACATACG
AAAAAATAGATTAGCATAACC
AAAAAATAGATGGACATAACC
AAAAAATAGATTGACATAACC
AAAAAATAGATTGATATAACC
AAAAAATAGATTGACATAACC
AAAAAATAGATTGACATAACC
AAAAAATAGATTGACATGCC

Nr of selected repeats 8 Similarity 0.900000

Consensus :

AAAAAATAGATTGACATAACC
>Cele-UNSB01_1:14166580-14166640 Satlength=61 Nr of Repeats=5 RepeatLength=12
seed=GCCTAAGCCT
GCCTAAGCCTGA
GCCTAAGCCTAC
GCCTAAGCCTAA
GCCTGAGCCTAA
GCCTAAGCCTAA

Nr of selected repeats 5 Similarity 0.866667

Consensus :

GCCTaAGCCTaa
>Cele-UNSB01_1:14168111-14168331 Satlength=221 Nr of Repeats=5 RepeatLength=63
seed=TTTTTGACTA
TTTTTGACTACTGGA
TTTTTGACTACATTGC

TTTTTGACTACGAGTGTCTTTTTTCGCTACTGAGCGAAAAATAGCTACATTTCGCACTTTTGTG
TTTTTGACTACGGAATGTCTTTTTTCGCTACTGACTGAAAAATAGCTACATTTCGCACTTTTGGC
TTTTTGACTACGGAATGTCTTTTTTCGCTACTGACTGAAAAATAGCTACATTTCGCACTTTTGGAA
Nr of selected repeats 3 Similarity 0.876736

Consensus :

TTTTTGACTACgGaaTGTCTTTTTTCGCTACTGACTgAAAAATAGCTACATTTCGCACTTTTgnc
>Cele-UNSB01_1:14174364-14175224 Satlength=861 Nr of Repeats=15 RepeatLength=64
seed=GTAGTCAAAA

GTAGTCAAAAAGTCAAAAAGTGCGAATGTAGCTATTTTTTCAGTCAGTAGCGAAAAAGACATTCA
GTAGTCAAAAAGTCAAAAAGTGCGAATGTAGCTATTTTTTCAGTCAGTAGCGAAAAAGACATTCA
GTAGTCAAAAAGACAAAAGTGCGAATGTAGCTATTTTTTCAGTCAGTAGCGAAAAAGACATTCA
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GTAGTCAAAAAGACAAAAGTGCGAATGTAGCTATTTTTTCGGTCAGTAGCGAAAAAGACACTC
GTAGTCAAAAAGCAAT
GTAGTCAAAAATCCA

Nr of selected repeats 10 Similarity 0.982870

Consensus :

ATCAAAGGATCAAAGG
ATCAAAGGATCAAAGA
ATCTAAGGATCTAAGG
ATCTAAGGATCTAAGG
ATCTAAGTATCTAAGT
ATCTAAAGATCTAAAG
ATCTAAGGATCTAAGG
ATCTAAGGATCTAAGG
ATCTAAGGATCTAAGT
ATCTAAGTATCTAAAG
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ATCTAAGGATCTAAGG
ATCTAAGGATCTAAGG
ATCTAAGGATCTAAGG
ATCTAAGGATCTAAGG
ATCTAAGGATCTAAGA
ATCTAAGGATCTAAGG
ATCAAAGGATCAAAGG
ATCAAAGGATCAAAGGATCAAAGA
ATCTAAGGATCTAAGG
ATCTAAGGATCTAAGG

Nr of selected repeats 145 Similarity 0.924178

Consensus:

ATCTAAGGATCTAAGG

>Cele-UNSB01_1:14245984-14247232 Satlength=1249 Nr of Repeats=59

RepeatLength=16 seed=AGATCCTTAG

AGATCCTTAGGCTTAGGTTGCAAAGCTAAATTTCTTTGGGCTTATTTTGTCAAGCGAGTTCATGCAAATTCTCTTACAA
CTAGGGGAATTATGTTTACTATCAGTCTTTTAGGCTTCAGACTCTTACTATTAGGCTCAGACTCTTTGACGCAAATTAT
CAAGCTAGGGCCCTGAAAATTTCAATTTTGATAGTTATACATTTTGGATCAGCCCCCTTCGTTTTGGACCTAAGATTAA
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AGATCCTTAGTTCCCTT
AGATCCTTAGATCCTT
AGATCCTTAGATCCTT
AGATCCATAGATCCATAGATACCT
AGATCCATAGATCCTT
AGATCCTTAGATCCTT
AGATCCTTAGATCCTT
AGATCCATAGATCCATAGATACCT
AGATCCATAGATCCTT
AGATCCTTAGATCCTT
AGATCCTTAGATCCTT
AGATCCATAGATCCATAGATACCT
AGATCCATAGATCCTT
AGATCCTTAGATCCTT
AGATCCTTAGATCCTT
AGATCCATAGATCCATAGATACCT
AGATCCATAGATCCTT
AGATCCTTAGATCCTT
AGATCCATAGATCCATAGATACCT
AGATCCATAGATCCTT
AGATCCTTAGATCCTT
AGATCCATAGATCCAT
AGATCCTTCGACCCAT
AGATCCTTAGATCCTT

Nr of selected repeats 48 Similarity 0.862780
Consensus:

AGATCctTAGATCCTT

>Cele-UNSB01_1:14248002-14248098 Satlength=97 Nr of Repeats=6 RepeatLength=16

seed=AGGATCTAAG

AGGATCTAAGGATCTA

AGGATCTAAGGATCTA

AGGATCTAAGGATCTA

AGGATCTAAGGATCTA

AGGATCTAAGGATCTA

AGAATCTAAGGATCTA

Nr of selected repeats 6 Similarity 0.972222

Consensus:

AGGATCTAAGGATCTA

>Cele-UNSB01_1:14266018-14266935 Satlength=918 Nr of Repeats=5 RepeatLength=179

seed=CTACCCAAAT

CTACCCAAATTTTTGAAATTTGGAAATTTTTCAAAAATTCTCAAATTTTAAAAATCCCATAATTCAGCCAATTTTTGAG

ATTTTCAGATATTTTTTAATTTGAAAATTTCTGTTTGTCTTATCCATTAAACTATATCGCTGCATCTACATTTTTTCACAGT

ACCCCATGACTTTTCCCGATT

CTACCCAAATTTTTGAAATTTGGAAATTTTTCAAAAATTCTCAAATTTTCAAAAATCCCATAATTCAGCCAATTTTTGAG

ATTTTCAGATATTTTTTAATTTGAAAATTTCTGTTTGTCTTATCCATTAAACTATATCGCTGCATCTACATTTTTTCACAGT

ACCCCATGACTTTTCCCGATT

CTACCCAAATTTTTGAAATTTGGAAATTTTTCAAAAATTCTCAAATTTTCAAAAATCCCATAATTCAGCCAATTTTTGAG

ATTTTCAGATATTTTTTAATTTGAAAATTTCTGTTTGTCTTATCCATTAAACTATATCGCTGCATCTACATTTTTTCACAGT

ACCCCATGACTTTTCCCGATT

CTACCCAAATTTTTGAAATTTGGAAATTTTTTCAAAAATTCAAACCTGCAAAACCCATAACTCTGCCAAATTTGAAGA

TTTTTCAGATATTTTCTAATTTCAATTTACACATGAATTTCTAGTTTTTTTTTCCAAAAAAAATTGCCGCATCTACATCTTC

CACAGTACCCCATGACTTTTTCGCATAAATAG

CTACCCAAATTTTTGAAACTTTGGAGATTTTTCAAAAATTTCAAATTTTAAAAATCCCATAATTCAGCCAATTTTTGAGA

TTTTTCCAATACTTTTTACTTTCAAATTTACACATGAATTTCTAATTTTTTTTTTACTAAAAAATATATTGCCGCATCTAC

ATTTTCCACACTACCCCAAGAACTTTTCGCAATG

Nr of selected repeats 3 Similarity 0.995034

Consensus:

CTACCCAAATTTTTGAAATTTGGAAATTTTTCAAAAATTCTCAAATTTTcAAAAATCCCATAATTCAGCCAATTTTTGAG

ATTTTCAGATATTTTTTAATTTGAAAATTTCTGTTTGTCTTATCCATTAAACTATATCGCTGCATCTACATTTTTTCACAGT

ACCCCATGACTTTTCCCGATT

>Cele-UNSB01_1:14275073-14275913 Satlength=841 Nr of Repeats=24 RepeatLength=40

seed=TTCTGGAAA

TTCTGGAAAAGTCGGTAAAAATTTTGGAGTGTTCCTGAACT

TTCTGGAAAATTTTAGAAAAATTCGGGAATGTTCTGGAACC

TTCTGGAAAATTCGAGGAAATTCGGGAATGTTCTAGAACC

TTCTGGAAAATTCGATAAAGAACTGGAGTGTTCAGAACT

TTCTGGAAAATTCGATAAAAAATTCGGGAATGCTCTGGAACC

TTCTGGAAAATTCAGAAAAATTCGGGAATGCTCTAGAACC

TACTGGAAAATTTGATAAAA

TTCTGGAATATTCTACAACA

TTCTGCAAAAGTCGGTAAAAATTCGGGAATGTTCTAGAACC

TTCTGGAAAATTCAGAAAAATTCGGGAATGCTCTAGAACC

TTCTGGAAAATTCGCTAAAA

TTCTGGAATATTCTACAACA

TTCTGGAAAAGTCGGTAAAAATTCGGGAATGCTCTGGAACC

TTCTGGAAAATTTTAGAAAAATTCGGGAATGTTCTGGAACC

TTCTGGAAAATTCGCAAAAAATTCGGAGCGTTCTAGAACC

TACTGGAAAATTTGATAAAAAATTCGGCATATTCTACAACA

TTCTGCAAAAGTCGGTAAAAATTCGGGAATGTTCTAGAACC

TTCTGGAAAATTCAGAAAAATTCGGGAATGCTCTAGAACC

TTCTGGAAAATTTCGGTAAAA
TTCTGGAATATTGTACAACA
TTCTGGAAAAGTCGGAAAAATTTTGGAGTGTTCCCGAACT
TTCTGGAAAATTTTAGAAAAATTCCTGGAATGTTATGGAACC
TTCTGGAAAATTCAATAAAATTTCTGGAATGTTCCAGAACC
TTCTGGAAAATTTCGGTAAAATTCCTGGAATGTTCTGGAAC
Nr of selected repeats 18 Similarity 0.755338

Consensus:

TTCTGGAAAATCgatAAAAATCtGGAaTgtTctaGAACc

>Cele-UNSB01_1:14343732-14344621 Satlength=890 Nr of Repeats=4 RepeatLength=62
seed=GTAGTTTGTA

GTAGTTTGTAGCCTGAGCCTCACCAAATTCGATTCTGTGTTTAATTCTTGATTTCTAGTTGATTTTCGCCGTTTTT
TTTTGCTTTTTTCTTTCTTTTCTCCCGCAAACCCAATTTTCCCTTTAAAAAACCCCGTTTTTTCCAGATGGTGCAT
TCAAACGGAGCCATCACGAGCACAATTCTGAAGGCTCGTCACGCCGACGTCGTCGCAAGACGTCACCTCACACGCCA
ACGACTTGACACTCATCGATCTCGTGCTCAATGTGCAGCGGCTTTTGGCTCTCCCATCCGACGCGAATTTTCGTGTTGAA
GTACAAGGATGAAGGTAGGAATTGCACTGAAAATTGCGATTTTAATTCAATTTTGTCAATTTTAGAAGGCGATTTGGT
GACACTCGCCGAGGATAGCGACCTCCTGCTGGCTCTTACACGCTCTGGAGCCACGCTCGACGTGACCGTCGTTGTGAC
TCGAGAGCTCGTGAGGCTGTGCACGATGTGCAGAAGCAAGTCGAGCAGATTAAGGTAAGGAGGATTTTGAGCGAAAAA
AACGATTTTTGAGCTGAAAAGCGCAATTTTGTAGCGGAAAAATGCAAAATGTTGCAGAAATTTTCATCGAAAATGCTGCAT
TTTTGAGCTTTTTAGACAAAAAAAATCCGGAAAAACACTGAAAATGTTGGTTGAGGCTAAGAAACAAGT
GTAGTTTGTAGTGTGAGCCTCAACCAAAGCTTAGCTAAAGCTTGTAGTGAGGCTATGGTGATTTT
GTAGTTTGTAGCTTTAGCCTCAACCAAATTAGCTAAAGCTTGTAGTGAGGCTATGGTGATTTT
GTAGTTTGTAGCTTTAGCCTCAACCAAATTAGCTAAAGCTTGTAGTGAGGCTATGGTGATTTT
Nr of selected repeats 3 Similarity 0.928315

Consensus:

GTAGTTTGTAGCtTtAGCCTCAACCAAAtTAGCtAAAGCTTGTAGTGAGGCTATGGTGATTTT

>Cele-UNSB01_1:14381938-14382071 Satlength=134 Nr of Repeats=7 RepeatLength=19
seed=CCCTGATACC

CCCTGATACCCCTGGTCC
CCCTGATACCCCGGTCCC
CCCTGATACCCCTAGCCT
CCCTGATGCCCCCTAGTCT
CCCTGATACCCCTAGTCT
CCCTGATACCCCTAGTCC
CCCTGATACCCCGGGTCC

Nr of selected repeats 7 Similarity 0.788889

Consensus:

CCCTGATACCCCTaGTcC

>Cele-UNSB01_1:14392151-14393037 Satlength=887 Nr of Repeats=5 RepeatLength=177
seed=CTAACAAAAT

CTAACAAAATAATTAGCGTAAAAATTTCTACATTTTACTAGTTAACAATATTTTGTAGCATCAGTGGTTTTTGTAGATA
CAGAAGTTATAAGATGTACGTCCAAAAATGATTGTGAGCTGCTCTTATCAAAAAATACCATAACTTTTTACTACTAAC
GGTATCAAAAATGTTTTAA
CTAACAAAATAATCAGCGTAAAAATTTCTACATTTTACTAGTTAATAATATTTTGTAAACATCAGTGGTTTTTAAGTTA
CGCAAGTTTTAAGGTGAGCGCCAAAAATAGTTGTGAGAAGGTTAATCAAAAACCGGTATAATTTTTTACACACTAAC
GATATCAAAAATGTTTTAA
CTAACAAAATAATCAGCGTAAAAATTTCTACATTTTACTAGTTAACAATGTTTTGTAGCATTAGTGGTTTTTGTAGATA
CGCAAGTTTTAAGGTGGGCGCCAAAAATAGTTGTGAGCAGGTTAATAAAAAACCGACATAACTTTTTACTACTAAC
GGTATTA AAAATGTTTTAA
CTAACAAAATAATCAACGTAAAAATTTCTATATTTTATTAGTTAGCAACTTTCAAATAACATTACTGTTTTTTGTAGATA
AGCATGGTTAAAGGTAGACGCTCAAAAATGTCTGCGAGCGGCTTTTCTTTAGAGTGATATAACTCCTTGCTCATGAAC
GCTAGCAAAAATCTTTCAA

CTAACAAAATAATTAACGTAAAAATTTTTCTATATTTTCTTTCTGAACAACCTTTCTTAAAGCGTTAGTAGTTTTTAAGTT
ACGCAAGTTATAAGATATAGTGCCGAAAATGTCTGCGTGCTGCTTTAATCAAAAACCTACATAACTTTTTACAGAATAA
CGACATCAAAAATATTTTCAG

Nr of selected repeats 4 Similarity 0.721286

Consensus:

CTAACAAAATAATcAgCGTAAAAATTTcCTAcATTTtAcTAGTTAacAAaTtTtgATAaCATcAgTGgTTTTTgAGaTA
cgcAaGtTttAAGgTggaCGccCAAAAATagTTGtGAGcaGcTtTaatcaaAaAccgacATAAcTttTTaCtCActAAC
GgTAtcAAAAATgTTTTAA

>Cele-UNSB01_1:14511380-14511819 Satlength=440 Nr of Repeats=17 RepeatLength=22
seed=GCACGGCCTG

GCACGGCCTGGTAGTCCCTGAGGGCGCGACCTTTTCGGTCTGAGG
GCATGGCCTGACGGTCCTGAGG
GCATGGCCTGGCAGTCCAGAGG
GCATGGCCTGGCAGTCCGAGA
GCACGGCCTGGTGGTCTGAAAG
GCACGGCATGGCAGTCCGAGA
GCACGGCCTGTCATTACTGACG
GCACGGCCTGGCGGTCCGGAGG
GCACGGCCTGGCGGTCTGAGG
GCACGGCCTCACGGTCTGAGG
GCACGACCTGGGGGGCCCTGAAAACACTCTTTGGGGGCCAGAAAA
CACGGCCTGACGGTCCTGAGG
GCACGGCCTGAGAGTCCCTGAAGGCCGAGTGTTCGGTCTGAGG
GCATGGCCTGGTAGTCCCTGAGA
GCACGGCCTGGTGGTCTGATG
GCACGGCCTGTCATTACTGAGA
GCACGGCCTGGTGGTCTCAGG

Nr of selected repeats 13 Similarity 0.701226

Consensus:

GCACGGCCTGgcgGTCTGAGg

>Cele-UNSB01_1:14535288-14535435 Satlength=148 Nr of Repeats=8 RepeatLength=15
seed=GGGGCAACA

GGGGCAACAAAAA
GGGGCAACATTTGAACTCTCCCT
GGGGCAACAAATTA
GGGGCAACATTTTCATAAATGTA
GGGGCAGCAAAAAA
GGGGCAACATAATA
GGGTCAACATTTGAACTCTCCCC
GGGGCAACAAATTA

Nr of selected repeats 5 Similarity 0.822222

Consensus:

GGGGCAaCAaAatA

>Cele-UNSB01_1:14537614-14537761 Satlength=148 Nr of Repeats=8 RepeatLength=15
seed=TGTTGCCCCC

TGTTGCCCCCTAATT
TGTTGCCCCCGGGGAGAGTTCAAA
TGTTGACCCCTATTA
TGTTGCCCCCTTTTT
TGCTGCCCCCTACATTTATGAAAA
TGTTGCCCCCTAATT
TGTTGCCCCCGGGGAGAGTTCAAA
TGTTGCCCCCTTTTT

Nr of selected repeats 5 Similarity 0.822222

Consensus :

TGTTGcCCCCTatTt

>Cele-UNSB01_1:14566637-14566717 Satlength=81 Nr of Repeats=4 RepeatLength=20
seed=ATATCAAAAAA

ATATCAAAAAATAGATTGAC

ATACCAAAAAATAGATTGGC

ATATCAAAAAATAAATTGGC

ATATCAAAAAACAAATTGGC

Nr of selected repeats 4 Similarity 0.855556

Consensus :

ATAtCAAAAAAtAaATTGgC

>Cele-UNSB01_1:14568940-14569168 Satlength=229 Nr of Repeats=4 RepeatLength=14
seed=TGTAGTTTGT

TGTAGTTTGTAGTT

TGTAGTTTGTAGTG

TGTAGTTTGTAGTT

TGTAGTTTGTAGTTTGTAGAAAACCTTTCAAAGCTCTTTTGAGAGTTACCAAAAAACGTTTTTTTTGGGAATTTTGAATT

TTTCAAATTTATAATATTTTCAGTATTTTTTTTTTCTTTGTAACATTCCAAAAACTGTCAAAAAAAAACAACTCATCA

AATTCCAAGTTTTCTTAAATTTGAAGAT

Nr of selected repeats 3 Similarity 0.936508

Consensus :

TGTAGTTTGTAGTt

>Cele-UNSB01_1:14574460-14574865 Satlength=406 Nr of Repeats=4 RepeatLength=101
seed=GCATTTGCAT

GCATTTGCATATAGAGATCAGATAAAAAGTTAGAATTTTCCAGCCGTTGCAAGTGCGCTCTATTGAGAACATTTTGAAAA

TTGAATGTTTTCAAATTAGAGC

GCATTTGCATATCGAGATCAGATAAAAAGTTAGAATTTTCCAGCCGTTGCAAGTGCGCTCTATTGAGAACATTTTGAAAA

TTGAATGTTTTACATTAGAGC

GCATTTGCATATGAAGGTTCAGATAAAAATTTGAATATTCGAGTAGTTGCAAGTGCGCTTTAATGAGAAAATCTTAAAT

CTGCATGTTTTACATTAGAGA

GCATTTGCATATCGAGGTTAGATAAAAAGTTGAATTTTCCAGTTGTTGCAAGTCCGCTCTATTGAGAAAATCTTGAAA

ATTGAATGTTTTACATTAGAGC

Nr of selected repeats 3 Similarity 0.826797

Consensus :

GCATTTGCATATngAGaTCAGATAAAAgtTaGAATtTTCcAGccGTTGCAAGTGCGCTcTAtTGAGAAcAtTTgAAAA

TTGaATGTTTTCAcATTAGAGc

>Cele-UNSB01_1:14577219-14577388 Satlength=170 Nr of Repeats=5 RepeatLength=23

seed=GCACCATAAG

GCACCATAAGGATCACATAATCATAACGAACCTTAGAGCATCACAGTAGAT

GCATCATAAGGACTCTAGTTGAT

GCATCATAAGGATCATAGTTGAT

GCACCATAAGGATTATAGTAGAA

GCACCATAAGAACCACAGAACCATACGGATCTCAGAGCACCAGTGTAGAT

Nr of selected repeats 3 Similarity 0.726852

Consensus :

GCAtCATAAGGATcaTAGTtGAt

>Cele-UNSB01_1:14582954-14583490 Satlength=537 Nr of Repeats=26 RepeatLength=18
seed=TTGTAGATCA

TTGTAGATCAGCGGGGTC

TTGTAGATCAACGGGGGTC

TTGTAGATTAACGGGGGTC

TTGTAGATCAACGGGGGTA

TTGTAGATCAACGGGGGTC

TTATAGATCAACGGGGGTA

TCGTAGATCAACGGGGTC
TTATAGATCAACGGGGGA
TTGTAGATCAACGGGAGTC
TTGTAGATCATTGTTTCAGACTAGCTTAACGGGGTC
TTGTAGATCAACGGGGTC
TTGTAGATCATTGTTTCAGTGTAGCTTAACGGGGTC
TTGTAGATTAACGGGGTC
TTGTAAATCAACGGGGTC
TTGTAAATCAACGGGGTA
TTGTAGATCAACGGGGTG
TTGTAGATCAACGGGGTG
TTGTAGATCAACGGGAGTC
TTGTAGATCATTGTTTCAGACTAGCTTAACGGGGTC
TTGTAGATCAACGGGGTC
TTGTAGATCATTGTTTCAGTGTAGCTTAACGGGGTC
TTGTAGATTAACGGGGTC
TTGTAAATCAACGGGGTC
TTGTAAATCAACGGGGTA
TTGTAGATCAACGGGGTC
TTGTAGATCAACGGGGCC

Nr of selected repeats 22 Similarity 0.869489

Consensus:

TTGTAGATCAACGGGGTc

>Cele-UNSB01_1:14647518-14647641 Satlength=124 Nr of Repeats=4 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGA

GTACTGTAGGA

GTACTGTAGGATTACTGTAGTTTAGGAAGAATTGAGTTTTTGTCTTTTGAAGAGATATAGTTTTGCGGTTAGTGGTGGG
ATATGGTCGGG

GTACTGTAGTA

Nr of selected repeats 3 Similarity 0.919192

Consensus:

GTACTGTAGgA

>Cele-UNSB01_1:14648049-14648258 Satlength=210 Nr of Repeats=6 RepeatLength=35
seed=AATTTAAATT

AATTTAAATTTTCTGCGAAAAATGTTTTAGCGGGA

AATTTAAATTTTCTGAAAAAATATTTTGGAGGGA

AATTTAAATTTTCTGAAAAAATATTTTGGAGGGA

AATTTAAATTTTCTGTGAAAAAATATTTTGGCGGGT

AATTTAAATTTTCTGAGAAAAAATATTTTGGAGGGA

AATTTAAATTTTCTGAGAAAAAATATTTTGGCGGGA

Nr of selected repeats 5 Similarity 0.859048

Consensus:

AATTTAAATTTTCTgAgAAAAAataTTTTgGcGGGa

>Cele-UNSB01_1:14674978-14675094 Satlength=117 Nr of Repeats=10 RepeatLength=12
seed=ATATGTATAT

ATATGTATAT

ATATATATAT

ATATGTATTTGT

ATATGTATATGT

ATATGTATATGT

ATATGCATATGC

ATATGTATATGT

ATATGTATATG

TATGTATATGTAT

ATATGTATATGT

Nr of selected repeats 6 Similarity 0.888889

Consensus:

ATATGTATATGT

>Cele-UNSB01_1:14687699-14688279 Satlength=581 Nr of Repeats=8 RepeatLength=73

seed=TGTCGGCCGC

TGTCGGCCGCTACCAAATAAGCACCTTTTAGCACTACGTTGCGCACACACACCAAACCTGCGGAACCCCTAACA

TGTCGGCCGCTCTAAACTATTTTGCATACACACCAAGCTACTTGTTCACGCCAAGCTGCGGAACCTCGAAAG

TGTCGGCCGCTTCCAAATAACTACCTTTTACATAATGTTGCGCACACCTCAAGCTGCGGGACCCCTGAACG

TGTCGGCCGCTACCAAATAAGCACCTTTTAGCACTACGTTGCGCACACACACCAAACCTGCGGAACCCCTAACA

TGTCGGCCGCTCTAAACTATTTTGCATACACACCAAGCTACTTGTTCACGCCAAGCTGCGGAACCTCGAAAG

TGTCGGCCGCTTCCAAATAACTACCTTTTACATAATGTTGCGCACACCTCAAGCTGCGGGACCCCTGAACG

TGTCGGCCGCTACCAAATAAGCACCTTCTAGCACTACGTTGCGCACACACACCAAACCTGCGGAACCCCTAACA

TGTCGGCCGCTCTAAACTATTTTGCACACACACCAAGCTACTTGTTCACGCCAAGCTGCGGAACCTCGAAAG

Nr of selected repeats 6 Similarity 0.624829

Consensus:

TGTCGGCCGCTaCcAAAcTAtttaGCanACaCaccaAGcaCTACgTTgcGcacaCACaCCAAaCTGCGGAACCCgAAc

Ag

>Cele-UNSB01_1:14694045-14694325 Satlength=281 Nr of Repeats=8 RepeatLength=35

seed=AAAATTTCCG

AAAATTTCCGGCAAATCGGCAATTTACCGAAAGTG

AAAATTTCCGGCAAATCGGCAATTTACCGAAAGTG

AAAATTTCCGGCAAATCGGCAATTTACCGAAAGTG

AAAATTTCCGGCAAATCGGCAATTTACCGAAAGTG

AAAATTTCCGGCAAATCGGCAATTTACCGAAAGTG

AAAATTTCCGGCAAATCGGCAATTTGTGCGAAAACG

AAAATTTCCGGCAAATCGGCAATTTACCGAAAGTG

AAAATTTCCGGCAAATCGGCAATTTACCGAAAGTG

Nr of selected repeats 8 Similarity 0.952381

Consensus:

AAAATTTCCGGCAAATCGGCAATTTACCGAAAGTG

>Cele-UNSB01_1:14697056-14704541 Satlength=7486 Nr of Repeats=214

RepeatLength=35 seed=GAAATTTTCA

GAAATTTTCACTTTTCGGCGAAGTGCCGATTTGCCG

GAAATTTTCACTTTTCGGTAAACTGCCGATTTACCG

GAAATTTTCACTTTTCGGTAAATATTTGCCG

GAAATTTTCACTTTTCGGCGAAGTGCCGATTTGCCG

GAAATTTTCACTCTCGGTAAATGCGGATTTAGCCG

GAAATTTTCACTTTTCGGTAAATATCGGATTTGCCA

GAAATTTTCACTTTTCGGTAAATGCGGATTTGGCA

GAAATTTTCACTTTTCGGTAAATGCGGATTTGCCG

GAAATTTTCACTTTTCGGTAAATGCGGATTTGCCG

GAAATTTTCACTTTTCGGTAAATATCGGATTTGCCA

GAAATTTTCACTTTTCGGTAAATGCGGATTTGCCG

GAAATTTTCACTTTTCGGTAAATGCGGATTTGGCA

GAAATTTTCACTTTTCGGTAAATGCGGATTTGCCG

GAAATTTTCACTTTTCGGTAAATGCGGATTTGGCA

GAAATTTTCACTTTTCGGTAAATGCGGATTTGCCG

GAAATTTTCACTCTCGGTAAATGCGGATTTAGCCG

GAAATTTTCACTTTTCGGTAAATATCGGATTTGCCA

GAAATTTTCACTTTTCGGTAAATGCGGATTTGGCA

GAAATTTTCACTTTTCGGTAAATGCGGATTTGCCG

GAAATTTTCACTTTTCGGTAAATGCGGATTTGCCG

GAAATTTTCACTTTCCGGTAAATATCCGATTTGCCA
GAAATTTTCACTTTCCGGTAAATTGCCGATTTGCCG
GAAATTTTCACTTTCCGGTAAATTGCCGATTTGGCA
GAAATTTTCACTTTCCGGTAAATTGCCGATTTGCCG
GAAATTTTCACTTTCCGGTAAATTGCCGATTTGCCG
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GAAATTTTCACTTTCCGGTAAATATCCGATTTGCCA
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GAAATTTTCACTTTCCGGTAAATTGCCGATTTGCCA
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GAAATTTTCACTTTCCGGTAAATTGCCGATTTGGCA
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GAAATTTTCACTTTCCGGTAAATTGCCAATTTGCCG
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GAAATTTTCACTTTCCGGTAAATATCCGATTTGCCG
GAAAATTTCACTTTCCGGTAAATTGCCGATTTGCCG
GAAATTTTCACTTTCCGGTAAATATCCGATTTGCCA
GAAATTTTCACTTTCCGGTAAATTGCCGATTTGCCG
GAAATTTTCACTTTCCGGTAAATTGCCGATTTGCCG
GAAATTTTCACTTTCCGGTAAATATCCGATTTGGCA
GAAATTTTCACTTTCCGGTAAATATCCGATTTGGCA
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GAAATTTTCACTTTCCGGTAAATTGCCGATTTGGCA
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GAAATTTTCACTTTCCGGTAAATATCCGATTTGGCA
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GAAATTTTCACTTTCCGGTAAATGCGGATTTGCCA
GAAATTTTCACTTTCCGGTAAATGCGGATTTGCCG
GAAATTTTCACTTTCCGGTAAATGCGGATTTGCCA
GAAATTTTCACTTTCCGGTAAATGCGGATTTGCCG
GAAATTTTCACTTTCCGGTAAATATCCGATTTGCCG
GAAATTTTCACTTTCCGGTAAATGCGGATTTGCCG

Nr of selected repeats 213 Similarity 0.929447

Consensus:

GAAATTTTCACTTTCCGGTAAATtgCGGATTTGCCg

>Cele-UNSB01_1:14726982-14727102 Satlength=121 Nr of Repeats=6 RepeatLength=20

seed=GTGAAATTTT

GTGAAATTTTGAAGTTT TAG

GTGAAATTTTAAATTTT GA

GTGAAATTTTGATTTCCGA

GTGAAATTTTGCATTTTAA

GTGAAATTTTAAATTTTAA

GTGAAATTTTAAAGTTT TAG

Nr of selected repeats 6 Similarity 0.705820

Consensus:

GTGAAATTTTaaAtTTTTaa

>Cele-UNSB01_1:14731269-14731934 Satlength=666 Nr of Repeats=19 RepeatLength=35

seed=GAAAATTTCC

GAAAATTTCCGGCAAACCGGCAAATGCGGGAATT

GAAAATTTCCGGCAACCCGGCAAATGCGGGAATC

GAAAATTTCCGGCAAACCGGCAAATGTCGGAATT

GAAAATTTCCGGCAAACCGGCAAATGCGGGAATC

GAAAATTTCCGTCAAACCGGCAAATGCGGGAATT

GAAAATTTCCGGCAAACCGGCAAATGCGGGAATT

GAAAATTTCCGGCAAATCGGCAAATGCCGGAATC
GAAAATTTCCGGCAAACCGGCAAATGCCGGAATT
GAAAATTTCCGGCAAATCGGCAAATGCCGGAATT
GAAAATTTCCGGCAAACCGGCAAATGCCGGAATT
GAAAATTTCCGGCAAATCGGCAAATGCCGGAATC
GAAAATTTCCGGCAAACCGGCAAATGCCGGAATT
GAAAATTTCCGGCAAATCGGCAAATGCCGGAATC
GAAAATTTCCGGCAAACCGGCAAATGCCGGAATT
GAAAATTTCCGTCAAACCGGCAAATGCCGGAAGC
GAAAATTTCCGGCAAACCGGCAAATGCCGGAATC
GAAAATTTCCGGCAAACCGGCAAATGCCGGAATT
GAAAATTTCCGTCAAACCGGCAAATGCCGGAATC
Nr of selected repeats 19 Similarity 0.939850

Consensus:

GAAAATTTCCGGCAAACCGGCAAATGCCGGAATt
>Cele-UNSB01_1:14804070-14804449 Satlength=380 Nr of Repeats=9 RepeatLength=43
seed=TTTGCCGGTT

TTTGCCGGTTTGCCGATTTGCCGGAATTTTCATTTTCCGGCAA
TTTGCCGGTTTCGACGGAAATTTTATTTTCCGGCAC
TTTGCCGGTTTGCCGATTTGCCGGAATTTTATTTTCCGGCAC
TTTGCCGGTTTGCCGATTTGCCGGAATTTTATTTTCCGGCAC

Nr of selected repeats 8 Similarity 0.931340

Consensus:

TTTGCCGGTTTGCCGgTTCGaCGGAAATTTTATTTTCCGGCAC
>Cele-UNSB01_1:14869199-14869444 Satlength=246 Nr of Repeats=6 RepeatLength=35
seed=CAAATCGGCA

CAAATCGGCAAATTTTCGGTGTGAAAAATTCCGG
CAAATCGGCAAATTTTCGGAATTGAAAATTTCCGG
CAAATCGACAAGTTGGCGGAATTGAAAATTTCCGT
CAAATCGGCAAATGCGGGAATTGAAAATTTCCGG
CAAATCGGCAGCTTGCTGGAATTGAACATTTTCCGG
CAAATCGGCAAATTTTCGGAATTAATAATTTCCGGCAAATTGCCAAGTTGTCAGAATTGAAATTTCTGG

Nr of selected repeats 4 Similarity 0.733333

Consensus:

CAAATCGgCAaATtGtcGGaaTTGAAaAtTTcCGg
>Cele-UNSB01_1:14918515-14918575 Satlength=61 Nr of Repeats=4 RepeatLength=15
seed=CCACGATGGG

CCACGATGGGTCTCG
CCACGATGGGTCTCT
CCACGATGGGTCTTT
CCACGATGGGTCTCA

Nr of selected repeats 4 Similarity 0.881481

Consensus:

CCACGATGGGTCTct
>Cele-UNSB01_1:14918627-14918817 Satlength=191 Nr of Repeats=5 RepeatLength=40
seed=CCAGAAGGTT

CCAGAAGGTTCTAGAACAATCCAGAATTTTTTTCGAATTTT
CCAGAAGGTTCTAGAACAATCCAGAATTTTTTTCGAATTTT

CCAGAAGGTTTTGGAACATTCCAGAATTTTCTCGATTGTT
CCAGAAGGTTCTAAAGCTTTTCAGCATTTT
CCAGAAGGTTCTGGAACATTCTAGAATTTTCCAGAAATTC
Nr of selected repeats 4 Similarity 0.800000
Consensus:

CCAGAAGGTTcTaGAACAaTcCAGAATTTTctcGAattTt
>Cele-UNSB01_1:14936456-14937856 Satlength=1401 Nr of Repeats=35
RepeatLength=40 seed=TTTCTAGAAA

TTTCTAGAAAAGTTCTGGAACATTCCAGAACTTTTTTCGAAA
TTTCTAGAAAAGTTCTGGAGCATTCCAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACGTTCTAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAACTTTTTTCGAAA
TTTCTAGAAAAGTTCTGGAGCATTCCAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACGTTCTAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAATTTTCCCGATT
TTTCTAGAAAAGTTCTGGAACGTTCTAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACGTTCTAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAACTTTTTTCGAAA
TTTCTAGAAAAGTTCTGGAGCATTCCAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACGTTCTAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAACTTTTTTCGAAA
TTTCTAGAAAAGTTCTGGAGCATTCCAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACGTTCTAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAACTTTTTTCGAAA
TTTCTAGAAAAGTTCTGGAGCATTCCAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACGTTCTAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAATTTTCCCGATT
TTTCTAGAAAAGTTCTGGAACGTTCTAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAATTTTTCGAAA
TTTCTAGAAAAGTTCTGGAGCATTCCAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAATTTTCTCGATT
TTTCTAGAAAAGTTCTGGAACATTCCAGAATTTTCCCGATT

Nr of selected repeats 35 Similarity 0.907675
Consensus:

TTTCTAGAAAAGTTCTGGAACaTTCcAGAATTTTcTCGAtt

>Cele-UNSB01_1:15014974-15015203 Satlength=230 Nr of Repeats=5 RepeatLength=34
seed=GAAATTTCAA

GAAATTTCAAAAAAAAAAATATGCAAAACCTCAATTTGCCGAAAATTTCCAAATTTCCGGCAAATCGATAGTTTGCCGG
TTTTCTGATTTGCG
GAAACTTCAACTCCTGCAAATTGCCGATTTGCCG
GAAATTTCAACTCCGGCAATTAGCCAATTTGCCG
GAAATTTCAACTCCGGCAATTAGCCAATTTGCCG
GAAATTTCAACTCCGGCAATTAGCCAATTTGCCG

Nr of selected repeats 4 Similarity 0.901961

Consensus:

GAAAtTTCAACTCCgGCAAtTaGCCaATTTGCCG

>Cele-UNSB01_1:15023397-15024044 Satlength=648 Nr of Repeats=19 RepeatLength=34 seed=CGGAAATTTTC

CGGAAATTTCCAATTCCGGCAAATTGTTCGATTTAT
CGGTAATTTCAATTCCGGCAAGTTGCCGATTTCC
CGGAAATTTCCATTCCAGAAATTTGTTCGATTTGC
CGGAAATTTCAATTCCAGCAATTTGCCGATTTGC
CGGAAATTTCAATTCCAGCAATTTGCCGATTTGC

Nr of selected repeats 18 Similarity 0.965142

Consensus:

CGGAAATTTCAATTCCAGCAATTTGCCGATTTGC

>Cele-UNSB01_1:15062491-15062841 Satlength=351 Nr of Repeats=10 RepeatLength=35 seed=AATTCCGGCA

AATTCCGGCAAGTTGTTCGTTTTGTTCGGAAATTTTT
AATTACGGCACTTTGTTCGATTTTCTGAAATTTTC
AATTCCGGCAATGTGCCGATTTTCTGAAATTTTC
AATTCCGGCAAGTTGCCGTTTTGTTCGGAAATTTTT
AATTCCGGCAATGTGCCGATTTTCTGAAATTTTC
AATTCCGGCAATTTGACGATTTTCTGAAATTTTA
AATTCCGGCAAGTTGCCGATTTTCTGAAATTTTC
AATTCCGGCAATTTGCCGATTTTCTGAAATTTTC
AATTCCGGCAATTTGCCGAGTTGCCCTGAAATTTTC
AATTCCGGCACTTTGCCGATTTTCTGAAATTTTC

Nr of selected repeats 10 Similarity 0.804115

Consensus:

AATTCCGGCAattTGcCGaTTTTcCtGAAATTTTC

>Cele-UNSB01_1:15073460-15073709 Satlength=250 Nr of Repeats=7 RepeatLength=35 seed=CGGTTTTGGA

CGGTTTTGGAAAATTTCCGGCAATTTGATAAATTGC
CGGTTTTGGAAAATTTCCGGCAATTTGACAATTTTGT
CGGTTTTGGAAAATTTCCGGTAATTTGACAATTGC
CGGTTTTGGAAAATTTCCGGCAATTTGACAATTGC
CGGTTTTGGAAAATTTCCGGCAATTTGATAAATTGC
CGGTTTTGGAAAATTTCCGGCAATTTGATAAATTTC
CGGTTTTGGAAAATTTCCGGCAAATTTACAATTTTGT

Nr of selected repeats 5 Similarity 0.885714

Consensus:

CGGTTTTGGAAAaTTTCCGGcAATTTcGAtAATTgC

>Cele-UNSB01_1:15094323-15094532 Satlength=210 Nr of Repeats=6 RepeatLength=35
seed=TTTCAATTCC

TTTCAATTCCGACATTTTGCCGATTTGCCGAAAAC
TTTCAATTCCGGCAATTCGCCGATTTACCAAAAAC
TTTCAATTCCGGCAATTTGCCGATTTGCCGAAAAC
TTTCAATTCCGGCAATTTGCCGATTTGCCGAAAAC
TTTCAATTCCGGCAATTTGCCGACTTGCCGAAAT
TTTCAATTCCGGCAATTTGACGATTTACCGAAAA

Nr of selected repeats 5 Similarity 0.878095

Consensus:

TTTCAATTCCGgCAaTTtGCCGAtTTgCCgAAAc

>Cele-UNSB01_1:15278589-15278861 Satlength=273 Nr of Repeats=10 RepeatLength=21
seed=AACTTTTTGG

AACTTTTTGGCAGGTTTCCAAATTTGTTGGCAGAGTTTCAA
AACTTTTTCGGAAATTTTCAAAAATTTTCTGCAATTTTCCAA
ACCTTTTTGGCAGATTTTCAA
AACTTTTTGGCTATTTTCCGA
AACTTTTTCGGCAATTTTCCAG
AACTTTTTGGCAATTTTCCAA
AACGTTTTGGTAGATTTTCA
AACTTTTTGGCAATTTTCCAA
AACTTTTTGGCAATTTTCAA
AACTTTTTCGGCAATTATCCAAAATTTTATGGCAATTTTCCAA

Nr of selected repeats 6 Similarity 0.791919

Consensus:

AACTTTTTGGCAATTTTcCAA

>Cele-UNSB01_2:2-3054 Satlength=3053 Nr of Repeats=243 RepeatLength=12
seed=AAGCCTAAGC

AAGCCTAAGCCT
AAGCCTAGCCT
AAGCCTAAGGAGCCTAACT
AAGCCTAAGAGCCCCT
AAGCCTAAGCGAGCCTAA
AAGCCTAAGGCCTAGT
AAGCCTAAGCCTAGCT
AAGCCTAAGCCT
AAGCTAAGCCT
AAGCCCTAAGCTAGTGCC
AAGCTAAGCCT
AAGCCTAAGCCT
AAGCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAAGCCT
AAGCCTAAGCCGCCT
AAGCCTAAGCCT
AAGCCTTAAGCCTAAGCCCCT
AAGCCTAAGCTCCTAAGCCTAG
AAGCCTAAGCCT
AAGCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCCAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT

AAGCCTAAGCCT

Nr of selected repeats 197 Similarity 0.998872

Consensus:

AAGCCTAAGCCT

>Cele-UNSB01_2:3110-3266 Satlength=157 Nr of Repeats=6 RepeatLength=26

seed=GTTACCAAAA

GTTACCAAAAATTGTGACTCTGACC

GTTACCAAAAATAGTGACTCTGACC

GTTACCAAAAATAGTGACTCTGACC

GTTACCAAAAATAGTGACTCTGACC

GTTACCAAAATATAGTGACTCTGACC

GTTACCAAAAATTGTGACAATGACC

Nr of selected repeats 6 Similarity 0.921368

Consensus:

GTTACCAAAAATaGTGACTCTGACC

>Cele-UNSB01_2:146899-146982 Satlength=84 Nr of Repeats=6 RepeatLength=12

seed=ATTTCTTGCA

ATTTCTTGCAAC

ATTTCTTGCAAC

ATTTTTTGCAA

ATTTCTTGAAAATTTCCAGCAAC

ATTTCTTCCAAA

ATTTCTTGCAA

Nr of selected repeats 5 Similarity 0.844444

Consensus:

ATTTcTTgCAa

>Cele-UNSB01_2:236549-238078 Satlength=1530 Nr of Repeats=40 RepeatLength=35

seed=TTTCCGGCAA

TTTCCGGCAAATCGGCCACTTGCCGGATTTGAAAA

TTTCCGGCAAACGCCGGAATTGAATG

TTTCCGGCAAATTGGCAAGTTGTCGGAATTGAAAATGACAAATCGGCAAATTGCTGGAATTGAAAA

TTTCCGGCAAATCGGCAGCCTGTCGGCATTGAAAA

TTTCCGGAAAATCAGTATATTACCAGAATTGAAAA

TTTCCGGCAATCGACAAATTGCCGAATTTAAAAAA

TTCCGGCAAACCGCAAATTGCCGGATTTGAAAA

TTTCCGGCATATCGGCAGCCTGTCGGAATTGAAAA

TTTCCGGCAAATCGGCAGCCTGTCGGCATTGAAAA

TTTCCGGCAAATCAGTATATTACCAGAATTGAAAA

TTTCCGGCAATCGGCAAATTGCCGAATTTAAAAAA

TTCCGGCAAACCGCAAATTGCCGGATTTGAAAA

TTTCCGGCAAATCGGCAGCCTGTCGGAATTGAAAA

TTTCCGGCAAATCAGTAAACTGCCAGAATTGAAAT

TTTCCGGCAAATCGACAAATTTGCCGAAATTGAAAAATTCGACAAATCGGAAAATTGCCGGATTTGAAAT

TTTCCGGCAAATCGGTAGATTGCCGGATTTGAAAT

TTTCCGGCAAATCGGTAAATTGTCGTAATTGAAAA

TTTCCGGCAAACCGGTAAATTGTCGTAATTGAAAA

TTTCCGGCAAATCGGCATACCGGTAAATTGTCGGAATTGAAAA

TTTCCGGCAAATCGGCATACCGGAATATTTTCGGAATTGAAAA

TTTCCGGCAAATCGGCATACCGGAATATTTTCGGAATTGAAAA

TTTCCGGCAAATCGGCAGCCTGTCGGCATTGAAAA

TTTCCGGAAAATCAGTATATTACCAGAATTGAAAA

TTTCCGGCAATCGACAAATTGCCGAATTTAAAAAA

TTCCGGCAAACCGCAAATTGCCGGATTTGAAAA

TTTCCGGCATATCGGCAGCCTGTCGGAATTGAAAA

TTTCCGGCAAATCGGCAGCCTGTGCGACATTGAAAA
TTTCCGGCAAATCAGTATATTACCAGAATTGAAAA
TTTCCGGCAAATCGGCAAATTGCCGAATTTAAAAAA
TTCCGGCAAACCGGCAAATTGCCGGATTTGAAAA
TTTCCGGCAAATCGGCAGCCTGTGCGGAATTGAAAA
TTTCCGGCAAATCAGTAAACTGCCAGAATTGAAAT
TTTCCGGCAAATCGACAAATTGCCGAAATTGAAAAATTCCGACAAATCGGAAAAATTGCCGGATTTGAAAT
TTTCCGGCAAATCGGTAGATTGCCGGATTTGAAAT
TTTCCGGCAAATCGGTAAATTGTCATAAATTGAAAA
TTTCCGGCAAACCGGTAAATTGTCGTAATTGAAAA
TTTCCGGCAAATCGGCATAACCGGTAAATTGTCGGAATTGAAAA
TTTCCGGCAAATCGGCAAGTTACCGGAATTGAAAA
TTTCCGGCAAATTGGCAAGTTACCGGAATTGAAAA
TTTCCGGCAAATCGGCATAACCGGAATTTTTCGGAATTGAAAA

Nr of selected repeats 27 Similarity 0.708272

Consensus:

TTTCCGGCAaATCgGcAnatTgcCgGAATTGAAAA

>Cele-UNSB01_2:371286-371494 Satlength=209 Nr of Repeats=10 RepeatLength=18
seed=TAAGCCTAAG

TAAGCCTAAGAC

TAAGCCTAAGTT

TAAGCCTATGTCTAAGAA

TAAGCCTAAGCATCGCTC

TAAGTCTAAGTCCAAGTCTAATAAACCCAAGCCTAAATAGCGTCACTGACGCCAAGCCCACGCA

TAAGCCTAAGTC

TGAGCCTAAGCTTAAGTC

TACGCCTAAGCCTAAACC

TAAACCTAAGCCTAAGTC

TAAACCTAAGCCGAAGCC

Nr of selected repeats 6 Similarity 0.619753

Consensus:

TAAgCCTAAGCcTAAgtC

>Cele-UNSB01_2:454595-455440 Satlength=846 Nr of Repeats=32 RepeatLength=15
seed=TCTCACCACG

TCTCACCACGATGGG

TCTCGCCACGAAGGG

TCTCACCACGATGTG

TCTCACCACGATGGG

TCTCACCACGAAAGG

TCTCGCCACGAAGGG

TCTCACCACGATGTG

TCTCACCACGAAGGG

TCTCACCACGAAGGG

TCTCACCACGATAATTTGATTTTCCCGCCAAAATATTTTTCTGAGAAAATTTGAATTTCCCGCCAAAATATTTTTCTGA

GAAAATTTGAATTTCCACCAAAAATATTTTTCTCAGAAAATTTAAATTTCCCGCCAAAATATTTTTCTCAGAAAATTTG

AATTTCCCGCCAAAATATTTTTCTCAGAAAATTTGAATTTCCCGCCGGAATATTTTTCTGAGAAAATTTGAATTTCCCG

CCAAAATGTTTTTCTCAGAAAATTTAAATTTCCCGCTAAAGTTTTGGA

TCTCACCACGATGGG

TCTCACCACGATGGG

TCTCGCCACGAAGGG

TCTCACCACGATGTG

TCTCACCACGATGGG

TCTCACCACGAAAGG

TCTCGCCACGATGGG

TCTCACCACGAAGGG
TCTCGCCACGAAGGG
TCTCACCACGAAGGG
TCTCACCACGATGGG
TCTCGCCACGATGGG
TCTCGCCACGATGGG
TCTCACCACGATGGG
TCTCACCACGATGGG
TCTCGCCACGATGGG
TCTCACCACGATGGG
TCTCACCACGAAGGG
TCTCACCACGAAAGG
TCTCACCACGATGGG
TCTCACCACGATGGG
TCTCGCCACGAAAATTTGAATTTCCCGCCAAAATGTTTTTTTTTCAGAAAATTTGAATTTCCCGCCAAAATTTTTATCTGA
GAAAATTTGAATTTCCCGCCAAAATTTTGGG

Nr of selected repeats 30 Similarity 0.884138

Consensus:

TCTCaCCACGAtGGG

>Cele-UNSB01_2:466682-467257 Satlength=576 Nr of Repeats=9 RepeatLength=20
seed=CAATTTTTGA

CAATTTTTGAGCTGGAAATCAAGAAAATTTCAATTTTCTGTTTTTTTTTGTGCTGTAAAAATCTAATTTTTCTAATTTTT
AAGGAAAAAATGAGAAAATTTCTGGAAACGCCACAAAATCGGCGAAACTTCGATTTTCCGGAATTTTCACAAAAAAA
AATCGATTTTTCTCAATTTTCCAATTTTCAAGCTGGAAAATTCAGAATTTTATAAAAAATTCGGTACTTTCTTTTCGCT
GCAAAATGTTGTTTTCGTCTTTGGATCCACATAAATCTGCATTTGGCCTTGTGCTCCAAGGCGATGGCTCCAAGTGAAT
CTTGCTCAATAATTTCTCGTGTCTTCAATTTCTACTTCTTCCATCGGCATCGGCTCCATTGGCTCCTGAAAAATCGA
ATTTTTTGAATTTAAAAAAT
CAATTTTTGAGTTAAAAAAT
CAATTTTTGAGTTAAAAAAT
CAATTTTTGAGTTAAAAAAT
CAATTTTTGAATTTAAAAAAT
CAATTTTTGAGTTAAAAAAT
CAATTTTTGAATTTAAAAAAT
CAATTTTTGAATTTAAAAAAT
CAATTTTTGAGTTAAAAAAT

Nr of selected repeats 7 Similarity 0.942857

Consensus:

CAATTTTTGAgTTAAAAAAT

>Cele-UNSB01_2:577469-577719 Satlength=251 Nr of Repeats=20 RepeatLength=12
seed=TAGGCTTAGG

TAGGCTTAGGCA
TAGGCTTAGGCT
TAGGTTTAGGCT
TAGGCCTAGGCT
TAGGCCTAGGAT
TAGGCCTAGGCT
TAGGCCTAGGAT
TAGGCCTAGGCT
TAGGCCTAGGAT
TAGGCCTAGGCT
TAGGCCTAGGAT
TAGGCCTAGGCT
TAGGCTTAGGCC
TAGGATTAGGCTTAGGTTTAGCA
TAGGTTTAGGCA
TAGGTTAGGTT

TAGGCTTAGGCT
TAGGCTTAGGTT
TAGGCTTAGGCC
TAGGCTTAGGCC
TAGGCTTAGGCT
TAGGCCTAGGAT

Nr of selected repeats 18 Similarity 0.816993

Consensus:

TAGGCtTAGGct

>Cele-UNSB01_2:590141-590909 Satlength=769 Nr of Repeats=12 RepeatLength=64
seed=AAATTTTGTA

AAATTTTGTAGTTTGTAGTCTAGCAGACCCATATTGAATACCAGCAAGTTGGGTCTGCCAAATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAACAAGTTGGGTCTGCCAGATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAATAAATTTGGGTATGCCAAATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAATAAATTTAGGTCTGCCAGATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAACAAGTTGGGTCTGCCAGATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAACAAGTTGGGTCTGCCAGATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAACAAGTTGGGTCTGCCAGATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAACAAGTTGGGTCTGCCAGATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAACAAGTTGGGTCTGCCAGATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAGCAAGTTGGGTCTGCCAGATC
AAATTTTGTAGTTTGTAGTCTAGCAGACCCATTTAGAATACCAGCAAGTTGGGTCTGCCAGATC

Nr of selected repeats 12 Similarity 0.921402

Consensus:

AAATTTTGTAGTTTGTAGTCTAGcAGACCCAttTaGAATACCAAcAAaTTGGGTCTGCCAgATC

>Cele-UNSB01_2:636344-636664 Satlength=321 Nr of Repeats=8 RepeatLength=40
seed=TTTCTAGAAA

TTTCTAGAAAAGTTCTGGAACATTCGAGAATTTTCTCGATT
TTTCTAGAAAATTTCTGGAACATTCAGAAATTTCCCGATT
TTTCTAGAAAATTTCTGGAACATTCAGAAATTTTCCCGATT
TTTCTAGAAAAGTTCTGGAACATTCGAGAATTTTCTCGAGA
TTTCTAGAAAAGTTCTGGAACATTCGAGAATTTTCTCGATT
TTTCTAGAAAATTTCTGGAACATTCAGAAATTTTCCCGATT
TTTCTAGAAAAGTTCTGGAACATTCGAGAATTTTCTCGATT
TTTCTAGAAAATTTCTGGAACATTCAGAAATTTTCCCGATT
TTTCTAGAAAAGTTCTGGAACATTCGAGAATTTTCTCGATT
TTTCTAGAAAATTTCTGGAACATTCAGAAATTTTCCCGATT

Nr of selected repeats 8 Similarity 0.917857

Consensus:

TTTCTAGAAAaATTCTGGAACATTCcAGAATTTTCCCGATT

>Cele-UNSB01_2:635957-636850 Satlength=894 Nr of Repeats=4 RepeatLength=35
seed=GAAAATTTAA

GAAAATTTAAATATCTTTTAAAAAACCGAAATCAGCTTTTGCCAGTGCAAAACTAATAGAAAGCGTAATATTAATAGG
AAAACCTCTCTTTTCAGACAAAATAATATTTTGTCTGGAAAATGTTTTCCCAACAAAAAAACAACCTTTATTTGGGATTTTAA
AGATTTAAAAAATTTTATGACGAATCAGTGTATGACTAACTAAAAACATTGTTTCATTGTCATGGGTCCAAGCACAAAC
AATATTTATCAACTCAGACAAAAAAGGAAAACAATTTTTCAGCGTGAAAATTAGTTATTTTGGACCAGCCGCTGACCGCGC
CTACGGCGCGGGCAACGACTGGCACCATTAAAAGTATTTGACTCACATAACTTCCAGAATTTTCTCGATTTTCTAG
AAGTTCTGGAACATTCGAGAATTTTCTCGATTTTCTAGAAAATTCTGGAACATTCAGAAATTTTCCCGATTTTCTAG
AAAATTTCTGGAACATTCAGAAATTTTCCCGATTTTCTAGAAAAGTTCTGGAACATTCGAGAATTTTCTCGAGATTTCTA
GAAAGTTCTGGAACATTCGAGAATTTTCTCGATTTTCTAGAAAATTCTGGAACATTCAGAAATTTTCCCGATTTTCTA
AGAAAGTTCTGGAACATTCGAGAATTTTCTCGATTTTCTAGAAAATTCTGGAACATTCAGAAATTTTCCCGATTTTCTA
TAGAAAGTTCTGGAACATTCGAGAATTTTCTCGAAATTTCCAAAAGATTCTAGATTCCAGAAATTTTGTAACTTTCA
GAAAATTTAAATTTCCCTCCAAAATTTTTTCTCA
GAAAATTTAAATTTCCCGCCAAAATTTTTTCTCA
GAAAATTTAAATTTCCCTCCAAAATTTTTTCTCA

Nr of selected repeats 3 Similarity 0.923810

Consensus:

GAAAATTTAAATTTCCCTCCAAAATaTTTTTCaCA

>Cele-UNSB01_2:636908-637328 Satlength=421 Nr of Repeats=27 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAC

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACACCGCGGT

GGGTCTCACCGCGAT

GGGTCTCACCACGAT

GGGTCTCATCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACACCGCGGT

GGGTCTCACCGCGAT

GGGTCTCACCACGAT

GGGTCTCATCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAC

GGGTCTCACACCGCGGT

GGGTCTCGCCACGATGGGTCTTTCCACGAT

Nr of selected repeats 26 Similarity 0.898256

Consensus:

GGGTCTCACCACGAT

>Cele-UNSB01_2:637418-637568 Satlength=151 Nr of Repeats=4 RepeatLength=40

seed=CAGAAGGTTTC

CAGAAGGTTCTAGAACAAATCCAGAATTTTTTCGAATTTTC

CAGAAGGTTCTGCAACATTCCAGAATTTTCTAGAATTTTC

CAGAAGGTTCTAAAGCTTTTCAGAATTTTC

CAGAAGGTTCTGGAACATTCTAGAATTTTCCAGAAATTCC

Nr of selected repeats 3 Similarity 0.800000

Consensus:

CAGAAGGTTCTggAACAtTCcAGAATTTTctaGAAtTTtC

>Cele-UNSB01_2:637664-637798 Satlength=135 Nr of Repeats=4 RepeatLength=11

seed=GTACTCCTAC

GTACTCCTACA

GTACTCCTACAGTACTACAACAGTACCCCGACCATATCCACTACTAACCCCAAATCTATATCTCTTCAAAGACTAAA

ACACAATTTTTCTAAACTACA

GTAATCCTACC

GTACTCCTACA

Nr of selected repeats 3 Similarity 0.838384

Consensus:

GTACTCCTACA

>Cele-UNSB01_2:646191-646835 Satlength=645 Nr of Repeats=25 RepeatLength=23
seed=GGCCACCAAT

GGCCACCAATTTCTTAAAAAATTC
GGCCACCGATCTATAAAAAATCTA
GGCCACCAATTTCTTAAAAAGTTC
GGCCACCGATCTATAAAAAAGCTA
GGCCACCAATCTGTAAAAAATTC
GGCCACCGATCTATAAAAAAGCTA
GGCCACGAATCTGTAAAAAATTC
GGCCACCGATCTATAAAAAAGCTA
GGCCACCAATCTGTAAAAAATTC
GGCCACCGATCTATAAAAAATCTAA
GCCACCAATTTCTTAAAAAATTC
GGCCACCGATCTATAAAAAATCTA
GGCCACCAATTTCTTAAAAAATTCGGCCACCGGTCAATAAAAAAGCTA
GGCCACCAATCTGTAAAAAGCTCGTCCACCGATCTATAAAAAATCTA
GGCCACCAATTTGTAAAAAATTC
GGCCACCGATCTATAAAAAACTA
GGCCACCAATTTGTAAAAAATTC
GGCCACCGATCTATAAAAAATCTA
GGCCACCAATTTCTTAAAAAATTC
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GGCCACCAATTTCTTAAAAAATTC
GGCCACCGATCAATAAAAAAGCTG
GGCCACCAATCTGTAAAAAATTC
GGCCACCAATCTATAAAAAACCTT

Nr of selected repeats 20 Similarity 0.753776

Consensus:

GGCCACCcATcTaTaAAAAAcTc

>Cele-UNSB01_2:649028-649082 Satlength=55 Nr of Repeats=4 RepeatLength=12
seed=GGCTCAGGCT

GGCTCAGGCTCA
GGCTCAGGCTCA
GGCTCAGGCTCA
GGCTCAGGCTCAGGCTCC

Nr of selected repeats 3 Similarity 1.000000

Consensus:

GGCTCAGGCTCA

>Cele-UNSB01_2:677942-678110 Satlength=169 Nr of Repeats=9 RepeatLength=16
seed=CCTACGTGCC

CCTACGTGCCTTCGTG
CCTAGGTGCCTTCGTG
CCTACGTGCCTACGTG
CCTACGTTCCCTACGTGCCTGCGTA
CCTACGTTCCCTACGTGCCTGCGTA
CCTAAGTGCCTTCGTA
CCTACGTGCCTACGTG
CCTACGTACCTACGTGCCTTCGTA
CCTACGTGCCTAAGTG

Nr of selected repeats 6 Similarity 0.844444

Consensus:

CCTAcGTGCCTaCGTG

>Cele-UNSB01_2:694600-694660 Satlength=61 Nr of Repeats=4 RepeatLength=15

seed=GTAGATCTTG

GTAGATCTTGTTTTG

GTAGATCTTGAAAAT

GTAGATCTTGTTTTG

GTGGATCTTGTTTTC

Nr of selected repeats 4 Similarity 0.675347

Consensus:

GTaGATCTTGtttTg

>Cele-UNSB01_2:698255-706115 Satlength=7861 Nr of Repeats=432 RepeatLength=15

seed=GGTGAGACCC

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GGTGAGACCCACCGT
GGTGAGACCCATCGT
GGTGAGACCCATCGC
GGTGATACCCATCGTGACGATACCTTTCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGTGACGAGACCCATCGT
GGTGAGACCCATCGT
GATGAGACCCATCGT
GGTGAGACCCATCGT
GGTGAGACCCATCGT
GGTGAGACCCATCGT
GGTGAGACCCACCGT
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GGTGAGACCCATCGC
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GGTGAGACCCTTCGT
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GGTGAGACCCATCGT
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GGTGAGACCCATCGC
GGTGAGACCCATCGT
GGTGAGACCCATCGT
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GATGAGACCCATCGT
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GGAAATTCAAATTTTCAGTGAAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGAAAAACATTTTTGGCGGGAAATTTCA
AATTTTTCAGTGAAAAACATTTTGCCGGGAAATTCAAATTTCTGAGAAAAAATTTTTGGCGGGAAATTCAAATTTTCTGA
GAAACTTTTTGTAGCTTAAGTACCACCTGGAAGTGGCGAGACCTATCGT

Nr of selected repeats 346 Similarity 0.920561

Consensus:

GGTGAGACCCATCGT

>Cele-UNSB01_2:858289-858649 Satlength=361 Nr of Repeats=5 RepeatLength=31

seed=TGTCTAGCGA

TGTCTAGCGAGACCCAGATAAGAGCAGAGGTGCTTCTGAGAGGGTTGGTGATTCAGGGGTAGTGCGAGCACTATCTCCT
GTCTCTTATGTGGCACATTGTTGTGTTTCTGTGTTTATAATAATACTCTCTCCCCCATACTCCTACATATGGGGCGA
GTGAGAAGGCTGGAGT
TGTCTAGCGAGACCTCAGAAGAGAGCTGAGT
TGTCTAGCGAGATAGCAGAGAAGAGATGAGT
TGTCTAGCGAGACCTCAGAAGAGAGCTGAGT
TGTCTAGCGAGATAGCAGAGAAGAGATGAGTTGTCTGAGTGAGATAGCAGAGAAGAGATGAGTTGTGGAGTGAAACCTCA
GAAGAGAGCTGAGT

Nr of selected repeats 3 Similarity 0.799283

Consensus:

TGTCgAGCGAGAcctCAGAagAGAGcTGAGT

>Cele-UNSB01_2:863874-864986 Satlength=1113 Nr of Repeats=34 RepeatLength=32

seed=AATTCCCGCC

AATTCCCGCCAAAAATTTTTTCAGAAAATTTG
AATTCCCGCCAAAAATTTTTTCACAGAAAATTTG
AATTCCCGCCAAAAATTTTTTCAGAGAAAATTTG
AATTCCCGCCAAAAATGTTTTCAGAAAATTTG
AATTCAGCCAAAAATTTTTCAAAGAAAATTTG
AATTCCCGCCAAAAATTTTTGAAGAAAATTTG
AATTCAGCCAAAAATTTTTCAAAGAAAATTTG
AATTCCCGCCAAAAATTTTTGAAGGAAAATTTA
AATTCCCGCCAAAAATTTTTTCAGAGAAAATTTG
AATTCAGCCAAAAATTTTTTCAGAAAATTTG
AATTCCCGCCAAAAATTTTTTCACAGAAAATTTG
AATTCAGCCAAAAATTTTTTAAAGAAAATTTA
AATTCCCGCCAAAAATTTTTTCAGAGAAAATTTG
AATTCAGCCAAAAATTTTTTAAAGAAAATTTA
AATTCAGCCAAAAATTTTTTCAGAGAAAATTTG

AATTCCCGCCAAAAAATTTTAAAGAAAATTTA
AATTCCCGCCAAAAAATTTTCAGAGAAAATTTG
AATTCCCGCCAAAAATGTTTCAGAAAATTTG
AATTCACGCCAAAAATGTTTCAGAAAATTTG
AATTCACGCCAAAAAATTTTCAAAGAAAATTTG
AATTCCCGCCAAAAAATTTTCAGAAAATTTG
AATTCACGCCAAAAAATTTTCAGAGAAAATTTG
AATTCACGCCAAAAAATTTTAAAGAAAATTTA
AATTCACGCCAAAAAATTTTCAGAGAAAATTTG
AATTCACGCCAAAAATGTTTCAGAAAATTTG
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AATTCACGCCAAAAAATTTTCAAAGAAAATTTG
AATTCACGCCAAAAAATTTTGAAGGAAAATTTA
AATTCACGCCAAAAAATTTTCAGAGAAAATTTG
AATTCACGCCAAAAAATTTTCAGAAAATTTGAACAACCGCCAAAAAATTTTCACAGAAAATTTG
AATTCACGCCAAAAAATTTCAAAGAAAATTTA

Nr of selected repeats 26 Similarity 0.854615

Consensus:

AATTCCCGCCAAAAAATTTcAaAGAAAATTTg

>Cele-UNSB01_2:865003-865078 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=ATGGGTCTCG

ATGGGTCTCGCCACG

ATGGGTCTCGCCACG

ATGGGTCTCGCCACG

ATGGGTCTCGCCACGA

AGGGTCTCGCAACG

Nr of selected repeats 3 Similarity 1.000000

Consensus:

ATGGGTCTCGCCACG

>Cele-UNSB01_2:870904-873513 Satlength=2610 Nr of Repeats=35 RepeatLength=72

seed=TCCATCCAGC

TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACGAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGTGGTTGGTTCGATGGGTGGGTCTCGAGTAGTTCAGGGACTCTCGTTTGTCCACGAGTAATGCCATT
GGCTCTAATTG

TCCATCCAGCTGCGGTTGGTTCGCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGCGGTTGGTTCGCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGCGGTTGGTTCGTTGGGCGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGCGGTTGGTTCGTTGGGCGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGCGGTTGGTTCGTTGGGCGAATCCTCGAGAAGTATCACGAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGCGGTTGGTTCGTTGGGCGAATCCTCGAGAAGTATCACGAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGTGGTTGGTTCGATGGGTGGGTCTCGAGTAGTTCAGGGACTCTCGTTTGTCCACGAGTAATGCCATT
GGCTCTAATTG

TCCATCCAGCTGCGGTTGGTTCGCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTATGGTTGGTCTCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACGAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGTGGTTGGTTCGATGGGTGGGTCTCGAGTAGTTCAGGGACTCTCGTTTGTCCGCGAGTAATGCCATT
GGCTCCGTTTCG

TCCATCCAGCTATGGTTGGTCTCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTATGGTTGGTCTCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTTCG

TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCAATAGTAGTACCATTGGCTCCGTTCCG
TCCATCCAGCTATGGTTGGTCTCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTCCG
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACGAGTAGTACCATTGGCTCCGTTTCG
TCCATCCAGCTGTGGTTGGTCGATGGGTGGTCTCGAGTAGTTCCAGGGACTCTCGTTTGTCCGCGAGTAATGCCATT
GGCTCCGTTCCG
TCCATCCAGCTATGGTTGGTCTCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTCCG
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCAATAGTAGTACCATTGGCTCCGTTCCG
TCCATCCAGCTATGGTTGGTCTCTGGGTGAATCCTCGAGAAGTACCACTAGTAGTACCATTGGCTCCGTTCCG
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCAATAGTAGTACCATTGGCTCCGTTTCG
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACGAGTAGTACCATTGGCTCCGTTTC
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCAATAGTAGTACCATTGGCTCCGTTTCG
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TCCATCCAGCTGTGGTTGGTCGATGGGTGGTCTCGAGAAGTATCAATAGTAGTACCATTGGCTCCGTTTCG
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCAATAGTAGTACCATTGGCTCCGTTTCG
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCAATAGTAGTACCATTGGCTCCGTTTC
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACGAGTAGTACCATTGGCTCCGTTTC
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACGAGTAGTACCATTGGCTCCGTTTC
TCCATCCAGCTGTGGTTGGTCGATGGGTGGTCTCGAGTAGTTCCAGGGACTCTCGTTTGTCCGCGAGTAATGCCATT
GGCTCTAATTG

Nr of selected repeats 29 Similarity 0.928845

Consensus:

TCCATCCAGCTgTGGTTGGTctCTGGGTGAATCCTCGAGAAGTAtCActAGTAGTACCATTGGCTCCGTTcG
>Cele-UNSB01_2:882806-882988 Satlength=183 Nr of Repeats=12 RepeatLength=14
seed=TAGGATCTAG

TAGGATCTAGAGTA
TAGGATCTACGATC
TAGGGTCTAGGATC
TAGGATCTAGGATC
TAGGATCTAGGATC
TAGGATCTAGGGTC
TAGGGTCTAGGATC
TGGGATCTAGGATCTAGGGTG
TAGGATCTAGGATC
TAGGATCCAGAATC
TAGAATCTAGGATCTAGGCTC
TGGGATCTAGGCTC

Nr of selected repeats 10 Similarity 0.807407

Consensus:

TAGGaTCTAGgaTC
>Cele-UNSB01_2:885470-885668 Satlength=199 Nr of Repeats=15 RepeatLength=12
seed=ACCTAGACCT

ACCTAGACCTAGACCTATAACCGAGA
ACTAGACCTAG
ACCTAGACCTAG
ACCTGGACCTAG
ACCTAGACCTAG
ACCTAGACCTAG
ACCTAGACCTAG
ACCTAGACCTAG
ACCTAAACCTAG
ACCTAGACCTAG
ACCTAGACCTAA
ACCTAGAACTAG

ACCTAAACCTTG
ATCTAGACCTTG
ATCTAGACCTAGACCTAG

Nr of selected repeats 12 Similarity 0.858586

Consensus:

ACCTAGACCTAG

>Cele-UNSB01_2:889690-889842 Satlength=153 Nr of Repeats=5 RepeatLength=11
seed=TGTAGGGGTAC

TGTAGGGGTAC
TGTAGGGGTAC
TGTAGGGGTAC

TGTAGGGGTACTCTAGGAGTAATTTGGAAATGAACAGAAAGGATGGTAT

TGTAGGGGTACTGTAGGCCATCTTGGGAGCAGAGAAGGAGTATTGTAAGGGTTCATACTATAAAGGTTT

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TGTAGGGGTAC

>Cele-UNSB01_2:891851-892689 Satlength=839 Nr of Repeats=4 RepeatLength=184
seed=GTTCAAAGA

GTTCAAAGACCCCATACGGTGGTACGTAAGCTTCTGGTCAACTGGCATAATGTTAATGTAAGTTTCCCATAAAATTAA
CCTGCGCGGCCGACAATTTACGAGCCTAACCATAACATTGTCCGCTGCTAATTTCTAACAGTTTTTTTTTAGTATTTTTC
GGCGCAGAAGGTCCATATTCCTCTTTCTTCTCATTCTAGTTCTAATTTTATAAATTTGCTCCCGCATAACATTTTTTGCAT
ACATTTTTTATCTCATGACGCGGACATGCCACAAATGTCTAGTTAGGCTT

GTTCAAAGATACAAAATTTATCTACACATCTACAAGTTAAACTTGCAACTTAGTTAACCAAATTCAAAAGTTATGAGC
CGGGGAACTATAATAACCAACGTTTCACACTAAAAAAGCCAAAAAAATTCGAAAAATCATTTTTTATCTCATGACGCGGA
CAAGCTACAAATGTCTAGTTAGGCTT

GTTCAAAGATACAAAATTTATCTACACATCTACAAGTTAAACTTGCAACTTAGTTAACCAAATTCAAAAGTTATGAGC
CGGGGAACTATAATAACCAACGTTTCACACTAAAAAAGCCAAAAAAATTCGAAAAATCATTTTTTATCTCATGACGCGGA
CAAGCTACAAATGTCTAGTTAGGCTT

GTTCAAAGATACAAAATTTATCTACACATCTACAAGTTAAACTTGCAACTTAGTTAACCAAATTCAAAAGTTATGAGC
CGGGGAACTATAATAACCAACGTTTCACACTAAAAAAGCCAAAAAAATTCGAAAAATCATTTTTTATCTCATGACGCGGA
CAAGCTACAAATGTCTAGTTAGGCTT

Nr of selected repeats 3 Similarity 1.000000

Consensus:

GTTCAAAGATACAAAATTTATCTACACATCTACAAGTTAAACTTGCAACTTAGTTAACCAAATTCAAAAGTTATGAGC
CGGGGAACTATAATAACCAACGTTTCACACTAAAAAAGCCAAAAAAATTCGAAAAATCATTTTTTATCTCATGACGCGGA
CAAGCTACAAATGTCTAGTTAGGCTT

>Cele-UNSB01_2:894739-894896 Satlength=158 Nr of Repeats=8 RepeatLength=20
seed=CAATCTATTT

CAATCTATTTTTGTCTGT
CAATCTATTTTTCTGGTATGC
CAATCTATTTTTTCGTGTAA
CAATCTATTTTTTCGGTATGC
CAATCTATTTTTTTGGTATGA
CAATCTATTTTTTTGGTATGA
CAATCTATTTTTTTGGTATGT
CAATCTATTTTTTTGGTATGT

Nr of selected repeats 6 Similarity 0.902222

Consensus:

CAATCTATTTTTTTGGTATGn

>Cele-UNSB01_2:898652-902061 Satlength=3410 Nr of Repeats=58 RepeatLength=59
seed=TATGGAAAAT

TATGGAAAATATGGTGTTCCAAATGAGCAATGGTTTTCAAATTTTTTTAAACTGAGAAT
TATGGAAAATATGGATTTTTAAATGTGCACTGGTTTTCAAATTTTTTTAAACTGAGAAT
TATGGAAAATATGGATTTTTAAATGTGAACTGGTTTTCAAATTTTTTTAAACTGAGAAT

TATGGAAAATATGGATTTTTAAATGTGCACTGGTTTTCAAATTTTTTAAACTGAGAAT

Nr of selected repeats 56 Similarity 0.981848

Consensus:

TATGGAAAATATGGATTTTTAAATGTGcACTGGTTTTCAAATTTTTTAAACTGAGAAT

>Cele-UNSB01_2:1043954-1044457 Satlength=504 Nr of Repeats=17 RepeatLength=11

seed=GTACTGTAGG

GTACTGTAGGG

GTACTGTAGGGT

TACTGTAGGATTACTGTAGTTTGGGAAAAATGGACTTTTTGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGGCGGGA

TATGGTCAGG

GTACTGTAGTA

GTACTGTAGGG

GTACTGTAGGGT

TACTGTAGGATTACTGTAGTTTGGGAAAAATGGACTTTTTGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGGCGGGA

TATGGTCAGG

GTACTGTAGTA

GTACTGTAGAG

GTACTGTAGGA

GTACTGTAGGA

GTACTGTTGGATTACTGTAGTTTGGGAAAAATGGACTTTTTGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGGCGGG

ATATGGTCAGG

GTACTGTGGTA

GTACTGTAGAG

GTACTGTAGGA

GTACTGTAGGATTACTGTAGTTTGGGAAAAATGGCTTTTTCGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGGTGGG

ATATGGTTGGG

GTACTGTAGTT

Nr of selected repeats 11 Similarity 0.819284

Consensus:

GTACTGTAGna

>Cele-UNSB01_2:1044642-1047492 Satlength=2851 Nr of Repeats=181 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGACCCA

TCGTGGTGAGATCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGTCCA

TCGTGGTGAGACCCA

TCGTAGTGAGACCCA

TCGTTGTGAGACCCA

TCGTTGTGAGACCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

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TCGTGGTGAGACCCA
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TCGTGGTGAGACCCA
TCGTGGCGAGACCCA
TCGTGGTGAGACCCTTCGTGATGAAACCCT
TCGTGGTGAGACCCA
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TCGTGGCGAGACCCA
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TCGTGGTGAGACCTT
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TCGTGGCGAGACCCA
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TCGTGGTGAGACCCT
TCGTGGTGAGACCTT
TCGTGGTGAGACCCT

>Cele-UNSB01_2:1097712-1098091 Satlength=380 Nr of Repeats=5 RepeatLength=26
seed=GTCGGCTGCT
GTCGGCTGCTCACAAACCTCGAGGT
GTCGGCTGCTTTTTTTTTGCAAAAGT
GCCGGCTGCTTCAAACCTCTGATTT
GTCGTCTGCTACTAATTATAGCACACTTTATGTTCCCTTGTCTACTCCCCGCAATTCCCATTCCAATATCAAAATAAGAA
AGCAAATAACAATTCTAAGTGGGTTAGTAGTAATAGTAGCAGGAGACCTGTTTTACTATTTTTACCGAAAATTTTCAA
ATGCCTGCTAATCGATTAGAAGAATTAGGGAATTACAAGGCTTTTTAACTGTAATCTATTAAATTTGAGAACACTGTA
GCATTGCCTCAGAACCCATCAGGT
GTCGGCTGCTTAATCATGTATAAAATGTTGCCTGGGAGGT
Nr of selected repeats 3 Similarity 0.339869

Consensus:

GtCGGCTGCTtnCAAAccctgAgtt

>Cele-UNSB01_2:1142725-1142802 Satlength=78 Nr of Repeats=5 RepeatLength=15
seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA

CGAAAAGGGGATCTG

CAAAAAGGGGATCTG

CGAAAAGGGGAGATA

CGAAAAGGGGAGATA

Nr of selected repeats 4 Similarity 0.777778

Consensus:

CgAAAAGGGGAgTa

>Cele-UNSB01_2:1142992-1143084 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTCGCAGA

TCCCCTTTTCGTTCTGC

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTCgtagc

>Cele-UNSB01_2:1186731-1187015 Satlength=285 Nr of Repeats=8 RepeatLength=26
seed=TACTGTAGTT

TACTGTAGTTTGACCTTCTAAACGAT

TACTGTAGTTTGACTAACTTAGGACT

TACTGTAGTTTGACCTACTTGTGGTTACTGTAACTATACTTAAGTATACCTGCGGT

TACTGTAGTTTGACCTACTTAGGGGA

TACTGTAGTTTGATATTCATAAGGGT

TACTGTAGCTAGATCTAAGTAAAGCTACGGT

TACAGTAGTTTGACCTACTTAGGGGA

TACTGTAGATTGACCTAATTTCCATAAACCTTACTGCACCTTTGACCTACTATCTAAAAATATAAAT

Nr of selected repeats 5 Similarity 0.621429

Consensus:

TACTGTAGtTTGAcctaCttAngGat

>Cele-UNSB01_2:1212949-1213169 Satlength=221 Nr of Repeats=4 RepeatLength=55
seed=GGGATTATTG

GGGATTATTGGAGTTTCTTTTTCTAGAATTTTTTGAAAATTTTGGACAGTTTTTC

GGGATTATTGGAGTTTCTTTTTCTAGAATTTTTTGAAAATTTTGGACAGTTTTTC

GGGATTATTGGAGTTTCTTTTTCTAGAATTTTTTGAAAATTTTAGACCCTTTTCT

GGGATTATTGGAGTTTCTTTTTCTAGAATTTTTTGAAAATTTTGGAACAGTTTTTC

Nr of selected repeats 4 Similarity 0.903030

Consensus :

GGGATTATTGGAGTTTCTTTTTCTAGAATTTTtTGAAAATTTtggACagTTTTtt

>Cele-UNSB01_2:1233155-1233235 Satlength=81 Nr of Repeats=5 RepeatLength=12

seed=TTAGGCTTAG

TTAGGCTTAGGC

TTAGGCTTAGGT

TTAGGCTTATGCATAGGCTTATGCGC

TTAGGCTTAGGT

TTAGGCTTAGGATTATGT

Nr of selected repeats 3 Similarity 0.925926

Consensus :

TTAGGCTTAGGt

>Cele-UNSB01_2:1258661-1259567 Satlength=907 Nr of Repeats=73 RepeatLength=12

seed=CTATGCCTAT

CTATGCCTATAC

CTATGCCTATGC

CTATACCTATGCCCATAC

CTATGCCTATGCCTAAGCCAAAGC

CTATGCCTATGC

CTATGCCTATGC

CTATTCCTATGC

CTATGCCTATAC

CTATGCCCATAC

CTATGCCTATGCCTAAGCCAAAGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGT

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTCTGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGT

CTATGCCTATGC

CTATGCCTATGC

CTATGTCTATTC

CTATGCCTATGC

CTATGCCTATGT

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CTATTCCTATGC
CTATGCCTATGC
CTATGTCTATGC
CTATGCCTATGT
CTATGCCTATGC
CTATGCCTATGT
CTATGCCTATGC
CTATGCCTATGT
CTATGCCTATGC
CTATGCCTATGC

Nr of selected repeats 70 Similarity 0.936416

Consensus:

CTATGCCTATGC

>Cele-UNSB01_2:1261170-1261684 Satlength=515 Nr of Repeats=42 RepeatLength=12

seed=CTATGCCTAT

CTATGCCTATGCC

CTATGCCTATGC

CTATGCCTGTGC

CTATGCCTATGC

CTATTCCTATTC

CTATGCCTATGC

CTATGCCTATTC

CTATGCCTATGC

CTATGCCTTTGC

CTTTGCCTATGC

CAATGCCTATGC

CTATGCCTATGC

CTGTGCCTATGC

CTATGCCTATGC

CTATGCCTATGC

CTATGCCTATGC

TAGTTTGTAGTTTGTAGTCTGGCAGACCACCATAAACTTGGGTTTTTCAGGAGTTTGC GCGGAAGGAATTGACGACGC
AATTCGCTCTGAAGACTTTGAAACAGCTTCCCAACATATTCATCGCTTCTTAACTCGATCAGGCTGTATTTTCAGATT
CGAGAGTTCAAGCAGAAAAGGTTTTTTCGCCTTTAATAGCTAATTTTACGTCAAACTCCTGCCATTTTCCAGACGCCACT
GACTCAATTCGCCACAGCTACGAAGTGCTCTCATCGGCGAAAGAACGCTTGTGAAAAATCTGAAATCCCGTCTAACAG
AGTCTGTTCAAAAGGGAGACGTCGCAGAAATGCAGCGATTTATTAATAATGTTCCCGTTGATTCATGAACCCGACGAGGG
ATTACAGAGATATTCGGTTTTCTTGAATCAGAAAATCGATAAACTGGCCGAGGATAATTTGGCGGTAAGAAATCGGCTA
TTTTTGTAGGAAATATCTTTAAAAAGAGGAAAAAATACCAAAATTGATCAAAAAATGGGTCTGCTAATTATTTTTT
G

TAGTTTGTAGTCTAGCAGACCATATTTCTTCAAACCCCATAGGTCTGCTAAATCGAACTTT
TAGTTTGTAGTCTAGCAGACCGAATTTTCGACAAAACCCCATTTGGTCTGCTAAATCGAAATTTG
TAGTTTGTAGTCTAGCAGACCAAAGTTTCGACAAAACCCCATGGGTCTGCTAAATCGAACTTTG
TAGTTTGTAGTCTAGCAGACCAATATTTCTTCAAACCCCATTTGGTCTGCTAAATCGAACTTTG
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TAGTTTGTAGTCTAGCAGACCAAATTTCTTCAAACCCCATAGGTCTGCTAAATCGAAAAGTG
TAGTTTGTAGTCTAGCAGACCGAATTTCTTCAAACCCCATGGGTCTGCTAAATCGAACTTTG
TAGTTTGTAGTCTAGCAGACCAAATTTTCGCCAAAACCTCATGGGTCTGCTAAATATTTTATG
TAGTTTGTAGTCTAGCAGACCGAATTTCTTCAAACCCCATTTGGTCTGCTAAATCGAACTTTG
TAGTTTGTAGTCTAGCAGACCAATACATTTTTTTTTCTTCAATTATCCATCAAAACAACGCGAGAAAAATTTCAAATTT
ACCCAAAATTAGTGTAGCGCACTAATTTTTTCAGGAAAATTACGAAAATTGCCACTTCTGCTAGATTTTTTGCTGCAA
TTTGCAGCCATTGGTCTGCGAAATGCGCTTTG
TAGTTTGTAGCCTAGCAGACCAAATCTATTTTTCTTCAATTTTCAGCAAGAAATCTACGAAAAATATCAAAAACTATT
GATTTTGTCTCTTAAATTTGCTATTAACCTGTTTTTAATTAATAATTTGGAAAAAATCCCGATATTGGTCTGCTAAA
TCGAAATTCG

Nr of selected repeats 8 Similarity 0.873016

Consensus:

TAGTTTGTAGTCTAGCAGACCaaATTTcttCAAACcCCcAtTGGTCTGCTAAATCGAAActTG

>Cele-UNSB01_2:1416594-1416934 Satlength=341 Nr of Repeats=5 RepeatLength=59
seed=CTACAAACTA

CTACAAACTACAGAAATATTTAGCAGACCCGCTCTAGAAATTCAAAAAAGTTGAGAAAAATTGAAAAAATGGCAA
TTTTCTCTTGGGTCTGCTAGA

CTACAAACTACAAAAGCCTATTTAGCAGACCCACGCCAACTTCTGATGGGTCTGCTAGA
CTACAAACTACAAAAGCCTATTTAGCAGACCCACGCCAACTTCTGATGGGTCTGCTAGG
CTACAAACTACAAAAATATTTAGCAGACCCAACTAATGTCTTATAAATTTGGGCCTGCTAGA
CTACAAACTACAAAAGCCTATTTAGCAGACCCACGCCAATTTCTGATGGGTCTGCTAGA

Nr of selected repeats 3 Similarity 0.969868

Consensus:

CTACAAACTACAAAAGCCTATTTAGCAGACCCACGCCAAcTTCTGATGGGTCTGCTAGa

>Cele-UNSB01_2:1422798-1423926 Satlength=1129 Nr of Repeats=9 RepeatLength=63
seed=TTGGTCTGCT

TTGGTCTGCTCTGGACAACAACTACAACTTTTGATTTAGCAGACCCATGGGGTTTTGAAGAAAA
TTGGTCTGCTAGACTACAACTACAACTTTTGATTTAGCAGACCCATGGGGTTTTGAAGAAAA
TTGGTCTGCTAGACTACATACTACAACTTTTGATTTAGCAGACCCATGGTGTTTTGAAGAAAA
TTGGTCTGCTAGACTACAACTACAACTTTTGATTTAGCAGACCCATGGGGTTTTGAAGAAAA
TTGGTCTGCTAGACTACATACTACAACTTTTGATTTAGCAGACCCATGGTGTTTTGAAGAAAA
TTGGTCTGCTAGACTACAACTACAACTTTTGATTTAGCAGACCCATGGTGTTTTGAAGAAAA
TTGGTCTGCTAGACTACAACTACAACTTTTTTTTCCAAAATCTGAAGAAAAGTCAATTTTTCTATGTTTTTTTTTTG
AAGAAAAAGCTAAAAAATATTTTTAAAAACAAGATTTTTTTTCAGAAAATCAAAAAAACCCTCCGAAAATTGTT
GTTTTCTAGTGTTTTTTAACAAAAAATTTCCAATTTTCAGAAAATAAAGTACAAATATGAAAATTTTCCAAAAATC
GGAATTTCAATGTTTTTTTAGAAAAAGTTGGAAAAATCAAAAAAATGAAATGTAGATTTTTTTGTGTTTTTTTAG
AGAAAAAATGAAAAAATCTATCAAATTTATTAATTTTTTTTTGTCAATTTAAATGTTTTTTATTAATTTAAACAAA
T

TGGGTCTGCTAGTAGACTACAACTACACATTTTCTATTAATAACTGGAACAATTTTCGATTTTCAAATAATCCCAGGA
AAAACGATAATTATCGATTTTTTGTCTATCTTTGAAAAAATCGGAAACATTTTTTTCTGAAAAATGAAATTTAAAA

AAATAGAAAAAATGGCTGAAAAACTCAATTTTCAAAGCAATAAATCAAAAAAATGTTAGATTTTGTAGTTTTTTAGTTTTTTTTTAAAGAAAAAATCCATTTTAAACGATTTTATATTTTTTCAACAACAAAAAATTT

Nr of selected repeats 6 Similarity 0.976014

Consensus:

TTGGTCTGCTAGACTACAaACTACAACTTTTGATTTAGCAGACCCATGGgGTTTTGAAGAAAA

>Cele-UNSB01_2:1429641-1430207 Satlength=567 Nr of Repeats=41 RepeatLength=12

seed=CCTATGCCTA

CCTATGCCTATG

CCTATGCCTATG

CCTATGCCTATG

CCTATGCCTATG

CCTATGCCTATG

CCTATGCCTAAA

CCTAAGCCTATGCTTGAGCCTATGAT

CTATGCCTATGCCTAAA

CCTAAGCCTATG

CCTATGCCTATG

CCTATGCCTATG

CCTATGACCTATG

CCTAAGCCTATG

CCTATGCCTAAG

CCTATGCCTAAG

CCTATGCCTAAG

CCTATGCCTAAG

CATATGCCTATGCCAAAGCATATT

CCTATGCCTAGGCCATA

CCTATGCCTATC

CCTATGCCTAAG

CCTATGCCTATG

CCTATGCCTAAG

CCTAAGCCTATG

CCTATGCCTATG

CCTATGCCTATG

CCTAAGCCTATG

CCTAAGCCTAAG

CCTATGCCTATG

CCTATGCCTCAGCCTAAGCCTGTGT

CTATGCCTATG

CCTATGCCTATG

CCTAAGCCTATG

CCTAAGCCTAAG

CCTATGCCTATG

CCTATGCCTCAGCCTAAG

CCTGTGCCTATG

CCTATGCCTATGCCCAAGA

CTATGCCTATGCCATA

CCTATGCCTAAA

CCTAAGCCTAAGCCTATG

Nr of selected repeats 30 Similarity 0.874585

Consensus:

CCTAtGCCTAtG

>Cele-UNSB01_2:1488365-1488455 Satlength=91 Nr of Repeats=5 RepeatLength=18

seed=GGAGGTCCAG

GGAGGTCCAGGTACCCCG

GGAGGTCCAGGAACCCCT
GGAGGTCCAGGTACTCCA
GGAGGTCTAGGTACCCCG
GGAGGTCCAGGTACCCCG

Nr of selected repeats 5 Similarity 0.859259

Consensus:

GGAGGTCCAGGTACCCG

>Cele-UNSB01_2:1507976-1508324 Satlength=349 Nr of Repeats=19 RepeatLength=15

seed=GGGGCAACA

GGGGCAACAAAATA

GGGGCAACATTTTCATAAATGTA

GGGGCAACAAAAA

GGGGCAACAAAAAT

GGGGCAACATTTTCATAAATGTA

GGGGCAGCAAAAAA

GGGGCAACATAATA

GGGGTCAACATTTGAACTCTCCCC

GGGGCAACAAATTA

GGGGCAACATTTGAACTCTCCCT

GGGGCAACAAATTA

GGGGCAACATTTTCATAAATGTA

GGGGCAACAAAAA

GGGGCAACAAAAAT

GGGGCAACATTTTCATAAATGTA

GGGGCAGCAAAAAA

GGGGCAACATAATA

GGGGTCAACATTTGAACTCTCCCC

GGGGCAACAAATTA

Nr of selected repeats 12 Similarity 0.807407

Consensus:

GGGGCAACAAAaA

>Cele-UNSB01_2:1517382-1518287 Satlength=906 Nr of Repeats=6 RepeatLength=150

seed=TTGCAACATG

TTGCAACATGCGGTGGCGGAAATTCAAATTTTTAGATCAAAAACAGGTTTTTCGACCAATTTTTTCATATTTTCTAGT

GAAATTATGCTAGAAAAATCAATTTTTCACTCAAAATCTTCAGTTTTTCGACATTTTCTCATTGGAGCGCAC

TTGCAACATGCGGTGGCGGAAATTTGAATTTTTGGGTCCAAAACACGTTTTTCGACTATTTTTCTATATTTTCAAG

TAAAATTAGGTAGAAAAATCCAATTTTCACGAAAAATCACCAATTTTCGACATTTTCTCATTGGGGCGCGC

TTGCAACATGCGGTGGCGGAAATTTGAATTTTTGGGTCCAAAACACGTTTTTCGACTAATTTTTTCATATTTTCAAGC

TAAATTATGATAGAAAAATCCAATTTTCCTAAAAATCGGCAATTTTCAGGATTTTCTCACTGGGGCGCAT

TTGCAACATGCGGTGGCGGAAATTCGAATTTTTTCAGTCCAAAACAGGTTTTTCGACCAATTTTTTCATATTTTCTAGT

GAAATTATGCTCGAAAAGTCAATTTTTCACTAAAAATCGCCAATTTTCCACATTTTCTCATTAGAGCGCAC

TTGCAACATGCGATCCGCGGAAATTCGAAATTTTTGGGTCCAAAACACGTTTTTCGACTATTTTTTTTTCTATACTTTC

AAGTGAAATTATGCTCGAAAAGTCAATTTTTCACTAAAAATCGATATTTTCTACTTTTTCTCATTGGGGCGCGC

TTGCAACATGCGGTGGCGGAAATTCGAATTTTTTCAGTCCAAAACATGTTTTTCGACCAATTTTTTCATATTTTCAAGC

TAAATTATGATAGAAAAATCCAATTTTCATAAAAAACCGCCAATTTTCCACATTTTCTCATTGGGGCGCGC

Nr of selected repeats 4 Similarity 0.817145

Consensus:

TTGCAACATGCGGtCGGCGaAAATTCgAATTTTTcaGTCcAAAACAgGtTTTTCGACcAATTTTTTCATATTTTCaAGc

gAAATTATGaTaGAAAATTCaAaTTTTActaAAAAATCgcCAaTTTTTccacATTTTCTCatTgGaGCGCac

>Cele-UNSB01_2:1585165-1585860 Satlength=696 Nr of Repeats=7 RepeatLength=96

seed=GGCCTGCGGC

GGCCTGCGGCCCTCAAACCTGGTTATTAGGCTTGAGTGAATAACATATCTGCTTAGAATAGGATCAAAGCCAGCCATA

GTTACCAAGAGTGTTCG

GGCCTGCGGCCCTCGAACCTGGTTGTTAGGTTTGAGTAAATAACAACCGCGTCGCAGGCCTACAGCCTGCTCTGCTTAG
AATAGGATTAAGCCAGCCACAGTTTTTCGAGAGTATTCT
GGCCTGCGGCCCTCAAACCTGGTTATTAGGCTTGAGTGAATAACATATCTGCTTAGAATAGGATCAAAGCCAGCCCATA
GTTTCCAAGAGTGTTTCG
GGCCTGCGGCCCTCGAACCTGGTTGTTAGGCTTGAGTGAATAACATATCTGCTTAGAATAGGATCAAAGCCAGCCCATA
GTTTTCAAGAGTGTTTCG
GGCCTGCGGCCCTCGAACCTGGTTGTTAGGCTTGAGTGAATAACATATCTGCTTAGAATAGGATCAAACCAGCCCATA
GTTTCCAAGAGTGTTTCG
GGCCTGCGGCCCTCGAACCTGGTTGTTAGGCTTGAGTGAATAACATATCTGCTTAGAATAGGATCAAAGCCAGCCCATA
GTTTCCAAGAGTGTTTCG
GGCCTGCGGCCCTCGAACCTGGTTGTTAGGCTTGAGTGAATAACATATCTGCTTAGAATAGGATCAAAGCCAGCCCATA
GTTTTCAAGAGTGTTTCG

Nr of selected repeats 6 Similarity 0.968518

Consensus:

GGCCTGCGGCCCTCGAACCTGGTTGTTAGGCTTGAGTGAATAACATATCTGCTTAGAATAGGATCAAAGCCAGCCCATA
GTTTcCAAGAGTGTTTCG

>Cele-UNSB01_2:1599041-1599824 Satlength=784 Nr of Repeats=24 RepeatLength=23
seed=CGCTGTAAGA

CGCTGTAAGACCCTTCGCTGTATCGCTGCGAGACCCTCCGCTGTAC
CGCTGTAAGACCATTTGCTGTAT
CGCTGTAACACCCTTCTCTGTAT
CGCTGTAAGACCCTTCGCTGTATCGCTGCGAGCCCCTTCGCTATATCGTTGCGAGACCCTTCACTATTT
CGCTGTAAGACCCTTCGCTGTAC
CGCTGTAAGATCCTTCGCTGTTC
CGCAGTAAGATCCTTCGCTGTTC
CGCTGTAAGACACTTCACTATTC
CGCTGTAAGACCCTTCGCTGTAC
CGCTGTAAGATCCTTCGCTTTTC
CGTTGTAAGACCGTTTGCTGTATCGCTGCGAGCCCCTTTGCTGTAC
CGCTGTAAGATCTTTGCTGTTC
CGTTGTAAGACCCTTCGCTGTAC
CGCTGTAAGAGCCTTTGCTGTAC
CGCTGTAAGATCTTTGCTGTTC
CGTTGTAAGACCTTTGCTGTAC
CGCTGTAAGACCCTTTGCTGTAC
CGCTGTAAGATCTTTGCTGTTC
CGTTGTAAGACCCTTCGCTGTAC
CGCTGTAAGACCCTTTGCTGTATCGCTGCGAGCCCCTTCGCTGTATCGTTGTGAGACCCTTCACTATTTGCTGCGAGA
CCCTTCGCTGTACA
GCTGTAAGATCCTTCGCTGTTC
CGCTGTAAGACCCTTCGCTGTATCGTTGTGAGACCCTTCACTATTTGCTGCGAGACCCTTCACTATAT
CGCTGTAAGACTCTTTGCTGTATCGTCGCGAGACCCTTCGATGTAT
CGCTGCAAGACCTCTTCGCTCTTT

Nr of selected repeats 16 Similarity 0.806763

Consensus:

CGCTGTAAGAcCcTTCGCTGTaC

>Cele-UNSB01_2:1617453-1617521 Satlength=69 Nr of Repeats=4 RepeatLength=17
seed=TCATTCCGTG

TCATTCCGTGATTATTT
TCATTCCGTGATTATTT
TCATTCCGTGATTATTT
TCATTCCGTGATTATTT

Nr of selected repeats 4 Similarity 1.000000

Consensus:

TCATTCCGTGATTATTT

>Cele-UNSB01_2:1625642-1627656 Satlength=2015 Nr of Repeats=131 RepeatLength=14

seed=GATCCTAGAT

GATCCTAGATCCTG

GATCCTAGATCCTA

GATCCGAGATCCTA

GAGCCTAGATCCTA

GATCCTAGATCCTA

GATCCCAGATCCTA

GATCCCAGATCCTA

GATCCCAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGTTCTA

GATCCTAGATCCTA

GATCCTAGATCCCA

GATCCTAGATCCCA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTAGATCC

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATCCTA

GATACTAGATCATA

GAGCCTAGATCCTA

GATCCTAGATCCTA

GATCCTAGATACTAGATCATA

GAGCCTAGATCCTGGTGTCTA

GATCCTAGATCCTA

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GAGCCTAGATCCTGGTGTCTA

GATCCTAGATCCTA

GATCCTAGATCCTA
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ATCCTAGATCCTA
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GATCTAGATCCTA
GATCCTAGATCCTA
GATCCTAGATCCTA
GATACTAGATCATA
GAGCCTAGATCCTGGTGTCTA
GATCCTAGAACCTA
GATCCTAGATACTAAATCATA
GAGCCTAGATCCTGGTGTCTA
GATCCTAGATCCTA
GATCCTAGATCCTA
GATCCTAGTTCTA
GATCCTAGATCCTA
GATCCTAGATCCTA
GATCCTAGTTCTA
GATCCTAGATCCTAGAGCCTAGAGCCTAGAGCCTAAAGCCTAAAGCCTA
GATCCTAGATCCTAGAGCCTAGAGCTTA
GAACCTAGATCCTAGATCATAGAACCCTAAATCTTG
GATCCTAGATCCTAGATAATC
GATCCTAGATAATAGATCCTGAAGCCTAGAGCGTAGATCCAAGACACTT
GATCCTAGATTTTA
GATCCTAGATCCTAGGTCTTA
GATCCTAGATACTT

Nr of selected repeats 112 Similarity 0.963106

Consensus:

GATCCTAGATCCTA

>Cele-UNSB01_2:1652802-1653206 Satlength=405 Nr of Repeats=5 RepeatLength=42

seed=TTGCCGGTTG

TTGCCGGTTGCCGAAATTTTTTGAATCAGCAACTTCGGCAA
TTGCCGGTTGCCGAACTCCAAAAATTTTTGGAGTTCGGCAACTTCGGCAATTGCCGAACTTTTTTTCAGCAACTTCGGC
AATTGCTGATATCAATGTCAAACATTCGTAGCTCAGAAAAAGCATTAGAGAGCATGAAAAATGCTAATATTTTGCTG
TAAACGAGAAAAACAACCATTTGCTTTTTGCCAAAACCTCAAAAATATATTTTTCAACAGAAAACAAAAATTCGAAACCTGG
TTGCCGGTTGTGCGAAAAGTTGCCGAAGTTTCTGCAACCGAAAG
TTGCCGGTTGCCGAAGTTTTTTCAGCGTTTCGACAACCTTCGGCAA
TTGCCGGTTGCCGAAATGTTTTGGGTTTCGGCAACTTCGGCAA

Nr of selected repeats 3 Similarity 0.809524

Consensus:

TTGCCGGTTGCCGAAATTTTTGggTTCggCAACTTCGGCAA

>Cele-UNSB01_2:1657514-1657909 Satlength=396 Nr of Repeats=5 RepeatLength=42

seed=CAACCGGCAA

CAACCGGCAATTGCCGAAGTTGCCGAACCCAAAACATTTTCGG
CAACCGGCAATTGCCGAAGTTGTCGAACGCTGAAAACCTTCGG
CAACCGGCAACTTTTCGGTTCAGAACTTCGGCAACTTTTCGA
CAACCGGCAACCAGGTTTCGAATTTTTGTTTCTGTTGAAAATATATTTTTGAGTTTTGGCAAAAAGCAATGGTTGTTTT
CTCGTTTACAGCAAAAATATTAGCATTTTTTCATGCTCTCTGAATGCTTTTTCTGAGCTACAGAATGTTTGACATTGATAT
CAGCAATTGCCGAAGTTGCTGAAAAAAGTTTCGGCAATTGCCGAAGTTGCCGAACTCCAAAAATTCGG
CAACCGGCAATTGCCGAAGTTGCTGATTCCAAAAATTTTCGG

Nr of selected repeats 3 Similarity 0.809524

Consensus:

CAACCGGCAATTGCCGAAGTTGccGAaccCaaAAaAtTTTCGG

>Cele-UNSB01_2:1681965-1682083 Satlength=119 Nr of Repeats=7 RepeatLength=17
seed=GATGCCCCCT
GATGCCCCCTCTGAACG
GATGCCCCCTCTGAACG
GATGCCCCATTTGAACG
GATGCCCCCTACGAACAA
ATGCCCCCTTTGACCTA
ATGCCCCCTTAGAACGC
GATGCCCCCTCTCTC

Nr of selected repeats 5 Similarity 0.729630

Consensus:

gATGCCCCcTttGAaCg

>Cele-UNSB01_2:1815608-1815814 Satlength=207 Nr of Repeats=6 RepeatLength=34
seed=ATTTGAATTT

ATTTGAATTTCCCGCCAAAATTTTTTCACTGAAA
ATTTGAATTTCCCGCCAAAATTTTTTCACTGAAT
ATTTGAATTTCCCGCCAAAATTTTTTCACTGAAA
ATTTGAATTTCCCGCCAAAATTTTTTCACTGAAA
ATTTGAATTTCCCGGCAAAAATTTTTTCACTGAAA
ATTTGAATTTCCCGCCAAAATGCTTTTACAGAAC

Nr of selected repeats 4 Similarity 0.980392

Consensus:

ATTTGAATTTCCCGcCAAAAATTTTTTCACTGAAA

>Cele-UNSB01_2:1818966-1819342 Satlength=377 Nr of Repeats=11 RepeatLength=34
seed=CGGGAAATTC

CGGGAAATTCAAATGTTCTGTGAAAAGCATTTTGG
CGGGAAATTCAAATTTTTCAGTGAAAAAATTTTGC
CGGGAAATTCAAATTTTTCAGTGAAAAAATTTTGG
CGGGAAATTCAAATTTTTCAGTGAAAAAATTTTGG
CGGGAAATTCAAATATTTCAGTGAAAAAATTTTGG
CGGGAAATTCAAATTTTTCAGCGAAAAAATTTTGG
CGGGAAATTCAAATTTTTCAGTGAAAAAATTTTGG
CGGGAAATTCAAATTTTTCAGTGAAAAAATTTTGG
CGGGAAATTCAAATTTTTCAGTGAAAAAATTTTGG
CGGGAAATTCAAATTTTTCAGTGAAACAATTTTGG
CGGGAAATTCAAATTTTTCAGTAAAAAATTTTGG

Nr of selected repeats 9 Similarity 0.956427

Consensus:

CGGGAAATTCAAATTTTTCAGTGAAAAAATTTTGG

>Cele-UNSB01_2:1881035-1881350 Satlength=316 Nr of Repeats=5 RepeatLength=65
seed=TATCGAGAGA

TATCGAGAGAATTTCCAATGTTTCCAACAAAATCGATTTCCAGTTCCAATAAGACTCTCAGTAAG
TATCGAGAGAATGCTCTACATTCACTTTGAATTTCTTTTCCAATTTCAATAAGACTCTCAGTAAG
TATCGAGAGAATTCACATTCACTTTGAATGCCCCGTTCCAATTTTCAGTAAAACTCTCTATAAG
TATCGAGAGAATGTTCCAAAGAATTCAATTTCCAATTTTCAATAAGACTCCCAGTAGG
TATCGAGAGAATATTACATTCATTTTGAATGCCCATTTCCAATTTCAATAAGACTCTCAGTAAG

Nr of selected repeats 3 Similarity 0.658497

Consensus:

TATCGAGAGAATntTccAcATTcactttgAattcctntTTCCAaTTtCAATAAGACTCTCAGTAAG

>Cele-UNSB01_2:1915179-1915855 Satlength=677 Nr of Repeats=26 RepeatLength=26
seed=ATTTACGGAG

ATTTACGGAGGTTTCGATCCTGTGTCG
ATTTACGGAGCTTCAAGTTAATGTTG
ATTTACGGAGCTTCAAGCTTGTGCCAA

ATTACGGAGCTTCACGTTTGTGTCG
 ATTTATGGAGCTTCAAGCTTGTGTCG
 ATTTACGGAGTTTCAAGCTTGTGTCGG
 TTTACGGAGCTTCAAGCTTGTGCCA
 ATTTACGGAACTTCAAGGTTGTGTCG
 ATTTACGGAGCTTCAATCTTGTGTCG
 ATTTACGGATCTCCAAGCTTGTGTAG
 ATTTACGGAGCTTTAGGATTATGTCG
 ATTTACGGAGCTTCAAGGTTGTATCA
 ATTCACGGAGCTTTGGGATTGTGTTG
 ATTTACGGAGCTTCAAGCTTGTGTCG
 ATTTACGGAGCTTCAAGCTTGTGTCG
 ATTTACGGAGCTACAAGCTTGTGTCG
 ATTTACGGAGCTTCAAGCTTGTGTCG
 ATTTACGGAGCTTCGAGCTTGTGTCG
 ATTTACGGAGCTACAAGCTTGTGTCG
 ATTTATGGAGCTACAAGCTTGTGTCA
 ATTTACGGAGCTTCGAGCTTGTGTCG
 ATTTACGGAGCTTCAAGCTTGTGTCG
 ATTTACGGAGCTTCGAGCTTGTGTCG
 ATTTACGGAGCTACAAGCTTGTGTCG
 ATTTATGGAGCTACAAGCTTGTGTCA
 ATTTACGGAGCTTCGAGCTTGTGTCG

Nr of selected repeats 22 Similarity 0.829282
 Consensus :

ATTTACGGAGCTtCaAGcTTGTGTCG

>Cele-UNSB01_2:1984417-1985378 Satlength=962 Nr of Repeats=31 RepeatLength=31
 seed=AGAGCTGAGT

AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
 AGAGATGAGTTGTGCGAGCGAGACCTCAGAAG
 AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
 AGAGATGAGTTGTGCGAGTGAGACCTCAGAAG
 AGAGCTGAGTTGTCTAGCGAGATAGCAGAAA
 AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
 AGAGATGAGTTGTGCGAGTGAGACCTCAGAAG
 AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
 AGAGATGAGTTGTGCGGCGAGACCTCAGAAG
 AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
 AGAGATGAGTTGTGCGAGTGAGACCTCAGAAG
 AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
 AGAGATGAGTTGTGCGAGTGAGACCTCAGAAG
 AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA

AGAGATGAGTTGTTCGAGCGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGTGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGTGAGACCTCAGAAG
Nr of selected repeats 31 Similarity 0.809341

Consensus:

AGAGcTGAGTTGTcTAGCGAGAtagCAGAnA

>Cele-UNSB01_2:1991206-1991967 Satlength=762 Nr of Repeats=23 RepeatLength=32
seed=AATTCGGCC

AATTCGGCCAAAAATTTTTCAGAAAATTTG
AATTCGGCCAAAAATTTGTAAGAAAATTTA
AATTCGGCCAAAAATTTTTCAGAGAAAATTTG
AATTCGGCCAAAAATTTTTCAGAAAATTTG
AATTCGGCCAAAAATTTTTCACAGAAAATTTG
AATTCGGCCAAAAATTTTAAAGAAAATTTA
AATTCGGCCAAAAATTTTTCAGAGAAAATTTG
AATTCGGCCAAAAATTTTTCAGAAAATTTG
AATTCGGCCAAAAATTTTTCACAGAAAATTTG
AATTCGGCCAAAAATTTTAAAGAAAATTTA
AATTCGGCCAAAAATTTTTCAGAGAAAATTTG
AATTCGGCCAAAAATTTTTCAGAAAATTTG
AATTCAGGCCAAAAATTTTCAAAGAAAATTTG
AATTCGGCCAAAAATTTTGAAGGAAAATTTA
AATTCGGCCAAAAATTTTTCAGAGAAAATTTG
AATTCGGCCAAAAATTTTTCAGAAAATTTG
AATTCGGCCAAAAATTTTGAAGGAAAATTTA
AATTCGGCCAAAAATTTTTCAGAGAAAATTTG
AATTCGGCCAAAAATTTTTCAGAAAATTTG
AATTCGGCCAAAAATTTTTCACAGAAAATTTG
AATTCGGCCAAAAATTTTAAAGAAAATTTA
AATTCGGCCAAAAATTTTTCAGAGAAAATTTG
AATTCGGCCAAAAATTTTTCAGAAAATTTGAGCTACCGCCAAAAATTTTTCACAGAAAATTTG
Nr of selected repeats 16 Similarity 0.855208

Consensus:

AATTCGGCCAAAAAtTTTcAnAGAAAATTTg

>Cele-UNSB01_2:1992839-1994265 Satlength=1427 Nr of Repeats=46 RepeatLength=31
seed=AGAGCTGAGT

AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGCGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGTGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAAA
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGTGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGCGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAAA
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGTGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGCGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTTCGAGCGAGACCTCAGAAG

AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTCTAGCGAGACCTCAGAAG
AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA
AGAGATGAGTTGTCTAGCGAGACCTCAGAAG

Nr of selected repeats 46 Similarity 0.811262

Consensus:

AGAGcTGAGTTGTCTAGCGAGAtagCAGAnA

>Cele-UNSB01_2:2000093-2000918 Satlength=826 Nr of Repeats=25 RepeatLength=32
seed=AATTC³CGCC

AATTC³CGCCAAAAATTTTTCAGAAAATTTG
AATTC³CGCCAAAAATTTTAAAGAAAATTTA
AATTC³CGCCAAAAATTTTCAGAGAAAATTTG
AATTC³CGCCAAAAATTTTTCAGAAAATTTG
AATTC³CGCCAAAAATTTTTCACAGAAAATTTG
AATTC³CGCCAAAAATTTTAAAGAAAATTTA
AATTC³CGCCAAAAATTTTCAGAGAAAATTTG
AATTC³CGCCAAAAATTTTTCAGAAAATTTG
AATTC³CGCCAAAAATTTTTCACAGAAAATTTG
AATTC³CGCCAAAAATTTTAAAGAAAATTTA
AATTC³CGCCAAAAATTTTCAGAGAAAATTTG
AATTC³CGCCAAAAATTTTTCAGAAAATTTG
AATTC³CGCCAAAAATGTTTTCAGAAAATTTG
AATTCACGCCAAAAATTTTCAAAGAAAATTTG
AATTC³CGCCAAAAATTTTGAAGGAAAATTTA
AATTC³CGCCAAAAATTTTTCAGAGAAAATTTG
AATTC³CGCCAAAAATTTTTCAGAAAATTTG
AATTC³CGCCAAAAATTTTGAAGGAAAATTTA
AATTC³CGCCAAAAATTTTTCAGAGAAAATTTG
AATTC³CGCCAAAAATTTTTCAGAAAATTTG

AATTCCCGCCAAAAATTTTTCACAGAAAATTTG
AATTCCCGCCAAAAAATTTTAAAGAAAATTTA
AATTCCCGCCAAAAATTTTTCAGAGAAAATTTG
AATTCCCGCCAAAAAATTTTAAAGAAAATTTA
AATTCCCGCCAAAAATTTTTCAGAGAAAATTTG
AATTCCCGCCAAAAATGTTTCAGAAAATTTGAGCTACCGCCAAAAATTTTTCACAGAAAATTTG

Nr of selected repeats 18 Similarity 0.865196

Consensus:

AATTCCCGCCAAAAatTTTcAnAGAAAATTTg

>Cele-UNSB01_2:2015956-2016256 Satlength=301 Nr of Repeats=25 RepeatLength=12
seed=ATGTATATGT

ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTTTATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAA
ATGTAAATGTAA
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTTT
ATGTATATGTAT
ATGTATATGTAA
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT
ATGTATATGTAT

Nr of selected repeats 25 Similarity 0.948889

Consensus:

ATGTATATGTAT

>Cele-UNSB01_2:2017071-2017146 Satlength=76 Nr of Repeats=5 RepeatLength=15
seed=TCGTGGCGAG

TCGTGGCGAGACCCA
TCGTTGCGAGACCCT
TCGTGGCGAGACCCA
TCGTGGCGAGACCCA
TCGTGGCGAGACCCA

Nr of selected repeats 5 Similarity 0.928889

Consensus:

TCGTgGCGAGACCCa

>Cele-UNSB01_2:2017169-2017519 Satlength=351 Nr of Repeats=10 RepeatLength=32
seed=GGCGGGAATT

GGCGGGAATTTAAATTTTCTTTGAAATTTTTT
GGCGGGAATTCAAATTTTCTGTGAAAATTTTGGCGGTAGTTCAAATTTTCTTCAAATTTTTT
GGCGGGAATTCAAATTTTCTTTGAAATTTTTT

Nr of selected repeats 42 Similarity 0.826558

Consensus:

GACAACCTCAgCTCTttTCTGctaTCTCgCTa

>Cele-UNSB01_2:2065528-2066342 Satlength=815 Nr of Repeats=5 RepeatLength=162
seed=AGTTTTATGA

AGTTTTATGAAATAAAAAAGAATGACTCCATATGATTTTCCAGGACTTTTGCATTTTGGAAAAATCAGCTTTTATATA
TTTTTATCATTAAAAAATACTTCCGTACAAGCTATTATAATTTGATTAGCATATCTGGTATTTTGGACTATG
CTGAAG

AGTTTTATGAAATAAAAAAGAATGACTCTATATGATTTTCCATACTTTTGAATTTTGGAAAAATCAGCTTTTATATA
TTTTTATCCATTTTAAAAAATACTTCCGTACAAGCTATTATACTTTGTTTAGCATTTCTGGTATTTTGGACTATGCT
GAAG

AGTTTTATGAAATAAAAAAGAATGACTCTATATGATTTTCCATACTTTTGAATTTTGGAAAAATCAGCTTTTATATA
TTTTTATCCATTTTAAAAAATACTTCCGTACAAGCTATTATACTTTGTTTAGCATTTCTGGTATTTTGGACTATGCT
GAAG

AGTTTTATGAAATAAAAAAGAATGACTCTATATGATTTTCCATACTTTTGAATTTTGGAAAAATCAGCTTTTATATA
TTTTTATCATTAAAAAATACTTCCGTACAAGCTATTATAATTTGATTAGCATATCTGGTATTTTGGACTATG
CTGAAG

AGTTTTATGAAACAAAAAGAATGACTCCATATGATTTTCCATACTTTTGAATTTTGGAAAAATCAGCTTTTATATA
TTTTTATCCATTTTAAAAAATACTTCCGTACAAGCTATTATACTTTGTTTAGCATTTCTGGTATTTTGGACTATGCT
AAAG

Nr of selected repeats 3 Similarity 0.983539

Consensus:

AGTTTTATGAAAtAAAAAGAATGACTCtATATGATTTTCCATACTTTTGAATTTTGGAAAAATCAGCTTTTATATA
TTTTTATCCATTTTAAAAAATACTTCCGTACAAGCTATTATACTTTGTTTAGCATTTCTGGTATTTTGGACTATGCT
gAAG

>Cele-UNSB01_2:2125481-2125594 Satlength=114 Nr of Repeats=5 RepeatLength=22
seed=TGGTCAGTGC

TGGTCAGTGCAAAAAAAAAACTAA

TGGTCAGTGCAAAAAATACTGAT

TGGTCAGTGCAACAATTTTAT

TGGTCAGTGCAACATTTTAT

TGGTCAGTGCAACATTTTAT

Nr of selected repeats 3 Similarity 0.959596

Consensus:

TGGTCAGTGCAAACAtTTTTAT

>Cele-UNSB01_2:2168167-2168227 Satlength=61 Nr of Repeats=4 RepeatLength=11
seed=ACCGCAACGCA

ACCGCAACGCA

ACCGCAACGCA

ACCGCAACGCA

ACCGCAACGCAACCGCACCTTAACGCG

Nr of selected repeats 3 Similarity 1.000000

Consensus:

ACCGCAACGCA

>Cele-UNSB01_2:2174137-2174267 Satlength=131 Nr of Repeats=5 RepeatLength=26
seed=TCAAGGCGAA

TCAAGGCGAAACGGGAGGTGAATCGC

TCAAGGCGAAACGGGAGGTGAATCGC

TCAAGGCGAAACGGGAGGTGAATCGA

TCAAGGCGAAACGGGAGGTGAATCGC

TCAAGGCGAAACGGGAGGTGAATCGC

Nr of selected repeats 5 Similarity 0.979487

Consensus:

TCAAGGCGAAACGGGAGGTGAATCGc

Nr of selected repeats 6 Similarity 0.936508

Consensus:

TGTGCCCTGGAAAGCTGGCAG

>Cele-UNSB01_2:2296694-2296754 Satlength=61 Nr of Repeats=4 RepeatLength=10

seed=CAGCAGAGTG

CAGCAGAGTG

CAGCAGAGTG

CAGCAGAGTG

CAGCAGAGTGCAGCGAAGTACAGCAGTGTG

Nr of selected repeats 3 Similarity 1.000000

Consensus:

CAGCAGAGTG

>Cele-UNSB01_2:2366031-2366422 Satlength=392 Nr of Repeats=13 RepeatLength=11

seed=CTACAGTACC

CTACAGTACCTTTACAGCACTA

CTACAGTACCCCGACCATACCCCATCACTAACCTCAAACCAATATCCCTTCAAAAAGGCGAAAAGTCAATTTTTCCCAA

CTACAGTAATC

CTACAGTACTC

CTACAGTACCT

CTACAGTACTA

CTACAGTACCCCGACCATATCCCACCACTAACCTCAAACCAATATCCCTTCAAAAAGGCGAAAAGTCAATTTTTCCCAA

CTACAGTAATC

CTACAGTAACC

CTACAGTACCT

CTACAGTACTA

CTACAGTACCCCGACCATATCCCACCACTAACCTCAAACCAATATCCCTTCAAAAAGGCGAAAAGTCAATTTTTCCCAA

CTACAGTAATC

CTACAGTACTC

CTACAGTACCT

CTACAGTACTA

Nr of selected repeats 9 Similarity 0.763889

Consensus:

CTACAGTACTn

>Cele-UNSB01_2:2379059-2380853 Satlength=1795 Nr of Repeats=9 RepeatLength=163

seed=TGAATTTTTG

TGAATTTTTGAAAATAATCTTCCGTACGAGCTACTATCAAATTTATGAATCGATCCTTCGATTTTTGCAAAAATCTTTG

CCGCACAGAAAGTTGGGCGGAGCGTCTTTTCGCAACACTGCCGCGCGGGGTTTGCCCCGCGCCTTTTCCGCTGCTTTT

CTTGTTGATTTTTTCAATAAAGTTTCGATTTTTCTTTTTTTTTTTTCAAATTTGGATAACATTTTCATTCGAAAAAAAAG

AAAAATCGAAAATTTATTGAAAAAATCAACAAGAAAAGCAGCGGAAAATGGCCGGGGGCAAACCCCGCGCGGCAGTGTT

GCGAAAGGACGCTCCTCCCAACTTTCTGTGCGCAAAGATTTTTGCAAAAATCGAAGGATCGATTCATAAATTTGATAG

TAGCACAATTTGTTTGGTATTTTCTGGTACATTTGACTATGCTGAACAGTTTTTATAAAAATAAAAAAGAATGACTTCATA

TAATTTTTGAGGTACTTT

TGAATTTTTGAAATATATCAGCTTTTGGTTAAATTTCTGCATTTTTTAAAAATAAACTTCCGTACGAGCTAGCACCTTTTT

TTAAGTATTTTCTGGTACATTTGACTATGCTGAACAGTTTTTATAAAAATAAAAAAGAATGACTTCATATAATTTTGGGT

ACTTT

TGAATTTTTGAAAATAACAGCTTTTGGTTAAATTTCTGCATTTTTTAAAAATAAACTTCCGTACGAGCTAGCACCTTTTT

TTAAGTATTTTCTGGTACATTTGACTATGTTGAACAGTTTTTATAAAAATAAAAAAGAATGACTTCATATGATTTTGGGT

ACTTT

TGAATTTTTGAAAATAAGAGCTTGTGGTTAAATTTCTGCATTTTTTAAAAATAAACTTCCGTACGAGCTATTGTATATTT

TTTGGTATTTTCTGGTACATTTGACTATGATGAACAGTTTTTATGAAATAAAAAAGAATGACTTCATATGATTTTGGGT

ACTTT

TGAATTTTTGAAAATAAGAGCTTTTGGTTAAATTTCTGCATTTTTTAAAAATAAACTTCCGTACGAGCTAGCACCTTTTT

TTAAGTATTTTCTGGTACATTTGACTATGCTGAACAGTTTTTATAAAAATAAAAAAGAATGACTTCATATAATTTTGGGT

ACTTT

TGAATTTTTGAAAAATACAGCTTTTGGTTAAATTCTGCATTTTTTAAAAATAAACTTCCGTACGAGCTAGCACCTTTTT
TTAAGTATTTTTCTGGTACATTTGACTATGCTGAACAGTTTTATAAAATAAAAAAATGACTTCATATGATTTTTGACGT
ACTTT

TGAATTTTTGAAAAATAAGAGCTTTTGGTTAAATTCTGCATTTTTTAAAAATAAACTTCCGTACGAGCTAGCACCTTTTT
TTAAGTATTTTTCTGGTACATTTGACTATGCTGAACAGTTTTATAAAATAAAAAAGAATGACTTCATATGATTTTTGACGT
ACTTT

TGAATTTTTGAAAAATAACAGCTTTTGGTTAAATTCTGCATTTTTTTTTTAAATAAACTTCCGTACGAGCTATTGTATATTTT
TTGGTATTTTTCTGGTACATTTGACTATGATGAACAGTTTTATGAAATAAAAAAGAATCGCTTCATATGATTTTTTTCAGTA
CTTT

TGAATTTTTGAATATATCAGCTTTTGGTTAAATTCTGCATTTTTTTTTTAAATAAACTTTGGTACGAGCTAGCATTCTTTG
TTTAgTATTTTTCTGGTATATTTGACTATGTTGAACAGTTTTATAAAATAAAAAAGAATGACTTCATATAATTTTTGAGGT
ACTTT

Nr of selected repeats 7 Similarity 0.906387

Consensus:

TGAATTTTTGAAaATAAcAGCTTTTGGTTAAATTCTGCATTTTTTAAAAATAAACTTCCGTACGAGCTAGCAcCTTTTT
TTaAGTATTTTTCTGGTACATTTGACTATGcTGAACAGTTTTATAAAATAAAAAAgAATGACTTCATATgATTTTTGAgGT
ACTTT

>Cele-UNSB01_2:2403604-2403679 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=TCGTGGCGAG

TCGTGGCGAGACCCA

TCGTTGCGAGACCT

TCGTGGCGAGACCCA

TCGTGGCGAGACCCA

TCGTGGCGAGACCCA

Nr of selected repeats 5 Similarity 0.928889

Consensus:

TCGTgGCGAGACCCa

>Cele-UNSB01_2:2547654-2548528 Satlength=875 Nr of Repeats=24 RepeatLength=35

seed=CCGGAATTT

CCGGAATTTTTCATTTTTCGGCAATTTGCCGATTTG

CCGGAAGTTTTAAATTCCGGCACTTTGTCGGTTTGCCGAAACTTTTTGTTTTCGGAAATGTGCCGCTTTG

CCGGAATTTTTCATTTTTCAACGATTTGCCGATTTG

CCGGAATTTTTAACT

CCGGCAATTTGCCGTTTG

CCGGAATTTTTCATTTTTGGTGATTTGCTGATTTT

CCGGAATTTTTCATTTTTCGTGATTTGCCGATTTG

CCGGAATTTTTCATTTTTGGTGATTTTCCGATTTG

CCGGAATTTTTCATTTTTCGACAATTTGCCGATTTG

CCGGAATTTTTAAATTCCGGCACTTTGCCGTTTGCCGAAACTTTTTATTTTTCGGAAATGTGCCGCTTTG

CCGGAATTTTTCATTTTTCAACGATTTGCCGATTTG

CCGGAATTTTTAACT

CCGGCAATTTGCCGTTTG

CCGGAATTTTTCATTTTTGGTGATTTGCTGATTTT

CCGGAATTTTTCATTTTTCGTGATTTGCCGAGTGT

CCGGAATTTTTCATTTTTGGTGATTTTCCGATTTG

CCGGAATTTTTCATTTTTCGACAATTTGCCGATTTG

CCGGAATTTTTAAATTCCGGCACTTTGCCGTTTGCCGAAACTTTTTATTTTTCGGAAATGTGCCGATTTG

CCGGAATTTTCATCATCGGCACATTATCGATTTG

CCGGAATTTTCATCATCGGCACATTGCCGATTTG

CCGGAATTTTCATTTTTGGTGATTTGCTGATTTG

CCGGAATTTTCATTTTTCGGCAATTTGCCGATTTG

CCGGAATTTTCATCATCGGCACATTGCCGTTTG

CCGGAATTTTCATTTTTGGTGATTTGCTGATTTG

Nr of selected repeats 16 Similarity 0.798413

Consensus :

CCGGAAATTTTCATTTTcggcgATTTGCcGATTtg

>Cele-UNSB01_2:2568294-2568366 Satlength=73 Nr of Repeats=6 RepeatLength=12

seed=TTAGGCTTAG

TTAGGCTTAGGA

TTAGGCTTAGGC

TTGGGCTTAGGT

TTAGGTTTAGTC

TTAGTCTTAGGC

TTAGGCTTAGGC

Nr of selected repeats 6 Similarity 0.785185

Consensus :

TTAGGCTTAGGc

>Cele-UNSB01_2:2602717-2603767 Satlength=1051 Nr of Repeats=24 RepeatLength=31

seed=CTGAAATTCC

CTGAAATTCCAATTTTCCAGTGTA AAAATGT

CTGAAATTCCAATTTTCCACAGTAAAAATGC

CTGAAATTCCAATTTTCCAGTGTA AAAATGT

CTGAAATTCCGATTTTCCAGTATAGAAATGT

CTGAAATTTTCGATTTTCCAGTGTA AAAATGTCTGGAATTTTCGATTTTCCAGTATAGAAATGT

CTGAAATTCCGATTTTCCAGTGTA AAAATGTCTGGAATTTCAAATTTCCACTGAAAAATGT

CTGAAATTCCGAATTTCCAGTGCA AAAATGT

CTGAAATTTTCGATTTTCCAATGTAAAAATCT

CTGAAAATCCGATTTTCCAGCGTAAAACGTCTGAAATTTTGATTTTCCACTGTAAAAATGTCTAAAATCCCGAATTTCC

ACTGAAAAAATGT

CTGAAATTCCGATTTTCCAGTGTA AAAATGC

CTGAAATTCCGAATTTCCAGTGCA AAAATGTCTGAAATTTTGATTTTCCAATGTAAAAATCT

CTGAAATTCCAATTTTCCAGTGTA AAAATGT

CTGAAATTCCAATTTTCCACAGTAAAAATGC

CTGAAATTCCAATTTTCCAGTGTA AAAATGT

CTGAAATTCCGATTTTCCAGTATAGAAATGT

CTGAAATTTTCGATTTTCCAGTGTA AAAATGTCTGGAATTTTCGATTTTCCAGTATAGAAATGT

CTGAAATTCCGATTTTCCAGTGTA AAAATGTCTGGAATTTCAAATTTCCACTGAAAAATGT

CTGAAATTCCGAATTTCCAGTGCA AAAATGT

CTGAAATTTTCGATTTTCCAATGTAAAAATCT

CTGAAAATCCGATTTTCCAGCGTAAAACGTCTGAAATTTTGATTTTCCACTGTAAAAATGTCTAAAATCCCGAATTTCC

ACTGAAAAAATGT

CTGAAATTCCGATTTTCCAGTGTA AAAATGC

CTGAAATTCCGAATTTCCAGTGCA AAAATGTCTGAAATTTTGATTTTCCAATGTAAAAATCT

CTGAAATTCCAATTTTCCACTGTAAAAATGT

CTGAAATTCCAATTTTCCAATGTAAAAATCT

Nr of selected repeats 16 Similarity 0.855556

Consensus :

CTGAAATTCCaATTTTCCAgTGTA AAAATGt

>Cele-UNSB01_2:2619434-2619682 Satlength=249 Nr of Repeats=8 RepeatLength=31

seed=AGAGCTGAGT

AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA

AGAGATGAGTTGTCTGAGCGAGACCTCAGAAG

AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA

AGAGATGAGTTGTCTGAGTGAGACCTCAGAAG

AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA

AGAGCTGAGTTGTCTGAGCGAGACCTCAGAAG

AGAGCTGAGTTGTCTAGCGAGATAGCAGAGA

AGAGCTGAGTTGTCTGAGCGAGACCTCAGAAG

Nr of selected repeats 8 Similarity 0.806548

Consensus:

AGAGcTGAGTTGTCgAGCGAGAcagCAGaAGa

>Cele-UNSB01_2:2625510-2625733 Satlength=224 Nr of Repeats=7 RepeatLength=32
seed=AATTCCCGCC

AATTCCCGCCAAAAATTTTTCACAGAAAATTTG
AATTCCCGCCAAAAAATTTTAAAGAAAATTTA
AATTCCCGCCAAAAATTTTCAGAGAAAATTTG
AATTCCCGCCAAAAATGTTTCAGAAAATTTG
AATTCCCGCCAAAAATTTTAAAGAAAATTTA
AATTCCCGCCAAAAATTTTCAGAGAAAATTTG
AATTCCCGCCGAAAAATTTCAAAGAAAATTTA

Nr of selected repeats 6 Similarity 0.855556

Consensus:

AATTCCCGCCAAAAAaTTTcAaAGAAAATTTa

>Cele-UNSB01_2:2625547-2626102 Satlength=556 Nr of Repeats=7 RepeatLength=32
seed=CCGCCAAAAA

CCGCCAAAAAATTTTAAAGAAAATTTAAATTC
CCGCCAAAAAATTTTCAGAGAAAATTTGAATTC
CCGCCAAAAATGTTTCAGAAAATTTGAATTC
CCGCCAAAAAATTTTAAAGAAAATTTAAATTC
CCGCCAAAAAATTTTCAGAGAAAATTTGAATTC
CCGCCGAAAAATTTCAAAGAAAATTTAAATTC
CCGCCAAAATGTAGGGGTCTCGCCACGATGGGTCTCGCCACGATGGGTCTCGCCACGATGGGTCTCGCCACGAAGGGTC
TCGCATCGATGGGTCTCGCCACGAAGGTGACTGGCCCCGCCACAACCTCTCAGTGACTTTAGGGGTGACGTCACAGAC
TACAAAGACTACATAGACTACAACTATGGACAGACCCACACTATTTTTTTATATATAAGTAATGATAATGATATGATC
ACATGTTTGTCTCTTAAATCCTTTGATATTCTTTTTTGCCTTGTCTTCAAATGTGAACGAATAAATACATATAATAT
AAATTATTTTCTTCAATTCTGATTTTCTGATTCCAAAAGATTGCAAAA

Nr of selected repeats 5 Similarity 0.866667

Consensus:

CCGCCaAAAAaTTTcAaAGAAAaTTTaAATTC

>Cele-UNSB01_2:2648748-2648862 Satlength=115 Nr of Repeats=6 RepeatLength=19
seed=AAAATCGATA

AAAATCGATAATTTTGAGA
AAAATCAATAGTTTCATCG
AAAATAGATAATTTTCGTCG
AAAATAGATAATTTTCATGG
AAAATCGATAATATCTTCA
AAAATCGATAACTTAATTG

Nr of selected repeats 6 Similarity 0.601058

Consensus:

AAAATcGATAATTTcaTcg

>Cele-UNSB01_2:2655599-2656120 Satlength=522 Nr of Repeats=10 RepeatLength=14
seed=CTACAAACTA

CTACAAACTATACTCTACAGAATACAATTTGAGCACAAAAAACTACAAAAAAATTTTGGCAATAGCTGAAATAGTTTC
CTTGTTTTTTCTCGCGATTTTATTGGAGAAATTCGATTTATTTTGAAACTCGAATTTGAATAACTTGTTTTGTTCTTG
AGTTTAAATTCAGTGACAG
CTACAACCTATAAA
CTACAAACTACAAG
CTACAAACTACAAAATACATA
CTACAAACTAGAACTACAACACAATAGAAAATGACTCTCATTTTGAIAAAAAAATGTTAGAATAGGTAGCCACTGTAG
TTAGAAAAGGTCACAACAATGAACAAGAATGAGCCCTAAA
CTACAGACTACAGA
CTACAAACTACAAA

CTACAGACTACAAACTACAACAACATAGAAAATAATTCTCATTTTTGAAAAAAGAAATGTGAGAAGCGGTGGCCACTGTT
GTTAGAAAAGATCACAAACAATGTTCAATAATGAACACTAAG

CTACAGACTACAAC

CTACAAACTACAAA

Nr of selected repeats 6 Similarity 0.796825

Consensus:

CTACAaACTACAAa

>Cele-UNSB01_2:2657840-2658242 Satlength=403 Nr of Repeats=31 RepeatLength=13

seed=TAAGCCTAAG

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTA

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TGAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCC

TAAGCCTAAGCC

TAAGCTCTAAGCC

TAAGCTCTAAGCC

TAAGCTCTAAGCC

TAAGCTCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

TAAGCCTAAGCTC

Nr of selected repeats 28 Similarity 0.872449

Consensus:

TAAGCCTAAGCTC

>Cele-UNSB01_2:2659185-2659251 Satlength=67 Nr of Repeats=5 RepeatLength=12

seed=CCTAAGCCTA

CCTAAGCCTAAG

CTTAAGCCTATG

CATAAGCCTAAGCCTAGT

CCTAAGCCTAAG

CCTAAGCCTAAC

Nr of selected repeats 4 Similarity 0.833333

Consensus:

CcTAAGCCTAag

>Cele-UNSB01_2:2738496-2739194 Satlength=699 Nr of Repeats=7 RepeatLength=95
seed=TTCGGGCCTG
TTCGGGCCTGCGGCCCTCAAACCTGACTTATTGGGCTCAGAATAGGTTTCACGGTTGCCCAACACTTCTTCGTGTATTGC
CTGTTTTGCTGAGAATGTGGTTAGAAGTTCCCTACAGTTTTAATGAGTA
TTCGGGCCTGCGGCCCTCAAACCTGGTTTGTAGGCTTGAGCGAATAACAATCTGCTTGAATAGGATTAAGTTGGCCC
ACAGTTTCCAAGAGTG
TTCGGGCCTGCGGCCCTCAAACCTGGTTTGTAGGCTTGAGCGAATAACAGTCTGCTTGAATAGGATTAAGCTGGCCC
ACAGTTTCCATGAGTA
TTCGGGCCTGCGGCCCTCAAACCTGGTTTGTAGGCTTGAGCGAATAACAATCTGCTTGAATAGGATTAAGCTGGCCC
ACAGTTTCCATGAGTA
TTCGGGCCTGCGGCCCTCAAACCTGGTTTGTAGGCTTGAGCGAATAACAATCTGCTTGAATAGGATTAAGCTGGCCC
ACAGTTTCCATGAGTA
TTCGGGCCTGCGGCCCTCAAACCTGGTTTGTAGGCTTGAGCGAATAACAATCTGCTTGAATAGGATTAAGCTGGCCC
ACAGTTTCCATGAGTA
TTCGGGCCTGCGGCCCTCAAACCTGGTTTGTAGGCTTGAGCGAATAACAATCTGCTTGAATAGGATTAAGCTGGCCC
ACAGTTTCCATGAGTA

Nr of selected repeats 6 Similarity 0.981287

Consensus:

TTCGGGCCTGCGGCCCTCAAACCTGGTTTGTAGGCTTGAGCGAATAACAATCTGCTTGAATAGGATTAAGCTGGCCC
ACAGTTTCCATGAGTA

>Cele-UNSB01_2:2756689-2756749 Satlength=61 Nr of Repeats=4 RepeatLength=12
seed=GCCTAAGCCT

GCCTAAGCCTAAGCCCAAACCTAG
GCCTAAGCCTAA
GCCTATGCCTAA
GCCTAATCCTGA

Nr of selected repeats 3 Similarity 0.777778

Consensus:

GCCTAagCCTaA

>Cele-UNSB01_2:2758878-2759540 Satlength=663 Nr of Repeats=24 RepeatLength=22
seed=ACTACAGTAA

ACTACAGTAATGCTACAGTACC
ACTACAGTAATTCTACGTCGCT
ACTACAGTAACCTAACAAATGACCCTACAGTAGCTCTATGGTACC
ACTACAGTAACCCTACATCACC
ACTACAGTAATCCTACAGTACCATAACAGTAGACCTCCATTGCCAATACATTAATCCAGTATC
ACTACAGTAAGCCTAGAGTATC
ATTACAGTAACCTATAACAGTACT
ACTACAGTAACCCTACATCAGC
ACTACAGTAATTCTACAATACC
ACTACAGTAACCCTACATCACC
ACTACAGTAATCCTACAGTACCATAACAGTAGACCTCCATTGCCAATACATCAATCCAGTATC
ACTACAGTAAGCCTAGAGTATC
ATTACAGTAACCTATAACAGTACT
ACTACAGTAACCCTACATCAAC
ACTACAGTAATTCTACAATACC
ACTACAGTAACCCTACATCACC
ACTACAGTACCATAACAGTAGACCTCCATTGCCAATACATTAATCCAGTATC
ACTACAGTAAGCCTAGAGTACC
ATTACAGTAACCTATAACAGTACT
ACTACAGTAACCCTACATCAGC
ACTACAGTAATTCTACAATACC
ACTACAGTAACCTAACAGTCATC
CTACAGTAACCTCTATAGAGCC

ACTACCGTAATCCTACATCACC

Nr of selected repeats 18 Similarity 0.729847

Consensus:

ACTACAGTAAccCTACAntAcc

>Cele-UNSB01_2:2787652-2787836 Satlength=185 Nr of Repeats=11 RepeatLength=16

seed=CACGTAGGCA

CACGTAGGCACGTAGG

CACGTAGGCAAGTAGG

CACGTAGGCACGTAGG

CACGTAGGCACATAGACACATAGA

CACGTAGGCACGTAGG

CACGTAGGCACGTAGG

CAAGTAGGCACGTAGG

CACGTAGGCACGTAGG

CACGTAGGCACGTAGG

CACGTAGGCACGTAGG

CACGTAGGCACGTAGG

Nr of selected repeats 10 Similarity 0.966667

Consensus:

CACGTAGGCACGTAGG

>Cele-UNSB01_2:2836927-2837967 Satlength=1041 Nr of Repeats=6 RepeatLength=144

seed=TGGCCTAGAA

TGGCCTAGAAATCCAAGTTTGCAAAAGTTAGTCCACCAACTTCAAATGCCTATAACTTTGCGGAAAATCAAGATTTTTTC

AGTGATTTTTAACGTAACATATGATGCTACTGGCTTTGCGCATCTTTTTGCCCTACTTAACGTTTGG

TGGCCTAGAAATCCAAGTTTGCAAAAGTTAGGCCATCAACTTCAAATGCCTATAACTTTGCGGAAAATCTATATTTCAA

ATTAATTTTTGAACTTCTGTGATGCCATTAACATTGCGCATTTTTTTTTGGCCTAGTTAACGTTTGA

TGACCTAGAAATTTAAAATTTGCAAAAGTTAGGTTATCAACTCAAAATATTTCTATCTTTGTGAAAAATCAAGATTTTTT

CTGTGATTTTTTACATTAACCTTCATGGCATTGTTTGTAGCGCATTTTTTTTTTGTAGTACAGACCGATTGG

TGGCCTAGAAATCCACAGTTTCGGCCACCAAATTCATCAACCATAACTTGGCTTAAAGTTCATATTTTTCCGTTCTGAA

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ACCACTGTTACGAATGTCTGTCAGATGTTTCAAGTGTGTTCTGGGCGCTGAAAATCTCACGGCAGGACCACTAATCAGTCA

TTTGAGTACCAAACACTCCTTCCAGTGTGTTCCATGGAAATGTGATGAGTGTGGATACAAAATGCGGTCCAGGTAAGC

GG

TGGCCTAGAAATCTCGATTTGCAAAAGTTAGGCCACCAACTTTAAATTTCTGTAATTCAGCTGAAAATCGATATTTTCC

TATGTTTTTAGTGCCAAGATGTAGCGAATTATGTAACGCTACTTTTTGGGGTACTTAACAATTGG

TGGCCTAGAAATCCCAACTTGCAAAAGTTAGGCCACCAACTTCAAATCGCCGTACTCAGCTGAAAATCAATATTTTCC

ATTGTTCTTGATGCTAAAATGTAGCCAATTTTGTAGCGCAACTTTTTGGGGTACTTAACAATTGG

Nr of selected repeats 4 Similarity 0.634815

Consensus:

TGGCCTAGAAATCnCaAgtTTGCAAAAGTTAGgCCaCAACTTcAAATGcCtaTaAcTcaGCgGAAAATCaAtATTTtc

catTgaTtTTaacTgCtaagATGtagCcAaTtacgTagCGCaacTTTTTGgccTAcTTAACaaTTGg

>Cele-UNSB01_2:2842834-2842918 Satlength=85 Nr of Repeats=6 RepeatLength=12

seed=CCTAAGCCTA

CCTAAGCCTAGT

CCTAAGTCTAAG

CCTAAACCTAAGCCTAATTCTAAGG

CCAAGCCTAAG

CCTAAGCCTACG

CCTAAGCCTACG

Nr of selected repeats 4 Similarity 0.754274

Consensus:

CCTAAGcCTAcG

>Cele-UNSB01_2:2923591-2929183 Satlength=5593 Nr of Repeats=231 RepeatLength=21

seed=CCAAAAATTG

CCAAAAATTGTGATTTTTAGT
CCAAAAATTGAGATTTTTAGT
CCTAAAATTGAGGCTTTTTAGT
CCAAAAATTGAGATTTTTAGT
CCAAAAATTGTGATTTTTAGT
CCAAAAATTGAGATTTGTAGT
CCTAAAATTGTGATTTTTAGT
CCATAAATTGAGGTTTTAGT
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CCAAAAATTGTGATTTTTAGT
CCTAAAATTGAGGCTTTTTAGT
CCAAAAATTGAGATTTATAGTCCTAAAATCGAGGTTTTTAGT
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CCTAAAATTGAGGCTTTTTAGT
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CCAAAATTTGGGCTTTTTTAGGCTAGAAATTGAGTGTTTTAGTATAAAAAGTTCAGGTTTTTAGCCTGAAAAATAGGGGTT
TTAGT
CCAAAATTTAAGGGTTTTTAGG
CCACAAATTGAGGGTTTTAAAACCTGAAAATTGAGGTTTTTCAGG
CCAAAATTTGACATTTATAAG
CCAAAATTTGAGATTTCAATA

Nr of selected repeats 201 Similarity 0.731595

Consensus:

CCaAAAATTGAGgtTtTAGT

>Cele-UNSB01_2:2979318-2980713 Satlength=1396 Nr of Repeats=9 RepeatLength=155
seed=TCCCGCTGTG

TCCCGCTGTGGTCAAAAAGTTTTTTGTGTGCTCAGTTCGTACGACAAATGTGTTAAAAATCTTCTGAAACTCAAATTC
CAAGTTTTCCAAAAATGGGTCAAATGGTACAGTGGGATTTTCCACGAATTC TAAGTAGATGGTTCGTGAGTTCAAC
TCCCGCTGTGGTCAAAATCTTTTTGCATGTTT CAGTTCGTGTGCGGTAAATATGTTTAAAATTTCTGAAACTTGAAAT
TCCAAGTTATTCAGAAATTTGTCCAAATGGCGCAGTGGGAAATTCGATTTCTCTGACCCAAGAGGCCACGGGTTCAAT
TCCCGCTGTGGTTAAAAGTTTTTTGCGTGCTCAGTTCGTACGGTAAATGTGTTAAAAACTTCTGAAACTTGAAATTC
CAAGTTATTCAGAAATTTGTCCAAATGGCGCAGTGGGAAATTCGATTTCTCTGACCCAAGAGGCCACGGGTTCAAT
TCCCGCTGTGGTTAAAAGTTTTTTGCGTGCTCAGTTCGTACGGTAAATGTGTTAAAAACTTCTGAAACTTGAAATTC
CAAGTTATTCAGAAATTTGTTCAAATGGCGCAGTGGGAAATTCGATTTCTCTGACCCAAGAGGCCACGGGTTCAAT
TCCCGCTGTGGTTAAAAGTTTTTTGCGTGCTCAGTTCGTACGGTAAATGTGTTAAAAACTTCTGAAACTTGAAATTC
CAAGTTATTCAGAAATTTGTTCAAATGGCGCAGTGGGAAATTCGATTTCTCTGACCCAAGAGGCCACGGGTTCAAT
TCCCGCTGTGGTTAAAAGTTTTTTGCGTGCTCAGTTCGTACGGTAAATGTGTTAAAAACTTCTGAAACTTGAAATTC
CAAATTTTTCAAAAAGTGTTCAAATAGCGCAGTGGGTTTTTCGAGTTCCTGTGCGAAAAGGTCACGGGTTCAAT
TCCCGCTGTGGATAAAAGGGTTTTTACATGTTT CAGTTCATATATGGTAAATATGTTTAAAATTTCTGAAACTTGAAATTC
CAAGATTTTTCGAAAAATCGTTCAAATGGCGCAGTGGGGTTTTTCGATTTCTTAGGCGCAAAGGTCACGGGTTCAAT
TCCCGCTGTGGATAAAAGGGTTTTTACATGTTT CAGTTCATATATGGTAAATATGTTTAAAATTTCTGAAACTTGAAATTC
CAAGATTTTTCGAAAAATCGTTCAAATGGCGCAGTGGGGTTTTTCGATTTCTTAGGCGCAAAGGTCACGGGTTCAAT

Nr of selected repeats 6 Similarity 0.781691

Consensus:

TCCCGCTGTGGtTAAAaGtTTTTTgCgTgCtCAGTTCtGtAcGGTAAATgTGTTaAAAAcTTCTGAAACTTGAAATTC
CAAGtTaTTCaGAAAaTtGTTCAAATGGCGCAGTGGGaaaTTCGATTTCTcaGaCcCAAgAGGcCACGGGTTCAAT

>Cele-UNSB01_2:2986853-2986937 Satlength=85 Nr of Repeats=7 RepeatLength=12
seed=ATAGGCATAG

ATAGGCATAGGC
ATAGGCATAGGC
ATAGGCATAGGC
ATAGGCATAGGC
ATAGGCATAGGC

ATAGGCATAGGC
ATAGGCATAGGC
Nr of selected repeats 7 Similarity 1.000000
Consensus:
ATAGGCATAGGC
>Cele-UNSB01_2:2995760-2997536 Satlength=1777 Nr of Repeats=53 RepeatLength=14
seed=CTACCTGCCT
CTACCTGCCTATGC
CTACCTGCCTATGGCTGCATGCATTTGC
CTACCTGCTTGTAC
CTAACTGCCTATGACCATCTGCCGTCGT
CTACCTGCCTATGC
CTACCTGTCTGTGC
CTACCTGCCTATGC
CTACCTGCCTATGCA
TACCTGCCTATGC
CTACCTGCCTATGC
CTACCTGCCTATGTCTTTCTGCTATGCACACCTGTTATAC
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CTACCTGCCCATGC
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TGTATCAAATGGTTTTTTCTGCGCCCCCCCCCCCCACCGCTTATAGGCTGCCTATAAACGTGTCTAGTAGTAAGTGTA
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CTACCTGCCTATGC
CTACCTGCCTAGAG
CTATCTGCCTAGCG
CTACCTGCTTATGCCTAACTGCTTAAGCCTTTCTGCCTATGC
CTACCTGCCAATGCCTACCTTCTTATGCT
TACCTGCCTATGC
CTACCTGCCTATGC

Nr of selected repeats 34 Similarity 0.798659

Consensus:

CTACCTGCCTATgC

>Cele-UNSB01_2:3009682-3009822 Satlength=141 Nr of Repeats=5 RepeatLength=28

seed=AATGTCGGCT

AATGTCGGCTGCTTCTAGAAGCCCGGCA

AATGTCGGCTGCTTCTAGAAACTAAGCA

AATGTCGGCTGCTTCTAGAAACTAAGCA

AATGTCGGCTGCTTCTAGAAGCCCGGCG

AATGTCGGCTGTTTCTAGAAACCAGGCA

Nr of selected repeats 5 Similarity 0.847619

Consensus:

AATGTCGGCTGcTTCTAGAAaCcagGCa

>Cele-UNSB01_2:3063296-3063566 Satlength=271 Nr of Repeats=18 RepeatLength=14

seed=TTAGGGCCTT

TTAGGGCCTTGGGT

TTAGGGCCTTGGGC

TTAGGGCCTTGGGT

TTAGGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGCCTTAGGCAAGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGC

TTACGGCCTTGGGC

TTAGGGCCTTGGGC

TTAGGGCCTTGGGA

TTAGGGCCTTGGGA

Nr of selected repeats 17 Similarity 0.949580

Consensus:

TTAGGGCCTTGGGc

>Cele-UNSB01_2:3065991-3066701 Satlength=711 Nr of Repeats=18 RepeatLength=19

seed=GCCAAGGCAC

GCCAAGGCACTTGATAAGG

GCCAAGGCACTGGAAATGC
GCCAAGGCACTGGAAATGC
GCCAAGGCACGAGAAACGC
GCCAAGGCACTAGGAATGG
GCCAAGTCACTAGAAACGC
GCCAAGGCACTGGAAATGT
GCCAAGGCACTGGAAATGCGCCAAATCACGAGAACTCGCCAATGCCTTAGAAATGCGTCAAGTCACTAGGAATGTGTC
AAGTCACAAAAGGAACAAAAACTC
GTCAAGGCACTACAAAAACGTCAAGTTACCAGAAACGTGCCAAGACATAAAGAATGC
GCCAAGGCACGCAAAAGGC
GCCAAGTCACAATAAATGCGCCAAGTCAGTAGAAACGAGTCAAAACACTAAGAGTGC
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GCCAAGGTACGATATATGTGTCAAGTCATTAATAAATGTGCAGTCACTAGAACTCGGCAAGTCACTAGGAATGC
GTCAAGGCACGCAAAAAAC
GCCAAGGCACGAGAAACGC
GCCAAGCACAAGAAATGCGTCAAGTCACGATAAATGC
GCCAAGGCACTCAAAACGAGCCAAGTCTTGATAAATGC
GCCAGGGCACCGAAAAAGCGTCAAGACACTACAAAAGCGTGAAGTTACTAAAAAGCGCCAGATGACTAAAAACGCGCC
AAGTCTTGATAATTGCGCCAGGTCACCAAAAAAGCGTTAAGTACGAAAAAGGC

Nr of selected repeats 11 Similarity 0.680606

Consensus:

GCCAAGGCACTnGAAAnGc

>Cele-UNSB01_2:3077809-3078033 Satlength=225 Nr of Repeats=15 RepeatLength=14

seed=CTTATACCTT

CTTATACCTTATAC
CTTATACCTTATAC
CTTATACATTATAA
CTTATGCCTTATAC
CTTATACCTTATAC
CTTATACCTTATACCTTATGCCTAATAT
CTTATACCTTATAC
CTTATACCTTATAC
CTTATACCTTATAC
CTTATACCTTATAC
CTTATACCTTATAC
CTTATACCTTATAC
CTTATACCTTATAC
CTTATGCCTTATAC

Nr of selected repeats 14 Similarity 0.947671

Consensus:

CTTATACCTTATAC

>Cele-UNSB01_2:3099938-3100072 Satlength=135 Nr of Repeats=4 RepeatLength=31

seed=ATCGATTTTT

ATCGATTTTTTCGGTAAAAAATCAATAAAAT
ATCGATTTTTTAGTGAAATTTAACAAAAAATTCAAATT
ATCGATTTTTTGGTTAAAAAATCAATAAAAT
ATCGATTTTTTCAGTGAAAAATAGTCCAAAAA

Nr of selected repeats 3 Similarity 0.700337

Consensus:

ATCGATTTTTTcGttAAAAAaTCaAtAAAAt

>Cele-UNSB01_2:3132033-3132195 Satlength=163 Nr of Repeats=6 RepeatLength=27

seed=GCTGCTGGAG

GCTGCTGGAGGATCCACTGCATCAACT

TGCTGGAGGATCCACTGCATCAACCGC
TGCTGGAGGATCAACTGCAACAACCGC
TGCTGGAGGATCAACTGCAACAACCGC
TGCTGGAGGATCCACTGCATCAACCGC
TGCTGGAGGATCAACTGCATCAACCGC
TGCTGGAGGATCAACTGCAACAACCGC
TGCTGGAGGATCAACTGCAACAACCGC
TGCTGGAGGATCAACTGCATCAACTGC
TGCTGGAGGATCAACTGCAACAACCGC
TGCTGGAGGATCCACTGCATCAACTGC
TGCTGGAGGATCCACTGCATCAACCGC
TGCTGGAGGATCAACTGCAACAACCGC
TGCTGGAGGATCAACTGCAACAACCGC
TGCTGGAGGATCCACTGCATCAACTGC
TGCTGGAGGATCCACTGCATCAACCGC
TGCTGGAGGATCAACTGCAACAACCGC

Nr of selected repeats 60 Similarity 0.923806

Consensus :

TGCTGGAGGATCaACTGCAtCAACcGC

>Cele-UNSB01_2:3141695-3142468 Satlength=774 Nr of Repeats=16 RepeatLength=43
seed=TTGCCGGAAT

TTGCCGGAATTGACAATTCCTCGGCAAACCTGCAAACCCAGCAAC
TTGCCGGAGTTGAAAATTTCTGTAAATCGGCAAACCCGGCAAC
TTGCCGGAATTGACAATTCCTGTAAATCGGCAAACCCGGGAAA
TTGTCCGAATTGAAAATTTCTGTAAATCGGCAAACCCGGGAAA
TTGCCGGAATTGAAAATTTCTGTAAATCGGCAAACCCGGCAAC
TTGCCGGAATTAATAATTTCTTTAAATCGGCAAACCCGGCAAG
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TTGCCGGAATTGAAAACCTTCTGTAAATCGGCAAACCCGGGAGT
TTGTCTGGAATTGAAAACCTTCTGTAAATCTGCAAACCCGGCAAC
TTGTCCGAATTGAAAATTTCCGGCAAATCTGCAAACCCGGGAAA

Nr of selected repeats 13 Similarity 0.825084

Consensus :

TTGcCGGAATTGAaAATTTCCtGtAAATCgGCAAACCCGGcAAc

>Cele-UNSB01_2:3154398-3154558 Satlength=161 Nr of Repeats=9 RepeatLength=16
seed=TAGGCACGTA

TAGGCACGTAGGCATG
TAGGCACGTAAGCATG
TAGGCATGTAGGCACG
TAGGCACATAGGCACA
TAGGCACGTAGGCACG
TAGGCACATAGGCACG
TAGGCACGTAGGCACG
TAGGCACGTAGGCACGTAGACATG
TAGGCACCTAGGCACCTATGCACC

Nr of selected repeats 7 Similarity 0.849206

Consensus :

TAGGCACgTAGGCACg

>Cele-UNSB01_2:3155808-3156160 Satlength=353 Nr of Repeats=18 RepeatLength=16

seed=TACGTGCCTA

TACGTGCCTACGTGCCTATGTACCTACCTGTT

TACGTGCCTACGTGCC

TACGTGCATAACGTGCA

TACGTGCATAACGTGCC

TACGTGCCTATGTGGCAATGTGCC

TACGTGCCTACGTGCC

TACGTGCCTACGTGCC

TACGTGCCTACGTGCC

TACGTGCCTACGTGCC

TATGTGCCTATGTGCC

TACGTGCCTATGTGCCAACGTGCC

TGCGTGCCTACGTACC

TACGTGCCTACGTGCCTATGTGCCAATGTGCC

TACGTGCCTACGTGCC

TACGTGCCTAGGTACC

TACGTGCCTAGGTTAC

TACGTGCCTACGCGACTACGCGAC

TACGTGCCTACGTGGCTACGTACC

Nr of selected repeats 12 Similarity 0.845960

Consensus :

TACGTGCCTAcGTgCC

>Cele-UNSB01_2:3166478-3166668 Satlength=191 Nr of Repeats=8 RepeatLength=12

seed=GGCTTAGGCT

GGCTTAGGCTTAGGTTTAGACTTAGGCCTAGACTTAAATTTA

GGCTTAGGCTTA

GGCTGAGGCTGAGGCTGAGCTTCGAAATTTGTTTTTTTTGTTTTAAATTTTTTTTTAAATACGATTTTGGTATG

GGCTTAGGCTTA

GGCTTAAGCTTA

GGCTTAGACTTA

GGCTTAGGCTAA

GGCTTTGGCTCG

Nr of selected repeats 6 Similarity 0.785185

Consensus :

GGCTTAGGCTtA

>Cele-UNSB01_2:3175289-3175339 Satlength=51 Nr of Repeats=4 RepeatLength=10

seed=AACTTTCGAA

AACTTTCGAA

AACTTTCGAA

AACTTTCGAA

AACTTTCGAAAACCTTTCGAA

Nr of selected repeats 3 Similarity 1.000000

Consensus :

AACTTTCGAA

>Cele-UNSB01_2:3182927-3183063 Satlength=137 Nr of Repeats=8 RepeatLength=16

seed=AGGCACGTAG

AGGCACGTAGGCAAGT

AGGCACGTAGGCATAT

AGGCACGTAGGCACGTAGGCATAT

AGGCACGTAGGCACGT

AGGCACGTAGGCAAGT

AGGCAAGTAGGCGCGT
AGGCACGTAGGCAAGT
AGGCAAGTAGGCACGT

Nr of selected repeats 7 Similarity 0.853175

Consensus:

AGGCACGTAGGCAnGT

>Cele-UNSB01_2:3184073-3184138 Satlength=66 Nr of Repeats=4 RepeatLength=14

seed=CCAAGGCCCA

CCAAGGCCCAAGGCCAAAACCC

CCAAGGCCCAAGGC

CCAAGGCCGAAGCC

CCAAGGCCCAATGC

Nr of selected repeats 3 Similarity 0.746032

Consensus:

CCAAGGCCcAAggC

>Cele-UNSB01_2:3220556-3221123 Satlength=568 Nr of Repeats=21 RepeatLength=16

seed=GTAGGCACGT

GTAGGCACGTAGGCGC

GTAGGCACGTAGGCAC

GTAGGCACGTAGGCAC

GTAGACACGTAGGCAC

GTAGGCAAGTAGGCAC

GTGGGCACGTAGGCAC

GTAGGCACGTAGGCAC

GTAGGCACGTAGGCAC

GTAGGCACGTAGGCAC

GTAGGCACGTTTTAATTTATACATTTATATTTTTAGACCTATGTATTTTTATATTAGAGCAAGTTTGGACACCCGTCGG

CTTCCTGAGGCAA

GTAGGCACGTAGACAC

GTAGGCACGTAGGCAC

GTAGACACGTAGGCAC

GTAGGCAGGTAGGCAC

GTAGGCACGTAGGCAC

GTAGGCACGTAGGCAC

GTAGGCACGTTTTAATTTATAAATTTATATTTTTAGACCTATTTTTATAGTAAAGCAAGTTTGGACACTCGTCGGCTTC

CTGAGGCAA

GTAGGCACGTAGGCAC

GTAGGCACGTAGGCAC

GTAGGCACGTAGGCAC

GTAGGCACGTTTTAATTTATAAATTTATATTTTTAGACCTATTTTTATAGTAAAGCAAGTTTGGACACTCGTCGGCTTC

CTGAGGCAAAGTAGGCAC

Nr of selected repeats 18 Similarity 0.936819

Consensus:

GTAGGCACGTAGGCAC

>Cele-UNSB01_2:3287465-3288008 Satlength=544 Nr of Repeats=19 RepeatLength=20

seed=GTAAATCTAC

GTAAATCTACAAGAAAACATTTACAATTTGGCAGAAATTTAA

GTAAATCTACATGAAAATCCGCAAGTCTACACAAAGATCCGTAAATCTTTACGTAGGTTC

GTAAATCTACACTTGCTTCC

GTAAATCTACACGTCCTTCC

GTAAATCTACACTGGCGTCC

GTAAATCTACACCTACCGTAAGTTCACACATTCCTCTT

GTAAATCCACATAGTCTTCC

GTAAATCTACACTATCTACTTCCCGTTTATCTACGCCACCTACCGCAAGTTCACTCATTCTTCC

CGTAGGCACGTAGGCA
CGTAGGCACGTAGGCA
CGTAGGCACGTAGGCA
CGTAGGCACGTAGGCA

Nr of selected repeats 39 Similarity 0.967611

Consensus:

CGTAGGCACGTAGGCA

>Cele-UNSB01_2:3331473-3331608 Satlength=136 Nr of Repeats=5 RepeatLength=27

seed=TTTACTCTCT

TTTACTCTCTGTGGCTTCCCACTATAT

TTTACTCTCTGTGGCTTCCCACTATAT

TTTACTCTCTGTGGCTTCCCACTATAT

TTTACTCTCTGTGGCTTCCCACTATAT

TTTACTCTCTGTGGCTTCCCACTATAT

Nr of selected repeats 5 Similarity 1.000000

Consensus:

TTTACTCTCTGTGGCTTCCCACTATAT

>Cele-UNSB01_2:3341963-3342088 Satlength=126 Nr of Repeats=4 RepeatLength=22

seed=ATTCTGCGCA

ATTCTGCGCACCCCTGCGCCG

ATTCTGCGCACATTGATGTTGTTGTGCCCTTTTTCTTGGTGGCATAGCCTCGTGCGCAC

ATTCTGCGCACCCCTGAGCGG

ATTCTGCGCACGTTTCAGCTCAC

Nr of selected repeats 3 Similarity 0.656566

Consensus:

ATTCTGCGCACcccCtGcgCng

>Cele-UNSB01_2:3406743-3406803 Satlength=61 Nr of Repeats=4 RepeatLength=15

seed=GGTGAGACCC

GGTGAGACCCATCGT

GGTGAGACCCATCGC

GGTGAGACCCATCGT

GGTGAGACCCGTCGT

Nr of selected repeats 4 Similarity 0.911111

Consensus:

GGTGAGACCCaTCGt

>Cele-UNSB01_2:3456136-3456276 Satlength=141 Nr of Repeats=4 RepeatLength=28

seed=TGCCTCGCCT

TGCCTCGCCTACGTGCCTATTTTCAGGAATTCCTTGCCTACGTGGCTATTTTCAGGCT

TGCCTCGCCTACGTGCCTATTTTCAGGCA

TGCCTCGCCTACGTGCTTATTTTCAGGCA

TGCCTCGCCTACGTGCTTATTTTCAGGCA

Nr of selected repeats 3 Similarity 0.968254

Consensus:

TGCCTCGCCTACGTGcTATTTTCAGGCA

>Cele-UNSB01_2:3460910-3461075 Satlength=166 Nr of Repeats=5 RepeatLength=16

seed=GCACGTAGGC

GCACGTAGGCACGCAGGTACATAAGAATCTAGGCGGATACCTAGGCACCTAACATCCTGGAACCTAGGCATCTAAACA

TCCAGGACACCCAG

GCACGTAAGCACGTAG

GCACGTAGGCACGTAG

GCACGTAGGCACGTAG

GCACGTAGGCATGTAGGCACGTAG

Nr of selected repeats 3 Similarity 0.944444

Consensus:

GCACGTAgGCACGTAG
>Cele-UNSB01_2:3500187-3500295 Satlength=109 Nr of Repeats=5 RepeatLength=18
seed=GGCTTAGGCT

GGCTTAGGCTTA
GGCTTAGGCTTAGGCTCA
GGATTAGGCTTAAGCTCA
GGCTTAGGCTTAAGCTCA
GGCTTAGGCTTGTGCTTGTGCTTAGGCCTAGGTCTTGGCTTA
Nr of selected repeats 3 Similarity 0.901235
Consensus:
GGcTTAGGCTTAaGCTCA

>Cele-UNSB01_2:3515774-3515844 Satlength=71 Nr of Repeats=4 RepeatLength=12
seed=ATACATATAC

ATACATATACAT
ATACATATACAT
ATACATATACAT
ATACATATACATATACAGTCCATATACAGTATAC
Nr of selected repeats 3 Similarity 1.000000
Consensus:

ATACATATACAT
>Cele-UNSB01_2:3535061-3535729 Satlength=669 Nr of Repeats=54 RepeatLength=12
seed=TAGGTATAGG

TAGGTATAGGTA
TAGGTAAAGGCA
TAGGCATAGGCA
TAGGTATAGGTTT
TGGTATAGGTA
TAGGTATAGGTA
TAGGTATAGGTATAGGAC
TAGGTATAGGTA
TAGGTATAGGTA
TAGGTATAGGTA
TAGGTATAGGTA
TCGGTATAGGTA
TCGGTATAGGTA
TAGGTATAGGTA
TAGGGATAGGTA
TAGGTATAGGTA
TAGGTATAGGAA
TAGGTATAGGTA
TAGGTATAGGTA
TAGGTATAGGTA
TAGGTATCGGTA
TAGGTATAGGTA
TCGGTATAGGTA
TAGGTAAAGGGA
TAGGTATAGGTAAAGGGA
TAGGTATAGGTA
TAGGTAAAGGGA
TAGGTATAGGTA
TAGGTAAAGGCA
TAGGCATAGGCA
TAGGTATAGGTTT
TGGTATAGGTA
TAGGTATAGGTA

TAGGTTTAGGTA
 TAGGTATAGGAA
 TAGGTATAGGTGTA
 TAGGAATAGGTA
 TAGGTATAGGTA
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 TAGGTATAGGTA
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 TAGGTAAAGGAA
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 TAGGTATAGGTA
 TAGGTAAAGGGA
 TAGGTATAGGTA
 TAGGTATAGGTA
 TAGGTATAGGTA
 TAGGTATAGGTA
 TAGGTATAGGTA
 TAGGTATAGGTA
 TAGGTATAGGTATAGGTA

Nr of selected repeats 46 Similarity 0.876973

Consensus:

TAGGTATAGGtA

>Cele-UNSB01_2:3539245-3539476 Satlength=232 Nr of Repeats=5 RepeatLength=39

seed=AATTTCCCGC

AATTTCCCGCCAAAAATTTTACGTTTTTCAGAAAATTCA
 AATTTCCCGCCAAAAATTGAATTTTTTAAAAGAAAATTTA
 AATTTCCCGCCAAAAATTGAATTTTTTAAAAGAAAATTTA
 AATTTCCCGCCAGAACTGTTTTTTTTGGGAAAATTTGAATTAGCCGCCTAAATTTAAAATTTTTTTTTTAGAAAATCTG
 AATTTCCCGCCAAAAATTAATTTTTTAAAAGAAAATTTCA

Nr of selected repeats 3 Similarity 0.769444

Consensus:

AATTTCCCGCCAAAAATTTgaAttTTTTtaaAGAAAATTTA

>Cele-UNSB01_2:3540761-3541492 Satlength=732 Nr of Repeats=18 RepeatLength=31

seed=GGTTACTGTA

GGTTACTGTTAGGACTACTGTAGCTTCCAA
 GGTTACTGTTACTGTACCTTTAAGACAAAGCCAACAGAATCTGCTCCGCACAGTGTACAGTGCATATGATTACATGAACC
 ATCGTTTTTCTTCAACAATTAATGTCTTGCAACGTGGACACGGGTGCGCTGAGACGTCTGAAAAAAAAACATTTGTAGG
 GGTTACTGTAGGAGTACTGTAGGGTTTTAAAAAACTCAGTGCAGTGCCTGTAG
 GATTACTGTATATCGTCTTAGGACACTTTG
 GGTTACTGTAACTCAAGCCTGAGATTCTTTCG
 GGTTACTGTAACTCAATCCTAGCCATCTAAAGGGTACTGTGGATCGGTTCTAGGATATGTTG
 GGTTACTGTAGATCGGTTCTAGGATACACTA
 GGTTACTGTATATCGATCCTAGAATACGTTG
 GGTTACTGTAGCTTAATCCTAAGGTTCTAGT
 GGTTACTGTAGATCGATCCTAGGATACTTTG
 GGTTACTGTAGATCGATCCTAGGATACTTTG
 GGTTACTGTAGATCGGTTCTAGGAAATTTTG
 GGTTACTGTAGCTTAATCCTAAGATTCTAAG
 GGTTACTGTAGATCGGTTCTAGGATACGTTG
 GGTTACTGTAGATCGGTTCTAGGATACGTCCG
 GGTTACTGTAGATCGATCCTAGAATTCTGAAG

GGTACTGTAGATCGATTTGGGGATGCTTTG
GGTTACTGTAGCCCAATCCTGGGATTCTAAG
Nr of selected repeats 11 Similarity 0.669318

Consensus:

GGTTACTGTAGaTCgaTcCTAgGATaCtttG

>Cele-UNSB01_2:3557247-3557399 Satlength=153 Nr of Repeats=9 RepeatLength=16
seed=GTAGGCACGT

GTAGGCACGTAGGCAC
GTAGGTACGTAGGCAC
GTAGGCACGTAGGCAC
GTAGGCACGTAGGCAC
GTAGGCTCGTAGGCAC
GTAGGCACGTAGGCAC
GTAGGCACGTAGGCAC
GTAGGCACGTAGGCAC
GTAGGCACGTAGGCAC
GTAGGCACGTAGGCAC

Nr of selected repeats 8 Similarity 0.958333

Consensus:

GTAGGCACGTAGGCAC

>Cele-UNSB01_2:3617397-3617684 Satlength=288 Nr of Repeats=6 RepeatLength=42
seed=TTTGAAAACC

TTTGAAAACCTGCAATATCCGGAATTGCCGATTGCCGAAAT
TTTGAAAACCTACATTTGCCGATTTGCCGATTTGCCAAAACATTCAATTTGCTCAATTTGCCGATTTGCCGATTTGCC
GAAAAT
TTTGAAAACCTACGTTTGCTGATTTGCCGAAAAA
TTTGAAAACCGGCAATTGCCGAAATTGTCGAGTGCCGAAAT
TTTGAAAACCTACAATTGCCGAAATTGCCGAGTGCCGAAAT
TTTGAAAACCGGCGATAGCCGGAATTGCCGATTTGCCGAAAT

Nr of selected repeats 4 Similarity 0.851852

Consensus:

TTTGAAAACCggCaATagCCGaAATTGcCGAgTGCCGAAAT

>Cele-UNSB01_2:3687013-3687103 Satlength=91 Nr of Repeats=5 RepeatLength=20
seed=CTATCGCCTG

CTATCGCCTGCTAGCGCCTA
CTATCGCCTGCTATTGCCTA
CTATTGCCTG
CTATCGCCTGCTGTCGCCTA
CTATCGCCTACTATCGCCTG

Nr of selected repeats 4 Similarity 0.833333

Consensus:

CTATCGCCTgCTatcGCCTa

>Cele-UNSB01_2:3736361-3736609 Satlength=249 Nr of Repeats=8 RepeatLength=31
seed=GCTGATTGGT

GCTGATTGGTTCGGCATGGTCTGCTCATCATC
GCTGATTGGTTCGGAATAACTCTCCCAGAATC
GCTGATTGGTTGGTGAGGTTTTCACATCTTT
GCTGATTGGTCAACGGGTTGCACCTACTGTT
GCTGATTGGTTCGGCGGGTTGCCTATCACC
GCTGATTGGTTCGGAGGGACTCGCCCAACGTT
GCTGATTGGTTCGGTGAGCTTTGCCCATCTTT
GCTGATTGGTTCGGCGGATTGCACCCACTGTT

Nr of selected repeats 8 Similarity 0.553571

Consensus:

GCTGATTGGTTCGGcgnGgtTcgCccAtcnTt

>Cele-UNSB01_2:3799242-3799338 Satlength=97 Nr of Repeats=4 RepeatLength=24
seed=TGCATCTGCC

TGCATCTGCCACAGGAGCTGGCGT
TGCATCTGCCGCTGGAGTTGTTGC
TGCATCTGCCGCTGGAACCTGGCGC
TGCATCTACCGCTGGAGTTGTTGC

Nr of selected repeats 4 Similarity 0.750000

Consensus:

TGCATCTgCCgCtGGAgcTGgcGc

>Cele-UNSB01_2:3989433-3989722 Satlength=290 Nr of Repeats=6 RepeatLength=45
seed=AAGGATCAGA

AAGGATCAGAAGGGTACCTCCTGATGATCTGATCCTTCAGCTTCA
AAGGATCATAAGGGGTATAAAAAGCAATAAATCCCCTTCTGTACCCCTTCTGATCCTTTGAAGCTG
AAGGATCAGATCATTAGGAGGTACCCTTCTGATCCTTCGGAGCTG
AAGGATCAGATCACCAGGAGGTACCCTTGTGATCCTTCGGAGCTG
AAGGATCAGATCACCAGGAGGTACCCTTGTGATCCTTCGGAGCTT
AAGGATCAGATCATCAGGAGGTACCCTTCTGATCCTTCGGAGCTG

Nr of selected repeats 5 Similarity 0.643210

Consensus:

AAGGATCAGatcAncAGGagGTACCCTTcTGATCCTTCggAGCTg

>Cele-UNSB01_2:3993365-3994945 Satlength=1581 Nr of Repeats=20 RepeatLength=79
seed=GTGAATCTCC

GTGAATCTCCTCTCTACCTAAATGAGTACTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTTTCTTCT
GTGAATCTCCTCTCCACCTAAATGATTCCTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGCTTTTAGTTTCTTCT
GTGAATCTCCTCTCAACCTAAATGATTCCTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTTTCTTCT
GTGAATCTCCTCTCAACCTAAATGATTCCTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTTTCTTCT
GTGAATCTCCTCTCCACCTAAATGATTCCTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTTTCTTCT
GTGAATCTCCTCTCCACCTAAATGATTCCTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTTTCTTCT

Nr of selected repeats 20 Similarity 0.984544

Consensus:

GTGAATCTCCTCTCcACCTAAATGATTCCTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTTTCTTCT

>Cele-UNSB01_2:4043072-4059727 Satlength=16656 Nr of Repeats=833

RepeatLength=20 seed=ATTGTTACAC

ATTGTTACACGAAAAATAG
ATTGTTACACGAAAAATAG
ATTGTTACACTAAAAATAG
ATTGTTACACGAAAAATAG
ATTGTTACACTAAAAATAG
ATTGTTACACTAAAAATAG
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ATTGTTACACTAAAAAATAG
ATTGTTACACGAAACATAG
ATTGTTACACGAAAAAATAG
ATTGTTACACTAAAAAATAG
ATTGTTACACTAAAAAATAG
ATTGTTACACTAAAAAATAG
ATTGTTACACTAAAAAATAG
ATTGTTACACTAAAAAATAG

Nr of selected repeats 812 Similarity 0.960325

Consensus:

ATTGTTACACTAAAAAATAG

>Cele-UNSB01_2:4095823-4096643 Satlength=821 Nr of Repeats=4 RepeatLength=16

seed=TGCCTACGTG

TGCCTACGTGCCTACG

TGCCTACGTGCCTACG

TGCCTACGTGCCTACG

TGCCTACCTGAAGTATGCGCAAGACCAGCAGGCAGGAACGTAAAAGGCATACTTTTTCTAGATTGTCCCCTGAAATTTT
TTAATATCTTCATATTTCTGTAGTTCAAAAAATTGTTTATTACATCTTCAAATTATTTATTATTATTAGGATTATCGTG
TGTCACAAAATAAAGAAATAAATTTATTCAATTATTTGTCTGTTTTAATTTTCACCAGCTCACGGACGTTGGGAATAAGG
ATAGAGAAATGAGAAATACAACAAAAATAATAAATATTTCAAATGAAAATGAAACTTGAGCAAAACAAAAAACA
TATTTATTTGATTTTGCCTGGCAGCGGAGGTGGCAAAAAGGCATTGTCTGGGGTGGGGGGAATTCATAATTTAGAATTTT
ATAAATTTCTTCGGGAAAAAATTTAAAAATCCATCATCTATAGTCAGATACGATAGCGTCCAAAGTTGAGAAGAAGT
CTTCTGGAGCGTAAATTCGGGAGTTTTGGAGCCGGAATTCCTTCGATTTCTCGACGTGTTGGACCCCGTCGCTTCTCGG
TTTGCCTTGAGTCGAAGACGGTTTTGAGCACGTTTACCATCTTCCAGAATGTGTAATCAGGTCGGAGAGCTACGATGTG
GGACGAGAAGCTGGAATAAAAAATTTGGTTTTTGAAGGAAATAAAATATTTGCCACAAGGTTTTGAGAATTTGTAAAT
ATTCAAAAATTATAATTTTAGATGTTAGGATTTTCATGATAGAAAACGCCTGCCTGCCTGCC

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TGCCTACGTGCCTACG

>Cele-UNSB01_2:4119390-4119751 Satlength=362 Nr of Repeats=4 RepeatLength=21

seed=CTACGTAAGA

CTACGTAAGAATGACACAGGA

CTACGTAAGAGTAGCGCAGGA

CTACGTAAGAGTAGCGCAGGA

CTACGTAGGAGCGGTTTCATGGCCATACTAGAAGTCCGATTTTCGAATCGGCTCCCCGGAAACCATTGTACAGGTAATATA
GTCATACGATCTGGAATAGTTGCACGATCGAGTTCCATGCCGAACCGTCCGGCAGATAATCCAGACTTAACATTGCAAGT
GTGATCTTCTCCAGGTTTACCGAGTGTTCGACATGGCGTTTCTGTATATTCCTTCTAGAGTCTATCTTGCCTCTC
TCCCGCGGACTTTACGTTTTTCAATGCCCCGTTCCCGCTACAGTCGTCAGG

Nr of selected repeats 3 Similarity 0.830688

Consensus:

CTACGTAAGAGTagCgCAGGA

>Cele-UNSB01_2:4146856-4147072 Satlength=217 Nr of Repeats=14 RepeatLength=12

seed=CTTAGGCTTA

CTTAGGCTTAGA

CTTAGGCTTAGA

CTGAGGCTTAAA

CTTAGGCTGAGACTGAGGT
TTAGGCTTAGG
CTTAGGCTGAGGCTTGGATTTAAGTTTGGG
CTTAGGCTTATG
CTTAGGCTCAGG
CTCAGGCTTAGG
CTTAGACTTAGA
CTTAGTCTTAGG
CTTAGGCTTAGG
CTTAAGCTTAGG
CATAGGCTTAGGCTTAGACATAGGCGTAGACTTAAG
Nr of selected repeats 10 Similarity 0.748148

Consensus:

CTtAGgCTTAgg

>Cele-UNSB01_2:4159337-4159593 Satlength=257 Nr of Repeats=13 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGACAGCTGTAGGG

GTACTGTAGGA

GTACTGTAGGAAAAGTGTAGGAGCACTGTAAGAGTACTGTAAAG

GTACTGTAGGA

GTACTGTAGGT

GTACTGTAGGG

GTACTTTAGGAGTTCTGTGAGATACTGTAACCTCTGAAAATTGAGTTTTTGGTTTTTGAAGAAAGAGTG

GTACTGTAGGA

GTACTGTAGAG

GTACTGTTGGAGTACTCTACGA

GTACTGTAGGT

GTACTGTAAGG

GTACTGTAGGA

Nr of selected repeats 9 Similarity 0.735043

Consensus:

GTACTGTAGGn

>Cele-UNSB01_2:4203805-4204480 Satlength=676 Nr of Repeats=4 RepeatLength=11

seed=TGCCTGCCTA

TGCCTGCCTAT

TGCCTGCCTAC

TGCCCCCCTAACCATGAAATAATTTTATAAACTGAAATAAATTTTGTTAATTTTCAGTATAAAATACAGGAATCTTGAAA

AAACTCCAACATCTAAAAATACTCTCAAAATATAGAAAACAAAGCGAAAAGAAAAAGAAAAAGAAAAAGAAGCGATAA

AGATTGGAACGGAACCTGAATATAATTAACCTAGAAATTTGGAGAAAGTGGGTGAGAGGGGCAAGGAAAATGAATGTGTT

GAAGAGGCAGAATGGTTTTGTTGGACATCAAATCCACGATTACTGTTCAACCACATTTTTTATTTATTTTGTGGCTTTAGT

GTTAATATTTTATTCCAGAAAAGAACTATATGTTCCGAAATAATGTTGCTCAAATTTTAATTATACGACCTAGAACTT

ATATTTTTCGCTGAAAATTCAAATTTTTTCATATGGAATTTCTAATGTTTCAAGCTAAAATTTTCACATTTTGACAGAAGT

TTCAGATTTAAGATTCTTGATTATGATTTTAAAAAAGGATTTAAAAATTTAACTAAACAGGTTTTGCAAAAGTTGAACT

TAAGGTTCTCAACTTTTTCAACTATTTTTTTGGATATAATATTAACCTCAGTCTCTTTTATATTACTCACATTGATAGCAG

TTTGCCTTTC

TGCCTGCCTAC

Nr of selected repeats 3 Similarity 0.919192

Consensus:

TGCCTGCCTAc

>Cele-UNSB01_2:4205915-4205959 Satlength=45 Nr of Repeats=4 RepeatLength=11

seed=GGCAGGCAGT

GGCAGGCAGTG

GGCAGGCAGTA

GGCAGGCAGTA

GGCAGGCAGTC

Nr of selected repeats 4 Similarity 0.898990

Consensus:

GGCAGGCAGTa

>Cele-UNSB01_2:4270872-4271040 Satlength=169 Nr of Repeats=5 RepeatLength=24

seed=GTGAGGTACG

GTGAGGTACGCA

GTGAGGTACGAGATGAGGTACAAG

GTGAGATACGATGTGAGGTCTGGG

GTGAGGTGCGAGGCGAGGCAGGAG

GTGAGGTACGAGGCCAGGTACTATGCGAGGTATGAGGTGAGGGGCGAGATGAGGTACTAGGCGAGGTGGGAGGCATGAT
ATGAG

Nr of selected repeats 3 Similarity 0.611111

Consensus:

GTGAGgTaCGAggtGAGGtangaG

>Cele-UNSB01_2:4272676-4272936 Satlength=261 Nr of Repeats=25 RepeatLength=10

seed=GCGTTAGCAG

GCGTTAGCAG

GCGTTAGCAG

GCATTAGCAG

GCGTTAGCAG

GCGTTAGCAG

GCGTAAGCAG

GCGTTAGCAG

GCGTTAGCAGGCGTTAGCAG

Nr of selected repeats 24 Similarity 0.977778

Consensus:

GCGTTAGCAG

>Cele-UNSB01_2:4275898-4276001 Satlength=104 Nr of Repeats=5 RepeatLength=18

seed=TGCAAGACTA

TGCAAGACTAATAGAGGC

TGCAAGACTAATTTTCGATTGATCCGTAGGGG

TGCAAGACTAATAGGGG

TGCAAGACTAATAGAGAC

TGCAAGACTAATAGAGAC

Nr of selected repeats 3 Similarity 0.950617

Consensus:

TGCAAGACTAATAGAGaC

>Cele-UNSB01_2:4325046-4325721 Satlength=676 Nr of Repeats=27 RepeatLength=25
seed=GAGAGTAAAA

GAGAGTAAAAATATACGGTGAAGCCA
GAGAGTAAAAATATACGGTGAAGCCA
GAGAGTAAAAACATACGGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATACGATGAAGCCA
GAGAGTAAAAATATACGGTGAAGCCA
GAGAGTAAAAATATACGGTGAAGCCA
GAGAGTAAAAATATACGGTGAAGCCA
GAGAGTAAAAATATACGGTGAAGCCA
GAGAGTAAAAATATACGGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATACGGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA
GAGAGTAAAAATATTCTGTGAAGCCA

Nr of selected repeats 27 Similarity 0.936486

Consensus:

GAGAGTAAAAATATaCgGTGAAGCCA

>Cele-UNSB01_2:4325748-4326453 Satlength=706 Nr of Repeats=45 RepeatLength=15
seed=CTCACCACGA

CTCACCACGACGGGT
CTCACCACGAAGGGT
CTCACCACGAAAGGA
CTTACCACGATGGGT
CTCACCACGATAAGT
CTCACCACGAAGGGTA
TCACCACGAAGGGTCTTACCATGAAGGGT
CTCACCACGAAGGGT
CTCACCACGATGGGTCTGACTACGATGCGT
CTCACCACGAAGGGC
CTCACCACGAAAGGT
CTCACCACGAAGGGC
CTTACCACGAAAGGT
CTCACCACGAAGGGT
CTCACCACGAAAGGT
CTCACCACGAATGGT
CTCACCACGAAGGGT
CTCATCACGAAAGGT
CTCACCACGAAGGGC

CTTACCACGAAAGGT
CTCACCACGAAGGGT
CTCACCACGAAAGGT
CTCACCACGAATGGT
CTCACCACGAAGGGT
CTCATCACGAAAGGT
CTCACCACGAAGGGC
CTCACCACGAATGGT
CTCACCACGAAGGGT
CTCACCACGAAAGGT
CTCACCACGATGGGT
CTCACCACGAAGGGT
CTCACCACGGAAGGT
CTCACCACGAAGGGT
CTCATCACGAAAGGT
CTCACCACGAAGGGCT
TCACCACGAATGGT
CTCACCACGAAGGGT
CTCACCACGGAAGGT
CTCACCACGAAGGGT
CTCATCACGAAAGGT
CTCACCACGAAGGGC
CTCACCACGAATGGT
CTCACCACGAAGGGT
CTCACCACGGAAGGT
CTCACCACGAAGTTC

Nr of selected repeats 40 Similarity 0.798251

Consensus:

CTCACCACGAAGGGT

>Cele-UNSB01_2:4361834-4362159 Satlength=326 Nr of Repeats=8 RepeatLength=35

seed=TTCCGGCAA

TTCCGGCAAATCGGCAAAACTGAACAT

TTCCGGCAAACCGCAAATTTGTCAAAATTGAAAAT

TTCCGGCAAATCCGCAATATGCCGAAATTGGAAAACGCCGGCAAACCGCAAAGCCAAAATTGAAAAC

TTCCGGCAAATGGCAAGTTGCCAAAATTTGAAAAT

TTCCGGCAAGACGGCAATATGCCAAAATTA

TTCCGGCAAACCGGCAAATTTGCCAAAATTTAAAAAATCCGGCAGAACGGCAAAC

TTCCGGGAAAACCGGCAAATTTGCCAAAATATGGAAAAT

TTCCGGGAAAACCGGCAAATTTGCCAAAATTA

Nr of selected repeats 5 Similarity 0.790476

Consensus:

TTCCGGcAAaAcGGCAAatTGcCAAaATgaAAAt

>Cele-UNSB01_2:4377229-4377482 Satlength=254 Nr of Repeats=23 RepeatLength=11

seed=CAGTTGTAC

CAGTTGTCACT

CAGTTATCACC

CAGTTGTCACT

CAGTTGTCACT
CAGTTGTCACC
CAGTTGTCACT
CAGTTGTCACT
CAGTTGTCACC
CAGTTGTCACC
CAGTTGTCACC
CAGTTGTCACTC
CGTTGTCACC
CGGTTGTCACT
CAGTTGTCACT
CAGTTGTCACC
CAGTTGTCACTC
CGTTGTCACC

Nr of selected repeats 19 Similarity 0.897927

Consensus:

CAGTTGTCACT

>Cele-UNSB01_2:4380400-4380472 Satlength=73 Nr of Repeats=4 RepeatLength=12
seed=AGCCTAAGCC

AGCCTAAGCCTA

AGCCTTAGCCTA

AGCCTAAGCCTG

AGCCTAGGCCTGAGCCTGATCCTAGGCCTGAGCCTG

Nr of selected repeats 3 Similarity 0.851852

Consensus:

AGCCTaAGCCTa

>Cele-UNSB01_2:4433247-4433329 Satlength=83 Nr of Repeats=4 RepeatLength=12
seed=TAAGCCTAAG

TAAGCCTAAGTCTATGCTTATGTCTAAGACTGAGCCTGAGCCTAGT

TAAGCCTAAGAC

TAAGCCTAAGAC

TAAGCCTAAGCC

Nr of selected repeats 3 Similarity 0.925926

Consensus:

TAAGCCTAAGaC

>Cele-UNSB01_2:4510577-4510967 Satlength=391 Nr of Repeats=36 RepeatLength=11
seed=TGCACATTTT

TGCACATTTT

TGCACATTTTGCACATTTT

TGCACATTTT

TGCACATTTT

TGCACATTTT

TGCACATTTT

TGCACATTTT

TGCACATTTT

TGCACATTTTT
TGCACACTTT
TGCACATTTTT
TGCACATTTTT
TGCACATTTTT
TGCACATTTTC
TGCACATTTTT

Nr of selected repeats 30 Similarity 0.991919

Consensus:

TGCACATTTTT

>Cele-UNSB01_2:4622617-4623337 Satlength=721 Nr of Repeats=18 RepeatLength=40
seed=TCCAGAACCT

TCCAGAACCTTCTGGAAAATTCGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT

Nr of selected repeats 18 Similarity 0.957734

Consensus:

TCCAGAACCTTCTGGAAAATtGAGAAAATTCGGAATGT

>Cele-UNSB01_2:4623470-4624110 Satlength=641 Nr of Repeats=20 RepeatLength=32
seed=CGGGAATTCA

CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAGAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTTGG

CGAGAATTCAAAATTTCTGTGAAAAAATTTGG
CGGGAATTCAAAATTTCTGTGAAAAAATTTGG
CGGGAATTCAAAATTTCTGTGAAAAAATTTGG
CGGGAATTCAAAATTTCTGTGAAAAAATTTGG
CGGGAATTCAAAATTTCTGTGAAAAAATTTGG
CGGGAATTCAAAATTTCTGTGAAAAAATTTGG
CGGGAATTCAAAATTTTATGAAAAAATTTGG
CGGGAATTCAAATTTCTGTGAAAAATATAA
CGGGAATTCAAGTTTTCTGTGAAAAATTTGG
CGGGAATTCAAATTTCTGTGAAAAATTTGG
CGGGAATTCAAATTTCTTTGAAAAATTTGG

Nr of selected repeats 20 Similarity 0.921491

Consensus:

CGGGAATTCAAAaTTTCTGTGAAAAATTTGG

>Cele-UNSB01_2:4637434-4637644 Satlength=211 Nr of Repeats=5 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATTTCAATTTTCGGAAAATGCCGG
TTTGCCGGAAAATTTAATTTTCGGAAATCACGGATTTTCCTGAAATATTCGATTCGGCAAATTTCTGA
TTTGCCAGAAAATTTCAATTTTCGGCAAATTACCGA
TTTGCCGGAAAATTTCAATTCGGCAAATTTACCGG
TTTCCCGGAAAATTTCAATTTTCGGCAAATTACCGA

Nr of selected repeats 4 Similarity 0.757716

Consensus:

TTTgCCgGaAAaTTTCaTtTtCGGcAAaTTaCCGa

>Cele-UNSB01_2:4751417-4751507 Satlength=91 Nr of Repeats=6 RepeatLength=15
seed=GAGACCCATC

GAGACCCATCGTGGC
GAGACCCAGCGTGGT
GAGACCCATCGTGGC
GAGACCCAGCGTGGT
GAGACCCATCGTGGC
GAGACCCATCGTGGT

Nr of selected repeats 6 Similarity 0.899259

Consensus:

GAGACCCAtCGTGGc

>Cele-UNSB01_2:4751413-4751956 Satlength=544 Nr of Repeats=21 RepeatLength=15
seed=TGGTGAGACC

TGGTGAGACCCATCG
TGGCGAGACCCAGCG
TGGTGAGACCCATCG
TGGCGAGACCCAGCG
TGGTGAGACCCATCG
TGGCGAGACCCATCG
TGGTGAGACCCATCG
TGGTGAGACCCATAAGTTTTGGCGGGAATTCAAATTTTCTGTGAAAATTTTTTGGTGGGAATTCAAATTTTATGTGAAA
AATTTTGGCGGCAATTCAAATTTTATGTGAAAAATTTTGGCGGGAATTCAAATTTTCTGTGAAAAATTTTCGGCGGGAAA
TTCAAATTTTCTGAGAAAAATTTTGGCGGGAATTAATAATTTTCTTAGAAATAATTTTGGCCGGGAAT
TGGTGAGACCCTTCG
TGGTGAGACCCTTCG
TGGTGAGACCCATCGT
TGTGAGACCCTTCG
TGGTGAGACCCTTAG
TGGTGAGACCCATCGT
TGTGAGACCCTTCG

TAGACCATTAGATGAATTCTCAAAGT
TAGACCATTAGATGAATTTCCAAAAT
TAGACCATTAGATGAATTTCCAAAAGT
TAGACCATTAGATGAATTCTCAAAGT
TAGACCATTAGATGAATTCTCAAAGT
TAGACCATTAGATGAATTTCCAAAAGT
TAGACCATTAGATGAATTTCCAAAAGT
TAGACCATTAGATGAATTTCCAAAAGT
TAGACCATTAGATAAAATTTCCAAAAGT
TAGACCATTAGATAAAATTTCCAAAAGT
TAGACCATTAGATGAATTTCCAAAAGT
TAGACCATTAGATGAATTCTCAAAGT
TAGACCATTAGATAAAATTTCCAAAAGT
TAGACCATTAGATGAATTTCCAAAAGT
TAGACCATTAGATGAATTCTCAAAGT
TAGACCATTAGATGAATTCTCAAAGT

Nr of selected repeats 155 Similarity 0.871050

Consensus:

TAGACCATTAGATGAATTTCCAAAAGT

>Cele-UNSB01_2:5217429-5217681 Satlength=253 Nr of Repeats=9 RepeatLength=25
seed=AGAGTAAAAT

AGAGTAAAATATAGTGGGAAGTCAG
AGAGTAAAATAATTGGTGAAGCCAG
AGAATAAAATATGGTGGGAAGCCACAG
AGAGTAAAATATAGTGGGAAGCCAG
AGAGTAAAATATTTGGGAAAAGCCAC
AGAGTAAAATAATTGGGAAAAGCCAG
AGAGTAAAATAATTGGGAAAAGCCAG
AGAGTAAAATAATTGGGAAAAGCCAG
AGAGTAAAATATTTGGGAAAAGCCACAGAGCAAATAATTGGTGAAGCCAG

Nr of selected repeats 6 Similarity 0.823932

Consensus:

AGAGTAAAATAATTGGGaaAGCCAG

>Cele-UNSB01_2:5217526-5241162 Satlength=23637 Nr of Repeats=927

RepeatLength=25 seed=AGCCAGAGAG

AGCCAGAGAGTAAAATATTTGGGAA
AGCCACAGAGTAAAATAATTGGGAA
AGCCAGAGAGTAAAATAATTGGGAA
AGCCAGAGAGTAAAATAATTGGGAA
AGCCAGAGAGTAAAATATTTGGGAA
AGCCACAGAGCAAATAATTGGTGA
AGCCAGAGAGTAAAATATCCTGTGA
AGCCAGAGAGTTACACGAAAAATAGATTGTTACACGAAAAATAGATTGTTACACGAAAAATAGATTGTTACACGAAAA
TAGATTGTTACACGAGAAATGGATTGTTACAAGAAAAATAGATTGTTACACGAAAAATAGATTGTTACACGAAAAATAG
ATTGTTACACGAAAAATAGATTGTTACACGAAAAATAGATTGTTACACGAAAAATAGATTGTTACACGAAAAATAGATT
GTTACACGAAAAATAGATTGTTACACGAAAAATAGATTGTTACACGAGAAATGGATTGTTACACGAAAAATAGATTGTT
ACACGAAAAATAGATTGTTACACGAAAAATAGATTGTTACACGAAAAATAGTAAAATATTTGGAAA
AGCCACAGAGTAAAATAATTGGTGA
ACCAGAGAGTAAAATAATTGGTGA
AGCCAGAGAGTAAAATAATTGGTGA
AGCCAGAGAGTAAAATAATTGGTGA
AGCCAGAGAGTAAAATAATTGGTGA
AGCCAGAGAGTAAAATAATTGGTGA
AGCCAGAGAGTGAAATATTGGGTGA

GGAATTGAAATTTCCAGCAAATCGGCAAATTGCC
GGAATTGAAATTTGCGGCAAATCGGCAAATTTCC
GGAATTGAAATTTCCGGCAAATCGGCAAATCTC
GGAATAGAAAATTTCCGGCAAATCGGCAAATCTG
GGAATTGAAATTTCCGGCAAATCGGCAAATCTG
GGAATTGAAATTTCCGGCAAATCGGCAAATTGCC
GGAATTGAAATTTCCGGCAAATCGACAAATTGCC
GGAATTGAAATTTCCGGCAAATCGACAAATTGCC

Nr of selected repeats 9 Similarity 0.831481

Consensus:

GGAATTGAAATTTCCgGCAAATCGgCAAAtTgCc

>Cele-UNSB01_2:5970897-5971730 Satlength=834 Nr of Repeats=4 RepeatLength=203
seed=GTTCAAGCAG

GTTCAAGCAGAACAAGTACATTTTCAGTTATACCTTTTAGATCGCATTTTGAGATTGAATGGAATAAACGAGTTATATG
CAAATTAGTAGACTTTCCAAACTTTGAAAATTAATATCTGGCTTCAAACCTAACTTTTCTGAAAATCCCCGTAGCCATT
TTGTTGCAAATTTGTGCTCTTTCAGAATTTAAAAACGGCATTCCAAACATTTCCGTATTTGCCGA
GTTCAAGCAGAACAAGTAGATCACATTTTGAGATTGAATAGAATAAACGAGTTATATGCAAATTAGTAGACTTTCCAA
ACTTTGAAAATTAATATCTGGCTTCAAACCTAACTTTTCTGAAAATCCCCGTAGCCATTTTGTGCAAATTTGTGCTCT
TTCAGAATTTAGAAACGGCATTCCAAACATTTCCATATTGCCAG
GTTCAAGCAGAACAAGTAGATCACGTTTTGAGATTGAATGGAATAAACGAGTTATATGCAAATTAGTAGACTTTCCAA
ACTTTGAAAATTAATATCTGGCTTCAAACCTAACTTTTCTGAAAATCCCCGAAGCCATTTTGTGCAAAGTTTTGTGCTCT
TTCAGAATTTAAAAAGGGCATTCCAAACATTTCCATATTGCCGA
GTTCAAGCAGAACAAGAAGATCACATTTTGAGATTGAATGGACTAAACGAGTTATATGCAAATTAGTAGACTTTCCAA
ACTTTGAAAATTAATATCTGGCTTCAAACCTAACTTTTCTGAAAATCCCCGTAGTCATTTTGTGCAAATTTGTGCTCT
TTCAGAACTTTAAAAGCGGCACTCCAAACATTTCCATATTGCCGA

Nr of selected repeats 3 Similarity 0.935730

Consensus:

GTTCAAGCAGAACAAGtAGATCACaTTTTGAGATTGAATgGAaTAAACGAGTTATATGCAAATTAGTAGACTTTCCAA
ACTTTGAAAATTAATATCTGGCTTCAAACCTAACTTTTCTGAAAATCCCCGTAgcCATTTTGTGCAAaTTTTGTGCTCT
TTCAGAAtTTAaAAacGGcAtTCCAAACATTTCCATATTGCCgA

>Cele-UNSB01_2:6168224-6172025 Satlength=3802 Nr of Repeats=21 RepeatLength=181
seed=TTTTTAACTT

TTTTTAACTTTTAAATCCACTAAAACCTTGAATGGTACAGAACATGCAAATTTGTAATTTTAAAGAACTGAATGTGGTTTC
GAATATTTATGGATTGCTTTATTTCGAACACTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGTCATATTATA
CCGAACACTACTAACTTTACTGG
TTTTTAACTTTTAAATCCACTAAAACCTTGAATGGTACAGAACATGAAAATTTGTAATTTTAAAAACTGAATGTGGTTTC
GAATATTTATGGATTGCTTTATTCTAAAACCTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGCCATATTATA
CCGAACACTACTAACTTTACTGG
TTTTTAACTTTTGAATCCACTAAAACCTTGAATGGTACAGAACATGCAAATTTGTAATTTCAAGAACTGAATGTAGTTTC
GAATATTTATGGATTGCTTTATTCTAAAGCTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGCCATATTATA
CCGAACACTACTAACTTTACTGG
TTTTTAACTTTTAAATCCACTAAAACCTCGGAATGGTACAGAACATGCAAATTTGTAATTTCAAGAACTGAATGTGGTTTC
GAATATTTATGGATTGCTTTGTTCCACACTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTGG
TTTTTAACTTTTAAATCCACTAAAACCTCGGAATGGTACAGAACATGCAAATTTGTAATTTCAAGAACTGAATGTGGTTTC
GAATATTTATGGATTGCTTTATTCTAAAACCTGACTCTGAAATATTTTGCATCCATATGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTGG
TTTTTAACTTTTAAATCCACTAAAACCTCGGAATGGTACAGAACATGCAAATTTGTAATTTCAAGAACTGAATGTGGTTTC
GAATATTTATGGATTGCTTTATTCTAAAACCTGACTCTGAAATATTTTGCATCCATATGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTGG

TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTAG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTAG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATATGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTTGGAA TGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTGTTC CCACTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTTGGAA TGGTACAG ATTATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATATGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTTGGAA TGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTAG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATATGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTTGGAA TGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTGTTC CCACTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTATTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAG ATTATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATATGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG
TTTTTAAC TTTTAAAT CCACTAAA ACTCGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTGG TTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATTTGACTACTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG

Nr of selected repeats 21 Similarity 0.964746

Consensus:

TTTTTAAC TTTTAAAT CCACTAAA ACTcGGAATGGTACAGA ACATGCAA ATTTGTAAT TTTCAAGA ACTGAATGTg GTTTC
GAATATTTATGGATTGCTTTATTCTAAA ACTGACTCTGAAATATTTTGCATCCATtTGACTAcTAATTGTCATATTATA
CCGAACACTACTAACTTTAGTG

>Cele-UNSB01_2:6176621-6177425 Satlength=805 Nr of Repeats=18 RepeatLength=45
seed=CTGAAGGATC

CTGAAGGATCAGA ACATCAGGAAGAGCCTCGTGATCCTTTGGAG
CTGAAGGATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTAT
CTGAAGGAC CAGA ACATCAGGAAGGTACCCATGTGATCCTTCGGAG
CTGAAGGATCAGA ACATCAGGAAGAGCCTCGTGATCCTTTGGAG
CTGAAGGATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTAT

AATAAAAATTTAATTTTTATTGGTGTCTCTATTTTATAAAGAAAATACATTTTCAAAATAGAGACA

Nr of selected repeats 38 Similarity 0.936325

Consensus:

AATAAAAATTTAATTTTTATTAGTGTCTCTAtTTTATcAAgAAAATAtATTTTCAAAATAGAGACG

>Cele-UNSB01_2:6532865-6533025 Satlength=161 Nr of Repeats=5 RepeatLength=32

seed=AAAAATTTTC

AAAAATTTTCACAAAAAATTTAAATTCCTGCA

AAAAATTTTCACAGAAAATTTGAATTCCTGCC

AAAAATTTTCACAGAACTTTGAATTCCTGCC

AAAAATTTTCACAGAAAATTTGAATTCCTGCC

AAAAATTTTCACAGAAAATTTGAATTCCTGCC

Nr of selected repeats 5 Similarity 0.916667

Consensus:

AAAAATTTTCACAgAAAaTTTgAATTCCcGCc

>Cele-UNSB01_2:6532865-6533618 Satlength=754 Nr of Repeats=6 RepeatLength=32

seed=AAAAATTTTC

AAAAATTTTCACAAAAAATTTAAATTCCTGCA

AAAAATTTTCACAGAAAATTTGAATTCCTGCC

AAAAATTTTCACAGAACTTTGAATTCCTGCC

AAAAATTTTCACAGAAAATTTGAATTCCTGCC

AAAAATTTTCACAGAAAATTTGAATTCCTGCC

AAAAATTTTCACAGAAAATTTGACACCACTAACCTCAAACCAATATCCCTTCAAAGACGAAAAGTCAATTTTTGCCAA

AGTACAGTAATCCTACAGAACTCCTACAGTACCTCTACAGTACTACTACAGTACCCCGACCATATCCCACCACTAACCT

CAAACCAATATCTCTTCAAAGACGAAAAGTCAATTTTTGCCAAAGTACAGTAATCCTACAGTACTCCTACAGTACCTC

TACAGTACTACTACAGTACCCCGACTATATCCCCTACTAACCAGCAAACCTATATCTCTTCAAAGACAAAACTCAAT

TTTTCTAAACTACAGTAATCCTACCGTACTCCTACAGTACTCCTACAGTACTACTACAGTACCCCGTCCATATCCCCT

TACTAAGCCCAAATAATATCCCTCCATCAGCCGAAAACGCCTTGCCTTTGTAAGCTATGACGTCCTACTTAAACAAAC

GGACACTATTTTTTATATATAGGTAATGATATTGTCTGATTTCTGAAAGCAATCGAAAAATTAATTTTTTAGCCTC

CTGCGTTTTGTTTCATTTTACACTAAAGATTAGAAAAAT

Nr of selected repeats 5 Similarity 0.916667

Consensus:

AAAAATTTTCACAgAAAaTTTgAATTCCcGCc

>Cele-UNSB01_2:7497139-7497311 Satlength=173 Nr of Repeats=4 RepeatLength=41

seed=AAAACGGGAA

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTTA

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTTA

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAGAATTTTA

AAAACGGGAAAACGGGATTTCCCGTTCCCGTGAAAATTTTAAAACGGG

Nr of selected repeats 3 Similarity 0.978320

Consensus:

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAaAATTTTA

>Cele-UNSB01_2:7497138-7497671 Satlength=534 Nr of Repeats=10 RepeatLength=41

seed=AAAACGGGAA

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTT

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTT

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAGAATTTT

AAAACGGGAAAACGGGATTTCCCGTTCCCGTGAAAATTTT

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTT

AAAACGGGACAACGGGAATTCCCGTTTTTTTTGAAAACACTCA

AAAACGGGACAACCTGGGCGTTTAAAAAAAAGAGTGCATAGTTGGCGTAAATTTTAGTGTATTCGAGGCAAATTATT

TAAAAAAACTGCATTATAACATTTTTATAGATTTTTTCAATATTAACAGATATTTAAAAAGCCAAAAAATGAGGGA

AAATGTCCCGTTCCCGTGAAAGTTTT

AAAACGGGACAACGGGAATTCCCGTTCCCGTGAAAATTTT

AAAACGGGACAACGGGAATTCCCGTTCCCGTGAAAACACCCC

AAAAACGGGACAACGGG

Nr of selected repeats 6 Similarity 0.956640

Consensus:

AAAAACGGGAAAACGGGAATTCCCGTTCCTCGTAAAATTTT

>Cele-UNSB01_2:7564245-7565607 Satlength=1363 Nr of Repeats=34 RepeatLength=14

seed=GAAGGATCGG

GAAGGATCGGGTCG

GAAGGATCGGGCCG

GAAGGATCAGGCCG

GAAGGATCAGGCCGAAAGATTGGGACGAGACGACGATGGTGAGAGGGAGTCCGGAAACGTGGACAATGGTAAGGAAAT

ATTTAAATGATGCTTCAGCTAAACTGATTTTTTACTGATCTACAATAAAGACGACGAA

GAAGGATCGGGTCG

GAAGGATCGGGCCG

GAAGGATCGGGCCG

GAAGGATCGGGTCG

GAAGGATCGGAACGAGACGACGATGGTGAGAGGGAGTCCGGAAACGTGGACAATGGTAAGAAAAGATTTAAATGATGCT

TCAGCTAAACTGATTTTTTACAGATCTAATAGAAAGACGACGAA

GAAGGATCGGGCCG

GAAGGATCGGGCCG

GAAGGATCAGGCCG

GAAAGATCGGGACGAGACGACGATGGGGAGAGGGAGTCCGGAAACGTGGGCAATGGTAAGAAAAGATTTAAATGATGCT

TCAGCTAAACTGATTTTTTACAGATCTACAATAAAGACGACGAA

GAAGGATCGGGTCG

GAAGGATCGGGTCG

GAAGGATCGGAACGAGACTACGATGGTGAGAGGGAGTCCGGAAACGTGGACAATGGTAAGAAAAGATTTAAATGATGCT

TCAGCTAAACTGATTTTTTACAGATCTAATAGAAAGACGACGAA

GAAGGATCGGGCCG

GAAGGATCGGGTCG

GAAGGATCGGAACGAGACGACGATGGTGAGAGGGAGTCCGGAAACGTGGACAATGGTAAGAAAAGATTTAAATGATGCT

TCAGCTAAACTGATTTTTTACAGATCTACAATAAAGACGACGAA

GAAGGATCGGGTCG

GAAGGATCGGGCCG

GAAGGGTCGGGCCG

GAAGGATCAGGCCG

GAAGGATCGGGACGAGACGACGATGGTGAGAGGGAGTCCGGAAACGTGGACAATGGTAAGAAAAGATTTAAATGATGCT

TCAGCTAAACTGATTTTTTACAGATCTACAATAAAGACGACGAA

GAAGGATCGGGTCG

GAAGGATCGGGTCG

GAAGGATCGGAACGAGACTACGATGGTGAGAGGGAGTCCGGAAACGTGGACAATGGTAAGAAAAGATTTAAATGATGCT

TCAGCTAAACTGATTTTTTACAGATCTACAATAAAGACGACGAA

GAAGGATCGGGTCG

GAAGGATCGGGCCG

GAAGGGTCGGGCCG

GAAGGATCAGGCCG

GAAGGATCGGGACGAGACGACGATGGGCAGAGGGAGTCCGGAAACGTGGACAATGGTAAGAAAAGATTTAAATGATGCT

TCAGCTAAACTGATTTTTTACAGATCTACAATAAAGACGACGAA

GAAGGATCGGGTCG

GAAGGATCGGGTCG

Nr of selected repeats 26 Similarity 0.910916

Consensus:

GAAGGATCGGGcCG

>Cele-UNSB01_2:7566750-7567567 Satlength=818 Nr of Repeats=42 RepeatLength=16

seed=CGGAAAAATT

CGGAAAAATTTTGCTG

CGGAAAAC¹TTTCGCTG
CGGAAAAATTGCGT²CGT
GGAAAAATTTTCCGCGACAAAAATTTGCTG
CGTAAAAATTCG³T⁴CG
CGGAAAAATTTGGTGTGGAGAAAAATTCG⁵T⁶CG
CGGAAAAATTTG⁷CCG
CGGAAAAATTTG⁸CTG
CGGAAAAATTTGT⁹GG
CGGAGAAAATTCG¹⁰T¹¹CG
CGGAAAAATTTGCTCGCGTGGAAAAATTCCT¹²TG
CGGAAACATTTGGCTGCAGAAAAATAAATTTGCTGCGGAAAAAAATTTG¹³T¹⁴CG
CGAAAAAATTTG¹⁵CCG
CGGAAAAATTTGCTGCGCGAAAAATTCG¹⁶T¹⁷CG
CGGAAAAATTTAG¹⁸CTG
CGGAAAAATTTG¹⁹CTGC
CGAAAAAATTTG²⁰CCG
CGGAAAAATTTGCTGCGCGAAAAATTCG²¹T²²CG
CGGAAAAATTTAG²³CTG
CGGAAAAATTTG²⁴CCG
CGGGAAAATTTGT²⁵GG
CGGAAAAATTTGG²⁶CTT
CGGAAAAATTTG²⁷CCG
CGGAAAAATTTACT²⁸G
CGGAAAAATTTGT²⁹AG
CGGAGAAAATTTGG³⁰CTG
CGGAATAATTTG³¹CCG
CGGAAAAATTTGCTCCGCGAAAAATTCG³²T³³CG
CGGAAAAATTTAG³⁴CTG
CGGAAAAATTTG³⁵CCG
CGGGAAAATTTGT³⁶GG
CGGAAAAATTTGG³⁷CTG
CGGAAAAATTTG³⁸CCG
CGGAAAAATTTGCG³⁹T⁴⁰CG
CGGAAACATTTAG⁴¹CTG
CGGAAAAATTTGCT⁴²GC
CGAAAAAATTTG⁴³CCG
CGGAAAAAATTTGG⁴⁴CTG
CGGAAAAATTTG⁴⁵CCG
CGGAAAAATTTGCTGCGCGAAAAATTCG⁴⁶T⁴⁷CG
CGGAAAAATTTAG⁴⁸CTG
CGGAAAAATTTGT⁴⁹GG

Nr of selected repeats 27 Similarity 0.719401

Consensus:

CGGAAAAATTTnGcnG

>Cele-UNSB01_2:7568262-7569624 Satlength=1363 Nr of Repeats=34 RepeatLength=14

seed=CCGATCCTTC

CCGATCCTTCCGAC

CCGATCCTTCCGAC

CCGATCCTTCTTCGTCTTTATTGTAGATCTGTAAAAATCAGTTTAGCTGAAGCATCATTTAAATCTTTTCTTACC

ATTGTCCACGTTTCCGGACTCCCTCTGCCATCGTCTCTCGTC

CCGATCCTTCCGGC

CTGATCCTTCCGGC

CCGACCCTTCCGGC

CCGATCCTTCCGAC

TCCATCCCGA
TCCATCCCAA
TCCATCCCAATCCGTCCCCA
TCCATCCCGA
TCCATCCCGA
TCCGTCCCGA
TCCATCCCGA
TCCGTCCCGA
TCCATCCCGA
TCCATCCCGA
TCCATCCCGA
TCCATCCCGA
TCCATCCCGA
TCCATCCCGA
TCCATCCCAATCCATCCCGA

Nr of selected repeats 19 Similarity 0.831650

Consensus:

TCCATCCCGA

>Cele-UNSB01_2:7594307-7594367 Satlength=61 Nr of Repeats=4 RepeatLength=15

seed=GTAGATCTTG

GTAGATCTTGTTTTG

GTAGATCTTGAAAAT

GTAGATCTTGTTTTG

GTGGATCTTGTTTTC

Nr of selected repeats 4 Similarity 0.675347

Consensus:

GTaGATCTTGtttTg

>Cele-UNSB01_2:8013550-8013642 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=CGAAAAGGGG

CGAAAAGGGGAGCAAAA

CGAAAAGGGGATCTG

CAAAAAGGGGATCTG

CGAAAAGGGGAGATA

CGAAAAGGGGAGATA

CGAAAAGGGGAGCAA

Nr of selected repeats 5 Similarity 0.768889

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_2:8013818-8013910 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=CCCCTTTTCG

CCCCTTTTCGTTGCT

CCCCTTTTCGTATCT

CCCCTTTTCGTATCA

CCCCTTTTCGCAGAT

CCCCTTTTTCGAGAT

CCCCTTTTCGTTCTGCT

Nr of selected repeats 5 Similarity 0.733333

Consensus:

CCCCTTTTcGtagct

>Cele-UNSB01_2:8406477-8418390 Satlength=11914 Nr of Repeats=144

RepeatLength=79 seed=TGACAGAATA

TGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTGTCGTTTCTTTTCTGAATCTCCACTCTTCCGAATGAGTCC

TGACAGAATACCGACAGTATTTTGGGGTCTCATTAGGTTTCTTTTCTTTTCTGAATCTCCACTCTTCCCTAATGAGTCC

TGACAGAATACCGACAGTATTTTGGGGTCTCATTAGGTTTCTTTTCTTTTCTGAATCTCCACTCTTCCCTAATGAGTCC

TGACCAAGGGTGTCAATTCCCCTTTCCCCTTTTCCCATTGTCCCGTTTTTGGGGTGTTTTCACGGGAACGGGAATTCC

Nr of selected repeats 10 Similarity 0.901482

Consensus:

AAAGTTCTGGAACATTCAGAatTTTCcCaATTTTTCTAG

>Cele-UNSB01_2:8586336-8586411 Satlength=76 Nr of Repeats=4 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGGTGGGTATTACCACGAT

GGGTCTCACCACGAC

GGGTCTCACCACGGT

GGGTCTCGCCACGAT

Nr of selected repeats 3 Similarity 0.822222

Consensus:

GGGTCTCaCCACGat

>Cele-UNSB01_2:9101090-9103530 Satlength=2441 Nr of Repeats=29 RepeatLength=86

seed=AGCCAGTATT

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCTTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCTTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATGC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCTTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATGC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCTTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCTACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCTACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATGC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATGC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATGC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATGC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCTACGACATTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCTACGACATTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC

AGCCAGTATTTGCGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCTACGACATTTTC
AAAATAC

AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC
AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATGC
AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC
AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATGC
AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC
AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
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AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC
AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCCACGACCTTTC
AAAATAC
AGCCAGTATTTTCGGGGTCTGGCAATAGTATTT

Nr of selected repeats 28 Similarity 0.980066

Consensus:

AGCCAGTATTTTCGGGGTCTGGCAATAGCTTCTCGTTAACTTCGAACTCTTCCATCTTTTCCCTATTGCcACGACCTTTC
AAAATaC

>Cele-UNSB01_2:9328143-9328548 Satlength=406 Nr of Repeats=27 RepeatLength=15

seed=TGGTGAGACC
TGGTGAGACCCATCG
TGGTGAGACCCTTCG
TGGTGAGACCCTTCG
TGGTGAGACCCATCG
TGGTGAGACCCTTCG
TGGTGAGACCCTTCG
TGGTGAGACCAATCG
TGGTGAGACCTTTCG
TGGTGAGACCCTTCG
TGGTGAGACCAATCG
TGGTGAGACCCTTCG
TGGTGAGACCCATCG
TGGTGATACCCTTCG
TGGTGAGACCCTTCG
TGGTGAGACCCATCG
TGGTGAGACCCTTCG
TGGTGAGACCCTTCG
TGGTGAGACCAATCG
TGGTGAGACCTTTCG
TGGTGAGACCCGTCG
TGGTGAGACCAATCG
TGGTGAGACCCTTCG
TGGTGAGACCCTTCG
TGGTGAGACCCATCG
TGGTGAGACCCTTCT
TGGTGAGACCCATCGC
GGTGAGACCCTTCG

Nr of selected repeats 25 Similarity 0.902519

Consensus:

TGGTGAGACCctTCG

>Cele-UNSB01_2:9328575-9329101 Satlength=527 Nr of Repeats=15 RepeatLength=35
seed=ATTCAAATTT

ATTCAAATTTTTAGTGAAAAAAAAATTTTGGAGGGAA
ATTCAAATTTTCAGTGAAAAAAAAATTTTGGCGGGAA
ATTCAAATTTTCTGTGAAAAAAAAATTTTGGCGGGAA
ATTCAAATTTTCAGTGAAAAAAAAATTTGGGCGGGAG
ATTCAAATTTTCAGTGAAAAAAAAATTTAGCGGGAA
ATTCAAATTTTCAGTGAAAAAAAAATTTTAGCGGGAA
ATTCAAATTTTCAGTAAAAAAAAATTTTGGAGGGAA
ATTCAAATTTTCAGTGAAAAAAAAATTTTGGCGGGAA
ATTCAAATTTTCAGTGAAAAAAAAATTTTGGCGGGAA
ATTCAAATTTTCAGTGAAAAAAAAATTTTGGAGGGAA
ATTCAAATTTTCAGTGAAAAAAAAATTTTGGCGGGAA
ATTAAAATTTTCAGTGAAAAAAAAATTTAGCGGGAA
ATTCAAATTTTCAGTGAAAAAAAAATTTTGGCGGGAA
ATTCAAATTTTCTGTGAAAAAAAAATTTTGGCGGGAA

Nr of selected repeats 10 Similarity 0.900952

Consensus:

ATTCAAATTTTCaGTGAAAAAAAAATTTTgGcGGGAA

>Cele-UNSB01_2:9328566-9329542 Satlength=977 Nr of Repeats=16 RepeatLength=35
seed=TGGCGGGAAA

TGGCGGGAAATTCAAATTTTCTGTGAAAAAAAAATTT
TGGAGGGAAATTCAAATTTTCAGTGAAAAAAAAATTT
TGGCGGGAAATTCAAATTTTCTGTGAAAAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTGGGCGGGAGATTCAAATTTTCAGTGAAAAAAAAATTT
TAGCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTT
TAGCGGGAAATTCAAATTTTCAGTAAAAAAAAATTT
TGGAGGGAAATTCAAATTTTCAGTGAAAAAAAAATTT
TGGCGGGAAATTTAAAATTTTCAGTGAAAAAAAAATTT
TGGAGGGAAATTCAAATTTTCAGTGAAAAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTT
TGGAGGGAAATTCAAATTTTCAGTGAAAAAAAAATTT
TGGCGGGAAATTTAAAATTTTCAGTGAAAAAAAAATTT
TAGCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTT
TGGCGGGAAATTCAAATTTTCTGTGAAAAAAAAATTT
TGGCGGGAAATTCAAATTTTCAGTGAAAAACAATTT
TGGCGGAAAATTCCAATTTCTGAGAAAAATCGAGAAATGTCTGCAATGTTCCAGAAGTTTCTAGAAAATTCGAGAAAAT
TCCGGAATGGTCCAGAATTTTCTAGAAAATTCAGAAAAGTTCTGGAATGGTCCAGAAGTTTCTAGAAAATTCGAGAAAA
TTCCGGAATGGTCCAGAATTTTCTAGAAAATCCGAGAAAAGTTCTGGAATGGTCCAGAATTTTCTAGAAAATTCGGGAAA
ATTCTGGAATATTCCAGAACTTTCTAGAAAATCCGGAAAAGTCTGCAATGTTCCAGAACTCTCTAAAAATTCGATAA
AATTCTGAAATGTTCAATTTTCGTGGAAAAATTCAGAAACTTCTGCAAAAGTTCTACACGAGGTTCTGGCTCGACCCCGC
GCTCCATTGGACACTGAAA

Nr of selected repeats 10 Similarity 0.909418

Consensus:

TgGCGGGAAATTCaAAATTTTCaGTGAAAAAAAAATTT

>Cele-UNSB01_2:9530992-9537371 Satlength=6380 Nr of Repeats=247 RepeatLength=25
seed=CTCTCTGGCT

CTCTCTGGCTTTCACAGAATAATTTA
CTCTCCGGCTTTCACAGTATATTTA
CTCTCTGGCTTTCACAGTATATTTA
CTCTCTGGCTTTCACAGAATAATTTA
CTCTCTGGCTTTCACAGTAAATTTA
CTCTCTGGCTTTCACAGTATATTTA

CTCTCTGGCTTCACAGAATAATTTA
CTCTCTGGCTTCACAGAATAATTTA
CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGAATAATTTA
CTCTCTGGCTTCACAGTATATTTTA
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CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGAATAATTTA
CTCTCTGGCTTCATAGTATATTTTTTTTTTTTTTTTTTATTTTAA
CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGTATATTTTACTCTCTTCACAGTATATTTTA
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CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGTATATTTA
CTCTCTGGCTTCACAGTATATTTTACTCCTCTGTTCTTGCTTCACAGAATAATTTA
CTCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGTAATTTA
CTCTCTGGCTTCACAGTATATTTTTCAAGAATTTTA
CTCTCTGGCTTCACAGTATATTTA
CTCTCTGGCTTCACAGTAATTTT
TCTCTGGCTTCACAGTATATTTTA
CTCTCTGGCTTCACAGAATAATTTA
CTCTCTGGCTTCACAGTATATTTTA
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CTCTCTGGCTTCACAGTATATTTTA
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CTCTCTGGCTTCACAGTAATTTA
CTCTCTGGCTTCAATATTTTA
CTCTCTGGCTTCACAGTATATTTTA

CTCTCTGGCTTCACAGAATAATTTA
CTCTCTGGCTTCACAGTATAATTTA
CTCTCTGGCTTCACAGATATTTTCTTTTTTTTTTTTTTTTTATTTTA
CTCTCTGGCTTCACAGAATAATTTA
CTCTCTGGCTTCACAGAATAATTTA
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CTCTCTGGCTTCATAGTATAATTTA
CTCTCTGGCTTCACAGTATAATTTA
CTCTCTGGCTTCACAGTACATTTA
CTCTCTGGCTTCACAGAATAATTTA
CTCTCTGGCTTCACAGTATAATTTA
CTCTCTGGCTTCACAGTATAATTTA

Nr of selected repeats 194 Similarity 0.906588

Consensus:

CTCTCTGGCTTCACAGtATAtTTTA

>Cele-UNSB01_2:9763711-9764616 Satlength=906 Nr of Repeats=23 RepeatLength=40
seed=TTCCAGAATT

TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTATCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTATCTAGAAATTTCTGGAACA
TTCCAGAATTTTCCCGATTTATCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTATCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTATCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTATCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCCCGATTTCTAGAT

Nr of selected repeats 22 Similarity 0.947763

Consensus :

TTCCAGAATTTTCcCGATTTtTCTAGAAAAGTTCTGGAACA

>Cele-UNSB01_2:9764656-9765286 Satlength=631 Nr of Repeats=18 RepeatLength=35
seed=CCAAAATATT

CCAAAATATTTTTCTCAGAAAATTTAAATTTCCCT
CCAAAATATTTTTCTCAGAAAATTTAAATTTCCCT
CCAAAATATTTTTCTCAGAAAATTTAAACTTCCCT
CCAAAATATTTTTCTCAGAAAATTTAAATTTCCCT
CCAAAATATTTTTCTCAGAAAATTTAAATTTCCCG
CCAAAATATTTTTTCACAGAAAATTTAAATTTCCCG
CCAAAATATTTTTTCACAGAAAATTTAAATTTCCCG
CCAAAATTTTTTTCACAGAAAATTTAAATTTCCCG

Nr of selected repeats 18 Similarity 0.925801

Consensus :

CCAAAATATTTTTtTCAGAAAATTTAAATTTCCCT

>Cele-UNSB01_2:9765369-9765639 Satlength=271 Nr of Repeats=17 RepeatLength=15
seed=CCACGATGGG

CCACGATGGGTCTCA
CCACGAAGGGTATCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCTCGATGGGTCTCA
CCACGATGGGTATCA
CCACGATGGGTCTCA
CCACGACGGGTTCACACGGTTGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTTT
CCACGATGGGTCTCT
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCG

Nr of selected repeats 16 Similarity 0.891852

Consensus :

CCACGATGGGTCTCa

>Cele-UNSB01_2:9765885-9766019 Satlength=135 Nr of Repeats=5 RepeatLength=11
seed=GTACTCCTAC

GTACTCCTACA

GTACTCCTACA

GTACTACTACAGTACCCCGACCATATCCCCCTACTAACCCCAAACCTATATCTCTTCAAAGACTAAAACACAATTTTT

CCTAAACTACA

GTAATCCTACC

GTACTCCTACA

Nr of selected repeats 4 Similarity 0.878788

Consensus:

GTAcTCCTACa

>Cele-UNSB01_2:9825153-9825520 Satlength=368 Nr of Repeats=4 RepeatLength=42

seed=CAGCCGACAG

CAGCCGACAGCCGAAAAATTGCGATTTTTTCGGCTGGTAGCAC

CAGCCGACAGCCGACTGATAGTGATAGGTCGGCTGGCGTTTTGAAAAAATAAACTGACTTTTTGGCATATTTTGAGAC

TGAGTGCAAGTTTTACAAGTGAAAAAGTACGGAAATTTGGTTTTTTGTTGAATAAAATGATGTAATATTTTGCTATAA

TTTGTTTTTGTACTAAAAGTATACTAAATAGCTCCGAACTTTGAAACAACCTCTAACCAAATCTCAGTCGGCTGGTG

GCGC

CAGCCGACAGCCGAAAAACTTGGAAATTTTTTCGGCTGGTAGCAC

CAGCCGACAGCCGACTGATAAAAAATTGCTCGGCTGTCGGTGT

Nr of selected repeats 3 Similarity 0.533769

Consensus:

CAGCCGACAGCCGAAAAAttggAaTtTTCGGCTGGTaGcac

>Cele-UNSB01_2:10367690-10367782 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTCGCAGA

TCCCCTTTTCGTTCTGC

Nr of selected repeats 5 Similarity 0.733333

Consensus:

TCCCCTTTtcGtagc

>Cele-UNSB01_2:10468271-10470517 Satlength=2247 Nr of Repeats=10

RepeatLength=225 seed=TTTTCGAAAT

TTTTCGAAATGTCTTTTCAGAACTTTGTTAGTAAATTTTAAGCTCTTTTCAGATTATATTAACAATATTCAGTAGGTACA

AGAAGCTTCAAGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTAATGAAAACCTAC

TATGTATAGGCAAAAATAGATGGATTTTACAACTTTGAAAATTCATAAACCTCTTCAAAGTAACTG

TTTTCGAAATGTCTTTTCAGAACTTTGTTAGTAAATTTTAAGCTCTTTTCAGATTATATTAACAATATTCAGTAGGTACA

AGAAGCTTCAAGTAGTTACAGAAATAGTATATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTTTATGAAAACCTA

CCATTTATAGGCAAAAAGATGGATTTTCCAATTTTGAATAATTCATAAATCTCTTCAATGTAACCTT

TTTTCGAAATGTCTTTTCAGAACTTTGTTAGTAAATTTTAAGCTCTTTTCAGATTATATTAACAATATTCAGTAGGTACA

AGAAGCTTCAAGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTAATGAAAACCTAC

TATGTATAGGCAAAAATAGATGGATTTTACAACTTTGAAAATTCATAAACCTCTTCAAAGTAACTG

TTTTCGAAATGTCTTTTCAGAACTTTGTTAGTAAATTTTAAGCTCTTTTCAGATTATATTAACAATATTCAGTAGGTACA

AGAAGCTTCAAGTAGTTACAGAAATAGTATATTTTCAGCCCTACCTTTTAGTGCGTATTTTTTTTATTTTATGAAAACCTA

CCATTTATAGGCAAAAAGATGGATTTTCCAATTTTGAATAATTCATAAATCTCTTCAATGTAACCTT

TTTTCGAAATGTCTTTTCAGAACTTTGTTAGTAAATTTTAAGCTCTTTTCAGATTATATTAACAATATTCAGTAGGTACA

AGAAGCTTCAAGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTAATGAAAACCTAC

TATGTATAGGCAAAAATAGATGGATTTTACAACTTTGAAAATTCATAAACCTCTTCAAAGTAACTG

TTTTCGAAATGTCTTTTCAGAACTTTGTTAGTAAATTTTAAGCTCTTTTCAGATTATATTAACAATATTCAGTAGGTACA

AGAAGCTTCAAGTAGTTACAGAAATAGTATATTTTCAGCCCTACCTTTTAGTGCGTATTTTTTTTATTTTATGAAAACCTA

CCATTTATAGGCAAAAAGATGGATTTTCCAATTTTGAATAATTCATAAATCTCTTCAATGTAACCTT

TTTTCGAAATGTCTTTTCAGAACTTTGTTAGTAAATTTTAAGCTCTTTTCAGATTATATTAACAATATTCAGTAGGTACA

AGAAGCTTCAAGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTAATGAAAACCTAC

TATGTATAGGCAAAAATAGATGGATTTTACAACTTTGAAAATTCATAAACCTCTTCAAAGTAACTG

TTTTCGAAATGTCTTTTCAGAACTTTGTTAGTAAATTTTAAGCTCTTTTCAGATTATATTAACAATATTCAGTAGGTACA

AGAAGCTTCAAGTAGTTACAGAAATAGTATATTTTCAGCCCTACCTTTTAGTGCGTATTTTTTTTATTTTATGAAAACCTA

CCATTTATAGGCAAAAAGATGGATTTTCCAATTTTGAATAATTCATAAATCTCTTCAATGTAACCTT

TTTTCGAAATGTCTTTCAGAACTTTGTAGTAAATTTTAAGCTCTTTCAGATTATATTAACAATATTCAGTAGGTACA
AGAAGCTTCAAGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTAATGAAAACCTAC
TATGTATAGGCAAAAATAGATGGATTTTACAACTTTGAAAATTCATAAACCTCTTCAAAGTAACTG
TTTTCGAAATGTCTTTCAGAACTTTGTAGTAAATTTTAAGCTCTTTCAGATTATATTAACAATATTCAGTAGGTACA
AGAAGCTTCAAGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTAATGAAAACCTAC
TATGTATAGGCAAAAATAGATGGATTTTACAACTTTGAAAATTCATAAACCTCTTCAAAGTAACTG

Nr of selected repeats 6 Similarity 1.000000

Consensus:

TTTTCGAAATGTCTTTCAGAACTTTGTAGTAAATTTTAAGCTCTTTCAGATTATATTAACAATATTCAGTAGGTACA
AGAAGCTTCAAGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTAATGAAAACCTAC
TATGTATAGGCAAAAATAGATGGATTTTACAACTTTGAAAATTCATAAACCTCTTCAAAGTAACTG

>Cele-UNSB01_2:10597740-10597833 Satlength=94 Nr of Repeats=5 RepeatLength=18

seed=TAAATAAGTG

TAAATAAGTGGCTATAAGT

TAAATAAGTGGCTATAAG

TAAATAAGTGGCTATAAT

TAAATAAGTGGCTATAAT

TAAATAAGTGGCTATATAAT

Nr of selected repeats 3 Similarity 0.950617

Consensus:

TAAATAAGTGGCTATAAT

>Cele-UNSB01_2:10844890-10845587 Satlength=698 Nr of Repeats=8 RepeatLength=35

seed=TTTCTGGCAA

TTTCTGGCAAATCGGCAGTTTGCCGAAAATTAAT

TTTCTGGCAAACCGGCAATTTGCCGAAAATTAATA

TTTCTGACAAACCGGCAAACCGGCACTTTGCCGAAAATTAAT

TTTCTGGCAAACCGGCAATTTGCCAAAAATTAATA

TTTCTGGCAAACCGGCAAACCGGCACTTTGCCGAAAATTAAT

TTTCTGGCAAACCGCAATTTGCCAAAAATTAACA

TTTCTGGCAAACCGGCAATTTGCCGAAAATTAATA

TTTCTGGCAAACCGGCCAATTTGCCAGAATTTGAAATTTTTCATAATTTTTCAGTATTATTCAAGTTTTTTTTTTGAGATT

TTCTTCGCTTCAACATACTTAACATCGATTTTATCCGTCGGTGCCTGTGACATGCTTCTCCAAAATGAACAAGAGCTG

TACAATCAGCGTGAGCAGCAGCGACTTCATCAACACAGCAGCTGGAAATTTCCATTATTTCTTTTTTTAATGAAAA

TCAAACCTTCTATAAGAAGTATCAGCTAGAACAATGTCTTCTTTGCACTTTCAGATCGAAATCTGCTTTTCGATGAGTT

TTGTGACTTTTTCCGAGTATGGAAGCAGAGAATCCGGGAATTGTAGAGCTATTTCGTTGATGATTTCCCTGTTTAATCCA

TTCAGATGTGGCGTCAATTTCAAAAAATGAATGAATATCGT

Nr of selected repeats 5 Similarity 0.900952

Consensus:

TTTCTGGCAAACCGgCAaTTTGCCgAAAATTAaAa

>Cele-UNSB01_2:10964073-10965096 Satlength=1024 Nr of Repeats=24

RepeatLength=11 seed=GTACTGTAGG

GTACTGTAGGA

GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTAGGAAAAATTGAGTTTTTGTATACAGAAGAGGTATTGGGTTGGGA

GTTGCTGGGGGATAATGTCAAG

GTACTGTAGTA

GTACTGTAGGA

GTACTTTAGGTATACGGTAGGGTTACTGTAGTTTAGGAAAAATTGAGTTTTTGTATACAGAAGAGGTATTGGGTTGGGA

GTTGCTGGGGGATAATGTCAAG

GTACTGTAGTA

GTACTGTAGGA

GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTAGGAAAAATTGAGTTTTTGTCTACAGAAGAGGTATTGGGTAGAGAG

TTGCTGGGGGATAATGTCAAG

GTACTGTAGTA

GTACTGTAGGA

AATTTTCAAAGTTTGGAAAAATCTATTAATTTTACATATAAAATTGTGGTCTACAAGGTATGACTGAAAATTCAC TTTTTTC
TGCTTGAAC TTTGGCGGTTTCAAAAATTTTTTGA AATTTCTGTTTTTA
AATTTTCAAAGAACATAAAAATTTGCTACAAAATGGCTCCGGAATTTCTAAAAAATTTAGTTTGAAGCCAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAATTTTATAAAATTTCTGAAAGAACATAAAAATTTGCTACATA
ATGGCTACGGAATTTCTAAAAAAGTTAGTTTGAAGCCAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAAATTGTGGTCTACAAGGTATGACTGAAAATTCAC TTTTTTC
TGCTTGAAC TTTGGCGGTTTCGAAATTTTTTGA AATTTCTGTTTTCAAATTTCTGAAAGAACATAAAAATTTGCTACAAAATG
GTTACGGGAATTTTTGAAAAAGTTAGTTTGAAGCCAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAAATTGTGGTCTACAAGGTATGACTGAAAATTCAC TTTTTTC
TGCTTGAAC TTTGGCGGTTTCAAAAATCTTTTGA AATTTCTGTTTTTA
AATTTTCAAAGAACATAAAAATTTGCTACAAAATGGCTACGGAATTTCTAAAAAATTTAGTTTGAAGACAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAATTTTATAAAATTTCTGAAAGAACATAAAAATTTGCTACAAA
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AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAATTTTATAAAATTTCTGAAAGAACATAAAAATTTGCTACAAA
ATGGCTACGGAATTTCTAAAAAATTTAGTTTGAAGACAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAATTTTATAAAATTTCTGAAAGAACATAAAAATTTGCTACAAA
ATGGCTACGGAATTTCTAAAAAATTTAGTTTGAAGACAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAATTTTATAAAATTTCTGAAAGAACATAAAAATTTGCTACAAA
ATGGCTACGGAATTTCTAAAAAATTTAGTTTGAAGACAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAATTTTATAAAATTTCTGAAAGAACATAAAAATTTGCTACAAA
ATGGCTACGGAATTTCTAAAAAAGTTAGTTTGAAGCCAGAAATG
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAAATTGTGGTCTACAAGGTATGACTGAAAATTCAC TTTTTTC
TGCTTGAAC TTTGGCGGTTTCAAAAATTTTTTGA AATTTCTGTTTTTA
AATTTTCAAAGAACATAAAAATTTGCTACAAAATGGCTACGGAATTTCTAAAAAAGTTAGTTTGAAGAGATTTATG
AATTTTCAAAGTTTGGAAAAATCCACCTATTTTGCCTATTAATGGTAGTTTTCATTAATAATAAAAATACGCACTAAAA
GGTAGGGCTGAAAATGTACTATTTCTGTAAC TACGTGAAGCTTCTGTACCTTCTGTAATATTGTTGTATATTCTAAAA
GAGCTCAGAATTTACTACAAAATTA AAAAAAAAAATTTCTTTCAAGATATTTATG

Nr of selected repeats 9 Similarity 0.708025

Consensus:

AATTTTCAAAGTTTGGAAAAATCTATTAATTTTGCATATAAATTTtTAtAAaTcTGAAaGAACATaAaaTTTgCTaCAAA
aTGGctaCgGGaaTTTCTaaAAAAATTTAgTTTGAAGnCaGaaaTT

>Cele-UNSB01_2:11366885-11367108 Satlength=224 Nr of Repeats=5 RepeatLength=44
seed=AAGGATCAGA

AAGGATCAGAACATCAGAAGGTACCCATGTGATCCTTCGGATCGG
AAGGATCAGATCATCAGGCAGAGCCTCATGCTCTTTTGGAGCTG
AAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCTA
AAGGATCAGACCATCAGGAGGTTCCCTTACGATCCTTCTTATCTGA
AAGATCAGAACATCAGAAGGTACCCATGTGATCCTTCGGAGCTG

Nr of selected repeats 3 Similarity 0.696296

Consensus:

AAgGATCAGAAcATCAGgaaGAgCCtcgTGaTCcTTtGGAGCTg

>Cele-UNSB01_2:11443617-11443668 Satlength=52 Nr of Repeats=4 RepeatLength=12
seed=ACTATAACTA

ACTATAACTACA
ACTATAACTACA
ACTATAACTACA
ACTATAACTATA

Nr of selected repeats 3 Similarity 0.851852

Consensus:

ACTAtAACTAcA

>Cele-UNSB01_2:11502184-11502280 Satlength=97 Nr of Repeats=5 RepeatLength=24
seed=GCTTAGGCTT

GCTTAGGCTTAG
GCTTAGGCTTAGGCTTGGGCTCAA

GCTTAGGTTTGGGCCTAGGCCTAG
GCTCAGGCTTGGGCTTATGCTAAA
GCTTAGGCATAC

Nr of selected repeats 3 Similarity 0.648148

Consensus:

GCTtAGGcTTgGGcTtagGcTnAa

>Cele-UNSB01_2:11560093-11560292 Satlength=200 Nr of Repeats=9 RepeatLength=20
seed=AAAAAATAGA

AAAAAATAGACTGGCATAACC
AAAAAATAGATTGGCATAACG
AAAAAATAGATTGGCATAACG
AAAAAATAGGTTGGCATAACG
AAAAAATAGATTGGCATAACG
AAAAAATAGATTGGCATAACG
AAAAAATAAGTTGACATAACC
AAAAAATAGATTGGCATAACG

AAAAAATAGATTGGCCTACGATAAAATAGATCGACATAACC

Nr of selected repeats 8 Similarity 0.892857

Consensus:

AAAAAATAGaTTGGCATAcG

>Cele-UNSB01_2:11664501-11665796 Satlength=1296 Nr of Repeats=29
RepeatLength=45 seed=TCTGATCCTT

TCTGATCCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT
TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG
TCTGATCCTTCAGCTCCAAAGGATCACGAGGCTCTTCCTGATGG
TCTGATCCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT
TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG
TCTGATCCTTCAGCTCCAAAGGATCACGAGGCTCTTCCTGATGT
TCTGATTCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT
TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG
TCTGATACTTCAGCTCCAAAGGATCACGAGGCTCTTCCTGATGT
TCTGATCCTTCAGCTCCAAAAGAACATGAGGCTCTGCCTGATGA
TCTGATCCTTCCGATCCGAAGGATCACATGGGTACCTTCTGATGA

Nr of selected repeats 19 Similarity 0.857050

Consensus:

TCTGATCCTTCAGaTccGAAGgATCacAtGGGTACCTtCTGATGn

>Cele-UNSB01_2:11667411-11669597 Satlength=2187 Nr of Repeats=49
RepeatLength=45 seed=GAAGGATCAG

GAAGGATCAGATCATCAGAAAGGTACCCATGTGATCCTTCGGATCG
GAAGGATCAGATCATCAGGCAGAGCCTCATGTTCTTTTGGAGCT
GAAGTATCAGACCATCAGGAGGTACCCATTACGATCCTTCTTATCT
GAAGGATCAGAACATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGATCATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGATCATCAGAAAGGTACCCATGTGATCCTTCGGATCG
GAAGGATCAGATCATCAGGCAGAGCCTCATGTTCTTTTGGCGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGTATCAGACCATCAGGAGGTACCCATTACGATCCTTCTTATCT
GAAGGATCAGAACATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGACCATCAGGAGGTACCCATTACGATCCTTCTTATCT
GAAGGATCAGAACATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGATCATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGATCATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGATCATCAGAAAGGTACCCATGTGATCCTTCGGATCG
GAAGGATCAGATCATCAGGCAGAGCCTCATGTTCTTTTGGCGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGTATCAGACCATCAGGAGGTACCCATTACGATCCTTCTTATCT
GAAGGATCAGAACATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
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GAAGGATCAGACCATCAGGAGGTACCCATTACGATCCTTCTTATCT
GAAGGATCAGAACATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGATCAGACCATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGACCATCAGGAGGTACCCATTACGATCCTTCTTATCT
GAAGGATCAGAACATCAGAAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGATCAGACCATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGACCATCAGGAGGTACCCATTACGATTCTTCTTATCT
GAAGGATCAGAACATCAGAAAGGTACCCATGTGATCCTTCGGAGCT

Nr of selected repeats 30 Similarity 0.857233
Consensus :

GAAGGATCAGAnCATCAGaAGGTACCCaTgtGATCCTTCggAgCT

>Cele-UNSB01_2:11673801-11673893 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=CGAAAAGGGG
CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAGATA
CGAAAAGGGGAGCAA

Nr of selected repeats 5 Similarity 0.768889

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_2:11674068-11674143 Satlength=76 Nr of Repeats=5 RepeatLength=15
seed=TCCCCTTTTC
TCCCCTTTTCGTTGC
TCCCCTTTTCGTATC
TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA
TCCCCTTTTTCGAGA

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTcGtagc

>Cele-UNSB01_2:11799205-11799469 Satlength=265 Nr of Repeats=8 RepeatLength=33
seed=AATTGAAAAT

AATTGAAAATCCAGCAAATGGGCAAATTGCCGT
AATTGAAAATCCGGCAAATGGGCAAATTGCCGT
AATTGAAAATCCGGCAAATGGACAAATTGCCGG
AATTGAAAATCCGGCAAATGGGAAAATTGCCGT
AATTGAAAATCCGGCTAATCCGCAGATTGTCGG
AATTGAAAATCCGGCAAATCAGCAAATGGCCGG
AATTGAGAATCCGGCAAATGGGCAAATTGCCGT
AATTGAAAATCCGGCTAATCCGCAGATTGTCGG

Nr of selected repeats 8 Similarity 0.834055

Consensus:

AATTGAAAATCCGGCaAATggGCAaATTGcCGg

>Cele-UNSB01_2:11872286-11872364 Satlength=79 Nr of Repeats=6 RepeatLength=12
seed=CTTAGGCTTA

CTTAGGCTTAGGGTCAGG
CTTAGGCTTAGG
CTTAGGCTTAGG
CTTAGACTTAGG
CTTAGACTTAGA
CTTAGGCTTGGG

Nr of selected repeats 5 Similarity 0.844444

Consensus:

CTTAGgCTTaGg

>Cele-UNSB01_2:12045935-12046042 Satlength=108 Nr of Repeats=8 RepeatLength=12
seed=AGGCTTAGGC

AGGCTTAGGCTT
AGGCTTAAGCTT
AGGTTTAGGCCT
AGGCTTAGGCAT
AGGCTCAGGCTT
AGACTTAGGCTC
AGGCTAGGCTC

AGGCTTAGGCTCAAGCTCAGGCTT

Nr of selected repeats 6 Similarity 0.748148

Consensus:

AGGCTTAGGCTT

>Cele-UNSB01_2:12047204-12047947 Satlength=744 Nr of Repeats=32 RepeatLength=20
seed=TAAATCTACA

TAAATCTACACGAGTTTCGTG

TAAATCTACACAGGGTGGTG

TAAATCTACAGGGCCTTGCG

TAAATCTACATATCGTGACGTAAGCCTACACTGATTCTTG

TAAATCTACACTGGTTTCGCG

TAAATCTACACTAGCTCGGCGCTCTCCTGCG

TAAATCTACAAAGCGTGACG

TAAATCTACACAGGCTGGTG

TAAATCTACAGGGCCTTGCG

TAAATCTACATATCGTGGCGTTAGCCTACACTGATTCTTG

TAAATCTACACTTGTTCGCG

TAAATCAACACAGGCCGGTG

TAAATCTACACTGACTTGCG

TAAATCTACACAGGGTGGTG

TAAATCTACAGGGCCTTGCG

TAAATCTACATATCGTGACGTAAGCCTACACTGATTCTTG

TAAATCTACACTGGTTTCGCG

TAAATCTACACTAGCTCGGCGCTCTCCTGCG

TAAATCTACAAAGCGTGACG

TAAATCTACACAGGCTGGTG

TAAATCTACAGGGCCTTGCG

TAAATCTACATATCGTGGCGTTAGCCTACACTGATTCTTG

TAAATCTACACTTGTTCGCG

TAAATCAACACAGGCCGGTG

TAAATCTACACTGACTTGCG

TAAATCTACACAGGGTGGTG

TAAATCTACAGGGCCTTGCG

TAAATCTACACTAGCTCGCG

TAAATCAACACCTTGTTCGCG

TAAATCTACACTGCCTTGTG

TAAATCGACATTTAGTTGCG

TAAATCTACACTAGCTAGCG

Nr of selected repeats 25 Similarity 0.700222

Consensus:

TAAATCTACAcnggcTnGcG

>Cele-UNSB01_2:12070558-12070690 Satlength=133 Nr of Repeats=10 RepeatLength=12
seed=AAGCCTAAGC

AAGCCTAAGCCT

AAGCCTAACCAT

AAGCCTAAGCCTA

AACCTAAGCCT

AAGCCTAAGCCT

AAGCTTAAGCCT

AAGCCTACGCCTTAGCTT

AAGCCTAAGCCC

AAGCCCAAGCCC

AAGCCTAAGCCTAAGCCT

Nr of selected repeats 6 Similarity 0.792593

Consensus :

AAGCCTAAGCCT

>Cele-UNSB01_2:12072605-12072779 Satlength=175 Nr of Repeats=10 RepeatLength=12

seed=AGGCTTAGGC

AGGCTTAGGCCAGGCTTTAGTTT

AGGCTTAGACTT

AGACTTAGGCTT

AGGCCTAGGCTT

AGGCATAGGCTT

AGGCTTAGGCTT

AGGCTAAGGCTTATGCTCA

AGCTTAGGCTAAGGAATATGCTTGAACCTTGGTTT

AGGTTTAGGCTT

ATGCTTAGGCTTAGTCTTAGGGTC

Nr of selected repeats 6 Similarity 0.822222

Consensus :

AGGCtTAGGCTT

>Cele-UNSB01_2:12142720-12142795 Satlength=76 Nr of Repeats=4 RepeatLength=15

seed=AAAACAAGAT

AAAACAAGATCTACG

AAAACAAGATCTACATTTTCAAGATCTACG

AAAAGAAGATCTACA

AAAACAAGATCCACC

Nr of selected repeats 3 Similarity 0.792593

Consensus :

AAAACaAGATCtACn

>Cele-UNSB01_2:12311843-12313532 Satlength=1690 Nr of Repeats=56

RepeatLength=30 seed=CAAACCTACAG

CAAACCTACAGTAGCACTGTAGTACCATAAC

CAAACCTACAGTAGTACTGTAGTACCATAACC

CAAACCTACAGTAGCACTGTAGTACCATAAC

CAAACCTACAGTAGTACTGTAGTACCATAAT

CAAACCTACAGTAGTACTTTTGTACCCTAAT

CAAACCTTCAGTAGTATTGTAGTACCATAAC

CAAACCTACAGTAGCACTGTAGTACCATAAC

CAAACCTACAGTAGTACTGTAGTATTATAACC

CAAACCTACAGTAGCACTGTAGTACCATAAC

CAAACCTACAGTAGTACTGTAGTACCATAAT

CAAACCTACAGTAGTACTTTTGTACCCTAAT

CAAACCTTCAGTAGTATTGTAGTACCATAAC

CAAACCTACAGTAGTACTGTAGTACCATAAT

CAAACCTACAGTAGTACTTTTGTACCCTAAT

CAAACCTTCAGTAGTATTGTAGTACCATAAC

CAAACCTACAGTAGCACTGTAGTACCATAAC

CAAACCTACAGTAGTACTGTAGTACCATAAT

CAAACCTACAGTAGTACTTTTGTACCCTAAT

CAAACCTTCAGTAGTATTGTAGTACCATAAC

CAAACCTATAGTAGTACTGTAGTACCATAAT

CAAACCTACAGTAGTACTTTTGTACCCTAAT

CAAACCTTCAGTAGTATTGTAGTACCATAAC

CAAACCTACAGTAGCACTGTAGTACCATAAC

CAAACCTACAGTAGTACTGTAGTACCATAAC

CAAACCTACAGTAGTACTGTAGTACCATAAT

CAAACCTACAGTAGTACTTTTGTACCCTAAT

CAAACCTTCAGTAGTACTGTAGTACCATAAC
CAAACCTACAGTAGCACTGTAGTACCATAAT
CAAACCTACAGTAGTACTTTTGTACCCTAAT
CAAACCTTCAGTAGTATTGTAGTACCATAAC
CAAACCTATAGTAGTACTGTAGTACCATAAT
CAAACCTACAGTAGTACTTTTGTACCCTAAT
CAAACCTTCAGTAGTATTGTAGTACCATAAC
CAAACCTACAGTAGCACTGTAGTACCATAAC
CAAACCTACAGTAGTACTGTAGTACCATAAC
CAAACCTACAGTAGTACTGTAGTACCATAAC
CAAACCTACAGTAGTACTGTAGTACCATAAT
CAAACCTACAGTAGTACTTTTGTACCCTAAT
CAAACCTTCAGTAGTACTGTAGTACCATAAC
CAAACCTACAGTAGCACTGTAGTACCATAAC
CAAACCTACAGTAGTACTGTAGTACCATAAC
CAAACCTACAGTAGTACTTTTGTACCCTAAT
CAAACCTTCAGTAGTATTGTAGTACCATAAC
CAAACCTACAGTAGCACTGTAGTACCATAAC
CAAACCTACAGTAGTACTGTAGTACCATAAC
CAAACCTACAGTAGTACTTTTGTACCCTAAT
CAAACCTTCAGTAGTATTGTAGTACCATAAC
CAAACCTACAGTAGCACTGTAGTACCATAAC
CAAACCTACAGTAGTACTGTAGTACCATAAC
CAAACCTACAGTAGTACTTTTGTACCCTAAT
CAAACCTTCAGTAGTATTGTAGTACCATAAC
CAAACCTACAGTAGCACTGTAGTACCATAAC
CAAACCTACAGTAGTACTGTAGTACCATAAT
CAAACCTACAGTAGTACTTTTGTACCATAAC

Nr of selected repeats 47 Similarity 0.880029

Consensus:

CAAACCTaCAGTAGtAcTGTAGTACCATAAc

>Cele-UNSB01_2:12381269-12381383 Satlength=115 Nr of Repeats=7 RepeatLength=12

seed=TTAGTCTTAG

TTAGTCTTAGTC

TTAGTCTTAGGC

TTAGGCTTAGCC

TTAGCCTTAGTTTTAGGCCCGGGTTCAGGC

TTAGCCTTAGGCTTAGGCTTTGGC

TTAGTCTTAGGC

TTAGTCTTAGGA

Nr of selected repeats 5 Similarity 0.833333

Consensus:

TTAGtCTTAGgc

>Cele-UNSB01_2:12388949-12389045 Satlength=97 Nr of Repeats=7 RepeatLength=12

seed=CCTAAGCCTA

CCTAAGCCTAAG

CCTAACCCTAAG

CCTAAGCCTACA

CCTAAGACTACA

CCTAAGCCTAAG

CCTAAGCCTATGCCCAAGTCTAAGA

CTAAGCCTAAG

Nr of selected repeats 5 Similarity 0.741026

Consensus:

CCTAAGcCTAAg

>Cele-UNSB01_2:12463695-12463773 Satlength=79 Nr of Repeats=5 RepeatLength=12

seed=TTAGGCTTAG

TTAGGCTTAGGT

TTAGGCTCAGGC

TTAGGCTTAGGC

TTAGGCGTAGAC

TTAGACTTAGGCTTAGGTGTAGACTTAGAC

Nr of selected repeats 4 Similarity 0.777778

Consensus:

TTAGGcTtAGgc

>Cele-UNSB01_2:12477614-12477893 Satlength=280 Nr of Repeats=4 RepeatLength=69

seed=AGGTAGGCCT

AGGTAGGCCTGTAGGCATTGACTGGCAGAAAAGTGTAGGCAGGCAGGCAGGTAAAAAGATACATGCGGC

AGGTAGGCCTGTAAGCACTGACATGCGCAAAAGCGTAGACAGGTAAACAGGTAAAAAGATAGTTGAGAC

AGGTAGGCCTGTAGGCATTGACTGTCAGAAAAGCGTAGACAGGCAAGCTGATAAAAAAGATACATGAGGC

AGGTAGGCCTGTAGGCATAGACTAGTCACAAAAATGTAGGCAAGCGGGTGAAAAGGTACCTGGACATGCGGA

Nr of selected repeats 3 Similarity 0.747619

Consensus:

AGGTAGGCCTGTAGcGCAtTGACTGnCagAAAAGcGTAGaCAGGcAagCaGgTAAAAaGATAcaTGaGgC

>Cele-UNSB01_2:12492091-12492147 Satlength=57 Nr of Repeats=5 RepeatLength=11

seed=CTACAGTACC

CTACAGTACCT

CTACAGTACCC

CTACAGTACCT

CTACAGTACCC

CTACAGTACCCC

Nr of selected repeats 4 Similarity 0.919192

Consensus:

CTACAGTACCc

>Cele-UNSB01_2:12494810-12494978 Satlength=169 Nr of Repeats=14 RepeatLength=12

seed=CCTATACCTA

CCTATACCTATG

CCTATACCTATA

CCTATACCTACA

CCTATACCTATA

CCTATACCTATA

CCTATACCTATA

Nr of selected repeats 14 Similarity 0.968254

Consensus:

CCTATACCTATA

>Cele-UNSB01_2:12522288-12522472 Satlength=185 Nr of Repeats=13 RepeatLength=12

seed=AGCCTAAGCC

AGCCTAAGCCTA

AGCCTAAGCCTA
AGCCTAAGGCTAACCCAA
AGCCTAAGCCTAAGCCT
AGCTCTAAGCCTT
AGCCTAAGCCTA
AGCCAAAGCCTA
AGCCAAAGCCTA
AGCCAAAGCCTA
AGCCTAAGTCTA
AGCCTAGCCT
AGCCTAAGCCTAAGAGTAAGCCTAACTCTA
AGCCTTAGCCTA
Nr of selected repeats 8 Similarity 0.884921
Consensus:
AGCCTAAGCCTA

>Cele-UNSB01_2:12544046-12545336 Satlength=1291 Nr of Repeats=30
RepeatLength=43 seed=TTTCCGGCAA

TTTCCGGCAAACCGGCAAACCGGTGATTTGCCGAAAATGCGAA
TTTCCGGCAAATCGGCAAACCGGCATATTGCCAAAAATAAAAA
TTTCCGGCAAATCGGCAAACCGGCAATTTGCCGAAAACAAAA
TTTCCGGCAAATCGGCAAACCGGCGATTTGCCGAAAATGAAAG
TTTCCGGCAAATCGGCAAACCGATGATTTGCCGAAAATGAAAA
TTTCCGGCAAATCGGCAAACCGGCAATTTGTGCGAAAATGAAAA
TTTCCGGCAAATCGGCAAACCGGCATTTTACCAAAAAATAAAAA
TTTCCGGCAAATCGGCAAACCGGCATATTGCCAAAAATAAAAA
TTTCCGGCAAATCGGCAAACCGGTGATTTGCCGAAAATGAAAG
TTTCCGGCAAATCGGCAAACCGTCAATTTGTGCGAAAATGAAAA
TTTCCGGCAAATCGGCAAACCGGCATTTTACCAAAAAATAAAAA
TTTCCGGCAAATCCGCAAACCGGCATTTTGCCGAAAATGAAAG
TTTCCGGCAAATCGGCAAACCGGTGATTTGCCGAAAATGAAAA
TTTCCGGCAAATCGGCAAACCGTCAATTTGTGCGAAAATGAAAA
TTTCCGGCAAATCGGCAAACCGGCGATTTGCCGAAAATGAAAG
TTTCCGGCAAATCGGCAAACCGATGATTTGCCGAAAATGAAAA
TTTCCGGCAAATCGGCAAACCGGCAATTTGTGCGAAAATGAAAA
TTTCCGGCAAATCGGCAAACCGGCATTTTACCAAAAAATAAAAA
TTTCCGGCAAATCGGCAAACCGGCATATTGCCAAAAATAAAAA
TTTCCGGCAAATCGGCAAACCGGTGATTTGCCGAAAATGAAAG
TTTCCGGCAAATCGGCAAACCGTCAATTTGTGCGAAAATGAAAA
TTTCCGGCAAATCCGCAAACCGGCATATTGCCAAAAATAAAAA
TTTCCGGCAAATCGGCAAACCGGCATTTTGCCGAAAATGAAAG
TTTCCGGCAAATCGGCAAACCGGTGATTTGCCGAAAATGAACA
TTTCCGGCAAATCGGCAAACCGGCATTTTGCCGAAAATGAAAG
TTTCCGGCAAATCGGCAAACCGGTGATTTGCCGAAAATGAACA
TTTCCGGCAAATCGGCAAACCGGCGATTTGCCGAAAATGAAAA

Nr of selected repeats 30 Similarity 0.867914
Consensus:

TTTCCGGCAAATCGGCAAACCGGcaaTTTGCCgAAAATgAAAA

>Cele-UNSB01_2:12597085-12597273 Satlength=189 Nr of Repeats=6 RepeatLength=31
seed=GACATCTCGC

GACATCTCGCAGGATCCTTACTGTTAGCGGCA
GACATCTCGCAGGACAATATAAAAAGCGACC

GACACCTCGCAGGACATTATAGGAAACGCC
GACATCTCGCAGGGCCTTACAATTAGCGACC
GACATCTCACAGGATCCCTATTGGTAGCGGCC
GACATGTGCGAAAACTTGAAAAGGTAGAGTTC

Nr of selected repeats 4 Similarity 0.584229

Consensus:

GACAtcTCGCaggaCattAtAagaAgcGacC

>Cele-UNSB01_2:12608492-12608559 Satlength=68 Nr of Repeats=5 RepeatLength=12

seed=GGCTTAGGCT

GGCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGGATTA

GGCTTAGGCTTA

GGCTTAGGCTCAGGCTTAG

Nr of selected repeats 4 Similarity 0.944444

Consensus:

GGCTTAGGcTTA

>Cele-UNSB01_2:12716681-12716766 Satlength=86 Nr of Repeats=5 RepeatLength=17

seed=ACTTGGTACA

ACTTGGTACATAGGCCA

ACTTGGTACATAGACCA

ACTTGGTACATAGGCCA

ACTTGGTACATAGACCA

ACTTGATACATAGGCCT

Nr of selected repeats 5 Similarity 0.890196

Consensus:

ACTTGgtACATAGgCCa

>Cele-UNSB01_2:12718309-12718687 Satlength=379 Nr of Repeats=8 RepeatLength=42

seed=TTGCCGAACC

TTGCCGAACCGTAAAAATTTTCGGCAAACGGGAATTGCCAAAG

TTGCCGAACCGTAAAAATTTTCGGCAACCTGGAACTGCCAAAG

TTGCCGAACCGTAAAAATTTTCGGCAACCGGAATTTGCCGAAA

TTGCCGAATCCAAAAATTTTCGGCAACCTGGAACTGCCAAAG

TTGCCGAACCGTAAAAATTTTCGGCAAACGGGAATTGCCAAAG

TTGCCGAACCCAAAAATTTTCGGCAACCGGAATTTGCCGAAA

TTGCCGAATCCAAAAATTTTCGGCAAACGGGAATTGCCAAAG

TTGCCGAACCCAAAAATTTTCGGCAACCGGCAACTGCCAAAGTTGCCGACTGTAAAAATTTTCGGCAACCGAAAATTGT
CGAAA

Nr of selected repeats 7 Similarity 0.797619

Consensus:

TTGCCGAAcCgtAAAAATTTTCGGCAAcCnGGAATTGCCAAAg

>Cele-UNSB01_2:12791702-12792113 Satlength=412 Nr of Repeats=11 RepeatLength=37

seed=ATTTTGGCGG

ATTTTGGCGGGAATTCAAATTTTAATTTTTTTTAAAAAT

ATTTTGGCGGGAATTAAAAATTTCAATTTTTTTGAAAAT

ATTTTGGCGGGAATTCAAATTTTAATTTTTTTGAAAAT

ATTTTGGCGGGAATTCAAATTTTAATTTTTTTGAAAAT

ATTTTGGCGGGAATTCAAATTTTAATTTTTTTGAAAAT

ATTTTGGCGGGAATTAAAAATTTTAATTTTTTTGAAAAT

ATTTTGGCGGGAATTCAAATTTTAATTTTTTTGAAAAT

ATTTTGGCGGGAATTAAAAATTTTAATTTTTTTGAAAAT

ATTTTGGCGGGAATTCAAATTTTAATTTTTTTGAAAAT

ATTTTGGCGGGAATTAAAAATTTTAATTTTTTTGAAAAT

ATTTTGGCGGGAATTCAAATTTTAATTTTTTTGAACAT

Nr of selected repeats 7 Similarity 0.951952

Consensus:

ATTTTGGCGGgAATTCAAATTTTAATTTTTTGAAAAT

>Cele-UNSB01_2:12792220-12794215 Satlength=1996 Nr of Repeats=131

RepeatLength=15 seed=TCGTGGTGAG

TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGAGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGGGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGAGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
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TCGTGGTGAGACCCA
TCGTGGTGAGACTCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
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TCGTGGTGAGACCCA
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TCGTGGTGAGACCCA
TCGTGATGAGACCCTTAGTGGTTAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCTTTCATGGAGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTTAGACCCA
TCGTGGTGAGACCTT
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TCGTGGTTAGACCCA
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TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCCT
TCGTGGTGAGACCAT
TCGTGGTCAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACTTT
TCGTGGTGAGACCAA
TCGTGGTGAGACCTT

Nr of selected repeats 129 Similarity 0.876421

Consensus:

TCGTGGTGAGACCca

>Cele-UNSB01_2:12843731-12843956 Satlength=226 Nr of Repeats=7 RepeatLength=11
seed=CTACAGTACC

CTACAGTACCCCGGCATATCCCCACTAACCCCAATCCAATACCTCTTTAAAAGACGAAAAGTCTTTTTTTTCCAAA
CTACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTG
CTACAGTACCCAGTCATAACCCCCCTACTAACCTCAAAGCAATATCACTTCAAAAAGACGAAAAGCCGATTTTTTCCAAA
A

CTACAGTACCT

CTACAGTACTA

Nr of selected repeats 5 Similarity 0.775000

Consensus:

CTACAGTACTn

>Cele-UNSB01_2:12862834-12863019 Satlength=186 Nr of Repeats=5 RepeatLength=43
seed=TATTTTCATT

TATTTTCATTTTCGGCAATTTGCCGTTTGCCGATTTGCCGGG
TATTTTCATTTTTTGGCAATTTGCCGGA
TATTTTCATTTTCGGCAATTTGCCGTTTGCCGATTTGCCGGG
TATTTTCATTTTTTGGCAATTTGCCGGA
TATTTTCATTTTCGGCAATTTGCCGTTTGCCGATTTGCCGGG

Nr of selected repeats 3 Similarity 0.979328

Consensus:

TATTTTCATTTTCGGCAAaTTGCCGGTTTGCCGATTTGCCGGG
>Cele-UNSB01_2:12892893-12893074 Satlength=182 Nr of Repeats=4 RepeatLength=45
seed=ATCTGATCCT

ATCTGATCCTTCAGCTCCGAAGGATCACAGGGGTACCTCCTGATG
ATCTGATCCTTCAGCTCCGAAGGATCAGAAGGGTACCTCCTGGTG
ATCTGATCCTTAAGCTCCGAAGGATCATAAGGGTACCTCCTGGTG
ATCTGATCCTTCAGCTCCGAAGGATCACAAGGGTACCTCCTGGTG
Nr of selected repeats 3 Similarity 0.950617

Consensus:

ATCTGATCCTTcAGCTCCGAAGGATCAnAAGGGTACCTCCTGGTG

>Cele-UNSB01_2:12900948-12901228 Satlength=281 Nr of Repeats=8 RepeatLength=35
seed=ATTTcAGGCA

ATTTcAGGCAATTTGCTGATTTGCCGAAATTACA
ATTTcAGGCAATTTACCGATTTGCCAGAAATGTTc
ATTTCCGGCAATTTGTGCGATTTGCCGAAATTTTc
ATTTcAGGCAATTTACCGATTTGCCAGAAATGTTc
ATTTCCGGCAATTTGTGCGATTTGCCAGAAATTTTc
ATTTcAGGCAACTTGCCAATTTGCTGGAAATTTTc
ATTTcAGACAATTTACCGATTTGGCAGAAATGTTc
ATTTCCGGCAATTCGCCGATTTGCCAGAAATTTTc

Nr of selected repeats 8 Similarity 0.791832

Consensus:

ATTTcAgGCAATTTGcCGATTTGCCaGAAATtTTC

>Cele-UNSB01_2:12905171-12905894 Satlength=724 Nr of Repeats=9 RepeatLength=14
seed=AACTACAAAC

AACTACAAACTACA
AACTATAAACTACA
AACTATAAACTACA
AACTACAAACTACA
AACTACAAACTATA
AACTACAAACTACC
AACTACAAACAGCA

AACTACAAACTACAATCTACAAAACTCTACCACACGGTCAAATTTTTTAAAGCTTTTTTTTTGTTAGTAAAATAAAGGA
CAGTCATTAGATGGCTGAAAAAAATTTGGGCAAAAATAAATATTTGCCTAAATTTATTGAAAACGGGTAATTCCTTGCGGA
TATATGCTTAATTCAGAAAACTAGGTTTATCTTATCAAACCTATTGAAAAGTGGCAAAATTTGGGCAATTTTGGCAAA
AATTCACAATTTTGAACCTCTCTAACATGGTTAATTTTGTAGTTAGAGGACTCAAAATTGATCTCAGAACCCTAAAA
TTGTCCTTTTTTcAGTTATCAGTAGTTTTTGTAAATTCGTTTTTAAAAAAATTTTTTGCCAAAAAAGGACAGTCAAAC
GAACAAAAAGGACAGGCTGAAAAAAATTTGGGCAAAAATAAATATTTGCCTAATTGTGTTGAAAACGGGAAATTCATATA
TGCCGAATTCAGAAAACTAGGTTTAACCCATCAAAAATTTTTAAAAAGTGGCAAAACTGAACAATTTATGGTAAAAAA
TCACAACCTCTCAAAGTTTTCGTTGCTGACTGTAGTGTAGATTAAACTATAACA

AACTACAAACTACAAACAACA

Nr of selected repeats 7 Similarity 0.845805

Consensus:

AACTAcAAACTACA

>Cele-UNSB01_2:12906532-12906652 Satlength=121 Nr of Repeats=7 RepeatLength=15
seed=ATTTCCGGAT

ATTTCCGGATCTACG
ATTTCCGGATCTATG
ATTTCCGGATCTACA
ATTTCCGGATCTATG
ATTTCCGGATCTACG
ATTTCCGGATCTACG

ATTTCCGGATCTATGATTTCCGAGTCTACG

Nr of selected repeats 6 Similarity 0.922963

Consensus :

ATTTCCGGATCTAcG

>Cele-UNSB01_2:12914019-12914481 Satlength=463 Nr of Repeats=11 RepeatLength=35
seed=TCAATTCCGG

TCAATTCCGGCAATTTTTGGATTTGCCGGAAATTT

TCAATTCCGGCAATTTTTCCGGTTTGCCGGAAAATT

TCAATTCCGGAAATTTGCCGATTTGCCGGAAATTT

TCAATTGCCGGCAATTTGCCGATTTGCCGGAAATTT

TCAATTCCGGCAATTTTTCCGGTTTGCCGGAAATTT

TCAATTCCGGAAATTTGCCGATTTGCCGGAAAATT

TCAATTCCGGAAATTTGCCGATTTGCCGCAAATTT

TCAATTCCGGCAATTTGCCGATTTGCCGGAAATTT

TCAATTCCGGCAATTTTTCCGATTTGCCGAAAGTTT

TCAATTCCGGCAATTTTTCCGATTCGCCGGAAATTTTTCTTTTTCCGGCAAATTGCCGATTTGCCGAAAATTTCAAATCCGA

CAATTCGCCGGTTTGCCGATTTTTCTGGAAAGTC

TCAATTCCGGCAATTTGTTGATTTGCCGGAAATTT

Nr of selected repeats 10 Similarity 0.869630

Consensus :

TCAATTCCGGcAATTTgccGaTTTGCCGgAAAtTT

>Cele-UNSB01_2:12938825-12939101 Satlength=277 Nr of Repeats=8 RepeatLength=35
seed=TGTGTAATAA

TGTGTAATAATAAAAATATCACTTTTTTTTTCAGGAT

TGTGTAATAATAAAAATTTACATTTTTTTTCACGAA

TGTGTAATAAGAAAAGTTTCGATTTTTTTTCACGAG

TATGTAATAAGAAAATTTACATTTTTTTTCACGAG

TGTGTAATAAGAAAATTTCAAATTTTTTTTCACGAG

TGTGTAATAAGAAAATTTCAAATTTTTTTTAAACGAA

TGTGTAATAAGAAAATTTCAAATTTTTTTTCAAAA

TATGTAATAAGAAAATTTCAAATTTTTTTTCACGTA

Nr of selected repeats 5 Similarity 0.794286

Consensus :

TgTGTAAAgAAAAAtTCaaaTtTTTTtcAcgaa

>Cele-UNSB01_2:12968710-12969129 Satlength=420 Nr of Repeats=28 RepeatLength=12
seed=GGCTTAGGCT

GGCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGGCTTG

GGCTTAGGCTTGGGTTTA

GGCTTAGGCTGA

GGCTTTGGCTTAGACTCA

GGCTTAGGCTAA

GGCTTAGGCTTATATTTATGTTTA

GGCTTAGGCTTAGACTCA

GGCTTAGGCTT

GGCTTAGGCTTA

GGCTGAGGCTTG

GGCTTAGACTCA

GGCTTGGGCTTA

GGCTGAGGCTGA

GACTTAGGCTTA

GGCTTGGGCTTAAGCTTG

GGCTTAGGCTTA

GGCTGAGGCTTG

GGCTTAGACTCA

GGCTAAGGCTTAGGATTAGGCGTC

GGCTTAGGCTTAA

GCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGGCTTA

GGCTTAGACTAAAGTTTAGGCATAAGTTTA

GGCTTAGGCTTA

GACTTAGGCTTATGCCTAGGCTTCTGCTTA

Nr of selected repeats 17 Similarity 0.799020

Consensus:

GGCTTAGGCTtA

>Cele-UNSB01_2:12988123-12990065 Satlength=1943 Nr of Repeats=72

RepeatLength=27 seed=GTGGGAAGCC

GTGGGAAGCCACAGAGAGTAAAAATATA

GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCACAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCACAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATG
GTGGGAAGCCAGAGAGTAAAAATATG
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCACAGAGAGTAAAAATATA
GTGGGAAGCCACAGAGAGTAAAAATATA
GTGGGAAGCCACAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCACAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA
GTGGGAAGCCACAGAGAGTAAAAATATA
GTGGGAAGCCACAGAGAGTAAAAATATA
GTGGGAAGCCATAGAGAGTAAAAATATA

Nr of selected repeats 71 Similarity 0.975358

Consensus:

GTGGGAAGCCAtAGAGAGTAAAAATATA

>Cele-UNSB01_2:12990090-13000798 Satlength=10709 Nr of Repeats=416

RepeatLength=25 seed=TGGCTTCCCA

TGGCTTCCC ACTATATTTTACTCTCTG
TGGCTTCCC ACTATATTTTACTCTCTG
TGGCTTCCC ACTATATTTTACTCTC
TGGCTTCCC ACTATATTTTACTCTC
TGGCTTCCC ACTATATTTTACTCTC
TGGCTTCCC ACTATATTTTACTCTC
TGGCTTCCC ACCATATTTTACTCTC
TGGCTTCCC ACCATATTTTACTCTC
TGGCTTCCC ACTATATTTTACTCTC
TGGCTTCCC ACCATATTTTACTCTC
TGGCTTCCC ACTATACTCTC
TGGCTTCCC ACCATATTTTACTCTC

TGGCTTCCCCTATATTTTTACTCTCTG
TGGCTTCCCCTATATTTTTACTCTCTG
TGGCTTCCCCTATATTTTTACTCTCTG
TGGCTTCCCCTATATTTTTACTCTCTG
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TGGCTTCCCCTATATTTTTACTCTC
TGGCTTCCCCTATATTTTTACTCTCTG
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TGGCTTCCCCTATATTTTTACTCTC
TGGCTTCCCCTATATTTTTACTCTC
TGGCTTCCCCTATATTTTTACTCTC
TGGCTTCCCCTATATTTTTACTCTC

TGGCTTCCCCTATATTTTACTCTC
TGGCTTCCCCTATATTTTACTCTC

Nr of selected repeats 292 Similarity 0.913730

Consensus:

TGGCTTCCCCTATATTTTACTCTC

>Cele-UNSB01_2:13043920-13044316 Satlength=397 Nr of Repeats=21 RepeatLength=18
seed=ACTACTGTAT

ACTACTGTATCTCAGGGG
ACTACTGTATCACAGGAGA
ATACTGTATCGCAGGAG
ACTACTGTATCGCAAGAT
ACTACTGTATCTCAGGAG
ACTACTGTATCACAGGAT
ACAACTGTATCACAGGAT
ACTACTGTATCACAGGAG
AGTACTGTATCGCAGGAG
ACTACTGTATCGCAAGAT
ACTACTGTATCGCAGGAG
ACTTCTGTATCGCACGAG
ACTAATGTATCACCGGAC
ACAACTGTATCACAGGAA
AGTACTGTATCGCAGGAT
ACTACGGTATCGCAGGAG
ACTACTCTATCGCAGGAG
ACTACTGTATCACAGGAG
ACTACTGTATCACAGGAT
ACTACTGTATCACAGGAGACTACGGCATCACAGGAT
ACAACTGTATCACAGGAT

Nr of selected repeats 18 Similarity 0.797628

Consensus:

ACTACTGTATCnCAGGAg

>Cele-UNSB01_2:13060029-13060418 Satlength=390 Nr of Repeats=5 RepeatLength=43
seed=GATTTGCCGG

GATTTGCCGGAAATTTTCAATCCCGCAAATTGCAGGTTTCGCC
GATTTGCCGGAAATTTTCAATCCCGCAAATTGCAGGTTTCGCC
GATTTGCCGGAAATTTTCAATCCCGCAAATTGTCGACTTTCGCC

GTTTGCCGGCTATCA
GATTTGCCGGAAATATTTAGAGGGATTTTGTATAAGACGAATGCACTTAAAACTGTGCAATTTTTCTCGTTTTTTCTAC
ATATTTTCATAGAATATGCTTAATTTTCAAAATAGATTTAGGAACATTCAAAGGATGCGTTTAATTTTGCCATTTGAAA
TTGAAATTCTGAACTTCCAAAACAAATAAGTACAAAACCACAATTTGCCGAAAAATTTAGGCAAATCGGAAATTTGCC
GATTCGCC

Nr of selected repeats 3 Similarity 0.875969

Consensus:

GATTTGCCGGAAATTTTCAATcCCGGCAAATTGcaGgtTtGCC

>Cele-UNSB01_2:13097657-13097799 Satlength=143 Nr of Repeats=5 RepeatLength=18

seed=CCTAAGCCTA

CCTAAGCCTAAG

CCTAATCCTAAGCCTAAATAGCGTCAGTAGCAAGCTCACGCTCGCCACTGACGCCAAGCATAAGTCTAGGTTTAGG

CCTGAGCCTAAGCTCAAC

CCTAAGCCTAAGACTAAA

CATAAGCCTAAGCCTAAG

Nr of selected repeats 3 Similarity 0.660819

Consensus:

CcTaAGCCTAAGnCTaAa

>Cele-UNSB01_2:13106081-13106253 Satlength=173 Nr of Repeats=4 RepeatLength=43

seed=CGGCAAATTA

CGGCAAATTACCGATTTGCCGTTTGGCCGAAATTTTCATTTT

CGGCAAATTACCAATTTGCCGATTTGCCGAAATTTTCATTTT

CGGCAAATTATAAGTTTGGCGTTTGGCCGAAATTTTCAGTTC

CGGCAATTTACCGATTTGCCGATATGTCGGAAATTTTCAATTC

Nr of selected repeats 4 Similarity 0.803618

Consensus:

CGGCAaATTAcCaTTTGGCGaTtTGcCGgAAATTTTCatTTc

>Cele-UNSB01_2:13133064-13133208 Satlength=145 Nr of Repeats=9 RepeatLength=16

seed=GCCTACATGC

GCCTACATGCCTGCAT

GCCTACATGCCTACAT

GCCTACATGCCTACAAG

GCTACATGCCTTCAT

GCCTACATGCATACAT

GCCTAAATGCCTACAT

GCCTACATGCCTACAT

GCCTATATGCCTGCAT

GCCTGCATGCCTGCAT

Nr of selected repeats 7 Similarity 0.861111

Consensus:

GCCTAcATGCCTaCAT

>Cele-UNSB01_2:13134300-13134450 Satlength=151 Nr of Repeats=4 RepeatLength=30

seed=TTCAGGCAGG

TTCAGGCAGGCATATGTCACATCGAATGTA

TTCAGGCAGGTATAGGTTTCTTTGAAAATT

TTCAGGCAGGCATAGGTTGACTTTGAGGTGTTAGTTAGGCAAAGAACACCTCAAAGGTA

TTCAGGCAGGCATTGATTACTTTGAAAAAT

Nr of selected repeats 3 Similarity 0.644444

Consensus:

TTCAGGCAGGcATaggTtaCtTtGAAaatt

>Cele-UNSB01_2:13161799-13161943 Satlength=145 Nr of Repeats=6 RepeatLength=19

seed=TATGGTGCAT

TATGGTGCATCTGACAAGT

TATGGTACATTTGACCAGTTACGGTGAATCTAACCAGT

TATGGTGCATTTAACTAGT
TATGGTACATTTGACCAGT
TACGGTGCATCTAACTTGA
TATGGTGCATCGACGGTGAATCTAGCCAGT
Nr of selected repeats 4 Similarity 0.707602
Consensus:
TAtGGTgCATcTaACTaGt
>Cele-UNSB01_2:13192718-13192854 Satlength=137 Nr of Repeats=4 RepeatLength=34
seed=TTCAATTCCG
TTCAATTCCGGCAATTTCCCGATTTGCCGAAAT
TTCAATTCCGGTAACCTCGTCGATTTTTCGGAAAT
TTCAATTCCGGCTTTTCGTTCGATTTGCCGACAT
TTCAATTCCGGCAATTCGTTCGATTTGCCGAAAT
Nr of selected repeats 4 Similarity 0.803922
Consensus:
TTCAATTCCGGcaatTcgtTCGATTTgcCGGAaAT
>Cele-UNSB01_2:13216705-13216849 Satlength=145 Nr of Repeats=8 RepeatLength=16
seed=TAGGCACGTA
TAGGCACGTAGACATGTAGCTACG
TAGGTACGTAGGCACA
TAGGCACGTAGGCACG
TAGGCACGTAGGCACG
TAGGCACGTAGGCACG
TAGGCACATAGGCACG
TAGGCACGTAGGCACG
TAGGCACGTAGGCACG
TAGGCACGTAGGCACG
Nr of selected repeats 6 Similarity 0.916667
Consensus:
TAGGCACGTAGGCACG
>Cele-UNSB01_2:13339084-13339231 Satlength=148 Nr of Repeats=7 RepeatLength=21
seed=AATCTAGCCA
AATCTAGCCAGACGCACCCCT
AATCTAGCCAGACGCACACCT
AATCTAGCCAGCCGCACACCT
AATCTAGCCAGACGCACACCT
AATCTAGCCAGACGCACACCT
AATCTAGCCAGACGCACACCA
AATCTAGCCAGACGCACACCC
Nr of selected repeats 7 Similarity 0.930461
Consensus:
AATCTAGCCAGACGCACACct
>Cele-UNSB01_2:13398823-13400207 Satlength=1385 Nr of Repeats=8
RepeatLength=165 seed=AAAATTC AAT
AAAATTC AATACCAATGATTA AAAACAAGATTGAAGTATAAAAACTGTGGGAAATTTTTTTTGGTTCGACTTCCAAAATTA
TTCCTCAGCTCCAGCCAAAATTTGAAAAGTATTATTATACATAATTTTCGGTCATTTTGGCAAGATAGGAATACTTTTT
AACATTTTTCCCACTGGCGCTGCTCAACCTTTGAGAATATTCAAACATCTAATAAAAAATCCCAAACTTA
AAAATTCGATTTTGGACTTATCTATTCTCTCTTTTTTTATAACATGTATTTTCAGTTGATAGAGGACTCAA AATTATAATG
CTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAATCAATTCTAAAAAACAGATTTTTTTTGGAAAGTTTAAGTAATATC
CGCGGAG
AAAATTC AATTTTGGGCATTTCTATTATCTTTTTTTTTTAAACATGTATTTTCAGTGAATAGAAGACTCAA AATTATAATG
CTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAATCAATTCTAAAAAACAGATTTTTTTTGGAAAGTTTAAGTAATTTTC
TGCGGAA

AAAATTCAATTTTGGACATTTCTATTATCTTTTTTTGAAAACATGTATTTTCAGTGAATAGAAGACTCAAATTATAATG
CTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAATCAATTCTAAAAAACAGATTTTTTTTGGAAAGTTTAAGTAATATC
CGCGGAG

AAAATTCAATTTTGGGCATTTCTATTATCTTTTTTTTTAAACATGTATTTTCAGTGAATAGAAGACTCAAATTATAATG
CTCGTAATTATTTATAAGTGTGTGTTGTCTGAGAATCAATTCTAAAAAACAGATTTTTTTTCGAAAGTTTAAGTAATTTCT
TGCGGAA

AAAATTCAATTTTGGACATTTCTATTATCTTTTTTTGAAAACATGTATTTTCAGTGAATAGAAGACTCAAATTATAATG
CTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAATCAATTCTAAAAAACAGATTTTTTTTGGAAAGTTTAAGTAATATC
CGCGGAG

AAAATTCAATTTTGGGCATTTCTATTATCTTTTTTTTTAAACATGTATTTTCAGTGAATAGAAGACTCAAATTATAATG
CTCGTAATTATTTATAAGTGTGTGTTGTCTGAGAATCAATTCTAAAAAACAGATTTTTTTTCGAAAGTTTAAGTAATTTCT
TGCGGAA

AAAATTCAATTTTGGACATTTCTATTATCTTTTTTTGAAAACATGTATTTTCAGTGAATAGAAGACTCAAATTATAATG
CTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAATCAATTCTAAAAAACAGATTTTTTTTGGAAAGTTTAAGTAATATC
CGCGGAG

Nr of selected repeats 7 Similarity 0.943050

Consensus:

AAAATTCAATTTTGGaCATTCTATTATCTTTTTTTtAAACATGTATTTTCAGTGAATAGAAGACTCAAATTATAATG
CTCGTAATTATTTATAAGTGTGTGTTGTCTcAGAATCAATTCTAAAAAACAGATTTTTTTtGAAAGTTTAAGTAATaTC
cGCGGAg

>Cele-UNSB01_2:13437444-13437847 Satlength=404 Nr of Repeats=10 RepeatLength=31
seed=CACGCCTATT

CACGCCTATTTTATGGGCGGAGTCTACAAGG
CACGCCTATTTTGTGGGAGGAGTCTACAAGC
CACGCCTATTTTGGGCGGAGTCTGCAAGT
CACGCCTATTTTCATGGACGAAGACTACAAGC
CACGCCTATTTTATGGGCGGAGAGTACAAGC
CACGTCTATTTTATGGGCGGGTCTACAAGGCGCGTCTATTTTCACGGGCGGAGCCTACAAGC
CACGCCATTTTTTGGACGGAGACTACAAGA
CACGCCTATTTTCATGGGCGGAGTCTACAAGCCACGCCGTTTTGTGGACGGAGACTACAAAT
CACGCCTATTTTATGGGCGAGTCTGCAAGGCGCGCATATTTTATGGGCGGAGCCTGCAAGC
CACGCCTATTTTATGGGTGGAGTCTACAAGC

Nr of selected repeats 7 Similarity 0.811572

Consensus:

CACGCCTATTTTaTGGgcGGAGtCTACAAGc

>Cele-UNSB01_2:13440285-13440859 Satlength=575 Nr of Repeats=12 RepeatLength=48
seed=TGCCTACGTG

TGCCTACGTGCCTACATAAGAAGCGTAGGTAGCTTCAAAGGTGTTGCG
TGCCTACGTGCCTGCAAAACAGGCGTGGGCAGCTTTAAAGGTGATGTA
TGCCTACGTGCCTACAAAATAAGCATAGGTAGCTCTAAAGGTAATGCA
TGCCTACGTGCCTACAAAACAGGCGTGGGCAGCTTTAAAGGTGATGTA
TGCCTACGTGCCTACAAAACAGGCGAATTAGCTTTGAAGGTGATGCA
TGCCTACGTGCCTACAAAACAGGCGTGGGCAGCTTTAAAGGTGATGCA
TGCCTACGTGCCTACAAAATAAGCATAGGTAGCTCTAAAGGTAATGCA
TGCCTACGTGCCTACAAAACAGGCGAATTAGCTTTGAAGGTGATGCA
TGCCTACGTGCCTACAAAACAGGCGTGGGCAGCTTTAAAGGTGATGCA
TGCCTACGTGCCTACAAAATAAGCATAGGTAGCTCTAAAGGTAATGCA
TGCCTACGTGCCTACATAAGAGGCATAGGTAACCTCAAAGGTGTTGCG
TGCCTACGTGCCTGCAAAACAGGCGTGGGCAGCTTTAAAGGTGTTGCG

Nr of selected repeats 10 Similarity 0.812346

Consensus:

TGCCTACGTGCCTaCAaAAcAgGCgTaGGcAGCTttAAAGGTgaTGca

>Cele-UNSB01_2:13459229-13459607 Satlength=379 Nr of Repeats=13 RepeatLength=14
seed=TAGTTTGTAG

TAGTTTGTAGTTTG
TAGTTTGTAGTTTA
TAGTTTGTATT
TAGTTTATAGTTTGTATATAAAATTGCATGCATGAAGTTCCAATTCCAATTTAAAAACGTTTTTTTATGATTATGACTTT
TTAATCTGTATTTTGAAGTTTA
TAGTATGTAGTATG
TAGTATGTAGTTTG
TAGTTGGTAGTTTGTAGTCTA
TGGTTTGTAGTTTG
TAGTTTGTAGCTTG
TAGTTTGTAGTTTTCTTATAGCTATGGAAATTAATTTTTGTAAGAATGAAATTCCTGCTCTGCCAAAATAACCCTAGTAT
GTTTCGTAGTTTTTTTATAAAGTCTG
TAGTATGTAGTTTG
TAGTTTATAGTTTG
TAGTTTGTAGTTTATACTTTTATAGTTTG

Nr of selected repeats 8 Similarity 0.829932

Consensus:

TAGTtTGTAGTTTG

>Cele-UNSB01_2:13460078-13460334 Satlength=257 Nr of Repeats=15 RepeatLength=16

seed=GGCATGTAGG

GGCATGTAGGCAGGTA

GGAATGTAGGCATGTA

GGCATGTAGGCATGTA

GGCATGTAGGCATGTAGGCATCTC

GGCATGTAGGCATCTA

GGCATATAGGCAAGTA

GGCATCTAGGCATGTA

GGCATGTAGGCATGTA

GGCATGTAGGCACTTA

GGCATGTAGGCATGTA

GGCATGTAGGCATGTA

GGCATCTAGGCATGTA

GGCATCTAGGCATATG

GGCAAGTAGGCATCTA

GGCATGTAGGCATGTAGGCATTTA

Nr of selected repeats 13 Similarity 0.840812

Consensus:

GGCATgTAGGCAtgTA

>Cele-UNSB01_2:13465788-13466109 Satlength=322 Nr of Repeats=20 RepeatLength=16

seed=GGCATGTAGG

GGCATGTAGGTAGGTA

GGCATATAGGCATGTA

GGTATGTAGGCATATA

GGCATGTAGGTATGTA

GGCATGTAGGCATGTA

GGCATGTTGGCATGTA

GGCATGTAGGTAGGTA

GGCATGTAGGCATGTT

GTCATGTAGGTATATA

GGCATATAGGTATGCA

GGCATGTTGGCATGTA

GGCATGTAGGTAGGTA

GGCATGTAGGCAGGTA

GGCACGTAGGCATCTA

GGCATGTAGGCATGTTA
GGCATTTAGGCATGTA
GGCAGGTAGGCATATA
GGCATATAGGTACGTA
GGCATATAGGCATGTA
GCCATGTAGGAATGTA

Nr of selected repeats 19 Similarity 0.773879

Consensus:

GGCATgTAGGcAtgTA

>Cele-UNSB01_2:13474627-13476516 Satlength=1890 Nr of Repeats=78

RepeatLength=20 seed=AAAATTTGAA

AAAATTTGAAATTTTGTCCAAAAATCATAGTTTTTTCCGAAAAAAAACCAGA

AAAATGTGAAAATTACCCCAAATTTCTAATTTTGAAGCGATTTTCTCCGAATTTTGAGCCCCAAACGTCGGAATTTCTC

CGCTCCCGTACCCTGTGCTCTTCCCTCCAGCAGCCGAGCCTTCCGTTTCCGTGTCTCGAGTGCTTTTACAATTGGAAT

CTCCTGTACATCGTCCATCGCCTCTTTTTCTTCCATTTTTTTCGTCAATTTTCTCTTTTTGCGACAAGCTGAATTCGTTCC

AAGGCTTCACGCACCATTCCCATAAAGACTTTGTGATTTTTTCGTTGGTATTCTCTGAAA

AAAATTTGAATTTTTAAGCC

AAAATTTGAATTTTTAAGTCA

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGCC

AAAATTTGAATTTTTCAGTCA

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTCAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTCTGCCA

AAAATTGAATTTTTAAGTC

AAAATTTGAATTTTTCTGCCA

AAAATTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGCC

AAAATTTGAATTTTTCAGTCA

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTCTGCCA

AAAATTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGCC

AAAATTTGAATTTTTCAGTCA

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTCTGCCA

AAAATTGAATTTTTAAGTC

AAAATTTGAATTTTTAAGTG

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTCAGTCA

AAAATATGAATTTTTAAGTG

AAAATTTGAATTTGTAAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTCAGTC

AAAATTTGAATTTTTAAGTC

AAAATTTGAATTTTTCTGCCA

AAAATTGAATTTTTAAGTC
AAAATTTGAATTTTCTGCCA
AAAATTGAATTTTTAAGTC
AAAATTTGAATTTTTAAGTC
AAAATTTGAATTTTTAAGCC
AAAATTTGAATTTTTCAGTCA
AAAATTTGAATTTTTAAGTC
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AAAATTTGAATTTTTCAGTC
AAAATTTGAATTTTACAGCC
AAAATTTGAATTTTACAGCC
AAAATTTGAATTTTTCAGTC
AAAATTTGAATTTTTCAGTC
AAAATTTGAATTTTTCTGCTGG
AAATTTGAATTTTTAGTAAAAAATTGGGTTCTCAGTC
AAAATTTGAATTTTTCAGCC
AAAATTTGAATTTTTCAGTCA
AAAATTTGAATTTTTCTGTC
AAAATTTGAATTTTTTAGTC

Nr of selected repeats 57 Similarity 0.826829

Consensus:

AAAATTTGAATTTTTaAGtC

>Cele-UNSB01_2:13490523-13491161 Satlength=639 Nr of Repeats=5 RepeatLength=122
seed=GATCTACAAA

GATCTACAAAAAGGCGGGAGAAGATCTTTTCGAGCCGAGAGTTCTCAACTGATTTGGTATGGTTTGACGTCACATAT
TTTTGAGCAAAAAAATTCCCGCATTTTTTGGAGATAAAACCGTGATGGGACAGCCTGGCGCCAAGTGCTTGATCTGCGT
A

GATCTACAAAAACGCGGAAAAGTGACGCAGAGTTTTGAACTGATTTTGCATAAAAAATTCCCGCATTTTTTGTAGATCA
AACCGTTATGGGACAGCCTGGTGCCACGTGCTTGATCTACGCA

GATCTACAAAAATGCGGAAAAGTGACACAGAGTTCTCAACTGATTTTGCATAAAAAATTCCCGCATTTTTTGGAGATCA
AACCGTGATGGGACAGCCTGGCACCACCTTGCTTGATCTACGTA

GATCTACAAAAATGCGGAAAAGTGACACAAGTATTTTGCATAAAAAATTCCCGCTTTTTTGTAGATCAAACCGTTAT
GGGACAGCCTGGTGCCACGTGCTTGATCTACGTA

GATCTACAAAAATGCGGAAAAGTGACACAGAGTTCTCAACTGATTTTGCATAAAAAATTCCCGCATTTTTTGGAGATCA
AACCGTGATGGGACAGCCTGGCACCACCTTGCTTGATCTACGTA

Nr of selected repeats 3 Similarity 0.927140

Consensus:

GATCTACAAAAAtGCGGGAAAAAGTGACaCAGAGTTcTcAACTGATTTTGCATAAAAAATTCCCGCATTTTTTgAGATCA
AACCGTgATGGGACAGCCTGGcaCCACtTGCTTGATCTACGtA

>Cele-UNSB01_2:13499104-13499209 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=CTAGAAAAAC

CTAGAAAAACCAGGCCATCAA

CTAGAAAAACTCGGCCATCAA

CTAGAAAAACTCGGCCATCAA

CTAGAAAAACTCGTCCATCAA

CTAGAAAAACTCGGCTATCAA

Nr of selected repeats 5 Similarity 0.898413

Consensus:

CTAGAAAAActcGgCcATCAA

>Cele-UNSB01_2:13500094-13501231 Satlength=1138 Nr of Repeats=46
RepeatLength=21 seed=TTTTCTAGTT

TTTTCTAGTTGATGGCCGAGT

TTTCCTAGTTGATAGCCGAGT

TTTTCTAGTTGATGGCCGAGT

TTTTCTAGTTGATGGCCGAGT

TTTCCTAGTTGACGGCCGATT

TTTTCTAGTTGATGTCCGAGC

TTTTCTAGTTGATGGCCTAGA

TTTTCTAGTTGCTGGCCGAAT

TTTTCTAGTTAATGTCAGAGTTTTTGGTGGCCTAGT

TTTCCTAGTTCATGGCAAAGT

TTTTCTAGTTGATGGCCGAGTTTTCTTTAGGTGACGGCCGAGT

TTTCCTAGTTGACGGCCGATT

TTTTCTAGTTGATGTCCGAGT

TTTTCTAGTTGATGGCCGAGTTTTCCTAGCTCATGGCCTAGG

TTTTCTAGTTGCTGGCCGAAT

TTTTCTAGTTGATGGCCGAGT

TTTTCTAGTTGATGGCCGAGT

TTTCCTAGTTGACGGCCGATT

TTTTCTAGTTGATGTCCGAGC

TTTTCTAGTTGATGGCCTAGA

TTTTCTAGTTGCTGGCCGAAT

TTTTCTAGTTAATGTCAGAGTTTTTGGTGGCCTAGT

TTTCCTAGTTCATGGCAAAGT

TTTTCTAGTTGATGGCCGAGTTTTCTCTAGGTGACGGCCGAGT

TTTCCTAGTTGACGGCCGATT

TTTTCTAGTTGATGTCCGAGT

TTTTCTAGTTGATGGCCGAGTTTTCCTAGCTCATGGCCAAGT

TTTTCTAGTTCATGGTCCGATTT

TTTTCTTGTGATGGCCTAGA

TTTTCTAGTTGATGGCCGAGT

TTTTCTAGTTGATGGCCGAGT

TTTCCTAGTTGACGGCCGATT

TTTTCTAGTTGATGTCCGAGC

TTTTCTAGTTGATGGCCTAGA

TTTTCTAGTTGCTGGCCGAAT

TTTTCTAGTTAATGTCAGAGTTTTTGGTGGCCTAGT

TTTCCTAGTTCATGGCAAAGT

TTTTCTAGTTGATGGCCGAGTTTTCTCTAGGTGACGGCCGAGT

TTTCCTAGTTGACGGCCGATT
TTTTCTAGTTGCTGGCCGAAT
TTTTCTAGTTAATGTCAGAGTTTTTGGTGTCCGAGC
TTTTCTAGTTGATGGCCGAGT
TTTTCTAGTTGATGGTTCGATTT
TTTTCTTGTGATGGTTCGATC
TTTTCTAGTTGATGGCCGAGTT
TTCTCTAGTTGATGGCCTAGG

Nr of selected repeats 34 Similarity 0.794245

Consensus:

TTTTtCTAGTTGATGGCCgAgt

>Cele-UNSB01_2:13509974-13510060 Satlength=87 Nr of Repeats=6 RepeatLength=12

seed=CTTAGGCTTA

CTTAGGCTTAAG

CTTAGGCTTAGT

CTTAGGCTTAAG

CTTAGGCTTAGTCTTTGT

CTTAGGCTTGGA

CTTAGGCTTAGGTTTAGCGC

Nr of selected repeats 4 Similarity 0.743590

Consensus:

CTTAGGCTTaaGn

>Cele-UNSB01_2:13528433-13528477 Satlength=45 Nr of Repeats=4 RepeatLength=11

seed=TGGAAAATTG

TGGAAAATTGA

TGGAAAATTGA

TGGAAAATTGA

TGGAAAATTGA

Nr of selected repeats 4 Similarity 1.000000

Consensus:

TGGAAAATTGA

>Cele-UNSB01_2:13541965-13542724 Satlength=760 Nr of Repeats=8 RepeatLength=95

seed=GGCCTGCGGC

GGCCTGCGGCCCTCAAACCTGACTTATTGGGCTCAGAATAGGCTTGACGGTTGCCAACACTTCTTCGTGTATTGCCTGT

TCCGCTGAGAATGTGGTGAGAAGTTACCTATGTGGTGAGAAGTTACCTTCCAAGGGTATTTCG

GGCCTGCGGCCCTCAAACCTGGTTGGTAGGCTTGAGCGAATAACAATCTGCTTGGAATAGGATTAAGCTGGCCCTTAT

TTTTCATGAGTATTCA

GGCCTGCGGCCCTCAAACCTGGTTGGTAGGCTTGAGTGAATAACAACCTGCTTGGAAGAGGATTAAGCTGACCCACAG

TTTCCAAGAGTGTTTCG

GGCCTGCGGCGCTCAAACCTGGTTGGTAGGCTTGAGTAAATAACAACCTGCTTGGAATAGGATTAAGCCAGCCAGTT

TGCAAGACTAGTTCG

GGCCTGCGGCCCTCAAACCTGGTTGTTAGGCTTGAGTAAATAACAACCTG

GGCCTGCGGCCCTCAAACCTGGTTGTTAGTCTTGAGTAAATAACAACCTGCTTGGAATAGGATTAAGCTGGCCCTTAG

TTTCCATGAGTATTTCG

GGCCTGCGGCCCTCAAACCTGGTTGGTATTCTTGAGCGAATAACAATCTGCTTGGAATAGGATTAAGCTGGCCCTTAG

TTTCCATGAGTATTTCG

GACCTGCGGCCCTCAAACCTGGTTGGTATGCTTGAGCGAATAACAATCTGCTTGGAATATGATTAACCAGCTCACAG

TTTCCAAGAGTGTTTCG

Nr of selected repeats 5 Similarity 0.859649

Consensus:

GgCCTGCGGCCCTCAAACCTGGTTGgTAggCTTGAGcgAATAACAAtCTGCTTGGAAtAgGATTAAGCtggCcCttAg

TTTcCatGAGTaTTCg

>Cele-UNSB01_2:13551182-13551985 Satlength=804 Nr of Repeats=20 RepeatLength=35

seed=GATTTGCCGG

GATTTGCCGGAAAATTTTCGATTCTGGCAATTTGCTGATTTACCAAAAATTTTCAATTCGGCAATTTGTC
GATTTGCCGGAAAATGTTCAATTCGGCAATTTACT
GATTTGCTGGAAAATTTTATATTTTCGCAATTTGTC
GATTTGCCGGAAAATGTTCAATTCGACAATTTGCC
GATTTGCCGGAAAAGTTTAAATTCGGCAATTTCCC
GATTTGCCGGAAAAGTTAAATTCGGCAACTTGCC
GATTTACCGGAAAATTTCAAATCCGCCAATTTGTCAAAAAGCAGGAATTATTCAATTCAGCAATTTGCC
GATTTGCCGGAAAATTTCAATTCGGCAATTTACT
GATTTGCTGGAAAATTTCAATTCGGCAATTTGCC
GATTTGCCGGAAAATTTCAATTCGAACAATTTGCC
GATTTGCCGGAAAATTTCAATTCGAACAATTTGCC
GATTTGCCGGAAAATTTCAATTCGACAATTTGCC
GATTTGCCGGAAAATTTCAATTCGGCAATTTGCC
GATTTGCCGGAAAATTTCAATTCGGCAATTTGCC
GATTTGCCGGAAAATTTCAATTCGGCAATTTGTC
GATTTGCCGGAAAATTTCAAATCCGGCAATTTGCC
GATCTGCCGGAGAATTTCAATTCGGCAATTTACT
GATTTGCCGGAATTATAGAATTTCTGGCAATTTGCCGATCTATCGAAAGTGTTCATTCGGAAAATTTGCC
GATTTTCCGGAAATATTCAATTCGGCAATTTGCC
GATTTACCGGAAAATTTTAAATTCGGCATTCTACT
Nr of selected repeats 15 Similarity 0.816490

Consensus:

GATTTGCCGGAAAAtTTCAATTCGGgCAATTTgCc

>Cele-UNSB01_2:13571681-13571955 Satlength=275 Nr of Repeats=20 RepeatLength=11
seed=CCTACAGTACC

CCTACAGTACC
CCTTCAGTACTG
CTACAGTACACCTACAGTGTC
CCTATAGTACC
CCTATAGTACT
CCTACAGTACT
CCTACCGTACC
CCTACTGTACTT
CTACAGTACC
CATAACAGTACC
CCTACAGTATC
CCTACAGTTCTCTTATAGACCAGTACAGTACTAACACAGCACC
CCTACAGTACCCCTACACTCCC
CCTACAGTACTC
CCACAGTACC
CCTACAGTACC
CCTACAGTACC
CCTACAGTACC
CCTACAGTACT
CCTACAGTACC

Nr of selected repeats 12 Similarity 0.853076

Consensus:

CCTACAGTACC

>Cele-UNSB01_2:13579229-13580664 Satlength=1436 Nr of Repeats=41
RepeatLength=35 seed=GAATTTTTGA
GAATTTTTGAAACTCCGCGATTTGCCGATTTGCCA
GAGTTTTTGATTTTCGGCAATTTGCCAATTTGCCA
GAATTTTTGAAACTCCGCGATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGATTTGCCG

GAATTTTTGATTTTCGGCAGTTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGATTTGCCG
GAATTTTTGAAACTTGGCAATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAGTTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGGGTTGCCG
GAATTTTTGAAACTTGGCAATTTGCCGATTTGCCG
GATTTTTGATTTTCGGCTATTAGCCGATTTGCCG
GAATTTTTGAAACTCCGCGATTTGCCGATTTGCCA
GAGTTTTGATTTTCGGCAATTTGCCAATTTGCCA
GAATTTTTGAAACTCCGCGATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAGTTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGATTTGCCG
GAATTTTTGAAACTTGGCAATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAGTTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGGGTTGCCG
GAATTTTTGAAACTTGGCAATTTGCCGATTTGCCG
GATTTTTGATTTTCGGCTATTAGCCGATTTGCCG
GAATTTTTGAAACTCCGCGATTTGCCGATTTGCCA
GAGTTTTGATTTTCGGCAATTTGCCAATTTGCCA
GAATTTTTGAAACTCCGCGATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAGTTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGATTTGCCG
GAATTTTTGAAACTTGGCAATTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAGTTTGCCGATTTGCCG
GAATTTTTGATTTTCGGCAATTTGCCGGGTTGCCG
GAATTTTTGAAACTTGGCAATTTGCCGATTTGCCG
GATTTTTGATTTTCGGCTATTAGCCGATTTGCCG
GAATTTTTGAAACTCCGCGATTTGCCAATTTGCCA
GAATTTTTGATTTTCGGCAATTTGCCAATTTGCCA
GAATTTTTGAAACTCCGCAATTTGCCGATTTGCCA
GAATTTTTGATTTTCGGCAATTTGCCGATTTGCCG
GAATTTTTGAAACTCCGCAATTTGCCGATTTGCCA

Nr of selected repeats 41 Similarity 0.852172

Consensus:

GAATTTTTGAtttTCGGCaATTTGCCGATTTGCCg

>Cele-UNSB01_2:13658533-13659809 Satlength=1277 Nr of Repeats=26

RepeatLength=27 seed=AGCAGCCGAC

AGCAGCCGACACTGCACGGGTCCATAAAGATTTCCGCTGCTGTGAGACCTGTGAAGCGTCGGCTGCTAACCATTAGGCG
AATCTA

AGCGGCCGACGTTCCATAGGCCTGCAAGATGTCGGCTGCTTTACTTTGGCAGCCGATAGACGATTGTTCCAGCAAATCT
CGACCTTATTCAA

AGCAGCCGACATTTTACGGGACCCTAGGGAACCAGTGAAATGTCGGCTGCTAACTCATCTCAACAAAGTTAACCCATGT
TTTCTTACAGTAGCCTTCTGCTATTTGACCCGGCGCCCCACGAACCGGCGTTCGTCTACCGTACCTATCACACCCTGC
GGCGGTTGAGTCGACGCAATGGAGAAGCTCGAATTCGAATGTCATCAAATCAGAAGAGCAGGAGGAGAGCAACGA
CTCGCCGGCTCAAGTGCTATTTGTGTAGAGATCGAAATATTGCTTCTTCTTCTTCTACTTCTTCTTCTATACTAG
CAACCCCTCTGTCTGTAGTGTGTATGAATTTTGAAGCGCGCTTTTTGATGGGCTTTTTGAAAGGGTGAATACTCAT
TTTCTTGGTA

AGCAGCCGACATTTCCGCGGGTCCGGTCAAATTTCTAGGAGAGCTATAT

AGCAGCCGACGCTTGCAGGGTCCGCTCA

AGCAGCCGACATTTTGCAGTTTGCTTA
AGCAGCCGACATTTTGCAGGTTGTTTAAAAAGCCGACATTTTGCGGGTTTCTTG
AGCAGCCGACACCTTGCAGGTTGCTCA
AGCAGCCGACACCTTGTCTGGTCGCTTA
AGCAGCCGACACCTTGATGGTTGTTCA
AGCAGCCGACATCTTGCAGGTTTCTTA
AGCAGCCGACACCTTGATGGTTGTTCA
AGCAGCCGACATCTTGCAGGTTGCTTA
AGCAGCCGACACCTTGAAGGTTTCTTG
AGCAGCCGATACTTGCGGGTTGCTTA
AGCAGCCGACACCTTGATGGTTGCTCA
AGCAGCCGACACCTTGCTGGTCGCTTA
AGCAGCCGACACCTTGATGGTTGTTCA
AGCAGCCGACATCTTGCAGGTTTCTTA
AGCAGCCGACACCTTGATGGTTGTTCA
AGCAGCCGACACCTTGAAGGTTTCTTG
AGCAGCCGATACTTGCGGGTTGCTTA
AGCAGCCGACACCTTGATGGTTGTTCA
AGCAACCGACATCTTGCAGGTTGCTTA
AGCAGCCGACACCTTACAGGTTGCATAAGCAGATGACACTTTACAGGTTGCTTA

Nr of selected repeats 20 Similarity 0.791813

Consensus:

AGCAGCCGACACCTTGCAGGTTGCTTA

>Cele-UNSB01_2:13663688-13663784 Satlength=97 Nr of Repeats=6 RepeatLength=16
seed=ACATGCCTAC

ACATGCCTACATGACT
ACATGCCTACATGCCT
ACATGCCTACATGCCT
ACATGCCTACATGCCT
ACATGCCTACATGCCC
ACATGCCTACATACT

Nr of selected repeats 6 Similarity 0.888889

Consensus:

ACATGCCTACATGCCT

>Cele-UNSB01_2:13678541-13678601 Satlength=61 Nr of Repeats=5 RepeatLength=12
seed=AATACCAACC

AATACCAACCAC
AATACCAACCAC
AATACCAACCAC
AATACCAACCAG
AATACCAACCAG

Nr of selected repeats 5 Similarity 0.933333

Consensus:

AATACCAACCAC

>Cele-UNSB01_2:13684820-13685366 Satlength=547 Nr of Repeats=24 RepeatLength=20
seed=GTAAATCGAC

GTAAATCGACAAACGACAACCAGC
GTAAATCGACAAAAGACATC
GTAAATCGACACACAACGTC
GTAAATCTACACACAACAGC
GTAAATCGACAAACGACAGCGCAAATAAATAACGACGGC
GTAAATCGACACAGCACGTT
GTAAATCAACACTCCGTGTC

GTAAATCGACAAAAGCCATC
GTAAATCGACACACAACGTC
GTGAATCGACAAACGACAGCCAGC
GTCAATCGACAGACGCTATC
GTAAATCGACAAACGACAAGCAGC
GTAAATCGACATACAATGTC
GTAAATCGGCAAACGACAGC
GTAAATCGACAGGAGACATTGTTAGGAAACAGC
GTAAATCGACAAACGACAGTATGC
GTAAATCGACATAACGACTGG
GTAAATCGACAGAAGACATTGCTAGACAACAGC
GTAAATCGACAGACGCTATC
GTAAATTGACACACAACGTC
GTAAATCGGCATAACAACGTC
GTAAATCGACAAACGACAGCCCGC
GTAAATCGACACACAACGTC
GTAAATCCACACACTACGTC

Nr of selected repeats 16 Similarity 0.655886

Consensus:

GTAAATCGACAcACnAcgTC

>Cele-UNSB01_2:13754985-13755264 Satlength=280 Nr of Repeats=7 RepeatLength=35
seed=TTGCCGGAAT

TTGCCGGAATTGAATATTTGCGGCAAATCTGTAAT
TTGCCGGAATTGAATATTTGCGGCAAATCTGTAAT
TTGCCGGAATTAAATGTTTCCGGAACATCGGCAA
TTGCCGGTATTAAATGTTTCCGGAACATCGGCAA
TTGCCGGAATTGAGTATTTCCGTAATTCGGCAA
TTGCCGGAATTGAGTATTTCCGGCAAATCGGCAA
TTGCCGGAATTGAAATTTCCAGCAAATCGGCAAATGCGTAAATGATTATTTCCGGCAAATCGGCAA

Nr of selected repeats 6 Similarity 0.784127

Consensus:

TTGCCGGAATTgAaTaTTTcCGGcAaATCgGcAAa

>Cele-UNSB01_2:13755448-13762935 Satlength=7488 Nr of Repeats=166
RepeatLength=45 seed=ACCAGGAGGT

ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTGATCCTTCGGAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTTGAAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTGATCCTTCGGAGCTGAAGGATCAGATC
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTGATCCTTCGGAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTGATCCTTCGGAGCTGAATGATCAGATT

ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTTGATCCTTCGGAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
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ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATTTTTTTTTTTGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTGATCCTTCGGAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
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ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
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ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
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ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATT
ACCAGGAGGTACTCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTTGAAGCTGAAGGATCAGATC
ACCAGGAGGTACCCTTCTTATCCTTCGGAGCTGAATGATCAGATC
ACCAGGAGGTACCCTTATGATCCTTTGAAGCTGAAGGATCAGATC

Nr of selected repeats 165 Similarity 0.932682

Consensus :

ACCAGGAGGTACcCTTCTTATCCTTCGGAGCTGAAtGATCAGATc

>Cele-UNSB01_2:13794379-13794568 Satlength=190 Nr of Repeats=10 RepeatLength=16
seed=CCTACATGCC

CCTACATGCCTTCATG
CCTACATGCCTACATG
CCTACATGCCTACATG
CCTACATGCCTACATG
CCTACATGCCTACATGCCTAG
CCTACATGCCTACATG
CCTACATGCCTACATG
CCTACATGCCTACATG
CCTACATGCCTACATGCCTACATGAATACATG
CCTACATGCCTACATGCCTACATG

Nr of selected repeats 7 Similarity 0.976190

Consensus :

CCTACATGCCTACATG

>Cele-UNSB01_2:13805325-13805605 Satlength=281 Nr of Repeats=7 RepeatLength=35
seed=CTTGCCGATT

CTTGCCGATTTTTCAGAAATTTTCAATTCCGGCAA

CTTGCCGATTTGCCGAAATTTCTCAATTCGGCAATTTGTGCGATTTGCCGAAATTTTAATTCCGCCAA

CTTGCCGATTTGCCGAAATTTTCAATTCGGCAA

CTTGCCGATTTGCCAGAAATTTTCATTTTCGGCAA

CTTGCCGATTTGCCAGAAATTTTCATTTTCGGCAA

CTTGCCGATTTGCCAGAAATTTTCAATTCAGCAA

CTTGCCGATTTGCCGAAATTTCTGAATTCGGCAA

Nr of selected repeats 6 Similarity 0.862857

Consensus :

CTTGCCGATTTGCCaGAAATTTTCAaTTcCGGCAA

>Cele-UNSB01_2:13813351-13813423 Satlength=73 Nr of Repeats=6 RepeatLength=12
seed=TAGGCTTAGG

TAGGCTTAGGCT

Nr of selected repeats 6 Similarity 0.962963

Consensus :

TAGGCTTAGGCT

>Cele-UNSB01_2:13831609-13831953 Satlength=345 Nr of Repeats=12 RepeatLength=27
seed=TTCCGGCAAAA

TTCCGGCAAAAACGGCAATTGAAATT

TTCCGGCAAATCGACAAATTTGCCGGAATTGAAATTTGAAAT

TTCCGGCAAATCGTCAAATTTGCCGGAATTTAAAT

TTCCGGCAAATGGGCAATTGTAAAC

TTCCGGCAAATCGGCAATTTTGAAAT

TTCCGGCAAATCGGCAATTTTAAAT

TTCCGGCAAATCGGCATTTTGAAAT

TTCCGGCAAATCGGCAAATTGCAAAAT

Nr of selected repeats 8 Similarity 0.904762

Consensus :

TTCCGGCAAATCGGCAAAaTTgcAAAAT

>Cele-UNSB01_2:13844810-13844989 Satlength=180 Nr of Repeats=5 RepeatLength=36
seed=TTGCCTAAAA

TTGCCTAAAATTTAAATTTCCAGCAAATCGGCAAAT

TTGCCTAAAATGAAAATTTCCGGCAAATCAGCAAAA

TTGCCTAAAATTTAAATTTCCGGCAAATCAGCAAAT

TTGCCTAAAATTTAAATTTACCGCAAATCAGCAAAT

TTGCCTAAAATTTAAATTTCCGGCAAATCGGCAAAT

Nr of selected repeats 4 Similarity 0.938272

Consensus :

TTGCCTAAAATTTAAATTTCCgGCAAATCaGCAAAT

>Cele-UNSB01_2:13878619-13878763 Satlength=145 Nr of Repeats=10 RepeatLength=12
seed=GCCTAAGCCT

GCCTAAGCCTAAATAAGCGTAA
GCCGAAGCCTAA
GTCTAAGCCTAAAA
GCCTAATCCTAAATCTTA
GCCTAAGCCTAG
GCTTAAGCCTCA
GCCTAAGCCTAA
GCCTCAGCCTAA
GTCTAAGCCTCT
GCCTAAGCCTAAGCCTCA

Nr of selected repeats 6 Similarity 0.725926

Consensus:

GCCTAAGCCTaa

>Cele-UNSB01_2:13900624-13901003 Satlength=380 Nr of Repeats=15 RepeatLength=21
seed=CTCGTAAATC

CTCGTAAATCGACAGGGATCC
CTCGTAGATCGACAAGAACTC
CTCGCAAATCGACAAAAGCTC
CTCGTAAATCTACAAGAACTCCTTGTAATTTGACAATAACTC
CTCGTAAATCCACAAGACCTCTTCGTAAATAGACAAAGAATC
CTCGTAAATCTACAAGCAATC
CTCGTAAATCGACAAGAACTC
CTCGTAAATCGGCAAGAACTC
CTCGTAATTCGACAAGAACTC
CTCGTAAATCCACAAGGACTCCTTGTAATTTGACAATAACTC
CTCGTAAATCGACAAAAACTCA
TCGTAAATCGACAAGAAAAC
CTCGTAAATCGACAAAAAACTC
CTCGTAAATCGACAAGTACTC
CTCGTAAATCGACAAGGATCT

Nr of selected repeats 9 Similarity 0.754630

Consensus:

CTCGTAAATCGACAAGaAcTC

>Cele-UNSB01_2:13903082-13903160 Satlength=79 Nr of Repeats=5 RepeatLength=13
seed=GGCTTCTAGT

GGCTTCTAGTCCA
GGCTTCTAGTCTAGGCTTCGGGTCTA
GGCTTCTAGTCTA
GGCTTCTAGTCTC
GGCTTCTAGTCCA

Nr of selected repeats 4 Similarity 0.880342

Consensus:

GGCTTCTAGTCca

>Cele-UNSB01_2:13911573-13912594 Satlength=1022 Nr of Repeats=28
RepeatLength=35 seed=TTTGCCGGAA

TTTGCCGGAAATTTTGAATATTGGCATATTGCCGA
TTTGCTGGAAATTTTCAAATCCGGCAAATTGCTGC
TTTGCCGAAAATTTTGATTTCCGGCATTGCTGT
TTTGCCGGAAATTTTAATTCAGCAA
TTTGCCGGAAATTTTCGATTTTCGGCAACATGCCGA
TTTGCCGGAAATTTTGAATTTTCGGCATTGTCGATTTGCCGG
TTTGCCGAAAATTTTGAATTTTCGGTAATTTGTCGA
TTTGCCGGAAAGTTTGAATTTTCGGCATTGCTGT
TTTGCCGGAAATTTTCGAATATTGGCATTTCCTCCGA

TTTGCCGGAAATTTTCAATTCGGGCACATTGCCGA
TTTGTCCGGAAATTTTGATTTTTGGCAACTTGCCGA
TTTGCCGGATATTTTGGTTTTTCGGTAATATGCCGATTTGCCGG
TTTGCCGGAAATTTTAAAAATCCGGCAAATTGCCGGTTTTCTGTAAATTTTAAAAATCCGGCTAATAGCCGG
TGTGCCGGAAATTTTCAATTCAGCAACTTGCCGAT
TTTCCGGAAATTTTAAATTTTCGGTAATTTGCCGT
TTTGCCGGAAATTTTGATTTTCGGCATTGTCGA
TTCGCCGGAAATTTTGATTTTCGCCATTTGCCGT
TTTGCCGGAAATTTTGATTTTCGGCATTGTCGA
TTTGCCGGATATTTGAATTCGGCAAACCTCCGG
TTTGCCGGAAACTTTGATTTTCGCCATTTGTCGA
TTTGCCGGAAATTTTCAAATCCGGCAAATAGTCGA
TTCGCCGGAAATTTTGATTTTCGACAATTTGCCGT
TTTGCCGGAAATTTTCAATTCGGCAAATTTGCCGA
TTTGCCGGAAATTTCAATTTGACAATTTGCCGT
TTTGCCGGAAATTTTCAATTCGGCAAATTTGCCGT

Nr of selected repeats 18 Similarity 0.750016

Consensus :

TTTGCCGGAAATTTTgAaTTtCGGCAatTTGcCGa

>Cele-UNSB01_2:13932545-13934837 Satlength=2293 Nr of Repeats=68

RepeatLength=35 seed=CCGGAATTGA

CCGGAATTGAAATTTCCGGCGAATCGGCAAATTG
CCGGAATTGAAAATTTCTGGAAAATCGGCAAATTG
CCGGAATTGAAAATTTCTGGCATATCGACAATTTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG
CCGGAATTGAAAATTTCTGGAAAATTAACAAATTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG
CCGGAATTGAAAATTTTGGAAAATTAACAAATTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG
CCGGAATTGATAATTTCTGGCAAATCGGAAAAC TG
CCGGAATTGACAATATCCGGCAAGCGGCAAATTG
CCGGAATTGAAATTTCCGGCGAATCGGCAAATTG
CCGGAATTGAAAATTTCTGGAAAATGGGTAAATTG
CCGGAATTGAAAATTTCTGGAAAATGGGTAAATTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG
CCGGAATTGAAAATTTTGGAAAATTAACAAATTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG
CCGGAATTGAAAATTTCTGGAAAATTAACAAATTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG
CCGGAATTGACAATTTG
CCGGAATTGATAATTTCTGGCAAATCGGAAAAC TG
CCGGAATTGACAATATCCGGCAAGCGGCAAATTG
CCGGAATTGAAATTTCCGGCGAATCGGCAAATTG
CCGGAATTGAAAATTTCTGGAAAATGGGTAAATTG
CCGGAATTGAAAATTTCTGGAAAATGGGTAAATTG
CCGGAATTGAAAATTTCTGGAAAATCAACAAATTG

CCGCTACCGC
CCGCTACCGC

CCGCTACCGCCCGCTACCTC

Nr of selected repeats 19 Similarity 1.000000

Consensus:

CCGCTACCGC

>Cele-UNSB01_2:13967191-13967257 Satlength=67 Nr of Repeats=5 RepeatLength=11

seed=CCGCTACCGC

CCGCTACCGCC

CCGCTACCGCA

CCGCTACCGCCCGCTTTTCGCC

CCGCTACCGCC

CCGCTACCGCA

Nr of selected repeats 4 Similarity 0.919192

Consensus:

CCGCTACCGCa

>Cele-UNSB01_2:13968253-13968583 Satlength=331 Nr of Repeats=23 RepeatLength=12

seed=GCCTAAGCCT

GCCTAAGCCTAAGCTTAG

GCCTAAGCCTAA

GCCCAAGCCTAC

GCATAAGCCTAA

GCCTAAGCCTGA

GCCTAAGCCTAA

GCCTAAGCCTAA

GCCTAAGCCTAA

GACTAAGCCTAAGCCCAA

GCCCAAGCCTAC

GCCTAAGCCTAA

GCCTAAACCTGAGCCTAAGCAAAAGCCAAA

GCTTAAGCCTAAA

CCTAAGCCTAAGACTGA

GCCTTAGCCTAA

GCTTAAGCCTGA

GCCTAAGCCTAAGCCTGATCCTAG

GCCTAAGCCTAG

GCCTAAGCCTAG

GCCTAAGCCTAG

GCCTAAGACTAAACCTAAA

CCTAAGCCTAA

GCCTATGCCTAT

Nr of selected repeats 15 Similarity 0.803175

Consensus:

GCCTAAGCCTAa

>Cele-UNSB01_2:13971711-13972389 Satlength=679 Nr of Repeats=37 RepeatLength=18
seed=AATTTACCAA

AATTTACCAAATTTGACATTTTGTAAATTTGGCAATTTCCATAATTTGACAATTATTAATTTTCAA
AATTTACCAATTTACCAA
AATTTCCAAGTTCCCAA
AATTTACCAAATTTGGGC
AATTTACCAA
AATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCGA
AATTTACCAATTTACCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAAATTTGGGC
AATTTACCAA
AATTTACCAATTTACCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAAATTTGGGC
AATTTACCAA
AATTTACCAATTTACCAAAAATTTGGC
AATTTACCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAATTTTCCAA
AATTTACCAATTTACCAA
AATTTACCAAAAATTTGGGC
AATTTACCAA
AATTTACCAATTTACCAA

Nr of selected repeats 29 Similarity 0.745813

Consensus:

AATTTACCAATTTaCCaA

>Cele-UNSB01_2:13977826-13977988 Satlength=163 Nr of Repeats=10 RepeatLength=12
seed=GCCTAAGCCT

GCCTAAGCCTAACTTAAGGCTAACCCTAAGTTAAG
GCCTAAGCATGAGCCTAAGAATGA
GCCTAAGCCTTA
GCCTACGCCTTA
GCCTACGCCTAG
GCCTAAGCCTAA
GCCTAAGCCTAAGCTCAA
GCCTAAGCCTAA
GCCTAAGCTCAA
GCCTAAGCCTAA

Nr of selected repeats 7 Similarity 0.798942

Consensus:

GCCTAaGCCTaA

>Cele-UNSB01_2:13981365-13981461 Satlength=97 Nr of Repeats=7 RepeatLength=12
seed=TTAGGCTTAG

TTAGGCTTAGGCTTTGGCTTCGGC

TTCCGGCTTAGGA

TTAGGTTTAGGC

TTAGGCTTAGTC

TTAGGCTTCGGC

TTAGACTTAGGC

TTAGGCTTAGTC

Nr of selected repeats 6 Similarity 0.755556

Consensus:

TTAGGCTTAGgC

>Cele-UNSB01_2:14003653-14004477 Satlength=825 Nr of Repeats=18 RepeatLength=34
seed=AATTCCGGCA

AATTCCGGCAATTTGCTGATTCATCAGAAATTTTC

AATTCCGGCAACTTGCTATTTTCCGGAAATTTTC

AATTCCGGCAATTTGCTGATTTATCAGAAATTTTC

AATTCCGGCAACTTGCTATTTTCCGGAAATTTTC

AATTCTGGCAATTCGCTGATTTTCCGGAAATTTTC

AATTCCGGCAATTTGCTGATTTATCAGAAATTTTC

AATTCCGGCAATTTGCTGATTTATCAGTAACTTC

AATTCCGGCAATTTGCTATTTTCCGGAAATTTTC

AATTCCGGCAATTTGGCGAACTACCAGAACTTTCAATTTTGCCGGTTTACCGATTTTCCGGAAATTTTC

AATTCCGGCAATTTGCTGATTTATCAGAACTTC

AATTCCGGCAATTTGGCGATTTGCCAGAAATTTTCAATTTTGCCGGTTTACCGATTTTCCGGAACTTC

AATTCCGGCAATTTGGCGATTTGTCAGAACTTTCAATTTTGCCGGTTTACCGATTTTCCGGAACTTC

AATTCCGGCAATTTGCTGATTTATCAGAAATTTTC

AATTCCGGCAATTTGGCGATTTGCCAGAAATTTTCAATTTTGCCGGTTTACCGATTTTCCGGAAATTTTC

AATTCCGGCAATTTGGCGATTTGTCAGAAATTTTCAATTTTGCCGGTTTACCGATTTTCCGGAAATTTTC

AATTCCGGCAATTTTCTGATTAGTCAGAAATTTCAATCCTCCGGCAATTTTGCCGATTTGCCAGAAATTTTC

AATTCCGGCAATTTTCCAATTTGTCGGAAGTTTC

AATTCCGGCAATTTTCCGATTTGCCGAAATTTT

Nr of selected repeats 12 Similarity 0.808081

Consensus:

AATTCCGGCAATTTGCTgATTTatCgGAAATTTTC

>Cele-UNSB01_2:14078695-14078860 Satlength=166 Nr of Repeats=5 RepeatLength=33
seed=AAAATTTGAA

AAAATTTGAATTTCCCGTCAAAAATTTTCTCAG

AAAATTCGAATTTGGCGCAAAAATTTTTCACAA

AAAATCTGAATTTCTCGCAAAAATGTTTCTCGG

AAAATTTGAATTTCCCGCTAAAAATTTTCCCAG

AAAATTTGAACTTCTGCAAAAATGTTTCTCAG

Nr of selected repeats 5 Similarity 0.749495

Consensus:

AAAATttGAAtTTcccGccAAAAtttTtCtCag

>Cele-UNSB01_2:14106829-14106943 Satlength=115 Nr of Repeats=7 RepeatLength=12
seed=AGCCTAAGCC

AGCCTAAGCCTAAACCTGAATGCGAGCCTGAGTTTGA

ACCTAAGCCTAC

ACCTAAGCCTGAACCTG

AGCCTAAGCCCA

AGCTTAAGCCTA
AGCCTAAGCCTA
AGTCTAAGCCTA
Nr of selected repeats 5 Similarity 0.733333
Consensus:
AgccTAAGCctA
>Cele-UNSB01_2:14136989-14138428 Satlength=1440 Nr of Repeats=41
RepeatLength=14 seed=TACAAACTAC
TACAAACTACAAAC
TACAAACTACAAAC
TACAAACTACAAACTACAAATC
ACAAACTACCAACTACAACATAAACTGCTTTAAGGTAAAATGGCATTTCATGACGATTCATGTTGTACACGATTATACA
CTAGACTTTTAGCCTCTAATACTAGGAAAAAACTAGGAATGTTATAGAC
TACAACCTACAAAC
TACAATCTACAAAT
TACAAATTACAAAC
TACAAACTACAAAC
TACAAACTACAAAC
TACAAACTACAAATC
ACAAACTACCAACTACAACATAAACTGCTTTAAGGTAAAATGGCATTTCATGACGATTCATGTTGTACACGATTATACA
CTAGACTTTTAGCCTCTAATACTAGGAAAAAACTAGGAATGTTATAGAC
TACAACCTACAAAC
TACAATCTACAAAT
TACAAATTACAAAC
TACAAACTACAAAC
TACAAACTACAAAC
TACAAACTACAAATC
ACAAACTACCAACTACAACATAAACTGCTTTAAGGTAAAATGGCATTTCATGACGATTCATGTTGTACACGATTATACA
CTAGACTTTTAGCCTCTAATACTAGGAAAAAACTAGGAATGTTATAGACTACAAC
TACAAACTACAATC
TACAAATTACAAAT
TACAAACTACAAAC
TACAAACTACAAAC
TACAAACTACAAATC
ACAAACTACCAACTACAACATAAACTGCTTTAAGGTAAAATGGCATTTCATGACGATTCATGTTGTACACTATTATACA
CTAGACTTTTAGCCTCTAATACTAGGAAAAAACTAGGACTGTTATAGAC
TACAACCTACAAAC
TACAATCTACAAAT
TACAAATTACAAAC
TACAAACTACAAAC
TACAAACTACAAACTACAAATC
ACAAACTACCAACTACAACATAAACTGCTTTAAGGTAAAATGGCATTTCATGACGATTCATGTTGTACACTATTATACA
CTAGACTTTTAGCCTCTAATACTAGGAAAAAACTAGGACTGTTATAGAC
TACAACCTACAAAC
TACAATCTACAAAT
TACAAATTACAAAC
TACAAACTACAAAC
TACAAACTACAAACTACAAATC
ACAAACTACCAACTACAACATAAACTGCTTTAAGGTAAAATGGCATTTCATGACGATTCATGTTGTACACTATTATACA
CTAGACTTTTAGCCTCTAATACTAGGAAAAAACTAGGACTGTTATAGAC
TACAACCTACAAAC
TACAATCTACAAAT
TACAAATTACAAAC
TACAAACTACAAAC
TACAAACTACAAACTATAATC

TACAAACTACTTTATGAAATAAGGAAATTTTGGACTGTGCTTTTTAAAGTTTTTTTTTTGGCCTTTTAGTGGCCAGGTAG
GTAATGTGACGACACCTACAGACCTATAGCAGATAGGCACGAGGTAGGCAGGTATTTTAGGAGCATACTACAACC

Nr of selected repeats 27 Similarity 0.871659

Consensus:

TACAAacTACAAAc

>Cele-UNSB01_2:14141898-14142455 Satlength=558 Nr of Repeats=7 RepeatLength=62

seed=TGCTAACTAG

TGCTAACTAGGTAGAACCCGCTCGCGAAACGGCTAATGCGCGGTCCCAGTTGGTTGTTGGCCGCTAAATATCTAGGACC
CACGTAGCTGTCCGGCTGCACTTGCTGTCCCTGTTGGTTGTCCGGCTGCTAGCTCGGTAGGGTTCGCTTAGGTGTCCGGCTG
CATTAGCAGTCCCTGGTTTAATGTCCGGC

TGCTAACTAGCGCGGGCCTGCTTAGGTGCCGGCTGCGAAAGCAGTCCTGGTTTAATGTCCGGC

TGCTAACTAGGTAGCGGCCAGCTTAAATGTCCGGATGCACGAGTAGTCCTGGTTTAATGTCCGGT

TGCTAACTAGCTAGGTCCCCTTAGGTGCCGGCTGCACGAGCAGTCCTGGTTTAATGCCGGC

TGCTAACTAGGCACGGCCAGCTTAGGTGCCGGCTGCACGAGCAGTCCTGGTTTAATGTCCGGT

TGCTAACTAGCTAGGTCCCCTTAGGTGCCGGCTGCACGAGCAGTCCTGGTTTAATGCCGGC

TGCTAACTAGGCACGGCCAGCTTAGATGTCCGGATGCACGAGCAGTCCTGGTTTAATGTCCGGT

Nr of selected repeats 6 Similarity 0.822222

Consensus:

TGCTAACTAGcTAcGgCCaGCTTAGgTGcCGGcTGCACGAGCAGTCCTGGTTTAATGtCGGc

>Cele-UNSB01_2:14148263-14148341 Satlength=79 Nr of Repeats=6 RepeatLength=12

seed=GGCTTTGGCT

GGCTTTGGCTTT

GGCTTAGGCTTATGCTTC

GGCTTTGGCTTT

GGCTTTGGCTTT

GGCTTTGGCTTT

GGCTTTGGCTTT

Nr of selected repeats 5 Similarity 1.000000

Consensus:

GGCTTTGGCTTT

>Cele-UNSB01_2:14148276-14148504 Satlength=229 Nr of Repeats=14 RepeatLength=12

seed=GCTTAGGCTT

GCTTAGGCTTAT

GCTTCGGCTTTG

GCTTTGGCTTTG

GCTTTGGCTTTG

GCTTTGGCTTTG

GCTTTGGCTTTGGCTTTGGATTTG

GCTTAGGCTTAG

GCTTAGGATTTTCCGGTTTTTTTGATTTTTCAGCGGTTCCCTGTTGGCCGATTAT

GCTTATGCTTAG

GCTTAGGCTTAG

GCTTACGCTTAG

GCTTAGGCTTGA

GCTTAGTCTTAG

GCTTAAGCTTAGGCTTCG

Nr of selected repeats 11 Similarity 0.711888

Consensus:

GCTTaGGCTTaG

>Cele-UNSB01_2:14178132-14178499 Satlength=368 Nr of Repeats=11 RepeatLength=11

seed=GTAAGTGTAGG

GTAAGTGTAGG

GTAAGTGTAGGA

GTACTGTAGGAGGGTTACTGTAGTTTAGGAAAAATTGACTTTTCGTCTTTTGAAGAGATATTGGTTTGGGGTTAGTGGA
AGGATATGGTCGGG
GTACTGTAGGG
GTACTATAGGA
GTACTGTAGGAGGGTTACTATAGCTTAAGAAAAATTGACTTTTAGTCTTTTGAAGAGATAATGGTTTGGGGTCAGTGGA
AGGATATGGTCGGG
GTACTGTAGGG
GTACTGTAGGA
GTACTGTAGGAGGGTTACTGTAGTTTAGGAAAAATTGACTTTTCGTCTTTTGAAGAGATATTGGTTTGGGGTTAGTGGA
GAGATATGGTCGGG
GTACTGTAGGG
GTACTATAGGA

Nr of selected repeats 8 Similarity 0.878788

Consensus:

GTACTgTAGGa

>Cele-UNSB01_2:14178691-14179588 Satlength=898 Nr of Repeats=30 RepeatLength=30
seed=TTTCTAGAAA

TTTCTAGAAAAATCAGAAAACTTTTGGAAAC
TTTCTAGAAACATTTGGAACTTCTAGAAC
TTTCTAGAAAAATTTGGAATCTTCTAGAAC
TTTCTAGAAAAATCTGGAACTTCTAGAAT
TTTCTAGGAAAATCAGAAAACTTTTGGAAAC
TTTCTAGAAAAATCTGGAACTTCTAGAAT
TTTCTAGGAAAATTTGGAATCTTCTAGAAC
TTTCTAGAAAAATCAGAAAACTTCTAGAAC
TTTCTAGAAAAATTTGGAATCTTCTAGAAC
TTTCTAGAAAAATCTGGAACTTCTAGAAT
TTTCTAGAAAAATCAGAACTTCTAGAAC
TTTCTAGAAAAATTTGGAATCTTCTAGAAC
TTTCTAGAAAAATCTGGAACTTCTAGAAT
TTTCTAGAAAAATCAGAAAACTTCTAGAAC
TTTCTAGAAAAATCTGGAACCTCTAGAACAATTTGGAATCTTCTAGAAC
TTTCTAGAAAAATCAGAAAACTTCTAGAAC
TTTCTAGAAAAATTTGGAATCTTCTAGAAC
TTTCTAAAAAATCTTGACA
TTTCTAGAAT

TTTCTAGAAAAATCAGAACTTCTAGAAC
TTTCTAGAAAAATTTGGAATCTTCTAGAAC
TTTCTAGAAAAATCTGGAACTTCTAGAAC
TTTCTAGAAAAATTTGGAATCTTCTAGAAC
TTTCTAGAAAAATCTGGAACTTCTAGAAT
TTTCTAGGAAAATCAGAAAACTTTTGGAAAC
TTTCTAGAAAAATCTGGAACTTCTAGAAT
TTTCTAGAAAAATCAGAACTTCTAGAAC
TTTCTAGAAAAATTTGGAATCTTCTAGAAC
TTTCTATAAAAAATCTGGAACTTCTAGAAT
TTTCTAGGAAAATCAGAAAACTTTTGGAAAC
TTTCTAGAAAAATCTGGAACTTCTAGAAC

Nr of selected repeats 24 Similarity 0.857649

Consensus:

TTTCTAGAAAAATctGgAAaCTTCTAGAAC

>Cele-UNSB01_2:14194765-14194942 Satlength=178 Nr of Repeats=5 RepeatLength=14
seed=GTAGTTTGTA

GTAGTTTGTA
GTAGTTTGTA

GTAGTTTGTAGTCC
 GTAGTTTTAGCAG
 GTAGTTTGAAAGTATGCAGCTTTTTTTTGTAAAGTTTTGTATTTCGTATACTTAAATACTTGTAGAAATGTTCAATA
 GAAATTGTTCAAAAATATACATAGTTTGTGGTCATTGTAGTTT
 Nr of selected repeats 3 Similarity 0.809524
 Consensus:
 GTAGTTTGTAGttt
 >Cele-UNSB01_2:14195501-14195591 Satlength=91 Nr of Repeats=5 RepeatLength=12
 seed=TAGGCTTAGG
 TAGGCTTAGGCT
 TAGGCTTAGGCTTAACCG
 TAGACTTAGGTTTAGGCTCCGGCTTAGGTTTAGGCT
 TAGCCTTAGGCC
 TAGGCTTAGGCT
 Nr of selected repeats 3 Similarity 0.851852
 Consensus:
 TAGgCTTAGGcT
 >Cele-UNSB01_2:14213145-14213210 Satlength=66 Nr of Repeats=4 RepeatLength=12
 seed=TAGGCTTAGG
 TAGGCTTAGGCT
 TAGGCTTAGGTTTAGACTTATAT
 TAGGCTTAGGTT
 TAGGCTTAGGCT
 Nr of selected repeats 3 Similarity 0.925926
 Consensus:
 TAGGCTTAGGcT
 >Cele-UNSB01_2:14289556-14289862 Satlength=307 Nr of Repeats=8 RepeatLength=34
 seed=CCGTGCCTAC
 CCGTGCCTACTAACCTACCGACCTTGCCTGCCTCTCGTGGCTACTTACCTACCGACTTTACCTGCCAT
 CCGTGCCTACTAACCTACCGACCTTGCCTGCCTC
 CCGTGCCTACTTACCTACCGACTTTACCTGTCTT
 CCATGCCTACTTACCTACCGACTTTACCTGCCAT
 CCGTGCCTACTTACCTACCGACCTTGTCTGCCTT
 CCGTGCCTACTAACCTACCAACCCTGCCTGCCTT
 CCGTGCCTACTAACCTATCGACCTTGTCTGCCTT
 CCGTGCCTACTAACCTATCGACCTTGCCTGCCTC
 Nr of selected repeats 7 Similarity 0.828198
 Consensus:
 CCGTGCCTACTaACCTAcCGACcTTGcCTGCCTt
 >Cele-UNSB01_2:14294397-14294650 Satlength=254 Nr of Repeats=11 RepeatLength=18
 seed=CTAGGTGCCT
 CTAGGTGCCTATTTCGTACCTAGGCGCATATTCATAC
 CTAGGTACCTATCCATTC
 CTAGGTGCCTATAACATTC
 CTAGGCGCCTATGCATAC
 CTAGGTGCCTTTGCATAC
 CTAGGTGCCTTTGCATAC
 CTAGGTGCCTATTTCATACCTACGTGTATAACCATAT
 CTAGGTGTCTATCCATTA
 CTAGGTGCCTATCCATTC
 CTAGGTGCCTATCCATACCTACAGTGCCTATCCATTA
 CTAGGTGCCTATCCATTC
 Nr of selected repeats 8 Similarity 0.804233
 Consensus:

CTAGGTGCCTaTcCATtC

>Cele-UNSB01_2:14297875-14298051 Satlength=177 Nr of Repeats=10 RepeatLength=16

seed=TAGGCATATA
TAGGCATATAGGCATA
TAGGCATATAGGCTTA
TAGGCATATAGGCTTG
TAGGCACATAGGCATA
TAGGCATATAGGCATA
TAGGCATATATGCATA
TAGGCATGTAGGCATA
TAGGGATATAGACATG
TAGGCATATAGGCATA

TAGGCATATAGGCATATAGGCAAAAAGGCATG

Nr of selected repeats 9 Similarity 0.842593

Consensus:

TAGGCATATAGGCaTa

>Cele-UNSB01_2:14303812-14304194 Satlength=383 Nr of Repeats=12 RepeatLength=22

seed=CTACAGTAAC

CTACAGTAACCATATTATTGAA
CTACAGTAACCCTAGTTTTGAA
CTACAGTAACCCAACTATTGAA
CTACAGTAACCCTAGTATTGAA
CTACAGTAACCCTAGTGTAAA
CTACAGTAACCCTAGTATTGAA
CTACAGTAACCTTAGTGTGAA
CTAAAGTAACCCTAGTGTAAAG
CTACAGTAACCCTGGTGTACACAGCAACCTTGGTAGATAATAGTCACGCCGCAC
CTACAGTACTCTATACCTTACCAAATGATACATCTAGGCCACTTCACCA
CTACAGTACTTGTAAGATACAGTATACATCCTATACTCCTATAGATATTCCGTAACCGTAGCCAAGAGCAATC
CTACAGTAATCTTAAACCCTCAGGCCAAAT

Nr of selected repeats 8 Similarity 0.798395

Consensus:

CTACAGTAACCcTAgTaTTgAA

>Cele-UNSB01_2:14320079-14320251 Satlength=173 Nr of Repeats=4 RepeatLength=43

seed=GAAAACCTAGG

GAAAACCTAGGCCACAGAGTTCGAGTTGACGGCCTAGAAATCTA
GAAAACCTAGGCCACGGAGTTCAAATTGATGGCCGAGAAGTCTA
GAAAACGAGGCCACAAACTTGAAATTGGTGGCATAGAGCTCTC
GAAAACCTAGGCCATGGAGTTGAAGTTCCTGGCCTAGAAATCTA

Nr of selected repeats 4 Similarity 0.715762

Consensus:

GAAAACtAGGCCAcagAgTTcaAaTTgatGGCctAGAAaTCTa

>Cele-UNSB01_2:14326178-14326688 Satlength=511 Nr of Repeats=14 RepeatLength=34

seed=CGGAATTGAA

CGGAATTGAAATTTCCGGCAAATTTGGTAAAATGC
CGGAATTGAAATTTCTGGCAAATTTGGTAAAATGC
CGGAATTGAAATTTCCGGCAAATTTGGTAAAATGC
CGGAATTGAAATTTCCGGCAAATTTGGTAAAATGC
CGGAATCGAAAATTTCCGGCAAATTTGGTAAAATGC
CGGAATTGAAATTTCCGGCAAATTTGGTAAAATGG
CGGAATTGAAATTTCCGGCAAATTTGATGAATTGC
CGGAATGGAAACTTCTGGCAAATTTGGTACAATGC
CGGAATTGAAATTTCTGCCAAATTTGGTAAAATGG
CGGAATCGAAAATTTCCGGCAAATTTGGTAAAATGC

CGGAATTGAAATTTCCGGCAAATCGGCCAGTTGGCTGAATGGAAAATACCGGCAAATTGATGAAATGC
CGGAATTGAAATTTCCCAGCAAATCGGCAAGTTGG
CGGAATGGAAAATACCGGCAAATTGATGAAATGC
CGGAATTGAAACTTCCGGCAAATGGTAAATTGG

Nr of selected repeats 13 Similarity 0.833082

Consensus:

CGGAATtGAAAtTTCcGGCAAATTGGTAAAaTGc

>Cele-UNSB01_2:14355758-14355994 Satlength=237 Nr of Repeats=18 RepeatLength=12

seed=ATAGGCATAG

ATAGGCATAGAC

ATAGGCATAGGC

ATAGGCATAGGC

ATAGGCATAGGCATAGAC

ATACGCATAGGC

ATAGGCATAGGC

ATAGGAATAGGC

ATAGGCAAAGGC

ATAGGCATAGGCATTGTC

ATAGGCATTGTC

ATAGGCATAGGC

ATAGGCATAGGC

ATAGGCATAGGCATAGAC

ATACGCATAGGC

ATAGGCATAGGC

ATAGGCATAGGCA

AAGGCATAGGC

ATAGGCATTGTC

Nr of selected repeats 11 Similarity 0.834343

Consensus:

ATAGGCATAGgC

>Cele-UNSB01_2:14379544-14380198 Satlength=655 Nr of Repeats=13 RepeatLength=13

seed=TATACAAAAA

TATACAAAAAATA

TATACAAAAAGTATCAAATTTGTATTTCCGGCAATTCAGCAGTTGCCGGTTTTGTAAATTTTCGAGAATCGGCAATTC

CGGCAATTGCCCGTTTTGTGAATTTCCGGCACAATTCGGCGATTACCGGTTT

TATACAAAAATGAA

TATACAAAAAGTA

TATACAAAAAGTATCAGATTTGTATTTCCGGCAATTCGGCGATTTTTTTTTTGTGACTTTTTGGGAACCGGCAGTTTTG

GCAATCGCCGGTTTTGTGAATTTCCGGCAATCGGCAATTCGGAAATTTCCGGTTT

TATACAAAAAGAA

TATACAAAAAGTA

TATACGAAAAAATATCAAATTTATATTTCCGGTAATGCCGGCAGTTGCCGGTTTTGTAAATTTTCGGGAATCGGCAATT

CCGGCAATTGCCGGTTTTGTGAATTTTCGGCAATCGGCAATTCGGAAATCGCCGGTTT

TATACAAAAAGAA

TATACAAAAATTA

TATACAAAAAGTATCAAATTTGTATTTCCGGCGATTCCGGCAATTGCCGGTTTTGTAAATTTTCGAGAATCGGCAATTC

CGGCAATTGCCCGTTTTGTGAATTTCCGGCACAATTCGGCGATTACCGGTTT

TATACAAAAATGAA

TCTACAAAAAGTA

Nr of selected repeats 9 Similarity 0.837607

Consensus:

TATACAAAAagtA

>Cele-UNSB01_2:14381587-14382260 Satlength=674 Nr of Repeats=16 RepeatLength=42

seed=AAAACCGGCA

AAAACCGGCAATTGCTGGAATTGCCGATTGCCGAATATTACC
AAAACCTGGCAATTGCCAAAAATTGCCGATTGCCGGGAAGATTG
AAAACCGGCAATTGCTAGAATTGCCGATTGCCGAATATTACC
AAAACCTGGCAATTGCCAAAAATTGCCGATTGCCCGAAATATTG
AAAACCGGCAATTGCCGAAATTGCCCTATTGCCGGAAATATTA
AAAACCGGCAATCGCTGAAATTTAGGCTATTTGGCTGATCTTGGCAATTACCGAAATTGCTGACTGCCGGAAATATTG
AAAACCGGCAATTGCCGGAATTGCCAAAAATTTCC
AAAACCGGCAATTGCCGGAATTGCCGATTGCCGATTATTACC
AAAACCGGCAATTGCCGGAATTGCCGGAATCGCCAAAAATTTCC
AAAACCGGCAATTGCCGGAATTGCCGAGTGCCGATTATTACC
AAAACCGGCAATTGCCGAAAAATTTG
AAAACCGGCAATTGTCGCAATTGCCAAAAATTTCC
AAAACCGGCAATTACCGAAATTGCTGATTGCCGGGCATATTG
AAAACCGGCAATTGCCGGAATTGCCGAGTGCAGGAAAGATTA
AAAACCGGCAATTCCCAGAATTGCCGATTGCTGGAATATTG
AAAACCGGCAATTGCCGGAATTGCCAAAAATTTCC

Nr of selected repeats 10 Similarity 0.749832

Consensus:

AAAACcGGCAATTgCcggAATTGCCGAtTGCcgGnAatATTa

>Cele-UNSB01_2:14401364-14401594 Satlength=231 Nr of Repeats=10 RepeatLength=21
seed=CAATTTTCTG

CAATTTTCTGTCAGACTTTGA
CAATTTTCTGTTAACTTTGG
CAATTTTCTGTTAACTTTGG
CAATTTTCTGTTCAACTTTGA
CAATTTTCTGTTCAACTTTGA
CAATTTTCTGTTAACTTTGA
CAATTTTCTGTTCAACTTTGA
CAATTTTCTGTTCAACTTTGA
CAATTTTCCGCAAGATTTTGGTACTTCTCTGCCAAACTTTGG
CAATTTTCTGCCAAACTTTGG
CAATTTTCTGTCAGACTTTGA

Nr of selected repeats 8 Similarity 0.841270

Consensus:

CAATTTTCTGTtnaACTTTGa

>Cele-UNSB01_2:14428274-14428974 Satlength=701 Nr of Repeats=18 RepeatLength=35
seed=GCAAATCGGC

GCAAATCGGCAAGTTGCCGGAATTGAAAATTTCCAG
GCAAATCGGCAAATTTGTCGGCATGGAAATTTCCG
GCAAATCGGCAAATTTGCCGGAATTGAAAATTTCCAG
GCAAATCGGCAAGTTGCCGGAATTGAAAATTTCCAG
GCAAATCGGCAAATTTGCTGGAATTTCAAATTTCCGGCAATTCGGTTAAATTGCCGGAATTTCAAATTTCCG
GCAAATCGCCGGAATTCAAAAATTTCCG
GCAAATCGTCAAATTTGCCTGAATTGAAAATTTCCA
GCAAATCAGCAAATTTGCCGGAATTGAAATTTACCG
GCAAATCGGCAAATTTGCCGGAATTGAAAATTTCCA
GCAAATCGGCAAATTTGCTGGAATTTGAAAATTTCCG
GCAAATCGGCAAATTTGCCGGAATTGAAAATTTCCG
GCAAATCGGCAAATTTGTCGGTATTGAAATTTTCCG
GCAAATCGGCAAATTTGCCGGAATTTCAAATTTCCA
GCAAATCGGCAAATTTGCCGGAATTTAAAGATTTCCG
GCAAATCGGCAAATTTGCCGGAATTTAAAATTTCCG
GCAAATCGGCAAATTTGCCGGAATTTGAAAATTTCCG
GCAAATCGTCAAATTTGCCTGAATTGAAAATTTCCA
GCAAATCGGGAAATTTGCTGGAATTTCAAATTTCCGGCAAATG

Nr of selected repeats 14 Similarity 0.835060

Consensus:

GCAAATCGGCAAaTTGCCgGAATTgAAAaTTTCcg

>Cele-UNSB01_2:14453377-14453692 Satlength=316 Nr of Repeats=8 RepeatLength=35
seed=CGGCAAATCG

CGGCAAATCGGCAAATTGCCGGAATTGTTAATTTTC
CGGCAAATCGGCAAATTGCCGGAACGTGTTAATTTTC
CGGCAAATCGGCAATTTACCGGAATTGCAAATTTTC
CGGCAAATCGGCAAACGTCCGAATTGAAATGTTT
CGGCAAATCGGCAAACGTCCGGAATTGCAAATTTTC
CGGCAAATCGGAAAATTGCCGAAAATGAAAGCTTCCGAAAATCAGCAAATTGCCGGAATTGTTAATTTTC
CGGCAAATCGGCAATTTACCGGAATTGAAAATTTTC
CGGCAAATCGGCAAACGTCCGAATTGAAATGTTT

Nr of selected repeats 7 Similarity 0.780864

Consensus:

CGGCAAATCGGCAAaTgcCgGAATTGnaAATTTc

>Cele-UNSB01_2:14458676-14459058 Satlength=383 Nr of Repeats=11 RepeatLength=35
seed=CCGGCAAATC

CCGGCAAATCAGCAAA
CCGGCAAATGGGCAAATTGCCGAAAATGAAAGCAT
CCGGCAAATCGGCAATATGTCGGTATTGAAAATTTTCAGCCAAA
CCGGCAAATCGGTAAATTGGCGGAATTGAACTTT
CCGGCAAATCGGTAAATTGGCGTATTGAACTTT
CCGGCAAACCGGCAAATCGGTAAATTGGCGGAATTGAACTTT
CCGGCAAACCGGCGAATTATCGGAATTGAAAATTT
CCGGCAAATCGGCAAATGTCCGAATTGAAAATTT
CCGGCAAATCGGTAAATTGGCGTATTGAACTTT
CCGGCAAATCGGTAAATTGGCGTATTGAACTTT
CCGGCAAATCGGCAAATTTGCCGAAAATGAAAGCTT

Nr of selected repeats 8 Similarity 0.757275

Consensus:

CCGGCAAATCGGcAAATTGgCGgaAtTGAAAcTTt

>Cele-UNSB01_2:14462473-14462688 Satlength=216 Nr of Repeats=5 RepeatLength=35
seed=CGGCAAATTG

CGGCAAATTGCCGGAATTTAAATTTTC
CGGCAAATCGGCTAATTGCCGAAATTGAAAATTTTC
CGGCAATTTGTTGGTTTGCACTTTTTTTTGGAAAATTTTCAGAAATTTCAATTTAAATCTGGAAAATTGCACGCATCCAAGG
AAAAC
CGGCAAATTGCCGGAATTGAAAATTTCCGACAAAT
CGGCAAATTGCCGGAATTGAAAATTTCCGGTAAAT

Nr of selected repeats 3 Similarity 0.586563

Consensus:

CGGCaAATTGCCGgAATTGAAAATTTTCcgnaaat

>Cele-UNSB01_2:14464146-14465077 Satlength=932 Nr of Repeats=26 RepeatLength=32
seed=AACCAATCAG

AACCAATCAGCGTTGAGCTCTTCCCATTTTGA
AACCAATCAGCGTTGAGCTCTCCTACTTTTGA
AACCAATCAGCGATGGGCTCCACCCTTTTTGA
AACCAATCAGCGATCGGCTCCACCCATTTTGG
AACCAATCAGCACTCAGCTTCTCCCATTTTGA
AACCAATCAGAGCTCAGCTCCACTCATTTTGG
AACCAATCAGCGCTCAGCTCCACTCATTTTGG
AACCAATCAGCGCTCAGCTCCACTCATTTTGG
AACCAATCAGCGCTCAGCGCCGCCATTCTGG

AACCAATCAGCGATAAGCTACACCCACTTTTGGACTTATCAGCACTCAGCTCCTCCCATTTTGG
AACCAATCAGCGCTCAGCTCCACCCATTTTGG
AACCAATCAGCACTCAGCTTCACTCATTTTGG
AACCAATCAGCGCTCAGCTCCACTCATTTTGG
AACCAATCAGAGCTCAGCTCCACTCATTTTGG
AACCAATCAGCGCTCAGCTCCACTCATTTTGG
AACCAATCAGCGCTCAGCTCCACTCATTTTGG
AACCAATCAGCGCTCAGCGCCGCCATTCCTGG
AACCAATCAGCGATAAGCTACACCCACTTTTGGACTTATCAGCACTCAGCTCCTCCCATTTTGG
AACCAATCAGCGCTCAGCTCCACCCATTTTGG
AACCAATCAGCACTCAGCTTCACTCATTTTGG
AACCAATCAGCGCTCAGCTCCACTCATTTTGGG
ACCAATCAGCGCTCAGCTCCACTCATTTTGG
AACCAATCAGCGCTCAGCTCCACTCATTTTGG
AACCAATCAGGATTCAGTTCACCCACTTTTGG
AACCAATCAGAACTCAGCTCCTCCCATTTTGGGACCAATCACCGATTAGCTCCACCCACTTCTGG
AACCAATCAGCACTCAGCTCCACCCACTTTTGG
AACCAATCAGCGCTCAGCCCTCCAATTTCCG

Nr of selected repeats 19 Similarity 0.803296

Consensus :

AACCAATCAGCGcTCAGCTCCaCcCATTTTGG

>Cele-UNSB01_2:14513028-14524678 Satlength=11651 Nr of Repeats=63

RepeatLength=185 seed=CTCGGACATA

CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACATTGGCCAAGAGTGTTCTAGTAAGAGA
ATTTCAATTTAGAAATATGAACAATTTGGGTAATTGGAAAGTGTCTTCGGGAATCTTTATACATCCGACAAATTCGAGTAT
GTTAGTATTCTGAATTGGATTCTTTTT
CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACGTTGGCCAAGAGTGTTCTAGTAAGAGA
ATTTCAATTTAGAAATATGAACAATTTGGGTAATTGGAAAGTGTCTTCGGGAATGATTATTCGTCCGATGTATTTCGACTAT
GTTCAATTTCTGAGTCGGATCTTTTT
CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACGTTGGCCAAGAGTGTTCTAGTAAGAGA
ATTTCAATTTAGAAATATGAACAATTTGGGTAATTGGAAAGTGTCTTCGGGAATCTTTATACATCCGACAAATTCGAGTAT
GTTAATATTCTGAATTGGATTCTTTTT
CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACATTGGCCAAGAGTGTTCTAGTAAGAGA
ATTTCAATTTAGAAATATGAACAATTTGGGTAATTGGAAAGTGTCTTCGGGAATCTTTATACATCCGACAAATTCGAGTAT
GTTAGTATTCTGAATTGGATTCTTTTT
CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACGTTGGCCAAGAGTGTTCTAGTAAGAGA
ATTTCAATTTAGAAATATGAACAATTTGGGTAATTGGAAAGTGTCTTCGGGAATGATTATTCGTCCGATGTATTTCGACTAT
GTTCAATTTCTGAGTCGGATCTTTTT
CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACATTGGCCAAGAGTGTTCTAGTAAGAGA
ATTTCAATTTAGAAATATGAACAATTTGGGTAATTGGAAAGTGTCTTCGGGAATCTTTATACATCCGACAAATTCGAGTAT
GTTAATATTCTGAATTGGATTCTTTTT
CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACATTGGCCAAGAGTGTTCTAGTAAGAGA
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CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACATTGGCCAAGAGTGTTCTAGTAAGAGA
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CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACGTTGGCCAAGAGTGTTCTAGTAAGAGA
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GTTAGTATTCTGAATTGGATTCTTTTT
CTCGGACATAAATTGGTGTTCGTATTCACCTTATGATACGTTCCGGCTGCGTACATTGGCCAAGAGTGTTCTAGTAAGAGA
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TCGTAATTATTCATAAGTTTGTGTTGTCTCAGAGCCATGTCTGAAAAACAGATTTTTTTTCGAAAATTTTAAAAAGTT
CGTAAAAATTGGATTTTTGACAAATCTATGCTCTCTTTTTTTGTTTGAATTTAGTTCAGTGACATACAATTTCAAAAA
TATAATGT

Nr of selected repeats 53 Similarity 0.999091

Consensus:

TCGTAATTATTCATAAGTTTGTGTTGTCTCAGAGCCATGTCTGAAAAACAGATTTTTTTTCGAAAATTTTAAAAAGTT
CGTAAAAATTGGATTTTTGACAAATCTATGCTCTCTTTTTTTGTTTGAATTTAGTTCAGTGACATACAATTTCAAAAA
TATAATGT

>Cele-UNSB01_2:14535014-14566604 Satlength=31591 Nr of Repeats=1170

RepeatLength=27 seed=TGTGGCTTCC

TGTGGCTTCCCACTATATTTTACTCTC

CGAAAAGGGGAGATA

CGAAAAGGGGAGCAA

Nr of selected repeats 4 Similarity 0.748148

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_2:14573886-14573978 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTTCGAGA

TCCCCTTTTTCGAGA

TCCCCTTTTCGTTTTGC

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTcGcaga

>Cele-UNSB01_2:14582719-14582837 Satlength=119 Nr of Repeats=5 RepeatLength=18

seed=TAGTCTTGCA

TAGTCTTGcAGcCTCTAT

TAGTCTTGcACCCCTAGAGGTCAATCGAAAAA

TAGTCTTGcAGcCTCTAT

TAGTCTTGcAGTTTTCTAT

TAATCTTGcACCCCTACGGGTTGATTGAAAAAT

Nr of selected repeats 3 Similarity 0.901235

Consensus:

TAGTCTTGcAGccTCTAT

>Cele-UNSB01_2:14966230-14966326 Satlength=97 Nr of Repeats=6 RepeatLength=16

seed=GCAGTTTGCC

GCAGTTTGCCGAGTTT

GCCGTTTGCCGAATTG

GCAGTTTGCCGAGTTT

GCCGTTTGCCGAATTG

GCAGTTTGCCGAGTTT

GCCGTTTGCCGAAGTG

Nr of selected repeats 6 Similarity 0.794444

Consensus:

GCaGTTTGCCGAaTTg

>Cele-UNSB01_2:15007973-15008319 Satlength=347 Nr of Repeats=4 RepeatLength=35

seed=TCCGGCAAAT

TCCGGCAAATCGGCAAATTGGTGAAATTTAAAATT

TCCGGCAAATCGGAAATTTTTTTATTTTTTCTCAACATTTTTTAGATTTTTTACTACAAAAATCAAAAAAAAAATTTCAA

AAATCAAAAAAAAAATTTAATTTTTTTGAAAATCAATTTTTTTTTCTCTAAAAATCCAAAATTGCGATTAAAGATAAAAAA

TAATTTTTTAAAAAATATTTAATTTTTTTTCCGAAAAAAATCAGCAAAAATGCTGGCTATTCAATTAGCCGAAATTTT

CAAT

TCCGGCAATTTTCCGATTTGCCGGAACTTTCAAT

TCCGGCAAATCGGCAAATTGCCGGAATTGAGAATC

Nr of selected repeats 3 Similarity 0.586420

Consensus:

TCCGGCAaATcggCaAaTTGccGaAAtTtanAATn

>Cele-UNSB01_2:15030456-15030601 Satlength=146 Nr of Repeats=7 RepeatLength=21

seed=ATTGGATTAG

ATTGGATTAGATTTGTTCCAT

ATTCGATTAGATTTGTTCCAT

ATTGGATTAGAATTGTTCCAT

ATTGGATTAGATTCCGGCCAT
ATTGGATTAGATTTGTTCCAC
ATTGGATTAGATTTCAACCAT
ATTTGATTAGAAAATCCAT

Nr of selected repeats 6 Similarity 0.792593

Consensus:

ATTGGATTAGATTTcctCCAT

>Cele-UNSB01_2:15064033-15064173 Satlength=141 Nr of Repeats=5 RepeatLength=30

seed=TTCTGGAAAA

TTCTGGAAAATTCTAGAATGTTCCAGAACC

TTCTGGAAAATTCTAAAAAGCTTTAGAACC

TTCTGGAAAA

TTCTAGAAAATTCTGGAATGTTCCAGAACT

TTCTGGAAAATTCTGAAAAAATTTCTGGATTGTTCTAGAACC

Nr of selected repeats 3 Similarity 0.762963

Consensus:

TTCTgGAAAATTCTagAAtGtTccAGAAcC

>Cele-UNSB01_2:15064232-15064367 Satlength=136 Nr of Repeats=9 RepeatLength=15

seed=AGACCCATCG

AGACCCATCGTGGCG

AGGCCCATCGTTGTG

AGACCCATCGTGGTG

AGACGCATCGAGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGTA

AGACCCATCGTGGTG

AGACCCATCGTGGTG

Nr of selected repeats 9 Similarity 0.881481

Consensus:

AGACCCATCGTGGTG

>Cele-UNSB01_2:15064421-15065299 Satlength=879 Nr of Repeats=25 RepeatLength=35

seed=TTAAATTTTC

TTAAATTTTCTGTGAAAAAATATTTTGCGGGGAAAA

TTAAATTTTCTGTGAAAAAATATTTTGAGGGGAAAT

TTAAATTTTCTGTGAAAAAATATTTTGCGGGGAAAT

TTAAATTTTCTGAAAAAAAAATTTTGGCGGGAAAT
TTAAATTTTCTGAAAAAAAAATTTTGGCGGGAAAT
TTAAATTTTCTGTGAAAAAAAAATTTTGGAGGGAAAT
TTAAATTTTCTGTGAAAAAAAAATTTTGGCGGGAAAT
Nr of selected repeats 22 Similarity 0.939312

Consensus:

TTAAATTTTCTGtgAAAAATTTTGGaGGGAAAT

>Cele-UNSB01_2:15097668-15098195 Satlength=528 Nr of Repeats=13 RepeatLength=35
seed=TTTCCGGCAA

TTTCCGGCAAATCGGCAAATGTTGGACTTGAAAA
TTTCCGGCAAATCGGCGAATTGCATTAATTTAAAA
TTTCCGGCAAATTAGCCAATTGCCGGACTTTAGAA
TTTCCGGCAAATCGGCGAATTGCTGAAATTGAAAA
TTTCCGGCAAATCGGCAAATTGCCGGAGTTGAAAA
TTTCCGGCAAATCGGCAAATTGCAGTAATTGAAAA
TTTCCGGCAAATTGGTCAATTGCCGGACTTTAGAAT
TTTCCGGCAAATCGGCGAATTGCAGTAATTGAAAA
TTTCCGGCAAATTGACCAATTGCCAGAATTGAAAA
TTTCCGGCAAATCGGCAAATGTTGGACTTGAAAA
TTTCCGGCAAATCGGCAAATGTTGGACATGAAAA
TTTCCGGCAAATTGTGATTTTTTACATTTTTTTGATATATGAAAATATTTAAAGAAAACGGGAAAATTACAACAAAAAA
AACTCAGTGTTTTGCATTTTGA

TATCCGGCAAACGACAAACCGGCAATTTGCCAAAAATGAAAA

Nr of selected repeats 8 Similarity 0.791837

Consensus:

TTTCCGGCAAATcGGCaAATTGctggAaTTgAAAA

>Cele-UNSB01_2:15105694-15106081 Satlength=388 Nr of Repeats=11 RepeatLength=35
seed=CAGAAAATTT

CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTTT
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTTT
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTTT
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTTT
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTCA

Nr of selected repeats 9 Similarity 0.949206

Consensus:

CAGAAAATTTAAATTTCCCGcCCAAAATATTTTTTca

>Cele-UNSB01_2:15106134-15106254 Satlength=121 Nr of Repeats=7 RepeatLength=15
seed=CCACGATGGG

CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTTA
CCACGATGGGTCTCA
CCACGATGGGTCTCACCTCGATGCGTCTCA
CCACGATGGGTCTCA
CAACGATGGGCCTCG

Nr of selected repeats 6 Similarity 0.881481

Consensus:

CCACGATGGGTCTCA

>Cele-UNSB01_2:15106314-15106454 Satlength=141 Nr of Repeats=5 RepeatLength=30
seed=AATTTTCCAG
AATTTTCCAGAAGGTTCTAGAACAATCCAGAATTTTTTCG
AATTTTCCAGAAAGTTCTGGAACATTCCAG
AATTTTCTAG
AATTTTCCAGAAGGTTCTAAAGCTTTTCAG
AATTTTCCAGAAGGTTCTGGAACATTCTAG
Nr of selected repeats 3 Similarity 0.792593
Consensus:
AATTTTCCAGAAgGTTCTggAaCaTTccAG
>Cele-UNSB01_2:15121230-15121314 Satlength=85 Nr of Repeats=6 RepeatLength=12
seed=TTAGGCTTAGG
TTAGGCTTAGGT
TTAGGCTCAGGCTTAAGT
TTAGGCTAAGGT
TTAGGCTTAGGC
TTAGGCTTAGAC
TTAGGCTTAGGCTTAGGC
Nr of selected repeats 4 Similarity 0.814815
Consensus:
TTAGGCTtAGgc
>Cele-UNSB01_2:15182818-15182878 Satlength=61 Nr of Repeats=5 RepeatLength=12
seed=AAGCCTAAGC
AAGCCTAAGCCT
AAGCCAAGCCT
AAGCCTAAGCCC
AAGCCTAAGCCT
AAGCCAAGCCT
Nr of selected repeats 5 Similarity 0.888889
Consensus:
AAGCctAAGCct
>Cele-UNSB01_2:15212191-15212515 Satlength=325 Nr of Repeats=14 RepeatLength=20
seed=TTCAGTCAAAA
TTCAGTCAAAAATTTAGATTT
TTCAGTCAAAAATTAAGTTTTT
TTCAGTCAAAAATTTAGATTTTTCTGTATAAAAATTAAGTTC
TTCAGTCAAAAATTTAGATTTTTCTGTATAAAAATTAAGTTC
TTCAGTCAAAAATTTAGATTT
TTCTGTCAAAAATTAAGTTT
TTCAGTCGAAATTTTAATTT
TTCAGTCCAAATTTGAATTT
TTCGGTCAAAAATTTAGATTT
TTCTGTCAAAAATTAAGTTT
TTCAGTCAAAAATTTAGATTT
TTCAGTCAAAAATTAAGTTC
TTCAGTCAAAAATTTAGATTT
TTCAGTCAAAAATTAAGTTTTT
Nr of selected repeats 10 Similarity 0.802963
Consensus:
TTCaGTCaAAAtTTaaaTTT
>Cele-UNSB01_2:15219171-15219261 Satlength=91 Nr of Repeats=6 RepeatLength=15
seed=TCGTGGCGAG
TCGTGGCGAGACCCA
TCGTTGCGAGACCCT

TCGTGGCGAGACCCA
TCGTGGCGAGACCCA
TCGTGGCGAGACCCA
TCGTGGCGAGACCCA

Nr of selected repeats 6 Similarity 0.940741

Consensus:

TCGTGGCGAGACCCA

>Cele-UNSB01_2:15219280-15219502 Satlength=223 Nr of Repeats=7 RepeatLength=32

seed=TTTTGGCGGG

TTTTGGCGGGGAATTTAAATTTTCTTTGAAATT
TTTCGGCGGGGAATTCAAATTTTCTGTGAAAAT
TTTTGGCGGGGAATTTAAATTTTCTTTAAATTT
TTTTGGCGGGGAATTCAAATTTTCTGTGAAAAA
TTTTGGCGGGGAATTCAAATTTTCTGTGAAAAT
TTTTGGCGGGGAGTTCAAATTTTCTCTGAAAAA
TTTTGGCGGGGAATTCAAATTTTCTGTGAAAAT

Nr of selected repeats 5 Similarity 0.841667

Consensus:

TTTTGGCGGGGAATTCAAATTTTCTTnTgAAAAt

>Cele-UNSB01_2:15221118-15221238 Satlength=121 Nr of Repeats=8 RepeatLength=15

seed=GGTGAGACCC

GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGC

Nr of selected repeats 8 Similarity 0.926984

Consensus:

GGTGAGACCCaTCGT

>Cele-UNSB01_2:15221118-15221591 Satlength=474 Nr of Repeats=14 RepeatLength=15

seed=GGTGAGACCC

GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGC
GGTGAGACCCTTCGC

GGTGATACCCACATTTTTGGCGGGAAATTCAAATTTTCTGTGAAAACAATTTTGGCGGGAAATTCAAATTTTTCAGTGAA
AAAATTTTGGCGGGAAATTCAAATTTTTCAGTGAAAAATTTTGGTGGGAAATTCAAATTTTCTATGAAAAAATATCAT
TACTTATATATAAAAAAATACAGTTCGTCTGTCCATAGTTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTCACACC
CAAAGTCAGTGAGAGTTGTGGCGGGCCTGTCACCTTCGTC

GTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGC

Nr of selected repeats 12 Similarity 0.916498

Consensus:

GGTGAGACCctTCGt

>Cele-UNSB01_2:15221267-15222837 Satlength=1571 Nr of Repeats=42
RepeatLength=32 seed=TTTTGGCGGG
TTTTGGCGGGAAATTCAAATTTTCTGTGAAAACAA
TTTTGGCGGGAAATTCAAATTTTCAAGTGAACAAA
TTTTGGCGGGAAATTCAAATTTTCAAGTGAACAAA
TTTTGGTGGGAAATTCAAATTTTCTATGAAAAAATATCATTACTTATATATAAAAAAATACAGTTCGTCTGTCCATAG
TTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTCACACCCAAAGTCAAGTGAAGAGTTGTGGGCGGGCCTGTACACCTT
CGTCGTGAGACCCATCGTGGTGAGACCCTTCGTGGTGAGACCCATCGTGGTGAGACCCTTCGCGGTGAGACCCTTCGCG
GTGATAACCCACAT
TTTTGGCGGGAAATTCAAATTTTCTGTGAAAACAA
TTTTGGCGGGAAATTCAAATTTTCAAGTGAACAAA
TTTTGGCGGGAAATTCAAATTTTCAAGTGAACAAA
TTTTGGCGTGAATTCAAATTTTCTGAAACAT
TTTTGGCGGGAATTCAAATTTTCTCTGAAAAAT
TTTTGGCGGGAATTTAAATTTTCTTCAAAATT
TTTTGGCGGGAATTCAAATTTTCTTCAAAATT
TTTTGGCGGGAATTCAAATTTTCTTTGAAAAAT
TTTTGGCGTGAATTCAAATTTTCTGAAACAT
TTTTGGCGGGAATTCAAATTTTCTCTGAAAAAT
TTTTGGCGGGAATTTAAATTTTCTTTAAATTT
TTTTGGCGGGAATTCAAATTTTCTCTGAAAAAT
TTTTGGCGGGAATTTAAATTTTCTTTAAATTT
TTTTGGCGGGAATTCAAATTTTCTGTGAAAAA
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TTTTGGCGGGAATTCAAATTTTCTCTGAAAAA
TTTTGGCGGGAATTTAAATTTCTTCAAAATT
TTTTGGCGGGAATTCAAATTTTCTTTGAAAAAT
TTTTGGCGGGAATTCAAATTTTCTTAAATTT
TTTTGGCGGGAATTCAAATTTTCTCTGAAAAAT
TTTTGGCGGGAATTCAAATTTTCTTCAAAATT
TTTTGGCGGGAATTCAAATTTTCTTTGAAAAAT
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TTTTGGCGGGAATTCAAATTTTCTCTGAAAAAT
TTTTGGCGGGAATTTAAATTTTCTTTAAATTT
TTTTGGCGGGAATTCAAATTTTCTCTGAAAAAT
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TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
TTTTGGCGGGAGTTCAAATTTTCTCTGAAAAA
TTTTGGCGGGAATTTAAATTTCTTCAAAATT
TTTTGGCGGGAATTCAAATTTTCTTTGAAAAAT
TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
TTTTGGCGGGAATTCAAATTTTCTCTGAAAAAT
TTTTGGCGGGAATTTAAATTTTCTTTAAATTT
TTTTGGCGGGAATTCAAATTTTCTGTGAAAAA
TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
Nr of selected repeats 27 Similarity 0.855679
Consensus:
TTTTGGCGGGAATTCAAATTTTCTnTgAAAAAT
>Cele-UNSB01_2:15224452-15224572 Satlength=121 Nr of Repeats=8 RepeatLength=15
seed=GGTGAGACCC
GGTGAGACCCTTCGT
GGTGAGACCATCGT

GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGC

Nr of selected repeats 8 Similarity 0.926984

Consensus:

GGTGAGACCCaTCGT

>Cele-UNSB01_2:15224452-15225368 Satlength=917 Nr of Repeats=26 RepeatLength=15

seed=GGTGAGACCC

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGC

GGTGAGACCCTTCGC

GGTGATACCCACATTTTTGGCGGGAAATTCAAATTTCTGTGAAAACAATTTGGCGGGAAATTCAAATTTTCAGTGAA
AAAATTTGGCGGGAAATTCAAATTTTCAGTGAAAAAATTTGGTGGGAAATTCAAATTTCTATGAAAAAATATCAT
TACTTATATATAAAAAAATACAGTTCGTCTGTCCATAGTTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTCACACC
CAAAGTCAGTGAGAGTTGTGGCGGGGCCTGTCACCTTCGTC

GTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGC

GGTGAGACCCTTCGC

GGTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGC

GGTGAGACCCTTCGC

GGTGATACCCACATTTTTGGCGGGAAATTCAAATTTCTGTGAAAACAATTTGGCGGGAAATTCAAATTTTCAGTGAA
AAAATTTGGCGGGAAATTCAAATTTTCAGTGAAAAAATTTGGTGGGAAATTCAAATTTCTATGAAAAAATATCAT
TACTTATATATAAAAAAATACAGTTCGTCTGTCCATAGTTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTCACACC
CAAAGTCAGTGAGAGTTGTGGCGGGGCCTGTCACCTTCGTC

GTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGC

GGTGAGACCCTTCGC

Nr of selected repeats 22 Similarity 0.913805

Consensus:

GGTGAGACCCtTCGt

>Cele-UNSB01_2:15224601-15228185 Satlength=3585 Nr of Repeats=96

RepeatLength=32 seed=TTTTGGCGGG

TTTTGGCGGGAAATTCAAATTTCTGTGAAAACAA

TTTTGGCGGGAAATTCAAATTTTCAGTGAAAAAA

TTTTGGCGGGAAATTCAAATTTTCAGTGAAAAAA

TTTTGGTGGGAAATTCAAATTTCTATGAAAAAATATCATTACTTATATATAAAAAAATACAGTTCGTCTGTCCATAG
TTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTCACACCCAAAGTCAGTGAGAGTTGTGGCGGGGCCTGTCACCTT
CGTCGTGAGACCCATCGTGGTGAGACCCTTCGTGGTGAGACCCATCGTGGTGAGACCCTTCGCGGTGAGACCCTTCGCG

GTGAGACCCATCGTGGTGAGACCCTTCGTGGTGAGACCCATCGTGGTGAGACCCTTCGCGGTGAGACCCTTCGCGGTGA
TACCCACAT
TTTTGGCGGGAAATTCAAATTTTCTGTGAAAACAA
TTTTGGCGGGAAATTCAAATTTTTCAGTGAAAAAA
TTTTGGCGGGAAATTCAAATTTTTCAGTGAAAAAA
TTTTGGTGGGAAATTCAAATTTTCTATGAAAAAATATCATTACTTATATATAAAAAAATACAGTTCGTCTGTCCATAG
TTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTCACACCCAAAGTCAGTGAGAGTTGTGGGCGGGCCTGTACACCTT
CGTCGTGAGACCCATCGTGGTGAGACCCTTCGTGGTGAGACCCATCGTGGTGAGACCCTTCGCGGTGAGACCCTTCGCG
GTGAGACCCACAT
TTTTGGCGGGAAATTCAAATTTTCTCTGAAAAT
TTTTGGCGGGAAATTCAAATTTTCTGAAACAT
TTTTGGCGGGAAATTTAAATTTTCTTTGAAAAT
TTTTGGCGTGAATTCAAATTTTCTGAAACAT
TTTTGGCGGGAAATTCAAATTTTCTCTGAAAAT
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TTTTGGCGGGAAATTCAAATTTTCTGAAACAT
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TTTTGGCGGGAGTTCAAATTTTCTCTGAAAAT
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TTTTGGCGGGAGTTCAAATTTTCTCTGAAAAA
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TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
TTTTGGCGGGAATTCAAATTTTCTTAAAAAT
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TTTTGGCGGGAATTTAAATTTCTTCAAAAT
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TTTTGGCGGGAATTCAAATTTTCTGAAAAA
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TTTTGGCGGGAATTCAAATTTTCTTTGAAAAA
TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
TTTTGGCGGGAATTCAAATTTTCTTAAAAAT
TTTTGGCGGGAATTCAAATTTTCTCTGAAAAA
TTTTGGCGGGAATTCAAATTTTCTTCAAAAT
TTTTGGCGGGAATTCAAATTTTCTTTGAAAAA
TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
TTTTGGCGGGAATTCAAATTTTCTGAAAAA
TTTTGGCGGGAATTTAAATTTTCTTTAAAAAT
TTTTGGCGGGAATTCAAATTTTCTGTGAAAAA
TTTTGGCGGGAATTCAAATTTTCTGAAAAA
TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
TTTTGGCGGGAATTTAAATTTTCTTTAAAAAT
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TTTTGGCGGGAATTTAAATTTCTTCAAAAT
TTTTGGCGGGAATTCAAATTTTCTTTGAAAAA
TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
TTTTGGCGGGAATTCAAATTTTCTGTGAAAAA
TTTTGGCGGGAATTTAAATTTTCTTTAAAAAT
TTTTGGCGGGAATTCAAATTTTCTGTGAAAAA
TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
TTTTGGCGGGAGTTCAAATTTTCTGAAAAA

Nr of selected repeats 67 Similarity 0.850591

Consensus:

TTTTGGCGGGAATTcAAATTTTCTnTgAAAAA

>Cele-UNSB01_2:15229801-15229921 Satlength=121 Nr of Repeats=8 RepeatLength=15

seed=GGTGAGACCC

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT
GGTGAGACCCTTCGC

Nr of selected repeats 8 Similarity 0.926984

Consensus:

GGTGAGACCCaTCGT

>Cele-UNSB01_2:15229801-15230289 Satlength=489 Nr of Repeats=15 RepeatLength=15

seed=GGTGAGACCC

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGC

GGTGAGACCCTTCGC

GGTGATACCCACATTTTTGGCGGGAAATTCAAATTTTCTGTGAAAAAATTTTGGCGGGAAATTCAAATTTTTCAGTGAA

AAAATTTTGGCGGGAAATTCAAATTTTTCAGTGAAAAAATTTTGGTGGGAAATTCAAATTTTCTATGAAAAAATATCAT

TACTTATATATAAAAAAATACAGTTCGTCTGTCCATAGTTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTCACACC

CAAAGTCAGTGAGAGTTGTGGCGGGCCTGTCACCTTCGTC

GTGAGACCCATCGT

GGTGAGACCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCTTCGC

GGTGAGACCCTTCGC

Nr of selected repeats 13 Similarity 0.913390

Consensus:

GGTGAGACCctTCGt

>Cele-UNSB01_2:15229950-15234144 Satlength=4195 Nr of Repeats=125

RepeatLength=32 seed=TTTTGGCGGG

TTTTGGCGGGAAATTCAAATTTTCTGTGAAAACAA

TTTTGGCGGGAAATTCAAATTTTTCAGTGAAAAAA

TTTTGGCGGGAAATTCAAATTTTTCAGTGAAAAAA

TTTTGGTGGGAAATTCAAATTTTCTATGAAAAAATATCATTACTTATATATAAAAAAATACAGTTCGTCTGTCCATAG

TTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTCACACCCAAAGTCAGTGAGAGTTGTGGCGGGCCTGTCACCTT

CGTCGTGAGACCCATCGTGGTGGAGACCCTTCGTGGTGGAGACCCATCGTGGTGGAGACCCTTCGCGGTGAGACCCTTCGCG

GTGAGACCCACAT

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TTTTGGCGGGAATTCAAATTTTCTGAAACAT

TTTTGGCGGGAATTCAAATTTTCTTTGAAAAT

TTTTGGCGTGAATTCAAATTTTCTGAAACAT

TTTTGGCGGGAATTCAAATTTTCTCTGAAAAT

TTTTGGCGGGAATTTAAATTTTCTTTAAAAT

TTTTGGCGGGAATTCAAATTTTCTCTGAAAAT

TTTTGGCGTGAATTCAAATTTTCTGAAACAT

TTTTGGCGGGAATTCAAATTTTCTCTGAAAAT

TTTTGGCGGGAATTCAAATTTTCTGAAACAT

TTTTGGCGGGAATTCAAATTTTCTTTGAAAAT

TTTTGGCGTGAATTCAAATTTTCTGAAACAT

TTTTGGCGGGAATTCAAATTTTCTCTGAAAAT

TTTTGGCGGGAATTTAAATTTTCTTTAAAAT

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TTTTGGCGGGAATTCAAATTTTCTGAAACAT

TTTTGGCGGGAATTCAAATTTTCTCTGAAAAA

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TTTTGGCGGGAATTCAAATTTTCTCTGAAAA
TTTTGGCGGGAATTTAAATTTTCTTTAAAAAT
TTTTGGCGGGAATTCAAATTTTCTGTGAAAA
TTTTGGCGGGAATTCAAATTTTCTGAAAAAT
Nr of selected repeats 93 Similarity 0.859221
Consensus :
TTTTGGCGGGAATTCAAATTTTCTnTgAAAAAT

>Cele-UNSB01_2:15235758-15235848 Satlength=91 Nr of Repeats=6 RepeatLength=15
seed=GGTGAGACCC
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGC
GGTGAGACCCTTCGC

Nr of selected repeats 6 Similarity 0.905185

Consensus:

GGTGAGACCCTTCGT

>Cele-UNSB01_2:15235864-15236243 Satlength=380 Nr of Repeats=11 RepeatLength=34
seed=TTGGCGGGAA

TTGGCGGGAAATTCAAATTTTCTGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTTCAGTGAAAACATT
TTGGCGGGAAAGTTCAATTTTCTATGAAAAAATA
TTGGCGGGAAATTCAAATTTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTTCAGTGAAAAACAAT
TTGGCGGGAAATTCAAATTTTTCAGTGAAAAAGATT
TTGACGGGAAATTCAAATTTTCTGAGGAAAACAT

Nr of selected repeats 7 Similarity 0.880511

Consensus:

TTGGCGGGAAATTCAAATTTTTCAGTGAAAAaATT

>Cele-UNSB01_2:15242777-15242951 Satlength=175 Nr of Repeats=9 RepeatLength=15
seed=AGACCCATCG

AGACCCATCGTGGCG
AGACCCATCGTGGCG
AGACCCATCGTGGTG
AGACCCATCGTGGAA
AGACCCATCGTGGCG
AGACCCATCGTTGCG
AGACCCATCGTGGCGAGACCCAAAATTTGGCGGGAAATTTAAATTTTCGTGGCG
AGACCCATCGTGGTG
AGACCCATCGTGGTG

Nr of selected repeats 8 Similarity 0.895238

Consensus:

AGACCCATCGTGGcG

>Cele-UNSB01_2:15242891-15243160 Satlength=270 Nr of Repeats=5 RepeatLength=35
seed=ATTTTGGCGG

ATTTTGGCGGGAAATTTAAATTTTCGTGGCGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAGAC
CTATCGTGGTGAGACCCGTCGTGGTGAGACCCACCGTGGTAAGACCCAAA
ATTTTGGCGGGTAATTTAAATATTCGGAGAAAAAT
ATTTTGGCGGGAAATTTAAATTTTCTGTGAAAAAT
ATTTTGGCGGGTAATTTAAATTTTTCGGAGAAAAAT
ATTTTGGCGGGAAATTTAAATTTTCTGTGAAAAAT

Nr of selected repeats 4 Similarity 0.904762

Consensus:

ATTTTGGCGGGaAATTTAAATtTTCgGaGAAAAAT

>Cele-UNSB01_2:15286316-15286491 Satlength=176 Nr of Repeats=5 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATTTAAATTC AAGCAAGTTGCCGT
TTTGCCGGAAATTTTAAATTC TGGCAATTTGCCGA
TTTGCCGGAAATTTTAAATAC GGGACACTTTGTCTGA
TTTGCCGGAAATTTTGAATTT GGGCAGTTTGCCGA
TTTGCCGGAAATTTGCTAATTC CGGCAAATTTGCCGA

Nr of selected repeats 3 Similarity 0.771429

Consensus:

TTTGCCGGAAATTTtnAATTCnGGCAatTTGCcGA

>Cele-UNSB01_2:15290141-15290702 Satlength=562 Nr of Repeats=16 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATTTGAATTTTGGACAATTTTTCGGCAATTTCAAATTCAGCGATTTGCCGA
TTTGCCGGAAAGTTTCAATTCAGGCAACTTGTCTGT
TTTGCCGGAAATTTAAAATTCGGGCAA
TTTGCCGGAAAATTTCAATTCGGCCA ACTTTGCCGA
TTTGCCGGAAATTTAAAATTCGGGCAA
TTTGCCGGAAAATTTCAATTCGGCCA ACTTTGTTGA
TTTGTCTGGAAATTTTAAATTCGGGCAATTTGCAAA
TTTCCGGAAATTTTAAATTCAGCGATTTGCCAAT
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TTTGCCGGAAATTTTCAATTCGGGCAACTTTGCCGA
TTTGCCGGAAATTTCCAATTCGGGCAACTTTGCCGA
TTTGCCGGAAATTTTAAATTCAGCGAGTTGCCGG
TTTGCCGGAAAGTTCCAATTCGGGCAACTTTGCCGA
TTTGCCGGAAATTTTAAATTCAGCGAGTTGCCGT
TTTGCCGGAAATTTCCAATTCGGGCAACTTTGCCGA

Nr of selected repeats 11 Similarity 0.731650

Consensus:

TTTGCCGGAAATTTtcAATTCcGcCaanTTGCCGa

>Cele-UNSB01_2:15354583-15354863 Satlength=281 Nr of Repeats=8 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATTTTCAATTCGGGCAATTTGCCGG
TTTGCCGGAAATTTTCAATTCGGGCAATATACTGA
TTTGCCGGAAAATTTCAATTCGGGCAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGGGCAATTTGCCTT
TTTGCCGGAAATTTTCAATTCGGGCAATATACTGA
TTTGCCGGAAAATTTCAATTCGGGCAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGGGCAATTTGCCTT
TTTGCCGGAAATTTTCAATTCGGGCAATTTGCCGG

Nr of selected repeats 8 Similarity 0.858503

Consensus:

TTTGCCGGAAATTTTCAATTCcGcCAATtTgCgga

>Cele-UNSB01_2:15381973-15383739 Satlength=1767 Nr of Repeats=38
RepeatLength=15 seed=GGGTCTCACC

GGGTCTCACC GCGAA
GGGTCTCACC ACAAC
GGGTCTCACC ACGAA
GGGTCTCACC ACGAT
GGGTCTCACC ACGAT
GGGTCTCACC ACGAA
GGGTCTCACC ACGAT

GGGTCTCACGACGAAGGTGACAGGCCCGCCCAACTCTCACTGACTTTGGGTGTGACGTACAGACTACAAAGACTA
CATAGACTACAAACTATGGACAGACGAAGTGTATTTTTTTATATATAAGTAATGATATTTTTTTTCATAGAAAATTTGAA

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ATTTCCCGCCAAAATGT

GGGTCTCACCACGAA
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GGGTCTCACCACGAT
GGGTCTCACCACGAA
GGGTCTCACCACGAT
GGGTCTCACCACGAA
GGGTCTCACCACGAT
GGGTCTCACCACGAA
GGGTCTCACCACGAT
GGGTCTCACCACGAA
GGGTCTCACCACGAT

Nr of selected repeats 35 Similarity 0.915593

Consensus:

GGGTCTCACCACGAn

>Cele-UNSB01_2:15429658-15431122 Satlength=1465 Nr of Repeats=9

RepeatLength=163 seed=AAATAAAAAA

AAATAAAAAAGAATGACTCCATATGATTTTCCCATACTTTTGAATTTTGAAAAAATCAGCTTTTATATATTTTTTATCA
ACTTTTAAAAAATACTTCCGTACAAGCTAATACTCTGTTTGGCATTCTGTTAACTTTGACTATGCTGAACAGTT
TTATG

AAATAAAAAAGAATGACTCCATATGATTTTCCCATACTTTTGAATTTTGAAAAAATCAGCTTTTATATATTTTTTATCA
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TTATG

AAATAAAAAAGAATGACTCCATATGATTTTCCCATACTTTTGAATTTTGGAAAAATCAGCTTTTATATATTTTTATCA
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AAATAAAAAAGAATGACTCCATATGATTTTCCCATACTTTTGAATTTTGGAAAAATCAGCTTTTATATATTTTTATCA
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TTATG
AAATAAAAAAGAATGACTCCACATGATTTTCCAGTACTTTTTAATTTTGAATTAACAGCTTTCCGATACATTCTGTTT
TTTTTTTTAAATAAACTTCCGTAGAAGCTACCATTTTTTTTTGGTGTCTTAGTATATTGAACATGCTAAACAGTTTTG
TA

Nr of selected repeats 8 Similarity 0.966696

Consensus:

AAATAAAAAAGAATGACTCCATATGATTTTCCcATACTTTTGAATTTTGGAAAAATCAGCTTTTATATATTTTTATCA
ATTTTTAAAAAATACTTCCGTACAAGCTAATATACTtTGaTTGGCATATTCTGGTAAtTTTaACTATGCTGAACAGTT
TTATG

>Cele-UNSB01_2:15432049-15432695 Satlength=647 Nr of Repeats=18 RepeatLength=34
seed=TTTCAATTCC

TTTCAATTCCGGCAACTTTCCGATTTGGCGGAAA
TTTCAATTCCGGCAACTTGCCGATTTGCCAAAAAT
TTTAATTCCGACAACCTTGCCGATTTGCCGGATA
TTTCAATTCCGGCAATTTGTTCGATTTGCCGGAAA
TTTCAATTCCGGCAATTTACCGATTTGCCGGATA
TTTCAATTCCGGCAATTTGTTCGATTTGCCGGAAA
TTTCAATTCCGGCAATTTACCGATTTGCCGGATA
TTTCAATTCCGGGACCTTGCCGATTTGCCGGAAATTTCAATGTCCGCAATTTGCCGATTTGCCGGGAAA
TTTCAATTCCGGCAATTTGCCGATTTGCCGGAAA
TTTCAATTCCGGCAATTTGCCGATTTGCCGGGAAA
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TTTCAATTCCGGCAATTTGTTCGATTTGCCGGAAA
TTTCAATTCCGGCAATTTACCGATTTGCCGGATA
TTTCAATTCCGGCACCTTGCCGATTTGCCGGAAA
TTTCAATTCCGGCAATTTGCCGATTTGCCGGGAAA
TTTCAATTCCGGCAATTTGCCGATTTGCCGGAAA
TTTCAATTCCGGCAATTTGCCGATTTGCCGGGAAA

Nr of selected repeats 13 Similarity 0.912016

Consensus:

TTTCAATTCCGGCAATTTgCgGATTTGCCcGGAAa

>Cele-UNSB01_2:15437952-15438032 Satlength=81 Nr of Repeats=4 RepeatLength=20
seed=TGTAGATTTA

TGTAGATTTACGAAGGACAA
TGTAGATTTACGCGGGATGG
TGTAGATTTACAAAGAATAA

TATAGATTTACACAGGACAG

Nr of selected repeats 4 Similarity 0.688889

Consensus:

TgTAGATTTACaaaGgAcaa

>Cele-UNSB01_2:15454038-15454614 Satlength=577 Nr of Repeats=12 RepeatLength=35
seed=CCGATTTGCC

CCGATTTGCCGAAATTTTAAATTCGGCAATTTTCAGATTGCCGATAGCAGATTTCCCGAAATTTTATAGAGCGATT
TTGTATAAGGAGGGACCCTTAAAACCGCCTTTTGAATTTTAGGAAATTTCTGAAATTTTCATTTTAAAAAATGTGCAA
AACGACAATTTGCAGAAGATTTTCGGCAATTTG
CCGATTTGCCGAAATTTTGAATTCGGCAACTTC
CCGATTTGCCGAAATTTTCAACTACGGCTATTTG
CCGATTTGCCGAAATTTTGAATTCGGCAATTTG
CCGATTTGCCGAAATTTTGAATTCGGCAACTTC
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CCGATTTGCCGAAATTTTGAATTCGGCAACTTC
CCGATTTGCCGAAATTTTCAACTACGGCTATTTG
CCGATTTGCCGAAATTTTGAATTCGGCAATTTG
CCGATTTGCCGAAATTTTCAACTACGGCTATTTG
CCGATTTGCCGAAATTTTGAATTCGGCAATTTG
CCGATTTGCCGAAATTTTCAACTACGACTATTTG

Nr of selected repeats 11 Similarity 0.807446

Consensus:

CCGATTTGCCGgAAaTTTtgAAtTcCGGCaAtTTg

>Cele-UNSB01_2:15454990-15455468 Satlength=479 Nr of Repeats=9 RepeatLength=35
seed=TTGCCGGAAT

TTGCCGGAATTTAAAATTTCTGGAAAGTCGGCAAA
TTGCCGGAATTTGAAAAATTTCTGGCAAACCGCCAAA
TTGCCGGAATTTTAAATTTCCGGCAAATCGGCAAA
TTGCCGGAATCAGAAATTTCCGGCAAATCGGCAATTTCCGAAAATGATAATTTCTGAAAAATCGGCAAA
TTGCCGGAATTTAAAATTTCTGGCAAACCGCCAAA
TTGCCGGAATGTTTAAATTTACGGCAAATCGGCAAA
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TACCAAAAATGAAAATTTCCGGCACACCGCCAAA
TTGCCGGAATTTGAAAATTTCTGGCAAATCGGCAATTCGGCAATTTGCCGAAAATGAAAATTTCTGGCAAATCAGAAAAC
CGCCAAA

TTGTGCGGAATTTGAAAATTTCTGACAATCCGCCAAG

Nr of selected repeats 6 Similarity 0.740952

Consensus:

TTGCCGGAATTTaaAATTTCTGGCAAacCGcCAA

>Cele-UNSB01_2:15522229-15522469 Satlength=241 Nr of Repeats=12 RepeatLength=23
seed=GCTACAGTAC

GCTACAGTACCCAGCTTGACTT
GCTACAGTACTTTA
GCTACAGTACCCAGCTTGACTT
GCTACAGTACTTTA
GCTACAGTACCCATCTTGACAT
GCTACAGTACTATCTTGACCA
GCTACAGTACCACAGCTTGACTT
GCTACAGTACTTTA
GCTACAGTACCACAGCTTGACTT
GCTACAGTACTTTA
GCTACAGTACCCATCTTGACAT
GCTACAGTAACCTAGCTTGACCG

Nr of selected repeats 8 Similarity 0.821946

TAAATAATTAGCAGACCATTTTTGGGTATGC
TAAATAATTAGCAGACCAAAGTTGGGTCTGC
TAAATAATTAGCAGACCAAAGTTGGGTCTGC
TAAATAATTAGCAGACCAAAGTTGGGTCTGC
TAAATAATTAGCAGACCAAAGTTGGGACTGC
TAAATATTTAGCAGACCAAAGTTGGGTCTGC
TAAATAATTAGCAGATTATATTTGGGTATGC
TAAATAATTAGCAGACCAAAGTTGGGTCTGC
TAAATAATTAGCAGACCAAAGTTGGGACTGCTAAATATTCAGCAGACCAACGTTGGGTCTGC
TAAATAATTAGCAGATCATATTTGGGTATGC
TAAATAATTAAGTACCACAGTTGGGTCTGC
TAAATAATTAGCAGACCATTTTTGGGTATGC
TAAATAATTAGCAGACCAAAGTTGGGTCTGC
TAAATATTTAGCAGACCATTTTTGTGTCTGC
TAAATATTTAGCAGACCATTTTTGGGTATGC
TAAATAATTAGCAGACCAAAGTTGGGTCTGC

Nr of selected repeats 38 Similarity 0.865584

Consensus:

TAAATAATTAGCAGACCAaagTTGGGTcTGC

>Cele-UNSB01_3:83964-84341 Satlength=378 Nr of Repeats=14 RepeatLength=21
seed=AAATTTGGCT

AAATTTGGCTGGAAATCGTGA
AAATTTGGCTTAAAATGTTGA
AATTTTGGCTTAAAATGGTTC
AAATTTGGCTTTAAATAGTGA
AAATTTGGCTTAAAATGTTGA
AAATTTGGCTTAAAATGGTTC
AAATTTGGCTTTAAATAGTGAAAAATCGGCTTGAAATGGTG
AAATTTGGCTTGAAATGGTGA
AAATTTGGCTTAAAATGTTGA
AAATTTGGCTTAAAATGGTTC
AAATTTGGCTTTAAATAGTGAAAAATCGGCTTTAAATAGTGAAAAATCGGCTTGAAATGGTGA
AAATTTGGCTTGAAATGGTGA
AAATTTGGCTTGAAATGGTGA
AAATTTGGCTTTAAATAGTGAAAAATCGGCTTGAAATGTTGA

Nr of selected repeats 11 Similarity 0.774105

Consensus:

AAATTTGGCTTaAAATgGtTga

>Cele-UNSB01_3:86662-86935 Satlength=274 Nr of Repeats=13 RepeatLength=21
seed=CCATTTTAAG

CCATTTTAAGCCAATTTTGGGA
CCATTTTAAGCCAATTTTGGGA
CCATTTTAAGCCAATTTTGGGA
CCATTTTAAGCCAATTTTGGGA
CCATTTTAAGCCAATTTTGGGA
CCATTTTAAGCCAATTTTGGGA
CCATTTTAAGCCAATTTTGGGA
CCATTTTAAGCCAATTTTGGGA
CCATTTTAAGCCAATTTTGGG
CCATTTTAAGCCAATTTAGGA
CCATTTTAAGACAATTTAGGA
CCATTTTAAGACAATTTAGGA

Nr of selected repeats 13 Similarity 0.947904

Consensus :

CCATTTTAAGCCAATTTtGGA

>Cele-UNSB01_3:86662-87180 Satlength=519 Nr of Repeats=25 RepeatLength=21
seed=CCATTTTAAG

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGGA

CCATTTTAAGCCAATTTTGGG

CCATTTTAAGCCAATTTAGGA

CCATTTTAAGACAATTTAGGA

CCATTTTAAGACAATTTAGGA

CCATTTTAAGACAATTTAGAT

CATTTTAAGTCAATTTAGAT

CATTTTAAGTCAATTTAGAT

CATTTTAAGTCAATTTAGAT

CATTTTAAGTCAATTTAGAT

CATTTTAAGTCAATTTAGGA

CCATTTTAAGCCAATTTTGGAT

CATTTTAAGGCTATTTAGAT

CATTTTAAGGCTATTTAGAT

CATTTTAAGCCAATTTTGAA

CCATTTTAAGCCAATTTTGAA

CCATTTTAAGCCAATTTTGAA

Nr of selected repeats 16 Similarity 0.877588

Consensus :

CCATTTTAAGCCAATTTtGGA

>Cele-UNSB01_3:88388-88698 Satlength=311 Nr of Repeats=9 RepeatLength=31
seed=TGCTAAATAA

TGCTAAATAATTAGCAGACCATTTTGGGTC

TGCTAAATAATTAGCAGACCATTTTGGGTA

TGCTAAATAATTAGCAGACCATTTTGGGTA

TGCTAAATAATTAGCAGACCATTTTGGGTTTGCAAATATTTAACAGACCAAAGTTGGGTA

TGCTAAATAATTAGCAGACCAAAGTTGGGTA

TGCTAAATAATTAGCAGACCATTTTGGGTA

TGCTAAATAATTAGCAGACCAAAGTTGGGTA

TGCTAAATAATTAGCAGACCAAAGTTGGGTA

TGCTAAATAATTAGCAGACCAAAGTTGGGTC

Nr of selected repeats 8 Similarity 0.907834

Consensus :

TGCTAAATAATTAGCAGACCAaagTTGGGTa

>Cele-UNSB01_3:119691-119763 Satlength=73 Nr of Repeats=5 RepeatLength=12
seed=GCCTAAGCCT

GCCTAAGCCTAAGTCATG

GCCTAAGCCTAAGTCATA

GCCTAAGCCTAA

GCCTAAGCCTAG

GCCTCAGCCTAA

Nr of selected repeats 3 Similarity 0.851852

Consensus :

GCCTaAGCCTAa

>Cele-UNSB01_3:134796-135400 Satlength=605 Nr of Repeats=7 RepeatLength=34

seed=AATTCGGCA

AATTCGGCAATGTGTGGTTCGGATTGCGGAAATTTCTATTTATAGGATGCGTACAATTTGCGGATTGAAATT
TAAATTCTGAAATTTCCAAAAAATGCGAAATCACAATTTGCTGAAATTTTCGGAAAAAATCGTTTGCAGCCCACCC
CAAATTATTTTTTCGACA

AATTCGGCAGATCGATAAAATGCGGTTTATCGGTTTTCGGGAAATTTAATTTTTGGCAAATGATTTGCGGAAATGT
TTAGAGAGATTTTTTATAAGACGAAACACTTACAACGTGCTTTTTTTCATAGAATTTGCTTATTTTTCAAATAGAT
GTACATACATAGGAACATTTTCATTCATAGGATGCGTACAATTTGCGGATTGAAATTTCCAAAAAAGTGCAGAA
CCACAATTTGCGGAAATTTTC

AATTCGGCAATTTACCAATTTGCCAGAAATTTTC

AATTCGGCAATTTACCAATTTGCCAAAAATTTTC

AATTCGGCAATTTACCAATTTGCCAGAAATTTTC

AATTCGGCAATTTACCAATTTGCCAAAAATTTTC

AATTCGGCAATTTACCAATTTGCCAAAAATTTTC

Nr of selected repeats 5 Similarity 0.976471

Consensus :

AATTCGGCAATTTACCAATTTGCCAaAAATTTTC

>Cele-UNSB01_3:192738-193322 Satlength=585 Nr of Repeats=4 RepeatLength=31

seed=TTAGCAGACC

TTAGCAGACCCAACCTATGGTCTGCTAATTAT

TTAGCAGACCCAAGTATGGTCTGCTAATTAT

TTAGCAGACCCAACCTATGGTCTGCTAATTAT

TTAGCAGACCCAATTTTTATGTTTTCCAGTTATTTTTCTTCAATTTTTTCAGTATTTTCAGCCAGTACCTGAATAAAA
TCGCGGCGTTTTGTAGTTTTACATCCCAGCGAAGTCGTTGTCTGAGGAATTAATCCTTTAAATCACTGTATCCGCTCTG
AAAAGTTGAAATTTTAGCTTTTTTCCACGAATTTCCAAGCTTCAACAAACATTTATAGCTTCTCTTCGCTGCCGTTTAC
ACCTCAAGTGCCTGCTTCTTTCTATCCGAGCTAAATCCGCCGGAATTCGTCGCTGGCGTGTGGGGCCGATGGGGA
GCTCGCCGAGCCGTCGGCGCACATTAGGTCCATATCGTCCGGCTTTTGGAGAGGAGCTGGCAGCTGCGGAACGGCTTCGA
GACATTTTTGGGCTGAAAAACAGAGAATTTTCAGTAGAGTAATTTGGGAAAAAACGAAGAAAAACGCGGATTTTTGAAAT
TTGGGTCTGCTGATTAA

Nr of selected repeats 3 Similarity 0.942652

Consensus :

TTAGCAGACCCAACtTATGGTCTGCTAAtTAT

>Cele-UNSB01_3:194647-195253 Satlength=607 Nr of Repeats=5 RepeatLength=31

seed=TTAGCAGACC

TTAGCAGACCCAATCTTCCCTTATTTTTGTGTGTTTTTTTTGCGTATTTTGCCCCAAAAATTATCTATAATTTCCCATTT
TTCAGGCCAACTCGAGTTTTGAAGCGTCAAATTTGAGAAAATTCGATGGGAAACGTGCAAAATTCGTTAATTTCCGAAT
TTTGGAGACAATTCGACTGTTTTTACACTGAAATGCACGATTTTCTCGGAAAATTTATGATTTTTGCCCTGAAATTTCA
GAATTTGGCCGATTTTCTTTAGAATTTGGGTCTGCCAACTAATTAGCAGGCTTGTAAGAACGCCACGTGGTTTTTCGATG
GTCTGCTAATAT

TTAGCAGACCCAAGTATGGTCTGCTAATAA

TTAGCAGACCCAAGTATGGTCTGCTAATAA

TTAGCAGACCCAAGTATGGTCTGCTAATAT

TTAGCAGACCCTAATCCCGTATTTATCCTTTAAATTTAGTTTTTTTTCGCGGAATTTACTGGTTTTTTTTCTGTTTTTCAA
CCAGGAAATCGTTCAAATTCATCACTTTTTGTCCCAGAAGCCGAGAAAAATCAGTTTTTTCAGCTCATATCGAAATTTGT
TTTTCAAAAAGAAATTATAAAAAAGT

Nr of selected repeats 3 Similarity 0.971326

Consensus :

TTAGCAGACCCAAGTATGGTCTGCTAATAa

>Cele-UNSB01_3:196367-196735 Satlength=369 Nr of Repeats=7 RepeatLength=31

seed=GGTCTGCTAA

GGTCTGCTAAATATTTAGCAGACCCATTTTT

GGTCTGCTAAATATTTAGCATACCCAACCTTT

GGTCTGCTAATTATTTAGCAGACCCAAGTAT
GGTCTGCTAAATATTTAGCAGACCCAGTAT
GGTCTGCTAAATATTTAGCAGACCCAGTAT
GGTCTGCTAAATATTTAGCATACCCAATTTT
GGTCTGCTAAACATTTTGCAGACCCAATTTGAAAAATCTTAATTTTTTCTCAAAAACGGAATTTTCTTGGTTTTTAC
AGCAAAAATCGAGAATTTCCGCGATTTTCTGACTAGAAAACCTGAAAAATTCGTGAAATTCGTTGAAAAAACTCAATTT
GGAACAGAAATTCGAAAAAAAATG

Nr of selected repeats 6 Similarity 0.868100

Consensus:

GGTCTGCTAATATTTAGCAGACCCaAgTaT

>Cele-UNSB01_3:198288-198567 Satlength=280 Nr of Repeats=9 RepeatLength=31

seed=ACCCAAGTAT

ACCCAAGTATGGTCTGCTAAATATGTAGCAG
ACCCAAGTATGGTCTGCTAATTATTTAGCAA
ACCCAAGTATGGTCTGCTAAATGATTAGCAA
ACCCAAGTATGGTCTGCTAAATGATTAGCAG
ACCCAAGTATGGTCTGCTAAATGTTTAGCAG
ACCCAAGTATGGTCTGCTCAATGTTTAGCAG
ACCCAAGTATGGTCTGCTCAATGTTTAGCAG
ACCCAAGTATGGTCTGCTCAATGTTTAGCAG
ACCCAAGTATGGTCTGCTCAATGTTTAGCAG
ACCCAAGTATGGTCTGCTCAATGTTTAGCAG

Nr of selected repeats 9 Similarity 0.906810

Consensus:

ACCCAAGTATGGTCTGCTaAATgtTTAGCAG

>Cele-UNSB01_3:211856-211976 Satlength=121 Nr of Repeats=7 RepeatLength=16

seed=TAGGCATCTA

TAGGCATCTATGCACT
TAGGCATCTAGGCAGG
TAGGCACCTAGGCATCTATGCACA
TAGGCACCTAGGCACC
TAGGCATCTATGCATC
TAGGCATCTATGCACC
TAGGCATCTATGCACC
TAGGCATCTATGCACC

Nr of selected repeats 6 Similarity 0.827778

Consensus:

TAGGCATCTAtGCACC

>Cele-UNSB01_3:214401-214633 Satlength=233 Nr of Repeats=8 RepeatLength=12

seed=AAGCCTAAGC

AAGCCTAAGCCT
AAGCCTAAGCTCAACTATACGACTCTCTGTAAATTTGCTTTGATCGGCCAACGGGAACCCTTTGAAAAATGAAAAA
AAACGCTATAAACCCAAGCCTAAATAGTAAAAACGCTCGCCACTGACGCC
AAGCTTAAGCTTAAGCAT
AAGACTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCG
AAGCCTAAGATT
AAGACTAAGCCTAGGGTTAAGCGT

Nr of selected repeats 5 Similarity 0.822222

Consensus:

AAGcCTAAGcct

>Cele-UNSB01_3:249570-249725 Satlength=156 Nr of Repeats=4 RepeatLength=31

seed=AGCTCAAAAT

AGCTCAAAATCTGCAAAATGCTCATTTCG
AGCTCAAAATCCACAAAATTACTTATTTTTGAGCTTAAGATCTACAAAACCTGTTCCCTTATTG

AGCTCAAAATCTGTAAAAATGCCCATTTTTG
AGATCAAAATTCACAAAAATGCTCATTTTTA
Nr of selected repeats 3 Similarity 0.711806
Consensus:
AGcTCAAAAtTcTgaAAAAATGcTcATTTTTg
>Cele-UNSB01_3:260141-260567 Satlength=427 Nr of Repeats=12 RepeatLength=30
seed=TTTTTTGAGC

TTTTTTGAGCAAAAAATGCGAAAAATCTAA
TTTTTTGAGCTAAAAATTCAAAAATCTCAGTTTT
TTTTTTGAAGCTAGAAATGCAAAAAATGGAATCTTTCCAAGCTTAAAATCCAAAAATCTTG
TGTTTTGAGCCAAAAATTCAAAAATCTCG
TTTTTTGAGCCAAAAACTCAAAAAATCTCG
TTTTTTGAGCCAAAAACTCTAAAAAGCTCG
TTTTTTGAGCCAAAAATCCAAAAATCTTG
TGTTTTGAGCCAAAAATTCAAAAATCTCG
TTTTTTGAGCCAAAAATTCAAAAATCTCG
TGTTTTGAGCAAAAAATGCGAAAAATCTCA
TTTTTTGAGCTAAAAATTCAAAAATCTCAGT
TTTTTTGAAGCTAGAAATGCAAAAAATGGAATCTTTCCAAGCTTAAAATTCAAAAATCTCGT

Nr of selected repeats 9 Similarity 0.761574
Consensus:
TtTTTTGAGCcAAAAAttCaAAAAATCTcg
>Cele-UNSB01_3:265034-265468 Satlength=435 Nr of Repeats=11 RepeatLength=11
seed=CCTACAGTAC

CCTACAGTACC
CCTACAGTACA
CCTACAGTACCCCGACCATATCCCCACTAACCCCAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCTAAAA
CTACAGTAAT
CCTACAGTACC
CCTACAGTACC
CCTACAGTACCCCGACCATATCCCCACTAATCCCAAATAATATTCTTTCAAAAAGACGAAAAGTCAATTTTTCTAAAA
CTACAGTAAT
CCTACAGTACC
CCTACAGTACCCCGACCATATCTCCCACTAATCCCAAATAATATTCTTTCAAAAAGACGAAAAGTCAATTTTTCTAAAA
CTACAGTAAC
CCTACAGTACC
CCTACAGTACCCCGACCATATCCCCACTAACCCCAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCTAAA
ACTACAGTAAT
CCTACAGTACC

Nr of selected repeats 7 Similarity 0.965368
Consensus:
CCTACAGTACC
>Cele-UNSB01_3:272176-273482 Satlength=1307 Nr of Repeats=13 RepeatLength=101
seed=GGTTACTGTA
GGTTACTGTAGCCCCAGAAGTACGTAAACACTGACGAGGCACCGAATCTTACGACAAAATGCAGAAAATCGTCTAAAAA
TTGGTTTTTGGG
GGTTACTGTAGTTCCAAAAGTACGCAAACACTGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GGTTACTGTAGCTCGAGAAATACGCAAACACTGACTACGGTTCCTAATACATCAGATATTATGACAAAGTGCAGAA
AAATCGCTAAAAATGACTTTACTGG
GGTTACTGTAGCTCCAAAAGTACGCAAACACTGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGGACCCTAATACATCAGATATTATGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG

GGTTACTGTAGCTCCAAAAGTACGCAAACACTGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGGACCCTAATACATCGGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GGTTACTGTACCTCCAGAAATACGCAAACACCGACTACGTGACCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GATTACTGTACCTCCAGAAATACGCAAACACCGACTACGTGACCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG
GGTTACTGTACCTCCAGAAATACGCAAACACCGACTACGTGACCCTAATACATCAGATATTACGACAAAGTGCAGAAAT
TCTCTAAAAATGACTTTACTGG

Nr of selected repeats 11 Similarity 0.942394

Consensus:

GGTTACTGTAgCTCCAgAAaTACGCAAACACcGACTACGgttCCCTAATACATCAGATATTACGACAAAGTGCAGAAAA
TCGCTAAAAATGACTTTACTGG

>Cele-UNSB01_3:344303-344830 Satlength=528 Nr of Repeats=17 RepeatLength=31
seed=TGGTCTGCTA

TGGTCTGCTAAATAATTAGCATACCCAACCT
TGGTCTGCTAAATTTTTAGCAGACCCAACAT
TGGTCTGCTATATATTTAGCAGACCCAACAT
TGGTCTGCTAAATATTTAGCATACCCAACCTG
TGGTCTGCTAAATATTTAGCATACCCAATTT
TGGTCTGCTAAATAATTAGCATACCCAACCT
TGGTCTGCTAAATAATTAGCACACCCAACCT
TGGTATGCTAAATATTTAGCAGACCCAATTT
TGGTCTGCTAAATAATTAGCATACCCAACCT
TGGTCTGCTAAATAATTAGCATACCCAACCT
TGGTATGCTAAATATTTAGCAGACCCAATTT
TGGTCTGCTAAATATTTAGCAGACCCAATTT
TGGTCTGCTAAATTTTTAGCATACCCAACCT
TGGTCTGCTAAATATTTAGCAGACCAAAGATG
GGTCTGCTAAATATTTAGTATACCCAACCTG
TGGTCTGCTAAATATTTAGCATACCCAACCTG
TGGTCTGCTAAATATTTAGCAGACCCAATTT

Nr of selected repeats 15 Similarity 0.868920

Consensus:

TGGTCTGCTAAATAtTTAGCAAtACCCAACcTT

>Cele-UNSB01_3:347263-347821 Satlength=559 Nr of Repeats=17 RepeatLength=31
seed=TATGCTAAAT

TATGCTAAATATTTAGCAGACCAAAAATAGG
TATGCTAAATATTTAGCAGACCAAAAATAGG
TATGCTAAATATTTAGCAGACCAAAAATAGG
TATGCTAAATATGTAGCAGACCAAAAATAGG
TATGCTAAATATGTAGCAGACCAAAAGTATG
TATGCTAAATATTTAGCAGACCAAAAGTAGG
TATGCTAAATATTTAGCAGACCAAAAAGTGGG
TATGCTAAATATTTAGCAGACCAAAAATAGG
TATGCTAAATGTTTAGCAGACCAAAAAGTGGG
TATGCTAAATATTTAGCAGACCAAAAATAGG

CTGCTAAATATTTAGCATACCAACTTCGGGC

CTGCTAAATATTTAGCATACCAACTTTGGGT

Nr of selected repeats 7 Similarity 0.938556

Consensus:

CTGCTAAATATTTAGCATACCaACTTTGGGT

>Cele-UNSB01_3:356762-357146 Satlength=385 Nr of Repeats=13 RepeatLength=31

seed=TTAGCAGACC

TTAGCAGACCAAGATGGGTATGCTAAATAT

TTAGCAGACCCAAATAAATAT

TTAGCAGACCAAGTTGGGTATGCTAAATAT

TTAGCAGACCAAGTTGGGTATGCTAAATAT

TTAGCAGACCAAGTTGGGTATGCTAAATAT

TTAGCAGACCAAGTTGGGTATGCTAAATAT

TTAGCAGACCAAGTTGGGTATGCTAAATAA

TTAGCAGACCAAGTTGGGTATGCTAAATAT

TTAGCAGACCAAGTTGGGTATGCTAAATAT

TTAGCAGACCAAGTTGGGTATGCTAAATAT

TTAGCAGACCAAGTTGGGTATGCTAAATAT

TTAGCAGACCCATTCTGAATAT

TTAGCAGACCCAAGTTTGGTATGGTAAATAT

Nr of selected repeats 11 Similarity 0.960899

Consensus:

TTAGCAGACCAAGTTGGGTATGCTAAATAT

>Cele-UNSB01_3:415402-416126 Satlength=725 Nr of Repeats=7 RepeatLength=40

seed=TCCACGTGGA

TCCACGTGGAATTTTTAGAAATTTCTCAAAAAAATTGAAA

TCCACGTGAAGTTTCAGAATTTCCCAGGAAAATTGAAATCCCCTTAGAATTTTCTTAGGAAGTTTGAATTTCCCTGTGAA

ATTTTCAGAGGCACGACCCGAAAAGGAGAACAGGTGAAAAAGGAGAATTACGAAAAGGAGAACACAAAACCCCGCCATTTT

TCCGTGCCGTGCCAAGTTTTTGCAAAACTTTTGCAAATTTGTAATTTTCAAACGAAACAACGAAGCTCCGAAATAACG

CATTCGTGATAAAACAACAATTTTTACCTGTTCTCCTTTCCGTGGTGTCTCTGAAAATTTTCAGAATTTTCACAGGAAAT

TAAAA

TCTACGTGGAATTTTCAGAATTTTCTCAGAAATTTTGATT

TCCACGTGGAATTTCCGAATTTTCGTAGGAAATTTGAAA

TCCACGTGGAATGTTTAGAATTTTCTCAGAAAATTTGAATCAGTGGTGGGCGGCAATTGCCGTTCCGCAAATTTGATTTG

TCGACAAATTCGGCAAATCGGCTATTTGCCGGTGTGCCGATTTGCCGGAATTTCCATTACGGCAATTTGCCGATTTG

CCGATTCGCCGGAATAATCGCTTGCCGCCACCCTGCTATGAAT

TCCATGTGGAATTTTCAGAATTTCCCAGAAATTTTCAA

TCCACGTGGAATTTCCGGGATTTCCCTGGAAATTTGAAA

Nr of selected repeats 5 Similarity 0.650794

Consensus:

TCcAcGTGGAATTTtcaGaAtTTtCncagaAAatTTgAaa

>Cele-UNSB01_3:421701-421887 Satlength=187 Nr of Repeats=6 RepeatLength=31

seed=TTGGGTCTGC

TTGGGTCTGCTAAATATTTAGCAGACCATAA

TTGGGTCTGCTAAATAATTAGCAGACCATAA

TTGGGTCTGCTAAATATTTAGCAGATTACAC

TTGGGTCTACTAAATAATTAGCAGGCCATAAC

TTGGGTCTGCTAAATATTTAGCAGGCCATAAC

TTGGGTCTGCTAAATAATTAGCAGACCATAA

Nr of selected repeats 6 Similarity 0.868100

Consensus:

TTGGGTCTGCTAAATAaTTAGCAGaCCATAa

>Cele-UNSB01_3:437143-437747 Satlength=605 Nr of Repeats=6 RepeatLength=31

seed=TATTTAGCAG

TATTTAGCAGACCCAATTATGGTCTGCTAAT
TATTTAGCAGACCCAATTATGGTCTGCTAAT
TATTTAGCAGACCCAAGTATGGTTTGCTAAT
TATTTAGCAGACCCAAATATAGTCTGCTAAA
TATTTAGCAGACCCAATTATGATCTGCTAAT
TATTTAGCAGACCCAAGCTTACTGTAAATTTTAAATTATTCCGATAATTCATTCTAGAATAAATATACTTTGAATTGAA
GAACTATTGAAAAAAAAAAAACAAAATTAGTTTTTAAAAAGTTTTCAAAAAATATCATTTTGGTGAAATTTGAGATAATT
TGGAGCTTTTTTGAGCGATTTTTTGGGTTTTTACGAGGATTTCCATCATTTTTTAGCTTCAAAAACTGTGTAAATTGAGCT
AAACAATGATTAAGAGTCCCGAAATGCGGAAACCCGGAGAAAACTTAAAAATCAGACCAAGGGGTGCAGAAATAT
TTTTAAAATTTGGATTTTTCTGTGAAAAGTTTAGTTTTTAGAGTTTTTCGAGTAGTTTCTGGTACTAAAAAGTATTTAAA
AGTATTTTATATCATTTTTTCGTTTGTAAAATCCAGAAAACTGAGAAAAATA

Nr of selected repeats 5 Similarity 0.901075

Consensus :

TATTTAGCAGACCCAAtTATggTcTGCTAAt

>Cele-UNSB01_3:438816-440336 Satlength=1521 Nr of Repeats=38 RepeatLength=40
seed=TAGAAAGTTC

TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCCCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTCTTGATTTTTTC
TAGAAAGTTCTGGTACATTCCAGAAATTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTGGTACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCCCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTTCCCAATTTTTTC
TAGAAAGTTCTGGTACATTCCAGAAATTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTGGTACATTCCAGAAATTTTCCCAATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCAATTTTTTC
TAGAAAGTTCTGGTACATTCCAGAAATTTCTCGATTTTTTT
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTTGAACATTCCAGACTTTTCCCAATTTTTAC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATCTTCTCGATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTCCCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAAAAATTTCTCGATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTGGTACATTCCAGAAATTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTCCCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTCCCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTCCCGATTTTTTC
TAGAAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTTC
TAGAAAGTTCTGGAACATTCCAGAAATTTCTCGATTTTTTC
TAGAAAGTTCTTGAACATTCCAGAAATTTCCCGATTTTTTC

Nr of selected repeats 38 Similarity 0.903556

Consensus:

TAGAAAGTTCTgGAACATTCCAGAAtTTTCcCgATTTTTTC

>Cele-UNSB01_3:438790-441355 Satlength=2566 Nr of Repeats=43 RepeatLength=40
seed=ACATTCCAGA

ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAAATTTCCCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGACTTTTCCCAATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCTTGATTTTTCTAGAAAGTTCTGGT
ACATTCCAGAATTTTCCAAATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAAATTTCTCGATTTTTCTAGAAAGTTCTGGT
ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAAATTTCCCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGACTTTTCCCAATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCTCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAATTTTCCCAATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCTCGATTTTTCTAGAAAGTTCTGGT
ACATTCCAGAATTTTCCAATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCCCAATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCCCAATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAAATTTCCCAATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAAATTTCCCAATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAAATTTCTCAATTTTTCTAGAAAGTTCTGGT
ACATTCCAGAATTTTCTCGATTTTTTTAGAAAGTTCTGGA
ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTTGA
ACATTCCAGACTTTTCCCAATTTTACTAGAAAGTTCTGGA
ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAATCTTCTCGATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCCCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAAAATTTTCTCGATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCTCGATTTTTCTAGAAAGTTCTGGT
ACATTCCAGAATTTTCCAATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCCCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGACTTTTCCCAATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTTGA
ACATTCCAGAAATTTCCCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGACTTTTCCAATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTGGA
ACATTCCAGAAATTTTTCGAAATTTCCAGAAGATTCTAGATTTCCAGAATTTTAGAATTTTCAGAAAATTTCAATTTCC
CGCAAAAATATTTTTACAGAAAATTTAAATTTCCCGCCAAAATATTTTTACAGAAAATTTAAATTTCCCGCCAAAAT
ATTTTTACAGAAAATTTAAATTTCCCTCCAAAATATTTTTCTCAGAAAATTTAAATTTCCCGCCGAAATATTTTTAC
AGAAAATTTAAATTTCCCGCCAAAATATTTTTCTCAGAAAATTTAAATTTCCCGCCAAAATTTGGGTCTTACCACGGT
GGGTCTCACCACGACGGGTCTCACCACGTTGGGTCTCACCACGATGGGTCTCACCACGATGGGTCTTTTTCACGATGGGT
CTCACCACGGTGGGTCTCGCCACGATGGGTCTCGCCACGATGGGTCTCGCCACGAAGATCTCGCAGCAACATTTTTTTA
ATTTTCCAGAAGGTTCTAGA
ACAATCCAGAATTTTTTCGAATTTTCCAGAAGGTTCTGGA
ACATTCCAGAATTTTCTAGAATTTTCCAGAACCTTATTTCCCGCCAAAATATTTTTACAGAAAATTTAAATTTCCCGC
CAAAATATTTTTACAGAAAATTTAAATTTCCCTTCAAATATTTTTCTCAGAAAATTTAAATTTCCCGCCAAAATATT

TTTCACAGAAAATTTAAATTTCCCGCCAAAATTTTGGGTCTTACCACGGTGGGTCTCACCACGACGGGTCTCACCACGA
TGGGTCTCGCCACGATGGGTCTCGCCACGATGGGTCTCGCCACGATGGGTCTCACCACGATGGGTCTCACCACGATGGG
TCTTTTACGATGGGTCTCACCACGGTGGGTCTCGCCACGATGGGTCTCGCCACGATGGGTCTCGCCACGAAGATCTCG
CAGCAACATTTTTTAATTTTCCAGAAGGTTCTAGA
ACAATCCAGAATTTTTTCGAATTTTCCAGAAGGTTCTGGA

Nr of selected repeats 41 Similarity 0.892358

Consensus:

ACATTCCAGAAATTTTcTcGATTTTTCTAGAAAGTTCTgGA

>Cele-UNSB01_3:441483-441987 Satlength=505 Nr of Repeats=18 RepeatLength=11

seed=CTACAGTACT

CTACAGTACTC

CTACAGTACTA

CTACAGTACCCCGACCATATTCCTACTACTAACCAGCAAACCTATATCTCTTCAAAAAGACAAAAACACAATTTTTTCATAAA

CTACAGTAATC

CTACCGTACTC

CTACAGTACTC

CTACAGTACTACTGCAGTACCCCGACCATATCCCTACTACTAACCCTATATCTCTTCAAAAAGACAAAAGCTCA

ATTTTTTCCTAAA

CTACAGTAATC

CTACAGTACTC

CTACAGTACTC

CTACAGTACTC

CTACAGTACTA

CTACAGTACCCCGACCATATCCCACCTACTAACCCTATATCTCTTCAAAAAGACAAAAACTCAATTTTTTCCTAAA

CTACAGTAATC

CTACAGTACTCCTAAAGTACTC

CTACAGTACTA

CTACAGTACCCCGACCATATCCCACCTACTAACCCTATATCTCTTCAAAAAGACAAAAACTCAATTTTTTCCTAAA

CTACAGTAATC

CTACAGTACTCCTACAGTACTC

Nr of selected repeats 12 Similarity 0.773779

Consensus:

CTACAGTAcTc

>Cele-UNSB01_3:464201-477164 Satlength=12964 Nr of Repeats=79 RepeatLength=164

seed=ATATAATGCT

ATATAATGCTCGTAATTATTAATAAATGTGTGTTGTCTCAGAGCCACGTCTGAAAAACAGATTTTTTCTCGAAAATTT

CAAAAACCTTTGTAGAAATTCGATTTTTGACATAAATGATCTCTCTTTTTTTCTGACATGTATTTTCAGTGACAACCTGTAC

TCGAAA

ATATAATGCTCGTAATTATTAATAAATGTGTGTTGTCTCAGAGCCACGTCTGAAAAACAGATTTTTTCTCGAAAATTT

CAAAAACCTTTGTAGAAATTCGATTTTTGACATAAATGATCTCTCTTTTTTTCTGACATGTATTTTCAGTGACAACCTAAAC

TAGAAA

ATATAATGCTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAGCCACGTCTGAAAAACAGATTTTTTCTCGAAAATTT

CAAAAACCTTTGTAGAAATTCGATTTTTGACATAAATGATCTCTCTTTTTTTCTGACATGTATTTTCAGTGACAACCTAAAC

TAGAAA

ATATAATGCTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAGCCACGTCTGAAAAACAGATTTTTTCTCGAAAATTT

CAAAAACCTTTGTAGAAATTCGATTTTTGACATAAATGATCTCTCTTTTTTTCTGACATGTATTTTCAGTGACAACCTAAAC

TAGAAA

ATATAATGCTCGTAATAATTTATAAGTGTGTGTTGTCTCAGAGCCACGTCTGAAAAACAGATTTTTTCTCGAAAATTT

CAAAAACCTTTGTAGAAATTCGATTTTTGACATAAATGATCTCTCTTTTTTTCTGACATGTATTTTCAGTGACAACCTAAAC

TAGAAA

ATATAATGCTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAGCCACGTCTGAAAAACAGATTTTTTCTCGAAAATTT

CAAAAACCTTTGTAGAAATTCGATTTTTGACATAAATGATCTCTCTTTTTTTCTGACATGTATTTTCAGTGACAACCTAAAC

TAGAAA

ATATAATGCTCGTAATTATTTATAAGTGTGTGTTGCCTCAGAGCCACGTCTGAAAAACAGATTTTTCTCGAAAATTT
CAAAAATTTGTAGAAATTCGATTTTTGACATAAATGATCTCTCTTTTTTTTTCTGACATGTATTTTCAGTGACTACTGGAA
TCGAAA

Nr of selected repeats 68 Similarity 0.967912

Consensus:

ATATAATGCTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAGCCACGTCTGAAAAACAGATTTTTCTCGAAAATTT
CAAAAATTTGTAGAAATTCGATTTTTGACATAAATGATCgCTCTTTTTTTTTCTGACATGTATTTTCAGTGACAAaTggAn
TAGAAA

>Cele-UNSB01_3:495426-496459 Satlength=1034 Nr of Repeats=16 RepeatLength=31
seed=TTTAGCAGAC

TTTAGCAGACCAAAAGTTGGGTATGCTAAATA

TTTAGCAGACCCAAACCAATA

TTTAGCAGACCAAAAGTTGGGTATGCTAAATA

TTTAGCAGACCAATGCCAATA

TTTAGCAGACCCAAAGTTAGGTATGCTAAATA

TTTAGCAGACCCAAAGTTGGGTATGCTAAATA

TTTAGCAGACCAAAAGTTGGGTCTGCTAAATA

TTTAGCAGACCAATGCCAATA

TTTAGCAGACCCAAAGTTAGGTATGCTAAATA

TTTAGCAGACCAATGCCAATA

TTTAGCAGACCCAAAGTTAGGTATGCTAAATA

TTTAGCAGACCAAAAGTTGGGTCTGCTAAATA

TTTAGCAGACCAAAAGTTGGGTCTGCTAAATA

TTTAGCAGACCAAAAGTTGGGTGTGCTAAATA

TTTAGCAGACCCAAAGCCAAT

TTTAGCAGACCAATAGAATTTTATAAAAAGTGGAAATTTGAAAAAATTTGTCATTTTACTAGCCAATTTTTCCAAAATTT
TGAAAATTTCAATAGAATTTCCGAACAAAACCGTCGATCCTCACAATTTTCACAGCGACCCCATCATCCTCGTCAACT
TCGAACGGAACGTCTGGAAGCTGCGGAGCAAACCGCCCGGCTGAAATTTTCTGCGCCGCCATAATACTCCCTGTACAC
GTGGCAAATTTAGGAGCTCAACGAGTTGCTGAACCGACGAAGATTTGATATTTGAAATGTCCCAGTCGTCGAGAACGTT
CTGTGATAGTTCTTGAAATGAGATCTCTTGTCTGCTGTTGTTGAGAAATTCGCGAGAATGATACGGCTTTTTGT
TGCTTTTTCGTTAAACTTGTTCGTGGAGGCCTTTCGTCGTCTGGAATTTTCAGTAAATTTGGTGTATTGCCACTTTTTT
TTTCAAAGTAGCTAAAATTTGCTTAAAAACCATAAAAAAATTGATTTTTTTAAGATTTAAAAATGTTTAAACTAGCTTA
TTTATCTACTTAAATTTCTAAAAACCGTATTTTCAAAAAAAGTTATATTTGGGTCTGCCGAAATA

Nr of selected repeats 10 Similarity 0.931183

Consensus:

TTTAGCAGACCaAAGTTgGGTaTGCTAAATA

>Cele-UNSB01_3:503013-503261 Satlength=249 Nr of Repeats=8 RepeatLength=31
seed=TTGGGTATGC

TTGGGTATGCTAAATATTTAGCAGACCAAGG

TTGGGTATGCTAAATATTTAGCAGACCAAGG

TTGGGTATGCTAAATATTTAGCAGACCAAGG

TTGGGTATGCTAAATATTTAGCAGACCAAGG

TTGGGTATGCTAAATATTTAGCAGACCAAGG

TTGGGTATGCTAAATATTTAGCAGACCAAGG

TTGGGTATGCTAAATATTTAGCAGACCAATG

Nr of selected repeats 8 Similarity 0.970814

Consensus:

TTGGGTATGCTAAATATTTAGCAGACCAaG

>Cele-UNSB01_3:506857-507105 Satlength=249 Nr of Repeats=8 RepeatLength=31
seed=GTATGCTAAA

GTATGCTAAATATTTAGCAGACCAAGTTGG

GTATGCTAAATATTTAGCAGACCAAGTTGG

GTATGCTAAATATTTAGCAGACCAAGTTGA

GTATGCTAAATATTTAGCAGACCAAAGTTGG
GTATGCTAAATATTTAGCAGACCAAAGTTAG
GTATGCTAAATATTTAGCAGACCAAATTTGG
GTATGCTAAATATTTAGCAGACCAAAGTTGG
GTATGCTAAATATTTAGCAGACCAAAGTTGG

Nr of selected repeats 8 Similarity 0.967742

Consensus:

GTATGCTAAATATTTAGCAGACCAAAGTTGG

>Cele-UNSB01_3:516006-516440 Satlength=435 Nr of Repeats=14 RepeatLength=31

seed=GGTCTGCTAA

GGTCTGCTAAATATTTATCATAACCAACTTT
GGTCTGCTAAATATTTAGCATAACCAACTTT
GGTCTGCTAAATATTTAGCATAACCAACTTT
GGTCTGCTAAATATTTAGTAGACCAACTTT
GGTCTGCTAAATATTTAGCATGCCCAACTTT
GGTCTGCTAAATATTTAGCATAACCAACTTT
GGTCTGCTAAATATTTATCATAACCAACTTT
GGTCTGCTAAATATTTAGCATAACCAACTTT
GGTCTGCTAAATATTTAGCATAACCAACTTT
GGTCTGCTAAATATTTAGTAGACCAACTTT
GGTCTGCTAAATATTTAGCATGCCCAACTTT
GGTCTGCTAAATATTTAGCATAACCAACTTT
GGTCTGCTAAATATTTAGCATAACCAACTTT
GGTCTGCTAAATATTTAGCATAACCAACTTT

Nr of selected repeats 14 Similarity 0.954626

Consensus:

GGTCTGCTAAATATTTAGCATAACCAACTTT

>Cele-UNSB01_3:517798-519152 Satlength=1355 Nr of Repeats=34 RepeatLength=31

seed=TTAGCAGACC

TTAGCAGACCCAACCTCCCGAAACTGATTTTTAAAGCTAAAAATTATTAGAATTTTCAGACGTTTCTCTCCGAAATATA
GCATGCCAATAGAAAAATTGACAAAAATCAAGGTTTTCTCATCGAAAAATAGCAAAAATAACTTTTTAAAAATCTACAGAAA
CTCACAATTTTTGTTTAAAAATGCCAACATTTATAAATTTTCTAAATATTTAGTTTTAAATTTGTAATTTTCTCACTTTT
TTCTGTGAAAAATATGCAAAATGAAACTGAAAAATCCACTAAAAATGTTTTAAAAATTTATCTTGAAGAAAAACGTAG
GAAATTTCAAATTTGAGCTAAAAAATCAGCGAAAAAATTTTTTTTTTCAAATTTGAGGAGGTTGGGTATGCTAAATAT
TTAGCAGACCCAAGGAAAAAATAT
TTAGCAGACCAAAGATAGGTATGCTAAATAC
TTAGCAGACCAAAGATAGGTATGCTAAATAT
TTAGCAGACCAAAGAAGGGTATGCTAAATAT
TTAGCAGACCCAAGGTGGGTATGCTAAATAT
TTAGCAGACCCAAGGAAAAAATAT
TTAGCAGACCAAAGATAGGTATGCTAAATAT
TTAGCAGACCAAAGATGGATATGCTAAATAT
TTAGCAGACCAAAGATGGGTATGCTAAATAA
TTAGCAGACCAAAGATGGGTATGCTAAATAA
TTAGCAGACCAAAGATGGGTATGCTAAATAA
TTAGCAGACCCAAGGAAAAAATAT
TTAGCAGACCAAAGTTGGGTATGCTAAATAA
TTAGCAGACCAAAGTTGGGTATGCTAAATAT
TTAGCAGACCAAAGTTGGGTATGCTAAATAT
TTAGCAGACCAAAGATGGGTATGCTAAATAA
TTAGCAGACCAAAGTTGGGTATGCTAAATAT
TTAGCAGACCAAAGTTGGGTATGCTAAATAT
TTAGCAGACCCAAGGAAAAAATAT
TTAGCAGACCAAAGATGGGTATGCTAAATAT
TTAGCAGACCCAAGGAAAAAATAT
TTAGCAGACCAAAGATAGGTATGCTAAACAT

TTAGCAGACCCAAGGAAAAATAT
TTAGCAGACCAAAGATAGGTATGCTAAATAT
TTAGCAGACCAAAGATGGATATGCTAAATAT
TTAGCAGACCAAAGATGGGTATGCTAAATAA
TTAGCAGACCCAAGGAAAAATAT
TTAGCAGACCAAAGATAGGTATGCTAAATAT
TTAGCAGACCAAAGATGGATATGCTAAATAT
TTAGCAGACCAAAGATGGGTATGCTAAATAA
TTAGCAGACCAAAGTTGGGTATGCTAAATAT
TTAGCAGACCCAAGGAAAAATAT
TTAGCAGACCAAAGATAGGTATGCTAAATAT
TTAGCAGACCAAAGATGGGTATGCTAAATAT
TTAGCAGACCAAAGTTGGGTATGCTAAATAT

Nr of selected repeats 25 Similarity 0.924301

Consensus:

TTAGCAGACCAAAGaTgGGTATGCTAAATAT

>Cele-UNSB01_3:523916-525062 Satlength=1147 Nr of Repeats=37 RepeatLength=31
seed=GGTCTGCTAA

GGTCTGCTAAATATTTAGCATAACATTTTT
GGTCTGCTAATTATTCAGCATACCCAAATTT
GGTCTGCTAAATATTTAGCATAACCCAACATT
GGTCTGCTAATTGTTTAGCATACCAAATGT
GGTCTGCTAAAAATATTTAGCATAACCCAACTTTA
GTCTGCTAAATATTTAGCATAACCCAAATTT
GGTCTGCTAAAAATATTTAGCATAACCGAACTTT
GGTCTGCTAATTATTTAGCATAACCCAACTTT
GGTCTGCTAATTATTTAGCCTACCGAACTTT
GGTCTGCTAATTATTTAGCGTACCCAACTTT
GGTCTGCTAATTATTTAGCATAACCCAAATTT
GGTCTGCTAATTATTTAGCGTACCCAACTTT
GGTCTGCTAATTATTTAGCATAACCCAAATTT
GGTCTGCTAAAAATATTTAGCATAACCGAACTTT
GGTCTGCTAAATATTTAGCATAACCCATTTTT
GGTCTGCTAAATATTTAGCACACCAAACCTTT
GGTCTGCTAATTATTTAGCATAACCTAACTTG
GGTCTGCTATATATTTAGCATAACCCAACTTG
GGTCTGCTATATATTTAGCATAACCCAACTTT
GGTCTGCTAATTATTTAGCATAACCGAACTTT
GGTCTGCTAATTATTTAGCATAACCCAACTTT
GGTCTGCTAATTATTTAGCCTACCGAACTTT
GGTCTGCTAATTATTTAGCGTACCCAACTTT
GGTCTGCTAATTATTTAGCATAACCCAAATTT
GGTCTGCTAAAAATATTTAGCATAACCGAACTTT
GGTCTGCTAAATATTTAGCATAACCCATTTTT
GGTCTGCTAAATATTTAGCACACCAAACCTTT
GGTCTGCTAATTATTTAGCATAACCTAACTTG
GGTCTGCTATATATTTAGCATAACCCAACTTG
GGTCTGCTATATATTTAGCATAACCCAACTTT
GGTCTGCTAATTATTTAGCATAACCCAACTTT
GGTCTGCTAAATATTTAGCATAACCCATTTTT
GGTCTGCTAAATATTTAGCACACCAAACCTTT
GGTCTGCTAATTATTTAGCATAACCTAACTTG
GGTCTGCTATATATTTAGCATAACCCAACTTG
GGTCTGCTATATATTTAGCATAACCCAACTTT
GGTCTGCTAATTATTTAGCATAACCCAACTTT
GGTCTGCTAAATATTTAGCATAACCCATTTTT

GGTCTGCTAAATATTCAAATAT

Nr of selected repeats 31 Similarity 0.865048

Consensus:

GGTCTGCTAAAtTATTTAGCATACCcAAcTTT

>Cele-UNSB01_3:546017-546152 Satlength=136 Nr of Repeats=6 RepeatLength=11

seed=CTACAGTACC

CTACAGTACCC

CTAGAGTACCAC

CACAGTACCTTGACATTATCCCCACTAACTTCCAATCTAATACCTCTTCAAACGCTAAAAAATTCAAATTTTCCCCAA

CTACAGTAACC

CTACAGTACCA

CTACAGTACCA

Nr of selected repeats 4 Similarity 0.858586

Consensus:

CTACAGTAcCa

>Cele-UNSB01_3:611245-611586 Satlength=342 Nr of Repeats=11 RepeatLength=31

seed=GGTCTGCTAA

GGTCTGCTAATTATTTAGCATACCCAACTTC

GGTCTGCTAATTATTTAGCATACCGAACTTC

GGTCTGCTAATTATTTAGCATACCCAACTTC

GGTCTGCTAATTATTTAGCATACCGAACTTC

GGTCTGCTAATTATTTAGCATACCCAACTTC

GGTCTGCTAATTATTTAGCATACCGAACTTC

GGTCTGCTAATTATTTAGCATACCGAACTTC

GGTCTGCTAATTATTTAGCATACCGAACTTC

GGTCTGCTAATTATTTAGCATACCGAACTTC

GGTCTGCTAATTATTTAGCATACCGAACTTC

GGTCTGCTAATTATTTAGCATACCCAACTTT

Nr of selected repeats 11 Similarity 0.968719

Consensus:

GGTCTGCTAATTATTTAGCATACCcAACTTC

>Cele-UNSB01_3:614340-614495 Satlength=156 Nr of Repeats=5 RepeatLength=31

seed=TGGGTATGCT

TGGGTATGCTAAATAATTAGCAGACCAAAGT

TGGGTATGCTAAATAATTAGCAGACCAAAGT

TGGGTATGCTAAATAATTAGCAGACCAAAGT

TGGGTATGCTAAATAATTAGCAGACCAAAGT

TGGGTATGCTAAATAATTAGCAGACCAAAGT

Nr of selected repeats 5 Similarity 1.000000

Consensus:

TGGGTATGCTAAATAATTAGCAGACCAAAGT

>Cele-UNSB01_3:660202-660394 Satlength=193 Nr of Repeats=6 RepeatLength=31

seed=TTAGCAGACC

TTAGCAGACCAATGAGGATAGGTCTGCTAAATAT

TTAGCAGACTCATGGTAGGTATGCTAAATAT

TTAGCAGACCCATAGGTGGTCTGCTAAATAA

TTAGCAGACCCATAGTTGGTCTGCTAAATAA

TTAGCAGACCAATGGGGATGGGTCTGCTAAATAT

TTAGCAGACCCAAGTTAGGTATGCTAAATAT

Nr of selected repeats 4 Similarity 0.781250

Consensus:

TTAGCAGACcCAtaGgTaGGTaTGCTAAATAa

>Cele-UNSB01_3:662174-662284 Satlength=111 Nr of Repeats=6 RepeatLength=18

seed=TAGGCTTAGG

TAGGCTTAGGTGTGAGCT
TAGTCTTAGGCTAACCTT
TAGGCTTAAGCTTAGGTG
TAGGCTTAGGTT
TAGGCCTAGGCTTATGCG

TAGGCTTAGGCTTGTGTCTCCAGGCA
Nr of selected repeats 4 Similarity 0.527778
Consensus:

TAGgCtTAgGcTtAgctg

>Cele-UNSB01_3:665955-666358 Satlength=404 Nr of Repeats=13 RepeatLength=31
seed=TGGGTCTGCT

TGGGTCTGCTAAATATTTAGCAGACCAACTA
TGGGTCTGCTAAATATTTAGCAGACCAACTA
TGGGTCTGCTAAATATTCAGCAGACCAACTG
TGGGTCTGCTAAATATTTAGCAGACCAACTG
TGGGTCTGCTAAATATTTAGCAGACCAACTG
TGGGTCTGCTAAATATTTAGCAGACCAACTA
TGGGTCTGCTAGATATTCAGTAGACCAACTG
TGGGTCTGCTAAATATTCAGCAGACCAACTG
TGGGTCTGCTAAATATTTAGCAGACCAACTG
TGGGTCTGCTAAATATTTAGCAGACCAACTG
TGGGTCTGCTAAATATTTAGCAGACCAACTG
TGGGTCTGCTAAATATTTAGCAGACCAACTA
TGGGTCTGCTAGATATTCAGCAGACCAACTG
TGGGTCTGCTAAATATTTAGCAGACCAACTA

Nr of selected repeats 13 Similarity 0.912876

Consensus:

TGGGTCTGCTAAATATTTAGCAGACCAACTg

>Cele-UNSB01_3:727287-727380 Satlength=94 Nr of Repeats=5 RepeatLength=15
seed=GGGGCAACA

GGGGCAACAAAAA
GGGGCAACATTTGAACTCTCCCT
GGGGCAACAAATTA
GGGGCAACATTTTATAAATGTA
GGGGCAGCAAAAAA

Nr of selected repeats 3 Similarity 0.822222

Consensus:

GGGGCAaCAAAaaA

>Cele-UNSB01_3:731921-732069 Satlength=149 Nr of Repeats=8 RepeatLength=15
seed=TGTTGCCCCC

TGTTGCCCCCTAATT
TGTTGCCCCCGGGAGAGTTCAAA
TGTTGACCCCTATTA
TGTTGCCCCCTTTTT
TGCTGCCCCCTACATTTATGAAAA
TGTTGCCCCCTAATT
TGTTGCCCCCCAGGGAGAGTTCAAA
TGTTGTCCCCTTTTT

Nr of selected repeats 5 Similarity 0.795556

Consensus:

TGTTGcCCCCTatTt

>Cele-UNSB01_3:882434-882682 Satlength=249 Nr of Repeats=7 RepeatLength=31
seed=TAAATATTTA

TAAATATTTAGCAGACCAAAGTTAGGTATGC
TAAATATTTAGTAGACCAAAGTTGGGTATGC

TAAATATTTAGCAGGCCAAAAGTTAGGTATGA
TAAATATTTAGCAGACCACAGTTAGGTATGCTATATGTTTAGCAGACCAAAGTTGGGTATGC
TAAATATTTAGCAGACCAAAAATTAGGTATGC
TATATATTTAACACACCAAAAGTTAGGTATCC
TAAATATTTAGCAGACCAAAGTTGGGTATGC
Nr of selected repeats 6 Similarity 0.862366
Consensus:
TAAATATTTAGCAGACCAAAGTTaGGTATGC
>Cele-UNSB01_3:949283-949630 Satlength=348 Nr of Repeats=8 RepeatLength=18
seed=TGCAAGACTA
TGCAAGACTAATAGAGAC
TGCAAGACTATTAGAAGC
TGCAAGACTAATTTTCGATAGCCAAATAATTTTGGAACAGTTATAAACTTTTGTGAAAACCTTAACCTAATACCGTTTA
AGTCATAAAAAATTATTTATTTTCCAATATTTTCATGAGCTATTTTATCATTTTCAAGTTCATTTTATCCAAAAAGTTAC
AAAATTTTAAAGTTTCCCTCATAGTATTGCTATCTAGGCAAAAATAGGAG
TGCAAGACTATTGGAGAC
TGCAATACTAATAGAGAC
TGCAAGACTATTTTTTGATAGACCTCTGGGGG
TGCATGACTAATAGGGG
TGCAAGACTAATAGAGGC
Nr of selected repeats 5 Similarity 0.822222
Consensus:
TGCAAgACTAaTaGAgAc
>Cele-UNSB01_3:949715-950024 Satlength=310 Nr of Repeats=5 RepeatLength=18
seed=TAGTGCTGCA
TAGTGCTGCACCAACAGGCCTTCCGAAAAAT
TAGTGCTGCAGTCTCTAT
TAGTGCTGCACCCATTTTCTACTGAAAGAGTGACTCAATAGTTTTGACATTTTGGGGAGTGTTTTTGTATATTTTTGA
AGATTTCTAGTTAATTTACAAATATAATTGGATTATTGGGTCATCTTTGTTACAAAAATTCACAATTTTAATGGATTTCC
TGCTTAAAGATGAGCATTTGTGACTAAAACTAGTGATCTCTAATTGAAAAAAGCCGTTCCGAAAAAT
TAGTGCTGCAGCCTCCAG
TAGTACTGCAGTCTCTAA
Nr of selected repeats 3 Similarity 0.777778
Consensus:
TAGTgCTGCAGtCTCtAn
>Cele-UNSB01_3:958005-958109 Satlength=105 Nr of Repeats=4 RepeatLength=26
seed=CGGCCAGAGT
CGGCCAGAGTCACTTCTTATGGTGAA
CGGCCAGAGTCACTATATTTGGTGAA
CGGCCAGAGTCACTTCTTATGGTGAA
CGGCCAGAGTCACTAATTTTGGTGAA
Nr of selected repeats 4 Similarity 0.863248
Consensus:
CGGCCAGAGTCACTactTaTGGTGAA
>Cele-UNSB01_3:958146-965823 Satlength=7678 Nr of Repeats=284 RepeatLength=27
seed=AGAGAGTAAA
AGAGAGTAAAATATAGTGGGAAGCCAC
AGAGAGTAAAATATAGTGGGAAGCCAC
AGAGAGTAAAATATAGTGAGAAGCCAC
AGAGAGTAAAATATAGTGGGAAGCCAC
AGAGAGTAAAATATAGTGGGAAGCCAC
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Nr of selected repeats 519 Similarity 0.929610

Consensus:

TGGGAAGCCACAGAGAGTAAAAATATAg

>Cele-UNSB01_3:1041359-1041618 Satlength=260 Nr of Repeats=12 RepeatLength=22
seed=TAAATCTACA

TAAATCTACATAGAGAGTTTCG
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TAAATCTACATAGAGAGCCCCG
TAAATCTACACAAATAGCCCCG
TAAATCTACACACTCGGTCCCCG
TAAATCTACACAGAGAGCTCCG
TAAATCTGCACACTTAGTCCCCG
TAAATCTACACAAAATCCTG
TGAATCTACAGACATAGTCCTG

TAAATCTACACACTTAACCCCG
TAAATCTACACAGAGAGTTCCCT
TAAATCTACACAGGACCCG

Nr of selected repeats 10 Similarity 0.692929

Consensus:

TAAATCTACAcAcataGcccCG

>Cele-UNSB01_3:1053032-1053110 Satlength=79 Nr of Repeats=5 RepeatLength=16

seed=TTATAGTGTT

TTATAGTGTTATAGTG

TTATAGTGTTATAGTG

TTATAATGTTATAGTA

TTATAGTTTATAGTA

TTATAGTTTACAGTG

Nr of selected repeats 3 Similarity 0.888889

Consensus:

TTATAgTGTTATAGTg

>Cele-UNSB01_3:1059346-1075750 Satlength=16405 Nr of Repeats=279

RepeatLength=59 seed=AACTGAGAAT

AACTGAGAATTATGGAGAATATGGAAAATTTAAATGTGCACTGGTTTTCAAAAATTTTTTA
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GAAAATATGAGAATTCAGGCATTTTTCCGGAAAATGCTTAGAAAATCGAT

Nr of selected repeats 12 Similarity 0.883838

Consensus:

AAAATCCACGTAGATTATtGATTTTTCATnGAATTTTGcA

>Cele-UNSB01_3:1112079-1113479 Satlength=1401 Nr of Repeats=16 RepeatLength=40
seed=TTTTGCAAAA

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GAT

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TT

TTTTGCAAAAATTCATGAAAAATCGATAATCCAAGTGGAT

Nr of selected repeats 11 Similarity 0.759596

Consensus:

TTTTGCAAAAATCCACGTAGATTATtGATTTTTTCATgGAA

>Cele-UNSB01_3:1175770-1176177 Satlength=408 Nr of Repeats=4 RepeatLength=96
seed=GAGGGCCGCA

GAGGGCCGCGAGGCCCGAACACTCTTGAAACTTTGGGCTGGCTTTGATCCTATTCTAAGCAGATATGTTATTTACTCAA
ACCTAACAACCAGGTTT
GAGGGCCGCGAGGCCCGAACACTCTTGAAACTATGGGCTGGCTTTGATCCTATTCTAAGCAGATATGTTATTTACTCAA
GCCTAATAACCAGGTTT
GAGGGCCGCGAGGCCCAATACTCTTGAAACTGTGGGCTGGCTTTAATCCTATTCTTAGCAGAGTAGGCTGTAGGCCTG
CGACGCGGTTGTTATTTACTCAAACCTAACAACCAGGTTT
GAGGGCCGCGAGGCCCGAACACTCTTGAAACTATGGGCTGGCTTTGATCCTATTCTAAGCAGATATGTTATTTACTCAA
GCCTAATAACCAGGTTA

Nr of selected repeats 3 Similarity 0.949074

Consensus:

GAGGGCCG CAGGCCCGAACACTCTTGAAACTaTGGGCTGGCTTTGATCCTATTCTAAGCAGATATGTTATTcACTCAA
gCCTAAAtAACCAGGTn

>Cele-UNSB01_3:1204553-1205580 Satlength=1028 Nr of Repeats=13 RepeatLength=35
seed=TTTAAAATTT

TTTAAAATTTCCGGCAAATCGCCAAATTGCCGGAA
TTGAAAATTTCCGGCAAATTGCCAACCTGCCGGAT
TTTAAAATTTCCGGCAAATCGTAAAATTGCCGGAA
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Nr of selected repeats 8 Similarity 0.863946

Consensus:

TTgAAAATTTcGGCAAATcGgcAAaTTGCCGGAA

>Cele-UNSB01_3:1210986-1211328 Satlength=343 Nr of Repeats=4 RepeatLength=21
seed=ACTACAGTAC

ACTACAGTACCCCGTACGACT
ACTACAGTACCCCCACTACC
ACTACAGTACCCCCAACCCT
ACTACAGTACCCCCAATCACCACAACATATTCTGAAGACATCATTGACTCGGAAGTGACAAAATCGCCCGAGGAGCTCA
TTGCAGAGCTCAAAAAGCTTTGAAAGTCGGAAATTTCTGAAAACCGAAAATTTCAAGGAAGCCGAGGAGCCCGAAAT
CGATTTTGTAGCTTTTGGAAACGAAAACCGAGAGATGAACGCAATTGACACTGAAAATTCGGAGGAAATTGAAAATTC
GAGCCAATCGGAGCGACACGGTTTGCTCAGTGCTCCGTGAGG

Nr of selected repeats 3 Similarity 0.788360

Consensus:

ACTACAGTACCCcnACnAct

>Cele-UNSB01_3:1301641-1302992 Satlength=1352 Nr of Repeats=116 RepeatLength=11
seed=TTTTTGACACA

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TTTTTGACACAA
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TTTTTGACACA
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Nr of selected repeats 73 Similarity 0.910060

Consensus:

TTTTTGACACAt

>Cele-UNSB01_3:1307999-1309276 Satlength=1278 Nr of Repeats=65 RepeatLength=20
seed=AAAAATAGAT

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AAAAATAAATTGGCAGACGA
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Nr of selected repeats 40 Similarity 0.893203

Consensus:

AAAAATAGATTGACAGACGA

>Cele-UNSB01_3:1312329-1312425 Satlength=97 Nr of Repeats=5 RepeatLength=12
seed=AGGCTTAGGC

AGGCTTAGGCTC

AGGCTTAGGCTT

AGGCTTAGGCTC

AGGCTTAGGCTTAGGCATATGCTG

AGGCTTAGGCTAAGACTTATGAAGAGGCTCAAGCTT

Nr of selected repeats 3 Similarity 0.925926

Consensus:

AGGCTTAGGCTc

>Cele-UNSB01_3:1320709-1320805 Satlength=97 Nr of Repeats=5 RepeatLength=12
seed=AGGCTTAGGC

AGGCTTAGGCTC

AGGCTTAGGCTT

AGGCTTAGGCTC

AGGCTTAGGCTTAGGCATATGCTG

AGGCTTAGGCTAAGACTTATGAAGAGGCTCAAGCTT

Nr of selected repeats 3 Similarity 0.925926

Consensus:

AGGCTTAGGCTc

>Cele-UNSB01_3:1329089-1329185 Satlength=97 Nr of Repeats=5 RepeatLength=12
seed=AGGCTTAGGC

AGGCTTAGGCTC

AGGCTTAGGCTT

AGGCTTAGGCTC

AGGCTTAGGCTTAGGCATATGCTG

AGGCTTAGGCTAAGACTTATGAAGAGGCTCAAGCTT

Nr of selected repeats 3 Similarity 0.925926

Consensus:

AGGCTTAGGCTc

>Cele-UNSB01_3:1364177-1382615 Satlength=18439 Nr of Repeats=734
RepeatLength=25 seed=CAGAGAGTAA

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CAGAGAGTAAAATAATTGGTGAAGC
CAGAGAGTAAAATAATTGGTGAAGT
CAGAGAGTAATTTATTTGGTGAAGC
CAGAGAGTAAAATAATTGGTGAAGCA
AGAGAGTAATTTATTTGGTGAAGC
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CAGAGAGTAAAATATTGGTGAAGC
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CAGAGAGTAAAATAATTGGTGAAGC
CAGAGAGTAAAATAATTAGTGAAGC
CAGAGAGTAAAATAATTAGTGAAGC
CAGAGAGTAAAATAATTGGTGAAGC
CAGAGAGTAAAATAATTAGTGAAGC

Nr of selected repeats 587 Similarity 0.896061

Consensus:

CAGAGAGTAAaTAaTTGGTGAAGC

>Cele-UNSB01_3:1391886-1392275 Satlength=390 Nr of Repeats=16 RepeatLength=21
seed=TTTTTGGTAA

TTTTTGGTAAAATTTGGTGAAATTTGGTAAC

TTTTTGGTAAAATTTGATAAT

TTTTTGGTAAAATTTGGTAACTTTTGATAAAAATTTGGTAACTTTTCGGTGAAAATTCGGTAAC

TTTTTGATAAAAATTCGGTAAC

TTTTTGGTAAAATTTGGTAAT

TTTTTGGTAAAATTTAGTAAC

TTTTTGGTAAAATTCGGTAAC

TTTTTGGTAAAATTTGGTAAC

TTTTTGGTAAAATTTGATAAT

TTTTTGGTAAAATTTGGTAAT

TTTTTGGTAAAATTTGGTAAT

TTTTTGATAAAAATTTAGTATT

TTTTTGGTAAAATTCGGTAAC

TTTTTGGTAAAATTTGGTAAC

TTTTTGGTAAAATTCGGTAAC

TTTTTGATAAAAATTCGGTAACT

Nr of selected repeats 13 Similarity 0.873016

Consensus:

TTTTTGGTAAAATTTGGTAAC

>Cele-UNSB01_3:1394199-1394513 Satlength=315 Nr of Repeats=12 RepeatLength=21
seed=CAAAAAGTTA

CAAAAAGTTACAAAATTTTACC AAAAATATGCCAAATTTTCC

CAAAAAGTTATCAAATTTTAC
CAAAAAGTTACCAAATTTTAG
CAAAAAGTTACTAAAAATTTATTTAAAAAACCCAATTTTGCCAAAAATATACCAAGTTTATAG
CAAAAAGTTACCAAATTTTAC
CGAAAAGTTACCAAATTTTAA
CAAAAAGTTACCAAATTTTAA
CAAAAAGTTACCAAATTTTAA
CAAAAAGTTACCAAATTTTAA
CAAAAAGTTACCAAATTTTAA
CAAAAAGTTACCAAATTTTAA
CAAAAAGTTACCAAGTTTAC

Nr of selected repeats 10 Similarity 0.923810

Consensus:

CAAAAAGTTACCAAATTTTAA

>Cele-UNSB01_3:1395088-1395322 Satlength=235 Nr of Repeats=5 RepeatLength=35
seed=CAAATCGGCA

CAAATCGGCAAATTGCCGGAATTAATAATTTTTTGG
CAAATCGGCAAATCGGCACATTACCTTAATTGAAATTTTTGA
CAAATCGACAAATTGCCGGAATTGAAAATTTCCGG
CAAACCGGCAAATCGGCAAATGACCAAATTTGTTGAATTTTCCGGAAAAACGGCAACTTGCCGGAATTGAAAATTTCTCTG
CAAATAAG

CAAACCGGCAAGTTACCGAAATTTGAAAAGATCCGA

Nr of selected repeats 3 Similarity 0.695238

Consensus:

CAAAtCGgCAAaTTgCCGgAATTgAAAattTccGg

>Cele-UNSB01_3:1399964-1400110 Satlength=147 Nr of Repeats=5 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGG

GTACTGTAGGAA

TACTGTAGGATTACTGTAGTTTTGGAAAACTAACTTTTTGTCTTTTGAAGGTATATTGGGGTGGGGGTTAGTAGGGAG
ATATTGTTTGGGTACTGTTGTA

GTACTGTAGGA

GTACTGTAGGA

Nr of selected repeats 3 Similarity 0.919192

Consensus:

GTACTGTAGGa

>Cele-UNSB01_3:1400275-1400335 Satlength=61 Nr of Repeats=4 RepeatLength=15
seed=TCGTGGTGAG

TCGTGGTGAGACCTT

TCGTGGTGAGACCCA

TCGTGGTGAGACCTT

TCGTGGTGAGACCTT

Nr of selected repeats 4 Similarity 0.955556

Consensus:

TCGTGGTGAGACCTt

>Cele-UNSB01_3:1400394-1400521 Satlength=128 Nr of Repeats=4 RepeatLength=31
seed=AATTCAAATT

AATTCAAATTTATTTAAAAAATTTGGCGGG

AATTCAAATTTCTTCAAAAAATTTGGCGGG

AATGCAAATTTCTTCAAAAAATTTGGCGGG

AATTCAAATTTCTGAGAAAAGAAATTTGGGCAGGA

Nr of selected repeats 3 Similarity 0.885305

Consensus:

AATtCAAATTTcTTcAAAAAAtTTTGGCGGG

>Cele-UNSB01_3:1406406-1406896 Satlength=491 Nr of Repeats=33 RepeatLength=11
seed=GGTACTGTAG

GGTACTGTAGG
GGTCTGTAGGGTTATGTAGGGATGCTGTAGGGGTACTGGGGGGGGGGGGGGGGGGGGGG
GGTACTGTAGGGGTGCTGTACG
GGTGCTGTAGG
GGTACTGTAGT
GGTTCTGTAGG
GGTACTGTAGG
GGTTCTGTAGGAATTCTGTAGG
GGTACTCTAGT
GGTACTGTAGT
GGTACTGTAGT
GGTACTGTAGG
GGTACTGTAGG
GGTACTGTTGT
GGTACTGTAGG
GGTACTGTAGG
GCTACTGTAGGGGAACAGTAGGGATATTGTAGG
GGTATTGTAGG
GGTACTGTAAG
GGTACTGTAGAGATCAAAACTATCTGTAGG
GATACTGTAGGA
GGTCTGTAGT
GGTACTGTAGG
GGTATTGTAGG
GGTACTGTAAG
GGTACTGTAGAGATCAAAACTATCTGTAGG
GATACTGTAGGA
GGTCTGTAGT
GGTACTGTAG
GGTAGTGTAGG
GGTACTGTAGG
GGTCTGTAGG
GGTTCTGTAGG

Nr of selected repeats 21 Similarity 0.844156

Consensus:
GGTACTGTAGg

>Cele-UNSB01_3:1413910-1414798 Satlength=889 Nr of Repeats=40 RepeatLength=14
seed=ATACCTAATA

ATACCTAATAACTA
ATACCTTATACCTT
ATACCTAATACCTA
ATACCTAATACCTA
ATACCTAATACCTTCTACCTCATACTTAA
AACCTAATACCTT
ATACCGAATACCTA
ATATCTAATACCTC
ATACCTAATACTTA
ATACCTAATAACTA
ATACCTTATACCTT
ATACCTTATACCTA
ATACCTAATAACTA
ATACCTAATACCTTCTACCTCATACTTAA

AACCTAATACCTT
ATACCTAATACCTA
ATATCTAATACCTTATTCCTTATATCTAATGCCGAACACCTTATATATTTAAACCTAATGTTTA
ATACCTAATACCTA
ATACCTAACACCTA
ATACCTAATACCTA
ATACCTAATTCCCTA
ATATCTAATACCTTACACCTTAAACCTCATACTCATGCCTT
ATACCTAATACCTAATTGCTAATA
ATATCTAATACCTA
ATACCAATACCTA
ATACCTAATACTTA
ATACCTAATACCTA
ATACCTAATACCTA
ATACCTAATACCTA
ATACCTAAAACCTTATTCCTT
ATACCTAATACCTA
ATACCTAATACCTA
ATACCTAATACCTAATACTTTATTCCTT
ATACCTAATACCTG
ATACCTAATACCTA
ATACCTAATACCTA
ATACCTAATACCTA
ATACCTAAAGCCTA
ATACCTAATACCTA
ATACCTTATACCTTATACCTACAAGGCATTTATATCCACTTCTACAACCTTCAAAGAGGGCGCATTTATCCGAAATGGT
CTCGTCACGCGCCCGAAAATCAATGGGTCGAACCATCGCGCGTGAACACGCCCTCTTTAAAGTTGCAGAAGTAGAAAA
AATGCGATGCAATATTTTATGCCTAGTATCGGATA
ATACCTAATACCTAATGCCTGATACCTT

Nr of selected repeats 28 Similarity 0.877047

Consensus:

ATACCTAATACCTA

>Cele-UNSB01_3:1466668-1467327 Satlength=660 Nr of Repeats=5 RepeatLength=43

seed=GGCTCTCGGC

GGCTCTCGGCTCGCGCCGAGGGCCGAGTTCCACTAAAAGTTTC

GGCTCTCGGCTTGCGCCGAGAGCCGAGGGCTGATTGCTTTATATTTTCGGTATCGATTTTCGCACGCTCCCTCCGATAAT

GAATAAAAATTATAATTACAACACTACGACTTTACAACCTATAAAAATAAATAGTTTCGCTGCTAACAATAAGGAATTGAGT

ACTTTTCCGATTTCTGCCCCAAAAACATTTGTATGTCATGTAGGGGGTTGTAAAGATATACTCAAAGGGTTCCACAG

GAAAGGATAACCATAATAGATACCCCAATAACAGATCTAATATTTGATTATATGGGTCATTGGGCTGTAAATATGTGTC

TCTTTATGGGGTAGGTGGCGATGTGTTGCCAGCTAACATTAACGTGTATTAATAAGAATTAGACTATGTAATAAGAATT

AGACTATGATAGTTATGAGAGAGAATATAAGAGGAAGGTGCGAGGATTCCGAAACCAATCGGCGTGAGCCGAAAAACAG

AAAAAAAAATTTGTC

GGCTCTCGGCTCGCGCCGAGAGCCGAGCTCTATTTTCCGGTTC

GGCTCTCGGCTTACGCCGAGAGCCGAGTTTAAATTTTTTTC

GGCTCTCGGCTTGTGCCGAGAGCCGAAAAATACCCAAATTGTC

Nr of selected repeats 3 Similarity 0.627907

Consensus:

GGCTCTCGGCTcGcGCCGAGaGCCGAgntctActnaaagttTC

>Cele-UNSB01_3:1616576-1616906 Satlength=331 Nr of Repeats=16 RepeatLength=20

seed=CATAAAAATT

CATAAAAATTCTGAAAAATG

CATAAAAATTCAGAAAAATG

CATAAAAATTCTGAAAAATG

CATAAAAATTCAGAAAAATG

CATAAAAATTCTGAAAAATCTGAAAAAAG

CATAAAAATG
CATAAAAATTCAGAAAAATA
CATAAAAATTCAGAAAAATA
CATAAAAATTCAGAAAAATA
CATAAAAATTCAGAAAAATA
CATAAAAATTCAGAAAAATG
CATAAAAATTCAGAAAAATA
CATAAAAATTCAGAAAAATG
CATAAAAATTCAGAAAAATG
CATAAAAATTCTGAAAAATCTGAAAAATG
CATAAAAATTCAGAAAAATG

Nr of selected repeats 13 Similarity 0.947009

Consensus:

CATAAAAATTCAGAAAAATg

>Cele-UNSB01_3:1617648-1618407 Satlength=760 Nr of Repeats=37 RepeatLength=20
seed=TTTCACTAAA

TTTCACTAAAATCCTAATT
TTTCAATAAAGTCTCAAAATTACACAAAATTCCTAAT
TTTCACTAAAATTTCAAAT
TTTCACTAAACATCTCAAAA
TTTCACTAAAATCTCAAAA
TTTCACTAAAATCTCAAAA
TTTCACTAAACATCTCAAAA
TTTCACTAAACATCTCAAAA
TTTCACTAAAATCTCAAAA
TTTCACTAAAATCTCAAAA

Nr of selected repeats 36 Similarity 0.904019

Consensus :

TTTCACTAAAaATCTCAAAA

>Cele-UNSB01_3:1642030-1642586 Satlength=557 Nr of Repeats=7 RepeatLength=21

seed=CCTAAAAATT

CCTAAAAATTTCAATTTTTGT

CCTAAAAATTTCAAATTTTAA

CCTAAAAATTTCAAATTTTAA

CCTAAAAATTTCAAATTTTAACTTAAATTTCAAATTTTAA

CCTAAAAATTTCCACTTTTTTCCAGGCGGCTTCGTAGATCACCTCTCAATTTGCTTCATTTGCTCAATGAGCCAACAG

GCTCCACCCTCACAGCTCAATCAATAGTCGAAAGTTTAAAGGCGCATGGTTGGAGTATTACTGTAGGCGTTGAACATGA

TCTCTACGAACTTTTCAATGATTTGTAACAACCTGGGAGGATGAATTGAAGAGTTCCGCGGTATTTTAAATGAATCAA

TCGATTGAAAATTGTCATAGTAGTAGTAGTGAAGATGATGAAGATGTGGTGGTGAATCGACGAGTTTAAAGAGGATCCC

CGTCAATTATCAGAAAATTGATGAGTTTTTCCAGAGTTTCGGACGTGGAAAATTAGCTAAAAATCGGGTTTTTTAA

CCTAAAAATTTGCCGTGTTTTGA

CCTAAAAATTCGCATTTTTTTTG

Nr of selected repeats 5 Similarity 0.695238

Consensus :

CCTAAAAATtnCaattTTTna

>Cele-UNSB01_3:1690415-1691093 Satlength=679 Nr of Repeats=5 RepeatLength=72

seed=ATGAATTTTA

ATGAATTTTAAATACAATTTTCTGACGATGAAGTCATAAAAATTCATTTTTTTGACCTTTCAACTTTAGTTTT

ATGAATTTTAACTAACAAATTCAGATTCAGCACCCAATTTTACCTCTAGACACACGGTTTTTGCAAAAATTTTGGAAAA

TTCTGCAATTTGTGCGTAAGCTGTTGGGTGTTTGCCTACTTTTTGAAGCTACAGTACCCCAAATGTTTGATATTTGCGCT

GTAAACTTACAAAAAAGGTTTCCAGGGTAAAATTTAACGAGGAATTTGAATTTTTACATAAAAATCTGCAAAA

ATGAATTTTAAATACAATTTTCTGACGATAAAGTCATAAAAATTCATTTTTTTGACCTTTCAACTTTAGTTTT

ATGAATTTTAACTAACAAATTCAGATTCAGCACCCAATTTTACCTCTAGACACACGGTTTTTGCAAAAATTTTGGAAAA

TTCTGCAATTTGTGCGTAAGCTGTTGGGTGTTTGCCTACTTTTTGAAGCTACAGTACCCCAAATGTTTGATATTTGCGCT

GTAAACTTACAAAAAAGGTTTCCAGGGTAAAATTTAACGAGGAATTTGAATTTTTACATGAAAATCTGCAAAA

ATGAATTTTAAATACAATTTTCTGACGATGAAGTCATAAAAATTCATTTTTTTGACCTTTCAACTTTAGTTTT

Nr of selected repeats 3 Similarity 0.975309

Consensus :

ATGAATTTTAAATACAATTTTCTGACGATgAAGTCATAAAAATTCATTTTTTTGACCTTTCAACTTTAGTTTT

>Cele-UNSB01_3:1715361-1716220 Satlength=860 Nr of Repeats=41 RepeatLength=11

seed=TACTGTAGGG

TACTGTAGGGG

TACTGTAGAGG

TACTGTAGGGGTTTATTGGGGTACTGTATAATTATTGTAGAGGTAGG

TACTGTAGGGA

TACTGTAGGGGTGCTGTAGAGG

TACTGTAGGGG

TAATGTAGGGG

TACGGTAGGGA

TACTGTTGGGG

TACTGTAGGAG

TACAGTAGGGC

TACTGTAGGGGTAACTGTATGAG

TACTGCAGGGG

TACTGTAGGGGGTGTGTAACCTCACCGTTTAGG

TACTGTAGGTC

TACTGTAGGGG

TACTGTAGGAA

TACGGTAGGGG

TACTGTAGGGA

TACTGTAGAGGTACTGTAGAACACGGTACATTAGTAAAATTACCTCCAACAAAATAGAAGCACTCATCATTTCATGAAAAT
TGAATGGTCAAAAACACAAGCGATAAACAATGAAAAATGAGGGGCGGGGATGGATAGATCTGCCTTTTTTTGCAAATTGCG
ATGCTATCTTGCACTTTTGTGCAAGATAGCAAACCTGCAAAGAGAG
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TACTGTAGGGA
TACTGTAGGGG
TGCTGTAGGGG
TAATGTAGGGG
TAATGTAGGGGTAAGTGTATGAG
TACTGTAGGGGGTACTGTAAGTTTACCGTTTAGG
TACTGTAGGTC
TACTGTAGGGG
TACTGTAGGGGATACGGTAAGG

Nr of selected repeats 30 Similarity 0.811076

Consensus:

TACTGTAGGGg

>Cele-UNSB01_3:1724995-1725361 Satlength=367 Nr of Repeats=4 RepeatLength=92

seed=CTGCGGAACC

CTGCGGAACCCCGAACGTGTCGGCCGCTTCCAAAAACAACCACCTCTTCACACTTCATTGCGCACACACCAAACACTACTA
GTTTCACGTCAA

CTGCGGAACCCCGAACGTGTCGGCCGCTTCCAAAAACAACCACCTCTTCACACTTCATTGCGCACACACCAAACACTACTAGT
TTCACGTCAA

CTGCGGAACCCCGAACGTGTCGGCCGCTTCCAAAAACAACCACCTCTTCACACTTCATTGCGCACACACCAAACACTACTA
GTTTCACGTCAA

CTGCGGAACCCCGAACGTGTCGGCCGCTTCCAAAAACAACCACCTCTTCACACTTCATTGCGCACACACCAAACACTACTA
GTTTCACGTCAA

Nr of selected repeats 3 Similarity 1.000000

Consensus:

CTGCGGAACCCCGAACGTGTCGGCCGCTTCCAAAAACAACCACCTCTTCACACTTCATTGCGCACACACCAAACACTACTA
GTTTCACGTCAA

>Cele-UNSB01_3:1738456-1739086 Satlength=631 Nr of Repeats=52 RepeatLength=12

seed=TGAGCCTGAG

TGAGCCTGAGCC

TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGCA
TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGTC
TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGCA
TGCGCCTGAGCC
TGAGCCTGAGCC
TGAGCCTGAGTC
TGAGCCTGAGCC
TGAGCATGAGCC
TGAGCATGAGCCTGAGCA

Nr of selected repeats 51 Similarity 0.969848

Consensus:

TGAGCCTGAGCC

>Cele-UNSB01_3:1753459-1753580 Satlength=122 Nr of Repeats=11 RepeatLength=11
seed=GCAAAAAATG

GCAAAAAATGT

GCAAAAAATGG

GCAAAAAATGT

GCAAAAAATGG

Nr of selected repeats 11 Similarity 0.960331

Consensus:

GCAAAAAATGT

>Cele-UNSB01_3:1796051-1796519 Satlength=469 Nr of Repeats=35 RepeatLength=12

seed=CTAAGCCTAA

CTAAGCCTAACC

CTAAGCCTGAGC

CTAAGCCTAAAC

CTAAGCCTGAGC

CTAAACCTAAAC

CTAAGCCTGACC

CTAAGCCTAAAC

CTAAGCCTAAGC

CTAAGCCTAAGC

CTAAGCCTAACC

CTAAGCCTGAGC

CTAAGCCTAAAC

CTAAGCCTGAGC

CTAAACCTAAAC

CTAAGCCTGAGC

CTAAGCCTAAAC

CTAAGCCTAAGC

CTAAGCCTAAGC

CTAAGCCTAACC

CTAATCCTAAGCCTGAAC

CTAAGCCTAAAC

CTAAGCCTAAGC

CTAAGCCTGAGC

CTAAGCCTAAGA

CTAAGCTTAAGTCTGAGCCTAAAC

CTAAGCCTAAGCT

TAAGCCTAAGC

CTAAGCCTAACC

CTAAGCCTGAGCCTAATCCTATGCCTGAGCT

TAAGCCTAAGCCCAAGCA

TAAGCCTAATT

CTAGGCCTAAGCCTAATC

CTAGGCCTAAGC

CTAAGCCAAGGT

CTAAGCCTAATC

Nr of selected repeats 27 Similarity 0.758492

Consensus:

CTAAGCCTaAgC

>Cele-UNSB01_3:1833347-1833868 Satlength=522 Nr of Repeats=14 RepeatLength=34

seed=AATTGAAATT

AATTGAAATTTCCGGCAAATCGGCAAATGTCCG

AATTGAAATTTTCGGCAAATCGGCAAATCGACCAAATTGCCGG

AATTGAAATTTCCGGTAAATCGGAAAATTGCCGG

AATTGAAATTTCCGGCAAATCGGCAAATTGCCGG

AATTGAAATTTTCGGCAAATCGGCAAATCGACCAAATTGCCTA

AATTGAAATTTCTGCAAATTGGGAAAATGTCCG

AATTGAAATTTCCGGCAAATCGGCAAATCCCAA
AATTGAAATTTTCCGGCAAATCGGCAAATGTCCG
AATTGAAATTTTGGCAAATCGGCAAATCGACCAAATTGCCTA
AATTGAGATTTCCGGCAAATCGGCAAATCGACCAAATTGCCTA
AATTGAAATTTCTGCAAATGGGAAAATGTCCG
AATTTAAATTTTGGCATATCGGCAAATCCCAA
AATTGAAATTTCCGGCAAATCGGCAAATGCCCCG
AATTGAAATTTCCGGCAAATGGGCAAATCGACCAAATTGCCTA

Nr of selected repeats 9 Similarity 0.808279
Consensus:

AATTGAAATTTcCgGCAAATcGGcAAAtTgcCgg

>Cele-UNSB01_3:1843958-1844048 Satlength=91 Nr of Repeats=6 RepeatLength=12
seed=AGGCTTAGGC

AGGCTTAGGCTC
AGGCTGAGGCTT
AGGCTCAGGCTC
AGGCTTATGCTTCCGGCTT
AGGTTTAGGCAT

AGGCTTAGGCCATCGTTGGGCTT
Nr of selected repeats 4 Similarity 0.668803
Consensus:

AGGcTtAGGCTc

>Cele-UNSB01_3:1887376-1889731 Satlength=2356 Nr of Repeats=56 RepeatLength=19
seed=AAAATCGATA

AAAATCGATATTTTATCGG
AAAATCAATATTTTATCGG
AAAATCGATACTTTATTGG
AAAATCTATATTTTCTGG
AAAATCTATATTTTATCGGAAAGTCGGTAATTTGCCGGAAGATCTATATTTAGTTGG

AAAATCGATAATCCTTTAG
AAAATCAATAAATTATCGT
AAAATCGATAATTCATCGA
AAAATCGATAATTTATAGG
AAAATTGATAAATTGTGCGA
AAGATCGATAATTTATCGGAAAATCTTTATTTTGCTGG

AAAATCGATATTTTATCGG
AAAATCGATAAATTTGTCCG
AAAATCGATAGTTTTCCGG
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AAAATCGATAAATTGCCGA
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AAAATCGATATTTCCCGAAAACCCGATTTTCCAATAACTTTTTCTGA

AAAATCAATATTTCGAAGTTAAAAAATCTTAGAACAGATATTTTTTTTTCAAATTTCAAGTCTCCCAATTTCCAGGTC
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GCCAATGCGGAAAGGTGTGCGTCTCGGATACACAGCAAATGATGAGAAAGTGAGCGTTGAAAAAATAATTGAA
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CTCCAGCGGAGGCCTTGAGGCGCGGTGGCGAGCGCCGCCGCGCCAGCGGAGGCATAAAACCGGTGGCGAAGAAGAGC
TCGGCAGGAAGCGCCGGCGCGGTGCAAAACCTCTGACGAAGAAGACCAGCGACGTTGAAAAGGTTAGGGAACTTTGTG
GTTTAA

AAAATCGATAATTTAAATTTTCAGTCGTCTGCTCCAAACGCTCGAAAACTAGTACAGCTGTCAAGAAGGCGGATACCG
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TAACAATTTTCAAATTAGATAATTTTATAAATTTAATTTATTGATTTTTTATTTAAAAATTTCAAAAATCCTTATTTAAA
AATCCCGCTGAAAAAATAAAAATAGGCGAATTTCTCTTGATCTCACTCTCTTTCCACCGAACAAAAGCTCATAATT
TGTGCATTTTTATTGATTTTGTGATTTTCCCCCATTTTCCCTAACAAAATTTGTGATACTATGCCTAATTTATGCGCT
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AAATCGATATTTACTTAATCGG
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AAAATCGATATCTTATCGG
AAAATCGATATTTTATCGG
AAAATCGATAATTCGCGG
AAAATCGATATCTTATCGG
AAAATCGATAATTTTATCGG
AAAATCGATAATTTCTCGG

Nr of selected repeats 36 Similarity 0.647665

Consensus:

AAAATCGATAaTTaTCGG

>Cele-UNSB01_3:1891974-1892414 Satlength=441 Nr of Repeats=36 RepeatLength=11
seed=ATTTTTTGCA

ATTTTTTGCAC
ATTTTTTGTAC
ATTTTTTGCAT
ATTTTTTGCAA
ATTTTTTGAAC
ATTTTTTGCAC
ATTTTTTGCAC
ATTTTTTGCAC
ATTTTTTGCAC
ATTTTTTGCAC
ATTTTTTGCAC

AAAATCGATAATTTCTCGG
AAAATCGATAATTTCTCAG
AAAATCGAAAATTGCTCGG
AAAATCGATAATTTCTCAG
AAAATCGATAAATTCGTTCGG
AAAATCGATAAATTCGTCAATA
AAAATCGATAATAGGTCGG
AAAATCGATAATTTCTCGG
AAAATCGATAATTTCTCAG
AAAATCGAAAATTGCTCGG
AAAATCGATAATTTCTCAG
AAAATCGATAAATTCGTTCGG
AAAATCGATAAATTCGTCAATA
AAAATCGATAATAGGTCGG
AAAATCGATAATTTCTCGG
AAAATCGATAATTTCTCAG
AAAATCGAAAATTGCTCGG
AAAATCGATAATTTCTCAG
AAAATCGATAAATTCGTTCAG
AAAATCGATAAATTCGTCAATA
AAAATCGAGAATAGGTCGG

Nr of selected repeats 39 Similarity 0.805668

Consensus:

AAAATCGATAAATnTCgG

>Cele-UNSB01_3:2017089-2018496 Satlength=1408 Nr of Repeats=57 RepeatLength=21
seed=TGGAAATTTT

TGGAAATTTTAGCCCAAAAAC
TGGAAATTTTACCCCAAAAAT
TGGAAATTTTGACCCAAAAC
TAGAAATTTTAGTCCAAAAC
TGGAAATTTTGACCTAAAAC
TGGGAATTTTGACCCAAAAT
TGGAAATTTTAGCCTAAAAC
TGGAAATTTTAACCCAAAAT
TGGAAATTTTAACCCAAAACCTAGAATTTTAGCCCAAAAAC
TGGAAATTTTAACCCAAAAT
TGGAAATTTTAACCCAAAACCTAGAATTTTAGCCCAAAAAC
TGGAAATTTTAACCCAAAACCTAGAATTTTAGCCCAAAAAC
TGGAAATTTTACCCAAAAT
TGGAAATTTTGACCCAAAAC
TAGAAATTTTAGTCCAAAAC
TGGAAATTTTGACCTAAAAC
TGGGAATTTTGACCCAAAAT
TGGAAATTTTAGCCTAAAAC
TGGAAATTTTAACCCAAAAT
TGGAAATTTTAACCCAAAACCTAGAATTTTAGCCCAAAAAC
TGGAAATTTTAACCCAAAAT
TGGAAATTTTAACCCAAAACCTAGAATTTTAGCCCAAAAAC
TGGAAATTTTAACCCAAAACCTAGAATTTTAGCCCAAAAAC
TGGAAATTTTAACCCAAAAC
TGGAAATTTTAGCCCAAAAAT
TGGAAATTTTGACCCAAAAT
TGGAAATTTTAACCCAAAAT
TGGAAATTTTGACCTAAAAC

TAGAAATTTTAGCTCAAAAAAT
TGGAAATTTTAACCCAAAAAC
TGGAAATTTTAACCCAAAAAT
TGGAAATTTTAACCCAAAAAC
TGGAAATTTTAGCCCAAAAAAT
TGGAAATTTTGACCCAAAAAT
TGGAAATTTTGACCTAAAAAC
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TGGAAATTTTAACCCAAAAAT
TGGAAATTTTAACCCAAAAAT
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TGGAAATTTTACCCAAAAACT
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TGGAAATTTTGACCCAAAAAT
TGGAAATTTTAGCCTAAAAAC
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TGGAAATTTTAGCCCAAAAAAT
TGGAAATTTTAACCCAAAAAT
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TGGAAATTTTGACCTAAAAAC
TAGAAATTTTAGCTCAAAAAAT
TGGAAATTTTAACCCAAAAACTAGAATTTTGTAGCCCAAAAAAC
TGGAAATTTTAGCCCAAAAAAT
TGGAAATTTTGACCCAAAAAC
TGGAAATTTTAGCCCAAAAAACTAGAATTTTGTAGCCCAAAAAAC
Nr of selected repeats 45 Similarity 0.855059

Consensus:

TGGAAATTTTaaCCcAAAAAt

>Cele-UNSB01_3:2046603-2047209 Satlength=607 Nr of Repeats=30 RepeatLength=12
seed=TAGGCTTAGG

TAGGCTTAGGATTTTCCGGTTTTTTATTTTTGAGGGGGTTCCTGTTTGCCGATTC
AGGCTTAGGCG
TAGGCTTAGGCT
TAGGCTTAGGCT
TAGGCATAGGCT
TAGGCTTAGGCT
TAGGCTTAGGCT
TAGGCATAGGCT
TAGGCTTAGGCTTAGGCGTAAGCTT
TGGCTTAGGTTTAGACCAACACTTAGGCCTGGTCTTAGACG
TAGGCTTTGGCT
TAGGCTTAGGTT
TAGGCGTAGGCTT
TGGCTTAGGTTTAGACCAACACTTAGGCCTGGTCTTAGACGTAGGCTC
TGGCTTAGGCT
TAGGTTTAGGCGTAGGCTTTGACT
TAGGCTTAGTCT
TAGGCTTAGGAA
TAGGTTTAGGCT

TAGGCTTAGGCTTTGGCTTTGGTTTAGACCAACACATAGGCCAAGTCTTAGGCCTAGTCTTAGTTTTACGCTTAGACAA
AGACGC
AGGCTTAGGCG
TAGGCCTAGGCT
TAAGCTTAGGCT
TAGGCTCAGGCA
TAGGCTTAGGCT
TAGGCTTAGGCG
TAGGCTTTGGCTTAGGTTTAGACCAACACTTAGGCCTGGTCTTAGATG
TAGGCTTTGGCT
TAGGCTTGGGTTTAGGAA
TAGGTTTAGGCT

Nr of selected repeats 18 Similarity 0.824256

Consensus:

TAGGCTTAGGCT

>Cele-UNSB01_3:2058475-2058618 Satlength=144 Nr of Repeats=11 RepeatLength=11
seed=GTCGCGTTGC

GTCGCGTTGCG
GTCGCATTGCG
GTCGCGTTGCG
GTCGCGTTGCG
GTCGCGTTGCA
GTCGCGTTGCG
GTCGCATTGCG
GTCGCGTTGCGGTCAAATTGTG
GTCGCGTTGCA
GTCGCCTTGCG
GTCGCGTTGCGATCACACTGCG

Nr of selected repeats 9 Similarity 0.885522

Consensus:

GTCGCGTTGCG

>Cele-UNSB01_3:2068206-2068691 Satlength=486 Nr of Repeats=44 RepeatLength=11
seed=TGTGCAAAAA

TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAAAT
TGTGCAAAAA
TGTGCAAAAAAT
TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAA
TGGGCAAAAA
TGTGCAAAAA

TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAA
TGTGCAGAAAAGGTGCAAGAAA
TGTGCAGAAA
TGTGCAAAAA
TGTGCAAAAAAG
TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAAAT
TATGCAAAAA
TGTGCAAAAA
TGTGCAAAAA
TGTTCAAAA
TGTGCAGAAAAG
GTGCAAAAATGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAA
TGTGCAAAAA

Nr of selected repeats 31 Similarity 0.939785

Consensus:

TGTGCAAAAA

>Cele-UNSB01_3:2092267-2093197 Satlength=931 Nr of Repeats=27 RepeatLength=31
seed=TGCGTCCGGAA

TGCGTCCGGAAATTTATTCCGATCATTGCCGG
TGCGTCCGGAAATGCATTCTTATCATCAGCGG
TGCGTCCGGAAATTTATTCCGATTATCGGCCGA
TGCGTCCGGAACACAACCTCCAATCATTGCCGG
TGCGTCCGGAAATTTATTTCGATCATCGCCGGTGCTTCGGACTTTAGTTCTGATCATCGCCGGTGCTTCGGACTTTAGTT
CTGATCATCGCCGGC
GCGTCCGGAAATTCATTCCGTTTATCGCCGA
TGCGTCCGGAACACAATTCCGATGATCGCCGG
TGCGTCCGGAAATTTATTCCGATCATTGCCGG
TGCGTCCGGAAATGCATTCTTATCATCAGCGG
TGCGTCCGGAAATTTATTCCGATTATCGGCCGA
TGCGTCCGGAACACAACCTCCAATCATTGCCGG
TGCGTCCGGAAATTTATTTTCGATCATCGCCGGTGCTTCGGACTTTAGTTCTGATCATCGCCGGC
GCGTCCGGAAATTCATTCCGTTTATCGCCGA
TGCGTCCGGAACACAATTCCGATGATCGCCGG
TGCGTCCGGAAATTTATTCCGATCACCGGCGA
TGCGTCCGGAACACAATTCCGATAATCGCCGG
TGCGTCCGAAAATTTATTCCGATCATCGGCCGA
TGCGACGGAAATTCATTCCGTTTATCGGCCGA
TGCGTCCGAAAACAATTCCGATTATCACCGG
TGCGTCCGAAAATAATTCCGATCATCGACGG
TACGTCCGAAGTTTATTCCGATCAACGCCGA
TGCGTTGGAAATTTATTCCGATCACCGCCGG
TGCATCGGAAATTCATTCCGATCATCGCCGG
TGCATCGGAAATTCATTCCGATCACCGCCGG
TGCATCGGAAATTCATTCCGATCATCGCCGA
TGCGTCCGGAAATTTATTCCAATCACCGGCGA

TGCGTCGGAAACACAATTCCAATCATTGCCGG

Nr of selected repeats 23 Similarity 0.733775

Consensus:

TGCGTCGGAAattnATTCCgATcAtcGcCGg

>Cele-UNSB01_3:2094174-2094918 Satlength=745 Nr of Repeats=17 RepeatLength=31
seed=TCCGATGCAT

TCCGATGCATTGCCGATAAATTGCCACCTGGT

TCCGATGCATTGGAAATGATCGGAAAATGGT

TCCAATGCATTGCCGATAGTCGGAACCTGTT

TCCGATGCATCGGCAATGATCGGAACTCTGC

TCCGACGCATCGGTAATGATCGGAACTGGT

TCCGATGCATCGCCGATAGTCAGAATCCGGT

TCCGATGCATCGGAAATAATCGGAACCAACTGCCGACGTATCGCCGATTATCGGAACTGGT

TCCGATGCATCGCCGATAGTCAGAATCCGGT

TCCGATGCATCGGCAATAATCGGAACCAACTGCCGACGTATCGCCGATTATCGGAACTGGTTCCAACCCATCGGCAAT
GATCGGAAATTGAT

TCCGATGCATCGCCGATGATCAGAGCCAGGTTCTGATGAATCGCCTATAATCGGAAATTGGTTTCGATGTATCGCCGGT
AGTTGGAATTTAGC

TCCGATGCATTGCCGATAATCGGCACCTGGT

TCCGATGTATTGGCAATAATCGGAACCTCGC

TCCGATGCATCGCCGATGATCGGAACTGGT

TCCGATGCATCGCAGATAGTCAGAATCCGGT

TCCGATGCATCGGCAATAATCGGAACCAACTGCCGACGTATCGCCGATTATCGGAACTGGTTCCAACCCATCGGCAAT
GATCGGAAATTGAT

TCCGACGCATTGCCGGCAGTCATAACCTAGT

TCGGATGCATTGCCGCCAGTCATAACCTGGC

Nr of selected repeats 13 Similarity 0.625486

Consensus:

TCCGATGCATtGccgATaaTCggAAcCtGgt

>Cele-UNSB01_3:2095462-2096950 Satlength=1489 Nr of Repeats=36 RepeatLength=19
seed=TATCGATTTT

TATCGATTTTTCGAAAAATCAAGTTTTTCAGGATATGGACAAAGGGAGATCACACTATCGGGTAAGTTTTTTGATGCATAA
CAGGGGTAGAAAACATTGGGTAAATCAAAAAAAAAAAGTCAATAATCACTCACTAAAAATTAATAATCAAAAC
CAAAACAAAATTATTTTTTGAAAAAAAAAAACAAATTAGGGACCCTGAAATTCAATTATGATGAAGAAAAGAAAAAAAAA
CTTTAAAAAAAAATTTTCTTGAAAAATTAAAAAAAAAAAGTTTTTCCCTAAAA

TATCGATTTTTAAAA

TATTGATTTTATAACAAAAAAGTTGATTTTTCGCTAAAA

TATCAATTTTATAGAA

TATTGATTTTTCGCTAAAA

TATTGATTTTTCACGGAAA

TATAGATTTTCTGCAAAAA

TATCGATTTTCTAATAAAAAATAAAATTAATAATTTTTTTCACAAT

TATCGATTATTCTCGAAAT

TATCGATTTTCACTCAAACTGAACAAAAAATCAATAAAACCCAAAATCACAAGAAAAACGACACCTGGCGGGGAAA
CAACACTCCATCACTACGACAGTCGGACAGGCACTGAAGGCGGAACTCTTCGAAAT

TATCGATTTTCCGGCAGCTGCAGAAGTTGCGGCTTCG

ATCGATTTTCTGCTGAATCGGCGGCGGCGGTGTCAGGGTACTGAAGGGGTTAGTGGTGTGTTGTCAGGAAAACGTGTT
CAACGCGATGCACGACGTGGCAGCAGCTAATTGCGAGCTACCGACGAGCATTGTTCAACAAAAGGTGAGCCGAGTCA
GAGTGGGAGCCTAAATTTTTAGCACCTGTGGTTGTGGCGGTGGCGAGCGGCGGATCCACAGAGGCGATTTCCAGTTTGA
TGCCGGATTTTAGGGAGGTAATGACGTTGCCGTACAAACCCGCCATCACAACCTAGCGGGATTACAAGTAGGACGACGGT
CATGTATACCTGAAAATATAT

TATCGATTTTAAGTGAAATTTCCGATTTTCTCGGAAAC

TATTGATTTTCCATTATGCTTCCAATTTTGGGAAAA

TCTCGATTTTCCGTAAAAAG

TATTGATTTTTAGTGAAAT
TATCGATTTTTAGTGGAAT
TATCAATTTTTCCGTAGAAG
TATTGATTTTTCCCTAAAAAT
TATCGATTTTTCGTAAAAA
TATTGATTTTTCGTAAAAAT
TATCGATTTTCCTTAAAAAT
TATCGATTTTTCCGTAGAAG
TATTGATTTTTCCCTAAAAAT
TATCGATTTTTCCGTAAAAG
TATTGATTTTTAGTGAAAT
TATCGATTTTCCTTAAAAAT
TATCGATTTTTCGTAAAAA
TATTGATTTTTAGTGAAAT
TATCGATTTTCCTTAAAAAT
TATCGATTTTTCGTAAAAA
TATTGATTTTTAGTGAAAT
TATCGATTTTCCTTAAAAAT
TATCGATTTTCGTAAAAG
TATTGATTTTTAGTGAAAT
TATCGATTTTCCATAAAAAAT

Nr of selected repeats 22 Similarity 0.729931

Consensus:

TATcGATTTTTcgTaAAAt

>Cele-UNSB01_3:2118334-2118593 Satlength=260 Nr of Repeats=20 RepeatLength=11
seed=CTACAGTACC

CTACAGTACCCAAAATAGATACAGTACTTTTAGAATAACC
CTACAGTACTT
CTACAGTATCC
CTACAGTACCT
CTACAGTACCA
CTACAGTACC
CTACAGTATCC
CTACAGTACCT
CTACAGTACCA
CTACAGTACCT
CTACAGTACCA
CTACAGTACC
CTACAGTACCC
CTACAGTACCCC
CACAGTACCC
CTATAGTACCCCTACAGTATTC
CTACAGTACCC
CTACAGTACCT
CTACAGTACCC
CTACAGTACCC

Nr of selected repeats 14 Similarity 0.795788

Consensus:

CTACAGTACCn

>Cele-UNSB01_3:2118949-2119137 Satlength=189 Nr of Repeats=9 RepeatLength=20
seed=TGTAGATTTA

TGTAGATTTACGCGGTTCTG
TGTGGATTTACAGGAATCTA
TGTCGATTTACGAGGTTTTTTAAA

TGTAGATTTAAAGGATTCTA
TGTAGATTTACGGGGTACTG
TGTAGGTTTACGGGGATGTTCCCT
TGTAGATTTACGGAGTTCTA
TGTAATTTACGAGGTTTTA
TGTAATTTACGGGGGTCATG

Nr of selected repeats 6 Similarity 0.697778

Consensus:

TGTAGATTTACggGgTTCTa

>Cele-UNSB01_3:2149341-2150059 Satlength=719 Nr of Repeats=12 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATCGTGATTGCGAGTTTTCCCTAAAAGTATATCTTTACTTAAAAAGTCTTAAGAAGAAAAAACCAACTT
GTCGTGGGTTTATAACAGCATCCTTTATTAGTGGCAATATTTTGGTAACATTTTTCATTTTATAGGTTGTGCCTGTTTC
CGATAAACCATATCGCTGGACACTGTAGATGATGGCTGGGATTTTAGATTTGTCAAACTTTGTGTTTGTCAACTTATGAT
ACTTATAACAGGGATGGGCGCAATTGCCACTCGGTAAATCGGCCAAATTGGCAGCTTGCCGATTTGTGAGAAATTTTCA
ATTCCGACAATTTGCCGA

TTTGCCGGAAATTTTCAATTCGACAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGAGAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAAGTTGCCGA

Nr of selected repeats 10 Similarity 0.926349

Consensus:

TTTGCCGGAAATTTTCAATTCGACAAtTTGCCGA

>Cele-UNSB01_3:2160246-2184061 Satlength=23816 Nr of Repeats=142

RepeatLength=168 seed=TTTATTTTTG

TTTATTTTTGTTTTTCTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTAAAACAATCTAGAATCCAAATCTATCAAACATTTCCGGAA
TTCCATAATG

TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTAAAACAATCTAGAATCCAAATCTATCAAACATTTCCGGAA
TTCCATAATG

TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTAAAACAATCTAGAATCCAAATCTATCAAACATTTCCATAA
TTCCAAAATT

TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTAAAACAATCTAGAATCCAAATCTATCAAACATTTCCGGAA
TTCCATAATG

TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTAAAACAATCTAGAATCCAAATCTATCAAACATTTCCGGAA
TTCCATAATG

TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTAAAACAATCTAGAATCCAAATCTATCAAACATTTCCGGAA
TTCCATAATG

TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTAAAACAATCTAGAATCCAAATCTATCAAACATTTCCATAA
TTCCAAAATT

TTTATTTTTGTTTTTCTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTTAAACAATCTAGAATCCAAATCTATCAAACATTTCCATAA
TTCCAAAATT
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ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTTAAACAATCTAGAATCCAAATCTATCAAACATTTCCGGAA
TTCCATAATG
TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTTAAACAATCTAGAATCCAAATCTATCAAACATTTCCGGAA
TTCCATAATG
TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTTAAACAATCTAGAATCCAAATCTATCAAACATTTCCATAA
TTCCAAAATT
TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTTAAACAATCTAGAATCCAAATCTATCAAACATTTCCATAA
TTCCAAAATT

Nr of selected repeats 110 Similarity 0.984798

Consensus:

TTTATTTTTGTTTTTGTGCCTACATATACCTGTTGAAATTGGAATTCAAGACAAAAACCCCTGTAGCGCGTCTGAAA
ATGGATATCTAGGTACAAAAACTTACCAATAATATTTTTAAACAATCTAGAATCCAAATCTATCAAACATTTCCgAA
TTCCAtAATg

>Cele-UNSB01_3:2204608-2205196 Satlength=589 Nr of Repeats=25 RepeatLength=21
seed=GCCTAAAAAC

GCCTAAAAACGTAAAATTTAGC
CCTAAAAACGTGAATTTTAGTCCTAAAAATGTAAATTTTAG
GCATAAAAAACGTAAAATTTTAG
GCATAAAAAACGTAAAATTTTAA
GCTTAAAAACGTGAATTTTAA
GCCTAAAACCGTGAATTTTAA
GCCTAAAACCGTGAATTTTAA
GCCTAAAACCGTGAATTTTAG
GCCTAAAACCGTAAAATTTAGC
CCTAAAAACGTGAATTTTAG
GCCTAAAACCGTAAAATTTTAG
GCCTAAAAACTTAAATTTTAAAGTGTGAAACCGTGAATTTTAA
GCCTAAAAACTTAAATTTTAA
GCCTAAAACCTTAAATTTTAG
GCCTGAAAACGTAAAATTTTAA
GCCTAAAACCGTAAAATTTTAA
GCCTAAAATGTAAAATTTTAG
GCCTAAAACCGTGAATTTTAG
GCCTAAAATGTAACTTTTAG
GCCTAAAACATACATTTTGG

GTCTAAAAACGTAAATTGTAGT
GCTAAAAACGCAAATTTAAA
GCCTAAAACCTTGATTTTTTAA
GCCTAGAAACTTGATTTTTAGC
CCTAAAAACGTGAATTTTAGGTCGTAAAAACGTGAAAATTAG
Nr of selected repeats 16 Similarity 0.805291
Consensus:

GCCTAAAAaCgTaAATTTTTAa
>Cele-UNSB01_3:2212231-2213000 Satlength=770 Nr of Repeats=22 RepeatLength=31
seed=ATTTCCCGCC

ATTTCCCGCCAAAAAATATTTGAAAATTTGA
ATTTCCCGCCAAAAAATATTTAAAAATTTGAATTTTTGTC
ATTTCCCGCCAAAAAATATTTAAAAATTTGAATTTTTGTC
ATTTCCCGCCAAAAAATATTTGAAAACCTTGA
ATTTCCCGCCAAAAAATATTTAAAAATTTGAATTTTTGTC
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ATTTCCCGCCAAAAAATATTTGAAAATTTGA
ATTTCCCGCCAAAAAATATTTGAAAATTTGA
ATTTCCCGCCAAAAAATATTTAAAAATTTGAATTTTTGTC
ATTTCCCGCCAAAAAATATTCGAAAATTTAA

Nr of selected repeats 14 Similarity 0.922486
Consensus:

ATTTCCCGCCcAAAAAATATTTGAAAATTTgA
>Cele-UNSB01_3:2214780-2216279 Satlength=1500 Nr of Repeats=39 RepeatLength=39
seed=TTTTTGGCGG

TTTTTGGCGGGAAATTCAAAAATTCAAATTTTTCAAATAT
TTTTTGGCGGGAAATTCAAAAATTTAAATTTTTTGAATAT
TTTTTGGCGGGAAATTCAAAAATTCAAATTTTTTGAATAT
TTTTTGGCGGGAAATTCAAAAATTCAAATTTTTTGAATAT
TTTTTGGCGGGAAATTCAAAAATTCAAATTTTTTGAATAT
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TTTTTGGCGGGAAATTTAAAAATTCAAATTTCTGAATA
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TTTTTGGCGGGAAATTCAAAAATTCAAATTTTCAAATAT
TTTTTGGCGGGAAATTCAAAAATTCAAATTTTAGAATAT
TTTTTGGCGGGAAATTCAAAAATTTAAATTTTCAAATAT
Nr of selected repeats 29 Similarity 0.914530
Consensus:

TTTTTGGCGGGAAATTCaAAAAATTCAAATTTTcaAATAT
>Cele-UNSB01_3:2219970-2221469 Satlength=1500 Nr of Repeats=39 RepeatLength=39
seed=TTTTTGGCGG

TTTTTGGCGGGAAATTCAAAAATTCAAATTTTCAAATAT
TTTTTGGCGGGAAATTCAAAAATTTAAATTTTGAATAT
TTTTTGGCGGGAAATTTCAAATTCAAATTTTGAATAT
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Nr of selected repeats 29 Similarity 0.914530

Consensus:

TTTTTGGCGGGAAATTCaAAAAATTCAAATTTTcaAATAT
>Cele-UNSB01_3:2223808-2223967 Satlength=160 Nr of Repeats=4 RepeatLength=40
seed=TCCCGCCAAA

TCCCGCCAAAAATATTCAAAAAATTTGAATTTTTGAATT
TCCCGCCAAAAATATTCAAAAAATTTGAATTTTGAATT
TCCCGCCAAAAATATTTGAAAAATTTAAATTTTTGAATT
TCCCGCCAAAAATATTCAAAAAATTTAAATTTTTGAATT
Nr of selected repeats 3 Similarity 0.866667

Consensus:

TCCCGCCAAAAATATTCAAAAAaTTtaAaTTTTtgAATT
>Cele-UNSB01_3:2325106-2325938 Satlength=833 Nr of Repeats=23 RepeatLength=32
seed=CTCAGCCAAT

CTCAGCCAATCAACGTTTAACTCCGCCTATTTTTTCAGCGAATCAACGTTTAGCTCCGCCTATTC
CTCAGCCAATCGACGT
CTCAGCCAATCAACGTTTGTCTCCGCCTATTTTTTCAGCGAATCAACGTTTAGCTCCGCCTATTC
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Nr of selected repeats 17 Similarity 0.871936

Consensus:

CTCAGCCAATCAACGTTTAgcTCCGCCTATtT
>Cele-UNSB01_3:2342333-2342437 Satlength=105 Nr of Repeats=5 RepeatLength=21
seed=CTGACCAAAT

CTGACCAAATTTGTTTCAGCG
CTGACCAAATTTGTTTTCAGCA
CTGACCAAATTTTTCAGCA
CTGACCAAATTTTTCAGCA
CTGACAAAATTTGTTCCAGCA

Nr of selected repeats 4 Similarity 0.841270

Consensus:

CTGACcAAATTTgTTtcAGCa

>Cele-UNSB01_3:2351961-2352192 Satlength=232 Nr of Repeats=9 RepeatLength=21

seed=GTCAGTGCTG

GTCAGTGCTGGAGTAAATTT
GTCAGTGCTGTAACACATTTT
GTCAGTGATGTAACAAATTTT
GTCAGTGCTGGGACAAATTTT
GTCAGTGCTGGGACAAATTTT
GTCAGTGCTGGAATACATTTT
GTCAGTGCTGGAACAAATTTT

GTCAGTGCTGGAGCAAATTTTGGCCAGAGCTGGAGCAACTTTG

GTCAGTGCTGGAAAAATTTTGTCCAGCACTGACCAACTTTT

Nr of selected repeats 6 Similarity 0.856085

Consensus:

GTCAGTGCTGgaACaAaATTTT

>Cele-UNSB01_3:2562874-2563954 Satlength=1081 Nr of Repeats=40 RepeatLength=10

seed=AGGCAGGCTT

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AGGCAGGCTTAGGCAAGCAT

AGGCAGGCTT

AGGCAGGCTT

AGGCAGGCTT

AGGCAGGCTT

AGGCAGGCTTACAGAGGTTTAGGCAGACTC

AGGCAGGCTT

AGGCAAGCTT

AGGCAGGCTT

AGGCAAGCTTGGGCAGGATTAAGCATGTGTAGGCAAGCGTAGGCAGGTGTTGGCAGGCATGGGCAGGCT

AGGTAGGCTT

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AGGCTGGCTT

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Nr of selected repeats 27 Similarity 0.883001

Consensus:

AGGCAGGCTT

>Cele-UNSB01_3:2564180-2564252 Satlength=73 Nr of Repeats=5 RepeatLength=12

seed=CCAAGCCCAA

CCAAGCCCAAGC

CCAAGCCCAAGCCTAAGT

CCAAGCCCAATC

CCAATCCCAAGC

CCAAGCCCAAGCCCAAGC

Nr of selected repeats 3 Similarity 0.851852

Consensus:

CCAAGCCCAAGC

>Cele-UNSB01_3:2578277-2578816 Satlength=540 Nr of Repeats=27 RepeatLength=20

seed=GACCCAGCCT

GACCCAGCCTACCCCAGGCA

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GACCCAGCCTACCCCAGGCA

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GGTCTCACCACGATG
GGTCTCGCCACGATG
GGTCTCACCACGATGGGTCTTTCCACGATA
Nr of selected repeats 26 Similarity 0.920957
Consensus:

GGTCTCACCACGATG
>Cele-UNSB01_3:2665588-2665980 Satlength=393 Nr of Repeats=11 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATTTTCAATTCGGCAATTTGCCGA
TTTGCTGGAAATGTTCAATTCGGCAAATTTGCCGA
TTTGCCGGAAAGTTTCAATTCGGCAATTTGCTGAA
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TTTGCCGGAAATTTCAATTCGAAAATTTGCCGA
TTTGCCGGAAATGTTCAATTCGGACAATTTCCGA
TTTACCGGAAATTTTCAATTCGGCAATTTGCCGG
TTTGCCGGAAAAGTTTAAATTCGGCAATTTGCTGA

Nr of selected repeats 7 Similarity 0.807710
Consensus:

TTTGCCGGAAATtTTCAATTCcGGCAAtTTGCCGA
>Cele-UNSB01_3:2911307-2911655 Satlength=349 Nr of Repeats=10 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAAATTCAAATTCGGCAATTTGCCGC
TTTGCCGGAAATTTTTAATTCGGCAATTTGCCGA
TTTGCCGGAAATTTTTAATTCGGCAATTTGCCAA
TTTGCCGGAAATTTTCAATTCGGTAATTTGCCAA
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TTTGCCGGAAATTTTTAAATCTGGCAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGGCAACTTGCCGT
TTTGCCGGAAATGTTTAAATACGGCAATTTGCCGA

Nr of selected repeats 8 Similarity 0.859864
Consensus:

TTTGCCGGAAATTTTTtAATTCcGGcAATTTGCCGg
>Cele-UNSB01_3:2955858-2957390 Satlength=1533 Nr of Repeats=44 RepeatLength=19
seed=AAAATCGATA

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AAAATCAATACTAAATTCGAATTTTCGATTTTCAAATAAAATTCGATTTTGTTCGCACAAAAGTTAATAATTTAGTCAT
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AAAATCAATATGGAAAATGTGAAAGCAGTGGTTTTTAATATTCCATCACGGACCCTCCTCACATTGTACAGGGGACGAC
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Nr of selected repeats 31 Similarity 0.912620

Consensus:

AAAATCGATAATTTCCGGA

>Cele-UNSB01_3:3099001-3099720 Satlength=720 Nr of Repeats=4 RepeatLength=180
seed=TGTCGGCCGC

TGTCGGCCGCTATATCTTTTGACTTAAACGTTCAAAAATTTTAAACATGTTTAACTTGTAGAACATATTATGAGCAAC
AGTTGGGTAGTTGAAATTTTATTTCTAAAGTTTTTAGTTTCTGAGTTATACTCATTTCAATATCCCCAAGTGAAATCG
CCTAAAAATGAACTCGCGAGG

TGTCGGCCGCTGTATCTTTTGCCTCAATTTTTTTTAAATTTTCAAACATACATATTCATTAGGTAACATTATGAGCTA
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CAGTTTGTAGTTAAAAATTTTATTTCTAAAATTACTAGTTTCTGAGTTATACTCATTTCCAACCCACCCCAAGAGAAAT
TCCTAAAAATAGACTCGCAAAG

Nr of selected repeats 3 Similarity 0.750153

Consensus :

TGTCGGCCGCTgTATCtTTTGCCTcAATTTTTTTTTnAAtttTnAaACATncaTAttCCagTAGatAAcAttAtGaGcTA
CagTTTGTAGTtaaAATTTtATTTCTAaAATTacTAGTTTCTGAGTTAtACTCATTcCAAcccaCCCCAAGaGAAATt
tCCTAAAAATgaACTCGCgAgG

>Cele-UNSB01_3:3140206-3140936 Satlength=731 Nr of Repeats=5 RepeatLength=16
seed=TGTATATATA

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TGTATATATATATATA

TGTATATATATATATA

TGTATATATATATATACAGTGCGTCCAACCTTCTATAGCACCCCCCTCTATTTTGTAGGGTTTGTAGGCTTTCTGGAAATTATT
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TGTATATATAGTGTCACTCA

Nr of selected repeats 3 Similarity 1.000000

Consensus :

TGTATATATATATATA

>Cele-UNSB01_3:3145893-3146730 Satlength=838 Nr of Repeats=18 RepeatLength=37

seed=ATTTTGGCGG

ATTTTGGCGGTGCTTCGAATCCATTTTAAACATCATTTACTATATATAAAGCGCGTGCCTTCCGTCCGTTTGTAGTTT
GTAGTTTGTAGCTTTGGTCTTTGAACTCTGTAGTTTGTAGTCTCAATCACCTAAGAGGGTCTTATAGCCCCCGCCCTT
TTGTGACGTCAACAAATTTGGCGGAAATTCAAATTTTCTGAGAAATC

ATTTTGGCGGGATTTCAAATTTGAATTTTTTAAAAAT

ATTTTGGCGGGAATTCAAATTTTAAATTTTTTAAAAAT

ATTTTGGCGGGAATTCAAATTTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTTAAAAATTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAATTTTAAATTTTTTAAAAAC

ATTTTGGCGGGAATTCAAATTTTAAATTTTTTAAAAAT

ATTTTGGCGGGAATTCAAATTTTAAATTTTTTAAAAAT

ATGTTGGCGGGAATTCAAAATTTTAAATTTTTTAAAAAT

Nr of selected repeats 16 Similarity 0.920120

Consensus :

ATTTTGGCGGGAATTCAAAaTTTAAATTTTTcGAAAAC

>Cele-UNSB01_3:3152376-3152920 Satlength=545 Nr of Repeats=14 RepeatLength=35

seed=AATTGCCGGA

AATTGCCGGAATTGAAACTTTCCGGCAAATTGGAA

AATTGCCGGAATTGAAACTTTCCGGCAAATTGGAA

AATTGCCGGAATTGAAAATTTCCGGCAAACGGCA

AATTGCCGGAATTTAAAAATTTCCGGCAAATTGGCA

AATTGCCGGAATTTAAAAATTTCCGGCAAATTGGAA

AAGTGCCGGAATTTAAAATTTTCAGGAAAATTGGCA
AATTGCCGGAATTTAAAATTTCCGGCAAATTGGAA
AATTGCCGGAATTTAAAATTTCTGTCAAATCAGAAAATTGTCATTTTGCCAGAAAACCGGCAAATCAGAAAATTTCCGG
CAAAACGGCA
AATTGCCGGAATTGAAAATTACCGGCAAAACGGCA
AATTGCCGGAATTTAAAATTTTCAGGAAAATTGGCA
AATTGCCGGATTTAAAATTTTCAGGAAAATTGACA
AATTGCCGGAATTTAAAATTTTCAGGAAAATTGGCA
AATTGCCGGAATTTAAAATTTCCGGCAAAACGGCA
AATTGCCGGACATTTAAAATTTCCGGCAAATCAGAA
Nr of selected repeats 11 Similarity 0.843463

Consensus:

AAATGCCGGAATTTAAAATTTCCGGCAAAttGGcA

>Cele-UNSB01_3:3159908-3160529 Satlength=622 Nr of Repeats=13 RepeatLength=35
seed=AAATCGGCAA

AAATCGGCAATTTGCCATTTTCAAATTTTCGGAAAATTTGGCATTTGCCCAAATTTGAAAATTTTAAATTTTCGGC
AAATCGGAAAATTGCCGGAATTGAAAATTTCCAGA
AAATCGGCAAATTCAGAAAATTGAAAATTTCCGGC
AAATCGGCAAATTCGGGAATTGAAAATTTCCAGC
AAATCGGCAATTTGCCGGAATTGAAAATTTCTGGC
AAATCGGCAATTTGCCGGAATTTAAAATTTCCAGA
AAATCGGCAAATTCGGGAATTGAAAATTTCCAGA
AAATCGGCAAATTTGTCCGGAATTGAAAATTTCCGGCAAATTTCCCGAACTGAAAATTTCCGGCAAACAGCA
AAGTCCGGCAATTTGCCGTTTTCCAAATTTTGGCAAATTTCTGC
AAACCGGCAACTAGTCGATTTGCCGGAA
AAACGGCAACTGCCGAAAGTTTCGGTAAATTTGGGGTTTTCGTAATTTAAAAAATCCCCTCAAAAAATCCGGCGAATTG
ATATCCGGCAAAATTTGCCGGAATTGAAAATTTCCGGC
AAATCGGCAAATTTGCCGGAATTGAAAATTTCCAGC
AAATCGGCAATTTGCCGGAATTGAAAATTTCCAGA
Nr of selected repeats 8 Similarity 0.885714

Consensus:

AAATCGGCAAaTTGCcGGAATTGAAAATTTCCaGa

>Cele-UNSB01_3:3164980-3165718 Satlength=739 Nr of Repeats=38 RepeatLength=18
seed=GTCGATTTAC

GTCGATTTACGAGATTTT
GTCGATTTACGAGATTTT
GTCGATTTACGAGTTTGG
GTCGATTTACGACATTGT
GTCGATTTACGAAAGTAT
GTCGATTTACGAGAGTTT
GTCGATTTACGACATTGT
GTCGATTTACGAAATTAT
GTCGATTTACGAGAGTTT
GTCGATTTACGACTTTGT
GTCGATTTACGAGAGTTT
GTCGATTTACTAGGACTTT
TCGATTTACGAGATTTT
GTCAATTTACTAGAACGT
GTCGATTTACGAAATTGTGTCGAGTTCCGAGATTTT
GTAGATTTACGAGATTTTGTCAAGTTACTAGAATGT
GTCGATTAACGAGATTTT
GTCGATTTACGAAAGTAT
GTCGATTTACGAAATTAT
GTCGATTTACGAGAGTTT

GTCGATTTACGACTTTGT
GTCGATTTACGAGATTTT
GTCGATTTACGAAATTAT
GTCGATTTACGAGATTTG
GTTGATTTACGACATTGT
GTCGATTTACGAAAGTAT
GTCGATTTACGACTTTGT
GTCGATTTACGAGAGTTT
GTCGATTTACGACTTTGT
GTCGATTTACGAGAGTTT
GTCGATTTACTAGCACTT
GTCGATTTACGAGATTTT
GTCAATTTACTAGAACGT
GTCGATTTACGAAATTGT
GTCGAGTTACGAGATTTT
GTAGATTTACGAGAATTT
GTAGATTTACGAGATTTT
GTAGATTTACGAGATTTTGTCAAGTTACTAGAATGT

Nr of selected repeats 33 Similarity 0.778900

Consensus :

GTCGATTTACGAgAtTnT

>Cele-UNSB01_3:3200630-3201398 Satlength=769 Nr of Repeats=4 RepeatLength=151
seed=TTTAAAGGCG

TTTAAAGGCGCATAGGTAGATCAAAACTCAAAGTTGGCGGATTCTAGTCAATATGGGGCTTATTTTAAAGCTCTCGGTA
AGCTGAATGTAGTTTACTGACTGAAAATTGAAAATTTAAACAATTTTTGGGTCTAGCAGCGAAAATTTTCGAA
TTTAAAGGCGCATAGGTAGGACAAAATTTCAAATTTGACGGAATCTAGTCAATATGGGGCTTATTTGAAAGCTCTCAATG
AGCTGAATCTAGTTTGGCTACTAAAAATCAAAAAATACTGAAAATTTTCGCGGCGAGACCCAAAATTTCTATTTTTCATC
AGATTTTAATGAAAAAAACCCGGATTTTTTTCGAATTTTTTTGATAAAATTTAAAAATTTAAATTTGAACCACTAATAACTT
CAAAATGGCACATCTGTGCGCTAGTTCTCGGGAATTTCTGTATATTTTGGGTCCCGCCACCAAAAAAAAAAATTTCTAAA
TTTAAAGGAGCATAACCCAATTTCCCTTCTCATTTTCGAGGAAATCACTTAAAAATTTGAATTCCTTTGAAAAATTTCCAG
TCAAAACACACTTTTATTAAGCCTCTAACGTCGATTTTTAACTATTTTCGGGTCTCGCCACGAAAAATTTGTAG
TTTAAAGGCGCATAGGTAGCTGAAAATTTCAAATTTGACGGAATCTAGTCAATATGGGGCACATTTTGAAGCTCTCAGTG
AGCTTAATATACTGCGGCTACTAAAAATTTGAATATTTTCAAATTTTTTGGGTCTCGCAGCGAAAGTTTCGAA

Nr of selected repeats 3 Similarity 0.500000

Consensus :

TTTAAAGGcGCATAggtAgnTcaaantTCAaanTtGacGgAtTctagTcAAtATggGgcttaTTTTaAAgcTctCaGTa
AgCtnAaTnTanTtnaGctaCtnAAAAatTtGaanATTTtnAaatTTTTGGGTCTcGCagCGAAAatTTcGaA

>Cele-UNSB01_3:3207516-3208428 Satlength=913 Nr of Repeats=5 RepeatLength=151
seed=TTTAAAGGCG

TTTAAAGGCGCATAGGTAGATCAAAACTCAAAGTTGGCGGATTCTAGTCAATATGGGGCTTATTTTAAAGCTCTCGGTA
AGCTGAATGTAGTTTACTGACTGACAATTGAAAATTTAAACAATTTTTGGGTCTAGCAGCGAAAATTTTCGAA
TTTAAAGGCGCATAGGTAGGACAAAATTTCAAATTTGACGGAATCTAGTCAATATGGGGCTTATTTGAAAGCTCTCAATG
AGCTGAATCTAGTTTACTGACTAAAAATAAAAAATACTGAAAATTTTCGCGGCGAGACCCAAAATTTCTATTTTTCAT
CAGATTTTAATGAAAAAAACCCGGATTTTTTTCGAATTTTTTTGATAAAATTTAAAAATTTAAATTTGAACCACTAATAACT
TCAAAATGGCACATCTGTGCGCTAGTTCTCGGGAATTTCTGTATATTTTGGGTCCCGCCACGAAAAAAAAAATTTCTAAA
TTTAAAGGCACATGACCCAATTTCCCCCTTCTCATTTTCGAGGAAATCACTTAAAAATTTGAATTCCTTTGAAAAATTTCCAG
TCAAAACACACTTTTATTAAGCCTCTAACGTCGATTTTTAACTATTTTCGGGTCTCGCCACGAAAAATTTGTAG
TTTAAAGGCGCATAGGTAGTTGAAAATTTCAAATTTGACGGAATCTAGTCAATATGGGGCACATTTTGAAGCTCTCAGTG
AGCTTAATATACTGCGGCTACTAAAAATTTGAATATTTTCAAATTTTTTGGGTCTCGCAGCGAAAGTTTCGAA
TTTAAAGGCGCATAACAGTCATTTTATGGCGGTTCTAGACAACTTTCTGAGTAAATTTTGATTTATTTTTCAATTTTCC
TTATAAACAGTCTCAGTCATTTATTTGACAAATTTTTGGTGGGTCCCGCCACGAAAATTTCAA

Nr of selected repeats 3 Similarity 0.500000

Consensus :

TTTAAAGGCgCATAggtAgtTcaaantTCAaanTtGacGgAtTCTagTcAAAtATggGgcttaTTTtaAAgcTctCaGTa
AgCtnAaTnTanTtnaGCTaCTaAcaaTtGaanATTTtnAaattTTTtGGGTCTcGCagCGAAAatTTcGaA
>Cele-UNSB01_3:3351031-3351269 Satlength=239 Nr of Repeats=7 RepeatLength=30
seed=TAGAACTTTC

TAGAACTTTCCAAATTCTTTCAGAAAACCTCTAGAAGTTTACAGAATTTTCTAAAAACTGT
TAGAACTTTTCAGTTTTTCTAGAAAACCTC
TAGAACTTTCCAAATTTCTCTGAAAATTC
TAGAACTTTCCAAAGTTTTCTAAAAAATTC
TAGAACTTTCCAAATTTCTCTAGAAAATTC
TAGAGCTTTCCAAAGTTTTCTAGAAAATTTT
TAGAACTTTCCAGATTTTTTCTAGAAAAG

Nr of selected repeats 5 Similarity 0.786667

Consensus:

TAGAACTTTcCAaatTTtTCTagAAAatTc

>Cele-UNSB01_3:3352849-3353088 Satlength=240 Nr of Repeats=8 RepeatLength=30
seed=TAGAACTTTC

TAGAACTTTCCAAATTTCTCTAGAAAATTC
TAGAACTTTCCAAAGTTTTCTAAAAAATTC
TAGAACTTTCCAAATTTCTCTAGAAAATTC
TAGAACTTTCCAAATTTCTCTAGAAAATTC
TAGAACTTTCCAAATTTCTCTAGAAAATTC
TAGAACTTTCCAAATTTCTCTAGAAAATTC
TAGAGCTTTCCAAAGTTTTCTAGAAAATTTT
TAGAACTTTCCAGATTTTTTCTAGAAAAC

Nr of selected repeats 6 Similarity 0.925926

Consensus:

TAGAACTTTCCAAATTTCTCTAGAAAATTC

>Cele-UNSB01_3:3356021-3356788 Satlength=768 Nr of Repeats=13 RepeatLength=19
seed=CTTGGCGCAA

CTTGGCGCAATTCTCGTGC
CTTGGCGCAATTCTCGTGC
CTTGGCGCATTTTTAGTGTCTTGATGCAATTTTGGTGCCTTGACGCGATTCTAGTGCA
TTGGCGCAATTTTTGATGCCTAGGCGCATTTTCGGTGTCTTTGCTCAATTCTCGTGCCTGACGCGATTTTTGATC
CTTGGCGCATTTTTAGTGTCT
TTGGCGCAACTCTCGATCCTTGACGCATTTCTCGATCCTTAAACATTTTTTGCAGAAAAAGCTCCACCAACTCTCCCAA
TCTCAACAGCCGAGTTTCTCCGATTCATCTGTCAAAAAACGCTCGAGTTCTATGAAAATCGCCCGTGAATCGTCCGGCGT
CGTCTACCGAGTCACAACGTGGAATCTACAGTAACCAACAGAGATCGATAGGAAATAATTTGTTACAACGAGTTGTGAA
GTTGCAGGCAGAATTGATGGCAAAGGACGAAAAAGTACGTTTTGGAGTACGAAATGGGAAAAACGATTGAAAAATTTGG
AAAATTCGGGGAATTTCCGGAATAGAGACAAAAACAATTGGAATTTGGAGATTGTTTCGCGCATTTTTTGTGCCTAGGCGC
AGTTTCGGTGTGTA

TTGGCGCAATTCTCGTGCCTTGGCGCTTTTTTGGTGCCTGGGGCAGATCTTTTTGC

CTTGACGCAACTTTAGTGC

CTTGGCGCAAGTTTGGTGT

CTTGGCGCAATTCTAGTGC

CTTGACGCAATTCTCGATC

CTTGGCGCAAATTTGGTGC

CTTGACGCAATTCTCGTGT

Nr of selected repeats 8 Similarity 0.764411

Consensus:

CTTGgCGCAAtTcTcGTGc

>Cele-UNSB01_3:3394846-3394930 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=TCCAGCACTG

TCCAGCACTGACAAAATTTGC

TCCAGCACTGACAAAATTTGT

TCCAGCACTGACAAAATTTGT

TCCAGCACTGACAAAATTTGT

Nr of selected repeats 4 Similarity 0.936508

Consensus:

TCCAGCACTGACAAAaTTTGT

>Cele-UNSB01_3:3456121-3456336 Satlength=216 Nr of Repeats=18 RepeatLength=12

seed=AAAATAAAAA

AAAATAAAAAATA

AAAATAAAAAATA

AAAATAAAAAATA

AAAATAAAAAACA

AAAATAAAAAATA

Nr of selected repeats 17 Similarity 0.986928

Consensus:

AAAATAAAAAATA

>Cele-UNSB01_3:3456392-3470370 Satlength=13979 Nr of Repeats=556

RepeatLength=25 seed=ACTCTCTGGC

ACTCTCTGGCTTCCCACATATATTTT

TAGTCTTAGGCTTCGTCT
TAGGATTAGGTT
TAGGCTTAGGCT
TAGGCTTAGGCT
TAGTCTTAGGCT
TAGGCTTAGGCT
TAGGCTTAGGCT
TAGGCTTAGGCT
TAGGCTTAGGCT

TAGGCTTAGGCTTAGGCTTACCCATGACG

Nr of selected repeats 9 Similarity 0.901235

Consensus:

TAGGCTTAGGCT

>Cele-UNSB01_3:3518362-3520167 Satlength=1806 Nr of Repeats=19 RepeatLength=95
seed=TAATCCTATT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAATCAGGTTTGAGGGCCGCAGGCCCGAATACTCTTGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAATCAGATTGTTATTCGCTCAAGCCTACAAATCAGGTTTGAGGGCCGCAGGCCCGAACAACACTCTTGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAATCAGGTTTGAGGGCCGCAGGCCCGAACAACACTCTTGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTAAGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAATCAGGTTTGAGGGCCGCAGGCCCGAACAACACTCTTGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTAAGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGGTTTGAGGGCCGCAGGCCCGAACAACACTCTTGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTAAGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGGTTTGAGGGCCGCAGGCCCGAACAACACTCTTGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTAAGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGGTTTGAGGGCCGCAGGCCCGAACAACACTCTTGGA
AACTGTGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTAAGGGCCAGCTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTGTGGGCCAGTTT

TAATCCTATTCCAAGCAGATTGTTATTCGCTCAAGCCTACAAACCAGGGTTTGAGGGCCGCAGGCCCGAACAACACTCTTGGA
AACTAAGGGCCAGCTT

TAATCCTATTTCAAGCAGATTGTTATTTGCTCAAGCATAACCAACCAAGTTTGAGGGCCGCAGGCCCGAATACTCATGGA
AACTAAGGGCCAGCTG

Nr of selected repeats 19 Similarity 0.948948

Consensus:

TAATCCTATTCCAAGCAGATTGTTATTGCTCAAGCCTACAAAcCAGGtTTGAGGGCCGCAGGCCCGAAAtACTCaTGGA
AACTgtGGGCCAGCTT

>Cele-UNSB01_3:3579672-3580411 Satlength=740 Nr of Repeats=47 RepeatLength=15

seed=GTGGTGAGAC

GTGGTGAGACCCATC

GTGGTGAGACCCGTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGCGAGACCCATC

GTGGTGAGACCCATA

GTGGTGAGGCCTTTC

GTGGTGAGACCTTTC

GTGGTGAGACCATTC

GTGGTGAGATCCATC

GTGATGAGACCTTTC

GTGGCGAGACCCATA

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGCGAGACCCATC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGCGAGACCCATC

GTGGTGAGACCTTTC TAGGTGAGACCATTC

GTGGTGAGACCCATC

GTGATGAGACCTTTC

GTGGCGAGACCCATA

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGCGAGACCCATC

GTGGTGAGACCATTC TAGGTGAGACCATTC

GTGGTGAGACCCATC

GTGGTGAGACCTTTC

GTGGCGAGACCCATC

GTGGTGAGACCCATA

GTGGTGAGGCCTTTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

GTGGCGAGACCCATC

GTGGTGAGACCCATA

GTGGTGAGAGCTTTC

GTCGTGAGACCATTC

GTGGTGAGACCTTTC

GTGGTGATACCCGTTGTTC

GTGGTGAGACCTTTC

GTGGTGAGACCTTTC

Nr of selected repeats 44 Similarity 0.837350

Consensus:

GTGGTGAGACcctTC

>Cele-UNSB01_3:3676441-3676612 Satlength=172 Nr of Repeats=5 RepeatLength=34
seed=AATTGAAATT

AATTGAAATTTCCGGCAAATCGACAAATTGCGGG
AATTGAAATTTACGGCAAATCGGCAAGTTGCCGG
AATTGAAATTTCTGCAAAGCGGCAAATTGCCGA
AATTGAAATTTCCGGCAAATCGGCAAGTTGTCCG
AATTGAAATTTCTGTAAAGCGGCAAATTGTCCG

Nr of selected repeats 4 Similarity 0.800794

Consensus:

AATTGAAATTTCCgGcAAAgCGgCAAaTTGtCGg

>Cele-UNSB01_3:3780853-3780925 Satlength=73 Nr of Repeats=4 RepeatLength=16
seed=CCTACATACC

CCTACATACCTACATA
CCTACATACCTACATA
CCTACATATCTACAAA
CCTACATACCTACATACCTACATA

Nr of selected repeats 3 Similarity 0.888889

Consensus:

CCTACATAcCTACAtA

>Cele-UNSB01_3:3795055-3795458 Satlength=404 Nr of Repeats=8 RepeatLength=35
seed=TTCCGGCAA

TTCCGGCAAATCGGCAAATGCCGGAATTGAATTTTCCGGCACTTTGACGGGATTGAAAAT
TTCCGGCAAATCGACAATTTTCCGAAAATGAAAAT
TTCCAGCAAATCGGCAAATGCCGGAATCGAAAAT
TTCCGGCAAATCGGCAAATGCCGGAATTGAAAATTTATGCAAATCGGCAAATGCCGGAATTGAAGTTTCCGGAAAA
TCGTAATTTTGTGAAATGGAAAA
TTCCGGCAAATCGGCAAGTTGCCGGAATTGAAAAT
TTCCGGCAAACCGACAAATGCCGGAATTTAAAAG
TTCCGGCAAATCGGAAGATTGCCGGAATTTGAAAT
TTCCGGCAAATTACCGGAATTAATAATTTCCGGGAAAGTCGGCAATTTTCCGAAAAGGAAAAT

Nr of selected repeats 5 Similarity 0.760000

Consensus:

TTCCgGCAAAtCGgcAaatTgCCGgAAttgaAAAt

>Cele-UNSB01_3:3799869-3800537 Satlength=669 Nr of Repeats=5 RepeatLength=65
seed=AAGACACTAA

AAGACACTAATAAAAATATTATTTTTTATTCGTCTTTTCCAATCAGTGTGTCCATTTTTAAAGTGTCTACTGGAAGCTT
CATTTTTTGAATTCATAAAATTAATAATTTTCAATTTCCAATCAGTGTGTCCACTTTTAAAGTGTCCACTGGAAGCTTCAT
TTTTTGAACCTCAGAAAATTAAGTTTCATTTCCAATCAGTGTCCCGTGGTGGAAAAATTTTTTTTTTCTTTTTTTTTGG
GATGAAAAAATTCGAAAAAATTTTTTCATCCAGAAAAAAGGGGGAAAAAAGGTTTCAGAAAAAACAAACAAACAT
TTTTGTCTGCTGGATGGACTTTAGTCCAACAAAGGTAACGAGGGTTTGAAATGATTTTGAAAAAAGTAAAATAAAATT
TTTGATGAAAATTA

AAGACACTAATAAAAATATTATTTTTTATTCGTCTTTTAATTTTACAAAATTTTCAATAAAAATTT
AAGACACTAATAAAAATATTATTTTTTATTCGTCTTTATAATTTTAGAAAATTTTCAATAAAAATTT
AAGACACTAATAAAAATATTATTTTTTATTCGTCTTTTAATTTTAGAAAATTTTCAATAAAAATTA
AAGACACTAATAAAAATATGATTTTTTATTCGTCTTTTAATTTTAGAAAATTTTCAATAAAAATTA

Nr of selected repeats 3 Similarity 0.945299

Consensus:

AAGACACTAATAAAAATATtATTTTTTATTCGTCTTtTAATTTTAgAAAATTTTCAATAAAAATt

>Cele-UNSB01_3:3818464-3818544 Satlength=81 Nr of Repeats=5 RepeatLength=12
seed=TAAGCCTAAG

TAAGCCTAAGCTTGTTGGAAAATATG
TAAGCCTAAGCC
TAAGCCAAAGCG
TAAGCCTAAACC

TAAGCCTAACCTATGAC

Nr of selected repeats 3 Similarity 0.777778

Consensus:

TAAGCCTAAgCc

>Cele-UNSB01_3:3873879-3874448 Satlength=570 Nr of Repeats=9 RepeatLength=30

seed=CCTTGTAGGC

CCTTGTAGGCAAGGAGGAAGACGTAGGTCACCTTGAAAAGTGCAAAAGTAGGCCG

CCTTGTAGGTAAGGAGGTAGGTGTAGGCCG

CCTTGTAGGCAGAGAGATAGGCGTAGGTTCG

CCTTGTAGGCAAGGAGTTAGGCGTAGGTCA

CCTTGTAGGCAAGGAGGTAGGTCGAGTTGTAGGCAAGGAGGTAGGCCGTAGGTTCG

CCTTGTAGGCAAGGAGGAAGGCGTAGGTCA

CCTTGTAGGCAGAGAGGTAGGCGCACGCGCCGCAAGTGGTACATCCATGCAAATGCGCTCTACTGATAATTTGAGTGT

AGACCAGTTTTGGGCGCGTGATAACGAAAAAGCTTTGGTCCAAAAAATTTAGAAATTAATTTTCGGACATTTTTTATA

TGCATCACAAAAAACTGGACCAACCGTTTTTTGAGATACACGCGCCCAAACGTCCAGGTATACGGTAGACAAATTGCGT

ACAGGTACCACTGCTCGGGCCGTGAGGCGTAGGTAG

CCTTGTAGGCAAGGAGGTAGGCGTAGGTCA

CCTTGTAGGCCAGGAGGTAGGCGTAGGTTCG

Nr of selected repeats 6 Similarity 0.842963

Consensus:

CCTTGTAGGCAAGGAGgTAGGCGTAGGTCa

>Cele-UNSB01_3:3880760-3880928 Satlength=169 Nr of Repeats=10 RepeatLength=16

seed=TAGGCATGTA

TAGGCATGTAGGCATG

TAGACATGTAGGCATG

TAGACATGTAGGCATG

TAGGCATGAAGGTACG

TAGGCATGTAGGCATG

TAGGCATGTAGGCATG

TAGGCATGTAGGCATG

TAGGCATGTAGGCATG

TAGGCATGTAGGCATG

TAGGCATGTAGGCATGTAGGCATG

Nr of selected repeats 9 Similarity 0.912037

Consensus:

TAGgCATGTAGGCATG

>Cele-UNSB01_3:3928597-3928907 Satlength=311 Nr of Repeats=5 RepeatLength=18

seed=TGCAGCACTA

TGCAGCACTAATTTCCAGGCTCTTTTTTAA

TGCAGCACTATTAGAGAC

TGCAGCACTAATTTTCGAACGGCTATTTTCAATTGAAGATCATTAGTTTTTAGTCACACAAGCTCATCTTTTAAGCAGA

TATTCATTAATAACTGTGTACTTTTGTAACAAGAATGACCCAATAATTTAATTATATTTGTAAAATAATAAGAAATCATC

AAAAATATACAGAAAATCTCCCCAAAATGTCGAAACTATTGAGTGACTTTTTTCAAAGAAAAAGGGGG

TGCAGCACTATTAGAGAC

TGCAGTACTACTGGAGAC

Nr of selected repeats 3 Similarity 0.851852

Consensus:

TGCAGcACTAtTaGAGAC

>Cele-UNSB01_3:4029920-4030220 Satlength=301 Nr of Repeats=8 RepeatLength=40

seed=AGAACCTTCT

AGAACCTTCTGGGAATTTCTGGAAAATTCTAGAATGTTCC

AGAACCTTCTGGAAAATTCTGAAAAGCTTT

AGAACCTTCTGAAAAATTCTAGAAAATTCTGGAATGGTCC

AGAACCTTCTGGAAAATTCGAAAAATTCTGGAATGTTCC

AGAACCTTCTGGGAATTTCTGGAAAATTCTAGAATGTTCC
AGAACCTTCTGGAAAATTCTGAAAAGCTTT
AGAACCTTCTGAAAAATTCTAGAAAATTCTGGAATGGTCC
AGAACCTTCTAGAAAATTCGAAAAATTCTGGATTGTTCT
Nr of selected repeats 6 Similarity 0.824444

Consensus:

AGAACCTTCTGgaAAaTTcTagAAAATTCTgGAATGtTCC

>Cele-UNSB01_3:4030293-4031043 Satlength=751 Nr of Repeats=50 RepeatLength=15

seed=CGTGGTGAGA

CGTGGTGAGACCCAT

CGTGGCGAGACCCAC

CGTGGTGAGACCCGT

CGTGGTGAGACCCAT

CGTGGTGAGACCCAT

CGTGGTGAGATCCAT

CGTGGTGAGACCCAT

CGTGGTGAGATCCAT

CGTGGTGAGACCCAT

CGTGGTGAGATCCAT

CGTGGTGAGACCCAT

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CAAAACCCAAGtaGATCCCCT

>Cele-UNSB01_3:4389614-4389732 Satlength=119 Nr of Repeats=7 RepeatLength=17

seed=AGGGGGCATC

AGGGGGCATCGAGAG

AGGGGGCATCGCGTTCTA

AGGGGGCATTAGGTCAA

AGGGGGCATTGTTCGT

AGGGGGCATCCGTTTCAG

AGGGGGCATCCATTTCAG

AGGGGGCATCCGTTTCAG

Nr of selected repeats 5 Similarity 0.749020

Consensus:

AGGGGGCATccgtTCag

>Cele-UNSB01_3:4392502-4392620 Satlength=119 Nr of Repeats=7 RepeatLength=17

seed=GATGCCCCCT

GATGCCCCCTCTGAACG

GATGCCCCCTCTGAATG

GATGCCCCCTCTGAACG

GATGCCCCCTACGAACAA

ATGCCCCCTTTGACCTA

ATGCCCCCTTAGAACGC

GATGCCCCCTCTCTC

Nr of selected repeats 5 Similarity 0.729630

Consensus:

gATGCCCCCTctGAacg

>Cele-UNSB01_3:4778835-4779093 Satlength=259 Nr of Repeats=5 RepeatLength=17

seed=ATTATTTTCA

ATTATTTTCATTCCGTG

ATTATTTTCATTCCGTG

ATTATTTTCATTCCGTG

ATTATTTTCATTCCGTG

ATTATTTTCACTCGGGAATCGCTCGCCCCTATGGGGAGTCTACGCAAGGACAACGCAAGGACAAGGACAACATTCTA

ATGGAATGGAACAATTGCCGACTGCACCAATTCTAGTTCAAGCGAACAAATGATAACTTTTGTATTCTGTATTCCTTC

ACGTCTCCCAGCGAGCGTAATAAATTATTATT

Nr of selected repeats 4 Similarity 1.000000

Consensus:

ATTATTTTCATTCCGTG

>Cele-UNSB01_3:5426163-5426753 Satlength=591 Nr of Repeats=28 RepeatLength=20

seed=CTAGGTCTGC

CTAGGTCTGCCTAGGGTAGGCTATGGTAGG

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CTAGGTCTGCCAGGGTAGA

CTAGGTCTGCCTGAGGTAGG

CTAGGTCTGCCTAGGGTAGG

CTAGGTCTGCCTAGGGTAGA

CTAGGTCTGCCTAGGGTAGA

CTAGGTCTGCCTGAGGTAGG

CTAGGTCTGCCTAGGGTAGGCTATGGTAGG

CTAGGTCTGCCTAGGGTAGG

CTAGGTCTGCCAGGGTAGA

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CTAGGTCTGCCAGGGTAGA

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CTAGGTCTGCCTGAGGTAGG
CTAGGTCTGCCTAGGGTAGG
CTAGTTCTGCCTAGGGTAGA
CTAGGTCTGCCTAGGGTAGA
CTAGGTCTGCCTGAGGTAGG
CTAGGTCTGCCTAGGGTAGG
CTAGGTCTGCCCAGAGCGGG
CTAGGTCTGCCTGGGGTAGG
CTAGGTCTGCCTGGGGTAGG

Nr of selected repeats 25 Similarity 0.872444

Consensus:

CTAGGTCTGCCTagGGTAGg

>Cele-UNSB01_3:5426187-5427065 Satlength=879 Nr of Repeats=40 RepeatLength=20
seed=GGTAGGCTAG

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GGTAGGCTAGGTCTGCCAG
GGTAGACTAGGTCTGCCTGA
GGTAGGCTAGGTCTGCCTAG
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GGTAGGCTAGGGGTAGTGCTGTCTAG

Nr of selected repeats 28 Similarity 0.844293

Consensus:

GGTAGgCTAGGTCTGCCTaG

>Cele-UNSB01_3:5494321-5534864 Satlength=40544 Nr of Repeats=1542

RepeatLength=26 seed=GTTAGAGTCA

GTTAGAGTCATTATTTTAGGTGAATG

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GTTAGAGTCATTATTTTAGGTGAATG

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GTTAGAGTCATTATTTTAgGTGAATA
GTTAGAGTCATTATTTTAgGCGAATG
GTTAGAGTCATTATTTTAgGTGAACG
GTTAGAGTCATTATTTTAgGTGAATGG

Nr of selected repeats 1416 Similarity 0.990443

Consensus :

GTTAGAGTCATTATTTTAgGTGAATG

>Cele-UNSB01_3:5534873-5535003 Satlength=131 Nr of Repeats=5 RepeatLength=26
seed=ACCATTCACC

ACCATTCACCTAACATAATGACTCTA

ACCATTCACCCAAAATAATGACTCTA

ACCATTCACCTAAAAATATGACTCTA

ACCATTCACCTAAAATAATGACTCTA

ACCATTCACCTAAAATAATGACTCTA

Nr of selected repeats 5 Similarity 0.917949

Consensus :

ACCATTCACcAAaAtaATGACTCTA

>Cele-UNSB01_3:6120416-6122897 Satlength=2482 Nr of Repeats=10 RepeatLength=228 seed=CCACCAGATC

CCACCAGATCAGCAGCGTCTCATCTTCGCCGGAAAGCAGCTCGAGGACGGCCGCACCCTGTCTGACTACAACATCCAGA
AGGAATCTACTCTTCACTTGGTTCTTCGTCTTAGAGGAGGAATGCAGATCTTTGTCAAGACTTTGACTGGAAAGACCAT
CACACTTGAAGTTGAAGCTTCCGACACGATCGAGAACGTCAAGGCCAAGATTCAGACAAGGAGGGAATC
CCACCAGATCAGCAGCGTCTTATCTTTGCTGGTATGTTACATATAACAAATTTTGTTCATGAGAGACTAATTTTTTCC
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CTCAGAGGAGGTATGCAGATCTTCGTCAAGACATTGACTGGAAAGACCATCACACTTGAAGTCAAGCTTCCGACACGA
TCGAAAATGTCAAGGCTAAGATTCAAGATAAAGAAGGAATC
CCACCAGATCAGCAAAGACTTATCTTCGCCGGAAAGCAGCTCGAGGACGGCCGCACCCTTTGACTACAACATCCAGA
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CACCTCGAAGTCAAGCCTCCGACACCATCGAAAATGTCAAGGCCAAGATCCAAGACAAGGAAGGAATC
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CTCAGAGGAGGTATGCAGATCTTCGTCAAGACTTTGACTGGAAAAACCATCACTCTCGAGGTCAAGCTTCCGACACCA
TTGAGAATGTCAAAGCCAAAATCCAGGATAAGGAGGGAATC

Nr of selected repeats 6 Similarity 0.843765

Consensus:

CCACCAGATCAGCAAcGtCTcATCTTCGCCGGAAAGCAaCTCGAgGAcGGCCGcACCCTtTCgGACTACAACATCCAgA
AGGAaTCAACTCTTCACTTGGTTCTCCGTcTgAGAGGAGGtATGCAGATCTTCGTCAAGACaTTGACcGGAAAGACCAT
CACcCTcGAAGTCAAGCCTCcGAcACCATCGAaAAtGtCAAGGCCAAGATcCAAGACAAGGAAGGAATc

>Cele-UNSB01_3:6192343-6192405 Satlength=63 Nr of Repeats=4 RepeatLength=15 seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGCAA

Nr of selected repeats 3 Similarity 0.762963

Consensus:

CgAAAAGGGGAtCtg

>Cele-UNSB01_3:6192580-6192657 Satlength=78 Nr of Repeats=5 RepeatLength=15 seed=TCCCCTTTTC

TCCCCTTTTCGTTGC
TCCCCTTTTCGTATC

TCCCCTTTTTCGCAGA
TCCCCTTTTTGCAGA
TCCCCTTTTTCGTTCTGC
Nr of selected repeats 4 Similarity 0.748148
Consensus:
TCCCCTTTTTcGcaga
>Cele-UNSB01_3:6364525-6365839 Satlength=1315 Nr of Repeats=65 RepeatLength=19
seed=AAAAATAGAT
AAAAATAGATTGTTACACG
AAAAATAGATTGTTATACGAAAAAATGCATTGTTACACA
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Nr of selected repeats 61 Similarity 0.968479

Consensus:

AAAAATAGATTGTTACACG

>Cele-UNSB01_3:6731291-6731428 Satlength=138 Nr of Repeats=9 RepeatLength=15

seed=CGAAAAGGGG
CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAAATA
CGAAAAGGGGAGATA
CGAAAAGGGGAGATA
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CGAAAAGGGGAGATA
CGAAAAGGGGAGATA

Nr of selected repeats 8 Similarity 0.847619

Consensus:

CGAAAAGGGGAgaTa

>Cele-UNSB01_3:6731603-6731679 Satlength=77 Nr of Repeats=5 RepeatLength=15

seed=TCCCCTTTTC
TCCCCTTTTCGTTGC
TCCCCTTTTCGTATC
TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA
TCCCCTTTTCGCAGA

Nr of selected repeats 4 Similarity 0.748148

Consensus:

TCCCCTTTTCgcaga

>Cele-UNSB01_3:6746945-6756350 Satlength=9406 Nr of Repeats=204 RepeatLength=11

seed=GTACTGTAGG
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GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTAGGAAAATTGAGTTTTTGTCTACAGAAGAGGTATTGGGTAGAGAG
TTGCTGGGGGATAATGCCAAG
GTACTGTAGTA
GTACTGTAGTA

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GTACTGTAGGA

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GTACTGTAGTG

GTACTGTAGGA

Nr of selected repeats 123 Similarity 0.909143

Consensus:

GTACTGTAGtA

>Cele-UNSB01_3:6807960-6808176 Satlength=217 Nr of Repeats=6 RepeatLength=21
seed=AAATCTAATC

AAATCTAATCCAATGTGGAAC

AAATCTAATCCAATATGGCCG

AAATCTAATCCAATATGGAAC

AAATCTAATCCAATATGGCCG

AAATCTAATCCAATATGGTCG

AAATCTAATCAAATATGGCTGAGATCGTGCCATATTGGATTAGATTTTCGACCATATTGGATTAGATTTTCGACCATATTA
GATTAGATTTGTCTTCTAATGAAATATGGAGG

Nr of selected repeats 5 Similarity 0.822727

Consensus:

AAATCTAATCCAATaTGGnCc

>Cele-UNSB01_3:7587437-7632311 Satlength=44875 Nr of Repeats=1482

RepeatLength=27 seed=GTGGGAAGCC

GTGGGAAGCCACAGAGAGTAAAAATA

GTGGGAAGCCACAGAGAGTAAAAATAG

GTGGGAAGCCACAGAGAGTAAAAATATA

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TGGAGCGGTTT
TGGAGCGGTTA
TGGAGCGGTTT
TGGAGCGGTAT
TGGAGCGGTTA
TGGAGCGGTGAAGGAGCGGTGAA
GGAGCGGTTTTGTAGCCGTTG
TGGAGCGGTTT
TGGAGCGGTTT
TGGAGCGGTTA
TGGAGCGGTTT
TGGAGCGGTGA
TGGAGCGGTTT
TGGAGCCGTTG
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TGGAGCGGTTT

Nr of selected repeats 122 Similarity 0.884864

Consensus:

TGGAGCGGTTt

>Cele-UNSB01_3:7825014-7825135 Satlength=122 Nr of Repeats=11 RepeatLength=11

seed=CGGATAATTA

CGGATAATTAA
CGGATAATTAA

Nr of selected repeats 11 Similarity 1.000000

Consensus:

CGGATAATTAA

>Cele-UNSB01_3:7826007-7841897 Satlength=15891 Nr of Repeats=610

RepeatLength=26 seed=CATTAGATGA

CATTAGATGAAATTCCAAAATTAGAC
CATTAGATGAATTTCCAAAAGTTAGAC
CATTAGATGAAATTCCAAAATTAGAC
CATTAGATGAATTTCCAAAAGTTAGAC
CATTAGATGAATTCCAAAAGTTAGAC
CATTAGATAAATTCCAAAAGTTAGAC
CATTAGATGAAATTCCAAAATTAGAC
CATTAGATGAATTTCCAAAAGTTAGAA
CATTAGATGAAATTCCAAAATTAGAC
CATTAGATGAATTTCCAAAAGTTAGAC
CATTAGATGAATTCCAAAAGTTAGACAATTAGATAAATTTCCAAAAGTTAGAC
CATTAGATGAATTTCCAAAAGTTAGAC
CATTAAATGAATTTCCAAAAGTTAGAC
CATTAGATGAATTTCCAAAAGTTAGAC
CATTAGATGAATTTCCAAAAGTTAGAC

CATTAGATGAATTTCCAAAAGTTAGAC

Nr of selected repeats 417 Similarity 0.923292

Consensus:

CATTAGATGAATTcCCAAAAGTTAGAC

>Cele-UNSB01_3:7846966-7847368 Satlength=403 Nr of Repeats=9 RepeatLength=45

seed=TCTGATCCTT

TCTGATCCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT

TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG

TCTGATCCTTTAGCTCCAAAAGGATCACGAGGCTCTTCCTGATGT

TCTGATCCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT

TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG

TCTGATCCTTTAGCTCCAAAAGGATCACGAGGCTCTTCCTGATGT

TCTGATCCTTCAGCTCCGAAGGATCACATGGGTACCTTCTGATGT

TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG

TCTGATCCTTTAGCTCCAAAAGGATCACGAGGCTCTTCCTGATGT

Nr of selected repeats 6 Similarity 0.857778

Consensus:

TCTGATCCTTCAGaTaaGAAGGATCacAaGGGTACCTcCTGATGg

>Cele-UNSB01_3:7847664-7848155 Satlength=492 Nr of Repeats=11 RepeatLength=45

seed=GAAGGATCAG

GAAGGATCAGAACATCAGGAGGTACCCATGTGATCATTTCGGCTCT

GAAAGATCAGATCATCAGGCAGAGCCTCATGTTCTTTTGGAGCT

GAAGGATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTATCT

GAAGGATCAGATCATCAGAAGGTACCCATGTGATCCTTCGGATCG

GAAGGATCAGATCATCAGGCAGAGCCTCATGTTCTTTTAGAGCT

GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT

GAAGGATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTATCT

GAAGGATCAGAACATCAGAAGGTATCCATGTGATCCTTCGGAGCT

GAAGGTTTCAAGATCAGGAAGAGCCTCGTGATCCTTTGGAGCT

GAAGTATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTATCT

GAAGGATCAGAACATCAGAAGGTACCCATGTGATCCTTCGGAGCT

Nr of selected repeats 7 Similarity 0.820811

Consensus:

GAAGGATCAGAnCATCAGgAGGTACCCaTgtGATCCTTCggAtCT

>Cele-UNSB01_3:7913456-7913988 Satlength=533 Nr of Repeats=28 RepeatLength=19

seed=AATCTATTTT

AATCTATTTTTCGTGTAAC

AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGCAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC

Nr of selected repeats 28 Similarity 0.920040

Consensus:

AATCTATTTTTTCGTGTAAC

>Cele-UNSB01_3:7922958-7923224 Satlength=267 Nr of Repeats=14 RepeatLength=19
seed=CAATCTATTT

CAATCTATTTTTTCGTGTAA
CAATCTATTTTTTCGTGGAA
CAATCTATTTTTTCGTGTAA
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CAATCTATTTTTTCGTGTAA
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CAATCTATTTTTTCGTGTAA
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CAATCTATTTTTTCGTGTAA

Nr of selected repeats 14 Similarity 0.974552

Consensus:

CAATCTATTTTTTCGTGTAA

>Cele-UNSB01_3:7953449-7953511 Satlength=63 Nr of Repeats=4 RepeatLength=15
seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA

Nr of selected repeats 3 Similarity 0.762963

Consensus:

CgAAAAGGGGAtcTg

>Cele-UNSB01_3:7953695-7953787 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCTTTTC

TCCCCTTTTCGTTGC
TCCCCTTTTCGTATC
TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA
TCCCCTTTTCGCAGA
TCCCCTTTTCGTTCTGC

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTCGtagc

>Cele-UNSB01_3:8499608-8499713 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=AAGTTTTACT

AAGTTTTACTTTGATTTTTTTT
AAGTTTTACTTTGATTTTTTTT
AAGTTTTACTTTGATTTTTTTT
AAGTTTTACTTTGATTTTTTTT
AAGTTTTACTTTGATTTTTTTA

Nr of selected repeats 5 Similarity 0.974603

Consensus:

AAGTTTTACTTTGATTTTTTTt

>Cele-UNSB01_3:8579889-8580089 Satlength=201 Nr of Repeats=12 RepeatLength=16

seed=AGGCACGTAG
AGGCACGTAGGCACGT
AGGAACGTAGGCACGT
AGGCACGTAGGCACAC
AGGCACGTAGGCACGT
AGCCACGTAGCCACGT
AGGCACGTAGGCACGT
AGGCACGTAGGCACGT
AGGCACGTAGGCACGT
AGGCACGTAGGCACGT
AGGCACGTAGGCACAC
AGGCACGTAGGCACGT
AGCCACGTAGGCACGT
AGCCACGTAGGCACGTAGCCACGT

Nr of selected repeats 11 Similarity 0.887879

Consensus:

AGGCACGTAGGCACGT

>Cele-UNSB01_3:8580701-8581151 Satlength=451 Nr of Repeats=29 RepeatLength=15

seed=ACCCATCGTG
ACCCATCGTGGCGAG
ACCCATCGTGGCGAG
ACCCATCGTGGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCACCGTGGTGAG
ATCCATCGTGGCGAG
ACCCATCGTGGCGAG
ACCCATCGTGGCGAG
ACCCATCGTGGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
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ACCCACCGTGGTGAG
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ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCATCGTGGTGAG
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ACCCATCGTGGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCACCGTGGTGAA
ACCCACCGTGGGGAG

ACCCGTCGTGGTGAGACGCACCGTGGTAAG
ACCCATCGTGGTAAG
Nr of selected repeats 28 Similarity 0.904762
Consensus:
ACCCATCGTGGtGAG
>Cele-UNSB01_3:8581179-8581353 Satlength=175 Nr of Repeats=5 RepeatLength=35
seed=GGGAAATTTA
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGa
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGC
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGa
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGC
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGC
Nr of selected repeats 4 Similarity 0.974603
Consensus:
GGGAAATTTAAATTTTCTGTGAAAAATATTTTGGa
>Cele-UNSB01_3:8581474-8581754 Satlength=281 Nr of Repeats=7 RepeatLength=40
seed=TCTGGAATGT
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAG
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAG
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGAGAAAAG
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAT
TCTGGAATGTTCCAAAACCTTTCTAGAAAAATGGGAAAAG
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAG
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAG
Nr of selected repeats 7 Similarity 0.971429
Consensus:
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAG
>Cele-UNSB01_3:8589669-8589949 Satlength=281 Nr of Repeats=7 RepeatLength=40
seed=TCTGGAATGT
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TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAG
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Nr of selected repeats 7 Similarity 0.971429
Consensus:
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAG
>Cele-UNSB01_3:8597864-8598144 Satlength=281 Nr of Repeats=7 RepeatLength=40
seed=TCTGGAATGT
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Nr of selected repeats 7 Similarity 0.971429
Consensus:
TCTGGAATGTTCCAGAACTTTCTAGAAAAATGGGAAAAG
>Cele-UNSB01_3:8606059-8606339 Satlength=281 Nr of Repeats=7 RepeatLength=40
seed=TCTGGAATGT
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TTCAAACCTTTTAAACTGAGATTTATGGAGAATATGGAAATTTCAAATGTGCACTGGTT
>Cele-UNSB01_3:9809905-9810297 Satlength=393 Nr of Repeats=13 RepeatLength=11
seed=GTACTGTAGG
GTACTGTAGGG
GTACTGTAGGGT
TACTGTAGGATTACTGTAGTTTTGGAAAAATTGACTTTTTGTCTTTTGAAGTGATATTGGTTTGGAGTTAGTGGTGGGA
TATGGTCGGGATACTGTAGTA
GTACTGTAGGG
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TATGGTCGGG
GTACTGTAGCA
GTACTGTAGTA
GTACTGTAGGA
GTACTGTAGGATTTCTGTATTTTTGAAAAAAATTGGCTTTTCGTCTTTTGAAGTGATATTGCTTTTGGGTTAGTGTCCG
GATATGGTTGGG
GTACTGTAGTT
GTACTGTAGAG
GTATTGTAGGA

Nr of selected repeats 8 Similarity 0.796537

Consensus:

GTACTGTAGga

>Cele-UNSB01_3:9810383-9810703 Satlength=321 Nr of Repeats=8 RepeatLength=40
seed=TCCAGAACCT

TCCAGAACCTTCTGGAAAATTCGAGAAAATTTCTGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTTCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTTCTGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATGCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTTCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTTCTGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTTCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT

Nr of selected repeats 8 Similarity 0.945238

Consensus:

TCCAGAACCTTCTGGAAAATtcGAGAAAATtCTGGAATGT

>Cele-UNSB01_3:9810418-9811039 Satlength=622 Nr of Repeats=9 RepeatLength=40
seed=AATGTTCCAG

AATGTTCCAGAACCTTCTGGAAAATCCGAGAAAATTTCTGG
AATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGG
AATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATTTCTGG
AATGTTCCAGAACCTTCTGGAAAATCCGAGAAAATGCTGG
AATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATTTCTGG
AATGTTCCAGAACCTTCTGGAAAATCCGAGAAAATTTCTGG
AATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGG
AATGTTCCAGAACCTTCTGGAAAATTCGAGAAAATTCGTGGTGAGACCCTTCGTGGTGAGACCCATCTTGGTGAGACCC
ATCTTGGCGAGACCCATAAGTTTTGGCGGAAATTCAAATTTTCTGATAAAAAATTTTGGCGGTAATTCAAATTTTCT
GAGAAAAAATTTGGCGGGAATTCAAATTTTCTGTGAAAAATTTTGGCGGGAATTCAAAATTTCTTTGAAAAATTTTGGC
GGGAATTCAAAATTTCTTTGAAACATTTTGGCGGGAATTCAAAGTTTCTGAAAAAAATTTCTGG

Nr of selected repeats 8 Similarity 0.903571

Consensus:

AATGTTCCAGAACCTTCTGGAAAATtcGAGAAAATtCTGG

>Cele-UNSB01_3:10130069-10130193 Satlength=125 Nr of Repeats=4 RepeatLength=31
seed=TCTGCTAAAT

TCTGCTAAATAATTAGAAGACCAATCTTGGG
TCTGCTAAATAATTAGCAGACCATACTTGAT
TCTGCTAAATAATTAGCAGACCATACTTGAT
TCTGCTAAATAATTAGTAGACCATACTTGAT

Nr of selected repeats 4 Similarity 0.878136

Consensus:

TCTGCTAAATAATTAGcAGACCAtaCTTGat

>Cele-UNSB01_3:10140093-10140163 Satlength=71 Nr of Repeats=4 RepeatLength=19

seed=TGGTTGAGGC

TGGTTGAGGCTCTCGATTT

TGGTTGAGGCTCT

TGGTTGAGGCTCTAGATTT

TGGGTGAGGCTCTAGATTT

Nr of selected repeats 3 Similarity 0.906433

Consensus:

TGGtTGAGGCTCTaGATTT

>Cele-UNSB01_3:10146078-10146173 Satlength=96 Nr of Repeats=5 RepeatLength=19

seed=ATTTTGGTTG

ATTTTGGTTGAGGCTCTAG

ATTTTGGTTGAGGTTGAGG

ATTTTGGTTGAGGCTGAGG

ATTTTGGTTGAGGCTCTAG

ATTTTGGTTGAGGCTCAGG

Nr of selected repeats 5 Similarity 0.818333

Consensus:

ATTTTGGTTGAGGcTcAGg

>Cele-UNSB01_3:10214948-10215134 Satlength=187 Nr of Repeats=6 RepeatLength=31

seed=TCTGCTAAAT

TCTGCTAAATATTTAGCATAACCCACATTGGG

TCTGCTAAATATTTAGCATAACCCACATTGGG

TCTGCTAAATATTTAGCATAACCCACATTGGG

TCTGCTAAATATTTAGCATAACCCACCTTGGG

TCTGCTAAATATTTAGCATAACCCACATTGGG

TCTGCTAAATATTTAGCATAACCCATCTTGGG

Nr of selected repeats 6 Similarity 0.962724

Consensus:

TCTGCTAAATATTTAGCATAACCCACaTTGGG

>Cele-UNSB01_3:10216874-10217114 Satlength=241 Nr of Repeats=12 RepeatLength=20

seed=AAAAATAGAT

AAAAATAGATTGACATACCAA

AAAAATAGATTGACATACCA

AAAAATAGATTGACATACCA

AAAAATAGATTGACATACCA

AAAAATAGATTGACATACCA

AAATATAGATTGACATACCA

AAAAATAGATTGACATACC

AAAAATAGATTGACATACC

AAAAATAGATTGACATACAAA

AAAAATAGATTGACATACCA

AAAAATAGATTGGCATAACCA

AAAAATAGATTGACATACAA

Nr of selected repeats 8 Similarity 0.950000

Consensus:

AAAAATAGATTGACATACCA

>Cele-UNSB01_3:10234987-10235185 Satlength=199 Nr of Repeats=4 RepeatLength=31
seed=TATGCTAAAT
TATGCTAAATAGCTAGCAGACCCAAGGTGGC
TATGCTAAATATTTAGCAGACCCAACGTTGG
TATGCTAAATATTTAGCAGACCCAATGTGGA
TATGCTAAATATTTTCGAGACCCAAGGTGGTAGGGCTGAAAACATGATTTTTCAAAAAATGGGCCGATTTTGCCTGTT
TTGAGGGAAAATTTAGGCTTTTTGTG
Nr of selected repeats 3 Similarity 0.812500

Consensus:

TATGCTAAATAtTTAGCAGACCCAAnGTGGn

>Cele-UNSB01_3:10399868-10399945 Satlength=78 Nr of Repeats=5 RepeatLength=15
seed=CGAAAAGGGG
CGAAAAGGGGAGCAGAA

CGAAAAGGGGATCTG

CAAAAAGGGGATCTG

CGAAAAGGGGAGATA

CGAAAAGGGGAGCAA

Nr of selected repeats 4 Similarity 0.748148

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_3:10400120-10400212 Satlength=93 Nr of Repeats=5 RepeatLength=15
seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATCTCCATTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTTCGAGA

TCCCCTTTTCGTTCTGC

Nr of selected repeats 3 Similarity 0.762963

Consensus:

TCCCCTTTTcGcaGa

>Cele-UNSB01_3:10519446-10519548 Satlength=103 Nr of Repeats=8 RepeatLength=12
seed=AAAACATAAAA

AAAACATAAAAAT

AAAACATAAAAAT

AAAACATAAACTA

AAAATAAACTA

AAAATAAACT

AAAACATAAAAAT

AAAACATAAAAAT

AAAACATAAACTAAAAAT

Nr of selected repeats 5 Similarity 0.815385

Consensus:

AAAACATAAAAaT

>Cele-UNSB01_3:10519570-10525291 Satlength=5722 Nr of Repeats=35
RepeatLength=164 seed=ATGCCAATCA

ATGCCAATCAAAGTATAATAGCTTATACGGAAGTATTTTTTTTAAAACTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTTATTGCATAAACTGTTTCAGCGTAGTCAAAAATAC
CAGAAT

ATGCCAATCAAAGTATAATAGCTTATACGGAAGTATTTTTTTTAAAACTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTTATTGCATAAACTGTTTCAGCTAGTCAAAAATAC
AGAAT

ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTTATTGCATAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT

ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAAATCATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AATATTCAAAGTATGGGAAAAATATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGCATAGTCAAAAATACC
AGAAT
ATGCCAATCAAGTATAATAGCTTTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTCAA
TATTCAAAAGTATGGGAAAAATATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGCATAGTCAAAAATACCAG
AAT
ATGCCAATCACAGTATAATAGCTTATACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAAATCATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAAATCATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
ATATATTCAAAGTATGGGAAAAATATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGCATAGTCAAAAATAC
CAGAAT
ATGCCAATCACAGTATAATAGCTTATACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAAATCATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAAATCATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
ACATATTCAAAGTATGGGAAAAATATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGCATAGTCAAAAATAC
CAGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAAATCATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AATATTCAAAGTATGGGAAAAATATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGCATAGTCAAAAATACC
AGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTATGGGAAAAATCATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT
ATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
ATATATTCAAAGTATGGGAAAAATATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGCATAGTCAAAAATAC
CAGAAT
ATGCCAATCACAGTATAATAGCTTATACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AAAAATTCAAAGTGTGGGAAAAATCATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGTATAGTCAAAAATAC
CAGAAT

Nr of selected repeats 23 Similarity 0.972621

Consensus:

ATGCCAATCAAAGTATAATAGCTTgTACGGAAGTATTTTTTTTTAAAAATTGATAAAAAATATATAAAAGCTGATTTTTTTC
AaAaATTCAAAGTATGGGAAAAATcATATGGAGTCATTCTTTTTTATTGCATAAAAACTGTTTCAGtATAGTCAAAAATAC
CAGAAT

>Cele-UNSB01_3:10614332-10615157 Satlength=826 Nr of Repeats=20 RepeatLength=40
seed=AAAAGTAGGT

AAAAGTAGGTCATGACCTAGTTTTTCATGTGACCTACTTC
AAAAGTAGGTCATGACCTAGTTTTTCATGTGACCTACTTCA
AAAAGTAGGTTTTTAACGTGACCTTCTTA
AAAAGTAGGTCATGGCCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCATGACCTAGTTTTTAACGTGACCTCCTTA

AAAAGTAGGTCATGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCAGGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCAGGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCATGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCATGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCAGGACCTAGTTTTTAACCTTGACCTCCTCA
AAAAGTAGGTCAGGACCTAGTTTTTAACGTGACCTCCTCA
AAAAGTAGGTCATGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCAGGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCATGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCAGGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCATGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCAGGACCTAGTTTTTAACGTGACCTCCTTA
AAAAGTAGGTCATGACCTAGTTTTTAACGTGACCTCCTTA

Nr of selected repeats 16 Similarity 0.951944

Consensus:

AAAAGTAGGTCatGACCTAGTTTTTAACGTGACCTCCTTA

>Cele-UNSB01_3:10733639-10733701 Satlength=63 Nr of Repeats=4 RepeatLength=15

seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA

CGAAAAGGGGATCTG

CAAAAAGGGGATCTG

CGAAAAGGGGAGCAA

Nr of selected repeats 3 Similarity 0.762963

Consensus:

CgAAAAGGGGAtCtg

>Cele-UNSB01_3:10733861-10733953 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTTCGAGA

TCCCCTTTTTCGTTCTGC

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTTCGtagc

>Cele-UNSB01_3:10778310-10778713 Satlength=404 Nr of Repeats=14 RepeatLength=16

seed=GTAGGCACGT

GTAGGCACGTGAGAAGGTAGACATGTAGGTAGGCAGGCCTAAGATAGGTAG

GTAGGCACGTAGAATGTTAATAAGCAGACAGGCATGCCGTTGGCGGGCTGGCTTGAGGTAGGTAGGCATAAGTCATGTA

GACGGTTTCATAGGCAGGCAGGCTAAAGAAGAATTTTAAAGACAATCAGGCTAAACGTAGGTACGGCAGGCAT

GTAGGCACGTAGGCACA

TAGGCACGTAGGCAC

GTAGGCAGGTAGGCAC

GTAGGCACGTAGGCAC

GTAGGCACGTAGGCACGTAGGCAC

Nr of selected repeats 9 Similarity 0.981481

Consensus:

GTAGGCACGTAGGCAC

>Cele-UNSB01_3:10787273-10787444 Satlength=172 Nr of Repeats=5 RepeatLength=34

seed=TTTCCGGCAA

TTTCCGGCAAACCTGGCAAATTGCTGGAATTTAAAA

TTTCCGGCAAATCGGCGAATTGCCGGAATTGAAT

TTTCCGGCAAATTGACAAATTGTCGGAATCAAAA

TTTCCGGCAAATTGACAAATTGCCGGAATCAGAA

TTTCCGGCAAATTGACAAATTGCCGGAATCAAAA

Nr of selected repeats 4 Similarity 0.819841

Consensus:

TTTCCGGCAAATtGaCaAATTGcCGGAATcaaAA

>Cele-UNSB01_3:10934450-10934819 Satlength=370 Nr of Repeats=11 RepeatLength=29

seed=GGCCTAGAAA

GGCCTAGAAATCCTACTGGGTTACCTTTTTCTAAGTTGGT

GGCCTAGAAAACCCATTTTTAAAGTTGGT

GACCTAGAAACTTCTATTTGAAAGTAGAT

GGCATAGAAATTTCAAGTTGAAATTTGGT

GGCCTAGAAACTTCTACTTGAAAGTTGAT

GGCATAGAAATTTCAATTTGAAAGTTGGTGGCCTAACAACTTCTATTTGAAAGTTGGT

GGCCTAGAAAACCCATTTTTAAAGTTGAT

GACCTAGAAACTTCTATTTGAAAGTAGAT

GGCCTATAAATTTCTACTTGAAAATTTGGT

GACCTAGAAAACCTCCATTTCAACAGCTGAT

GGCCTAGAAACTTCTATTCGATTCGAAAGTTGATATGGC

Nr of selected repeats 7 Similarity 0.700055

Consensus:

GgCCTAGAAAanttCtatTTgAAAgtTtGaT

>Cele-UNSB01_3:10975904-10976322 Satlength=419 Nr of Repeats=11 RepeatLength=35

seed=CCGCCAAAAT

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTCCCGCTATAATTTTTTTCACAAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

CCGCCAAAATATTTTTCACTAAAAATTTGAATTTTC

Nr of selected repeats 10 Similarity 0.943280

Consensus:

CCGCCAAAATATTTTTCACTAAAAATTTgAATTTc

>Cele-UNSB01_3:10980699-10982201 Satlength=1503 Nr of Repeats=43

RepeatLength=35 seed=AAATTCAAAT

AAATTCAAATTTTTTGTGAAAAATACTTTGGCGGG

AAATTCAAATTTTTTAGTGAAAAATACTTTGGCGGA

AAATTCAAATTTTTTAGTGAAAAATACTTTGGCGGG

AAATTCAAATTTTTTGTGAAAAATTATAGCGGG

AAATTCAAATTTTTTGTGAAAAATACTTTGGCGGA

AAATTCAAATTTTTTAGTGAAAAATACTTTGGCGGG


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>Cele-UNSB01_3:11094399-11094498 Satlength=100 Nr of Repeats=5 RepeatLength=20
seed=GTTACACGAA
GTTACACGAAAAATAGATT
GTTACACGAAAAATAGATT
GTTACACGAAAAATAGATT
GTTACACGAAAAATAGATT
GTTACACGAAAAATAGATT
Nr of selected repeats 4 Similarity 1.000000
Consensus:
GTTACACGAAAAATAGATT
>Cele-UNSB01_3:11109268-11109343 Satlength=76 Nr of Repeats=5 RepeatLength=15
seed=TCCCCTTTTC
TCCCCTTTTCGTATC
TCCCCTTTTCATATC
TCCCCTTTTCGCAGA
TCCCCTTTTTCGAGA
TCCCCTTTTTCGAGA
TCCCCTTTTTCGAGA
Nr of selected repeats 5 Similarity 0.751111
Consensus:
TCCCCTTTTCgcAga
>Cele-UNSB01_3:11222702-11222792 Satlength=91 Nr of Repeats=6 RepeatLength=12
seed=GGCTTAGGCT
GGCTTAGGCTTG
GGCTTAGGCTTA
GGCTTAGGTTTA
GACTTAGGCTTA
GGCTTAGGCTAA
GGCTTAGGCTTAGTCTTAGTCTAAGGCTTA
Nr of selected repeats 5 Similarity 0.822222
Consensus:
GgCTTAGGcTta
>Cele-UNSB01_3:11241850-11242636 Satlength=787 Nr of Repeats=15 RepeatLength=37
seed=TTGGCGGGAA
TTGGCGGGAAATTCAAATTTTCTGAGAAATCATT
TTGGCAGGAATTCAAATTTTAAATTTTTTAAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAAATTTAAATTTTTTCGAAAACATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTAAAAACCATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAACCATT
TTGGCGGGAAATTCAAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTTTGAAAATATT
TTGGCGGGAAATTCAAATTTTAAATTTTGTCAAATTTAAAATGTCAAGGTAAGTGTAGTGGTACTGTAAGGGT
ACTGTAGGATTACTGTAGGGTTATTGTAGTTTGTAGTAAAATCGAATTTTAAACATTTTAAAGAGATATTGGCTTGAAAGT
TGGTGAAGATAATGTCAAGGCACTGTAATGGTACTGTAGGACTGTAGGATTATGGTAGGGTACTGTAGTTAGGA
AAACTTTGAATTTTAAAGCATTGAAAACATT
Nr of selected repeats 10 Similarity 0.935135
Consensus:
TTGGCGGGAAATTCAAATTTTAAATTTTTTgAAAatATT
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>Cele-UNSB01_3:11273157-11273241 Satlength=85 Nr of Repeats=5 RepeatLength=12
seed=GGCTTAGGCT

GGCTTAGGCTTA

GGCTTAAGCTCA

GGCTCAGGCTTA

GGCTTCGGCTTAAGCGTA

GGCTCAGGCTTAGGGTTAGGGTTAGGGTTA

Nr of selected repeats 3 Similarity 0.777778

Consensus:

GGCTtAgGCTtA

>Cele-UNSB01_3:11300832-11300986 Satlength=155 Nr of Repeats=5 RepeatLength=31
seed=GCAGCCGACG

GCAGCCGACGATATACGCGTTCGCTGGAGTA

GCAGCCGACGCTCTGCGAGGTTTGTAGAATG

GCGGCCGACGCTATATGAGTCTGATGGGAAA

GCAGACGACGCTTCCGGGTGTTGGATT

GCAGCCGACGCCTTGTGGGTCTGATGGAGTT

Nr of selected repeats 4 Similarity 0.524411

Consensus:

GCaGCCGACGctaTacGgGTctGaTgGagta

>Cele-UNSB01_3:11302620-11306800 Satlength=4181 Nr of Repeats=209

RepeatLength=20 seed=TCTATTTTTT

TCTATTTTTTGGTATGCCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAG

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAG

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAG

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAG

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAG

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAG

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAG

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAG

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTGGTATGTCAA

TCTATTTTTTAGTATGTCAA

TCTATTTTTTTGGTATGTCAA
TCTATTTTTTTGGTATGCCAA
TCTATTTTTTTGGTATGTCAA
TCTATTTTTTTGGTATGCCAA
TCTATTTTTTTGGTATGTCAA
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TCTATTTTTTTGGTATGCCAA
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TCTATTTTTTTGGTATGCCAA
TCTATTTTTTTGGTATGCCAA
TCTATTTTTTTGGTATGTCAA
TCTATTTTTTTGGTATGTCAA
TCTATTTTTTTGGTATGTCAA

Nr of selected repeats 209 Similarity 0.952647

Consensus:

TCTATTTTTTTgGTATGTCAA

>Cele-UNSB01_3:11327560-11327604 Satlength=45 Nr of Repeats=4 RepeatLength=11

seed=AAACTTGGGC

AAACTTGGGCA

AAACTTGGGTA

AAACTTGGGCT

AAACTTGGGCT

Nr of selected repeats 4 Similarity 0.858586

Consensus:

AAACTTGGGca

>Cele-UNSB01_3:11452503-11452739 Satlength=237 Nr of Repeats=6 RepeatLength=35

seed=AATTGCCGGA

AATTGCCGGAATTATACATTTCTGGCAAATTGGCAAATTTTCAATTCCGAGAATTTGCCA

ATTTGCCGGAACCTCGAAAAGTTCCCTTGCAAATCGGCA

AATTGCCGGAATTAAGATTTCCGGCAAATTGGCC

AATTGACGGAGTTCAAAAATTTCTGGCAAATTGGAA

AATTGCCGGAATTGAAAATTTTCGGCAAAGTTGTCA

AATTGCCGGAATTATAAATTTCCGGCAAACCAGCA

Nr of selected repeats 4 Similarity 0.720635

Consensus:

AATTGcCGGAaTTaaAaATTTccGGCAAattggca

>Cele-UNSB01_3:11461018-11461218 Satlength=201 Nr of Repeats=5 RepeatLength=40

seed=TCCAGAACCT

TCCAGAACCTTCTGGAAAATTCGAGAAAATTTCTGGAATGT

TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT

TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT

TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT

TCCAGAACCTTCTGGAAAATTCGAGAAAATTTCTGGAATGT

Nr of selected repeats 5 Similarity 0.960000

Consensus:

TCCAGAACCTTCTGGAAAATTTtGAGAAAATgCTGGAATGT

>Cele-UNSB01_3:11461401-11461721 Satlength=321 Nr of Repeats=10 RepeatLength=32

seed=TTTCTGTGAA

TTTCTGTGAAAAATTATAACGGGAATTCAAGT

TTTCTGTGAAAAATTATAACGGGAATTCAAAA

TTTCTGTGAAAAATTTGGCGGGAATTCAAAA

TTTCTGTGAAAAATTTGGCGGGAATTCAAAA

TTTCTGTGAAAAATTTTGGCGGGAATTCAAAA
TTTCTGTGAAAAATTTTGGCGGGAATTCAAAA
TTTCTGTGAAAAATTTTGGCGGGAATTCAAAT
TTTCTGTGAAAAATTTTGGCGGGAATACAAAT
TTTCTGTGAAAAATTATAACGGGAATTCAAGT
TTTCTGTGAAAAATTTTGGCGGGAATTCAAAA

Nr of selected repeats 10 Similarity 0.896296

Consensus:

TTTCTGTGAAAAATTTtTggCGGGAATTCAAaa

>Cele-UNSB01_3:11489719-11490125 Satlength=407 Nr of Repeats=12 RepeatLength=31
seed=TCTGAGCTAC

TCTGAGCTACAGTACTCCTGTCAAGAACAAT
TCTGAGCTACAGTACTCCTGTCAAGAACAGT
TCTGAGCTACAGTACTCCTGTCAAGAACGAT
TCTGAGCTACAGTGCCCTGCCAAGAGCGAT
TCTGAGCTACAGTACTCCTGTCAAGAACAAT
TCTGAGCTACAGTACTCCTGTCAAGAACAGT
TCTGAGCTACAGTACTCCTGTCAAGAACGAT
TCTGAGCTACAGTGCCCTGCCAAGAACAAT
TCTGAGCTACAGTACCCCTGCCAAGAGCGAT
TCTGAGCTACAGTACTTCTGTCAAGAGCGAT
TCTGAGCTACAGTACTCCTGTCAAGAGCGATTTTGGGCTACAGTACCCCGGTGCCAAGAGCGAT
TCTGAGCTACAGTACCTCCAGGAGCCAGAAT

Nr of selected repeats 11 Similarity 0.755258

Consensus:

TCTGAGCTACAGTACTcCCTGtCAAGAAcAaT

>Cele-UNSB01_3:11508351-11508507 Satlength=157 Nr of Repeats=10 RepeatLength=12
seed=GCTTAGGCTT

GCTTAGGCTTAG
GCCTAGGCTTAGCGTTGAGCCAAG
GCTTAGGATTAGGCCTAT
GCTTAGGCTTGGGATTAG
GCCTAGGCTTAG
GCTTAGGCTTAT
GCTTCGGCTTAT
GCTTAGGATTAGGCCTATGTTTAG
GATTAGGCTTAG
GCTTATGCTTCG

Nr of selected repeats 6 Similarity 0.755556

Consensus:

GCTTAGGCTTAg

>Cele-UNSB01_3:11522131-11522299 Satlength=169 Nr of Repeats=11 RepeatLength=14
seed=GATAATTGAA

GATAATTGAAAATC
GATAATTGAAAATC
GATAATTGAAAATC
GATAATTGAAAATCGATAAATGGAAATC
GATAATTGAAAATC
GATAATTGAAAATC
GATAATTGAAAATC
GATAATTGAAAATA
GATAATTGAAAATC
GATAATTGAAAATC
GATAATTGAAAATC

Nr of selected repeats 10 Similarity 0.980952

Consensus:

GATAATTGAAAATC

>Cele-UNSB01_3:11543247-11543687 Satlength=441 Nr of Repeats=21 RepeatLength=21
seed=GGCAATTTTC

GGCAATTTTCCAGTGTAATTC
GGCAATTTTCCAGTGCAATTC
GGCAATTTTCCCGTGCAATTT
GGCAATTTTCCAGTGCAATTC
GGCAATTTTCCCGTGCAATTT
GGCAATTTTCCAGTGCAATTC
GGCAATTTTCCCGTGCAATTT
GGCAATTTTCCAGTGCAATTC
GGAAATTTTCCATTGCAATTC
GGCAATTTTCCAGTGCAATTC
GGCAATTTTCCAGTGTAATTC
GGCAATTTTCCCGTGCAATTC
GGCAATTTTCCAGTGCAATTC
GGCAATTTTCCCGTGCAATTT
GGCAATTTTCCAGTGCAATTC
GGCAATTTTCCCGTGCAATTT
GGCAATTTTCCAGTGCAATTC
GGAAATTTTCCATTGCAATTC
GGCAATTTTCCAGTGCAATTC
GGCAATTTTCCAGTGTAATTC
GGCAATTTTCCCGTGCAATTC

Nr of selected repeats 20 Similarity 0.903425

Consensus:

GGCAATTTTCCaGTGCAATTC

>Cele-UNSB01_3:11612201-11612410 Satlength=210 Nr of Repeats=6 RepeatLength=35
seed=GATTTGCCGG

GATTTGCCGGAAATATTCAAATCCGGCAAATTGCA
GATTTGCCGGAAATATTTAAATCCGGCAATTTATC
GATTTGCCGGAAATATTCAAATCCGGCAAGTTGCA
GATTTGCCGGAAATATTCAAACCCGGCAAACCTGTA
GATTTGCCGGAAATACTAAATCCGGCAATTTATC
GATTTGCCGGAAATATTTAAATCCGGCAATTTATC

Nr of selected repeats 5 Similarity 0.850926

Consensus:

GATTTGCCGGAAATAtTaAAATCCGGCAAtTTatC

>Cele-UNSB01_3:11614727-11615007 Satlength=281 Nr of Repeats=6 RepeatLength=35
seed=TTGCCGGATT

TTGCCGGATTGTAATATTTTCGGCAAATCGGTAAA
TTGCCGGATTGTAATATTTTCGGCAAATCTGCAGT
TTGCCGGATTGTAATATTTTCGGCAAACCGGCAAT
TTGCCGGATTGTAATATATTCGGCAAATCTGCACT
TTGCCGGATTGTAATAATTTGGGCAAATCTGCAATTTCCCAAAAATTAACATTTCCGGCAAATCTGCACT
TTGCCGGATTGTAATAATTTGGGCAAATCTGCAATTTCCCAAAAATGAACATTTCCGGCAAACCGGCACT

Nr of selected repeats 4 Similarity 0.815873

Consensus:

TTGCCGGATTggAATATtTTCGGCAAAtCgGcAat

>Cele-UNSB01_3:11631810-11631935 Satlength=126 Nr of Repeats=4 RepeatLength=11
seed=CTACAGTACT

CTACAGTACTT

CTACAGTACTC
CTACAGTACCT
CTACAGTACTACTTCAGTGCCCCGACCATATTCCCCCACTAACCTCAAACCATTAACTCTTCAAAGACAAAACTCAA
TTTTTTTTCTAAA

Nr of selected repeats 3 Similarity 0.838384

Consensus:

CTACAGTACTt

>Cele-UNSB01_3:11700261-11701084 Satlength=824 Nr of Repeats=59 RepeatLength=14

seed=AATTATAAAT

AATTATAAATTATA

AATTATAAATTAGA

AATTATAAATTATA

AATTTAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTTAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTGTA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTGTA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTGTA

AATTATAAATTATA

AATTATAAATTATA

AATTATAAATTGTA
AATTATAAATTATA
AATTATAAATTATA

Nr of selected repeats 56 Similarity 0.980334

Consensus:

AATTATAAATTATA

>Cele-UNSB01_3:11723112-11723392 Satlength=281 Nr of Repeats=6 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATTTAGATTTTTGGCAAATTGCCGA
TTTGCCGGAAATTTTTATTTTTGGCGATTTGCCAATTTCCCAAATTTTGATTTTCGGCACATTGCCGA
TTTGCCGGAAATTTTTATTTTTGTCGATTTGCCAATTTCCCAAATTTTGATTTTCGGCACATTGCCGA
TTTGCCGGAAATTTTTATTTCTGGCAATTTGACGA
TTTGCCGGAAATTATTATTTCTTGCAATTTGCCGA
TTTGCCGGAAATTTTGATTTTCGGTAAATGGCCGA

Nr of selected repeats 4 Similarity 0.790476

Consensus:

TTTGCCGGAAATTTtgATTTctgGcAAaTtGcCGA

>Cele-UNSB01_3:11725694-11725970 Satlength=277 Nr of Repeats=12 RepeatLength=12
seed=TTAGGCTTAG

TTAGGCTTAGGCTTAGCTTCAGGCTTAAGCTTCGGCTTAACTTCTGCGTAGTC
TTAGGCTTAGGC
TTAGGCTTAGGC
TTAGGCATAGGC
TTAGGCTTAGGCTTTGGCTTAAGCTTCTGTGTAGTCTTACAA
TTAGGCTTAACTTAGATTTAGGCTGATGCTCAGGCTTATGCTCGGGC
TTAGGCTTAGGC
TTAGGCTTAGGC
TTAGGCTTTGGC
TTAGGTTTAGGC
TTAGGCTTAGGC
TTAGGCTTAGGCTTAGGCTCATGCTCAAATTTAGGT

Nr of selected repeats 8 Similarity 0.916667

Consensus:

TTAGGCTTAGGC

>Cele-UNSB01_3:11779688-11779808 Satlength=121 Nr of Repeats=10 RepeatLength=12
seed=CTTAGGCTTA

CTTAGGCTTAGT
CTTAGACTTATG
CTCAGGCTTAGGA
TTAGGCTTAGT
CTTAGGCTTAGG
CTTAGTCTTAGG
CTTAGGCTTAAC

CTTAGGCTTAGG
CTTAGGCTTAGA
CTTAGGCATAGG

Nr of selected repeats 8 Similarity 0.797619

Consensus:

CTTAGgCTTAgg

>Cele-UNSB01_3:11779996-11780140 Satlength=145 Nr of Repeats=7 RepeatLength=16

seed=TACAAGCCTA

TACAAGCCTACTAGCC

TACACGCCTACAAGCC

TACAAACCTACAGATCTACAAATA

TACAAGCCTATAAGCC

TACAAGCCTACAAGCA

TACAAGTCTACAAGCCTACAAGTGTATAAGCCAACAAGTC

TACAAGCCTACAAGCC

Nr of selected repeats 5 Similarity 0.866667

Consensus:

TACAaGCCTAcaAGCc

>Cele-UNSB01_3:11800186-11800737 Satlength=552 Nr of Repeats=15 RepeatLength=34

seed=AAATTTCAAT

AAATTTCAATTCCGCTAATTTGCCGATTTGCCGG

AAATTTCAATTCCGCTAATTTGCCGATTTGCTGG

AAATTTCAATTCCGCTAATTTGCCGATTTGCCGG

AAATTTCAATTCCGGCAATTTGCCGATTTGCCGG

AAATTTCAATCCGGCAATTTGCCGATTCGCCGG

AAATCTCAATCCGGCAATTTGCCGATTTGCTGGA

AAATTTCAATCCGACAATTTTATAATTTTGCCGA

AAATTTCAATCCGGCAATTTGCCAATTTGCTGGA

AAATTTCAATCCGCTAATTTGTTCGATTTGCCGG

AAATTTCAATCTGGCAATTTGCCGATTTGCCGG

AAATTTCAATCCGGCAATTTGGCGATTTTCCGG

AAATTTCAATCCGGCAATTTGCCGATTTTCCGGA

AAATTTCAATCCAGCAATTTGCATATTTGTGCCGGAAGTTTCAAATCCGGCAACTTGCCGATTTGACGA

AAATTTCAATCTGGCAATTTTCCGATTTGCCGG

AAATTTCAATCCGGCAATTTGCTGACTTGCCGG

Nr of selected repeats 10 Similarity 0.841394

Consensus:

AAATTTCaAtTCcGgcAATTTGcCGATTTGCCGG

>Cele-UNSB01_3:11834269-11834616 Satlength=348 Nr of Repeats=10 RepeatLength=34

seed=TTTTTCGATTT

TTTTTCGATTTTTCAATTTTTTGAAAAATCGAGAA

TTTTTCGATTTTTTCGATTTTTTGAAAAATCGGGAA

TTTTTCGATTTTTCAATTTTTTGAAAAATCGGGAA

TTTTTCGATTTTTCAATTTTTTGAAAAATCGGGAA

TTTTTCGATTTTTTCGATTTTTTGAATAATCGGGAA

TTTTTCGATTTTTCAATTTTTTGAAAAATCGGGAA

TTTTTCGATTTTTCAATTTTTTGAAAAATCGAGAA

TTTTCTATTTTTTCGATTTTTTGAATAATCGGGAA

TTTTTCGATTTTTCAATTTTTTGAAAAATCGAGAATTTTCGAT

Nr of selected repeats 8 Similarity 0.935574

Consensus:

TTTTTCGATTTTTCaATTTTTTGAAaAATCGgGAA

>Cele-UNSB01_3:11851795-11852785 Satlength=991 Nr of Repeats=24 RepeatLength=35
seed=CGGCAAATCG
CGGCAAATCGGTAAATTTGCCGAAACTGAATATTTTC
CGGCAAATCGGTAAAC
CGGCAAATTGCCGGAATTGAAAAATTTCTGGTAAATCGGCAATTTGACGAAACTGAAACTTTTC
CGGCAAATCGGCAAGTTGCCAAAACTGAAAATTTCC
CGGCAAATCGGCAACTTGCCGGAATTGAAATTTTC
CGGCAAATCGATATATTGCCAAAACTGAAAATTTCC
CGGCAAATCGGCAACTTGCCGGAATTGAAATTTTC
CGGCAAATCGATATATTGCCAAAACTGAAAATTTTC
CGGCAAATCGGCAACTTGCCGGAATTGAAATTTTC
CGGCAAATCGATATATTGCCAAAACTGAAAATTTTC
CGGCAAATCGGCAAATTTGTGGGAACTGAAAATTTTCTGCAATATGGCAATATGCCGAAACTGAATATTTTC
CGGCAAATCGGTAAAC
CGGCAAATTGCCGGAATTGAAAAATTTCTGGTAAATCGGCAATTTGACGAAACTGAAACTTTTC
CGGCAAATCGGCAAGTTGCCAAAACTGAAAATTTCC
CGGCAAATCGGCAACTTGCCGGAATTGAAATTTTC
CGGCAAATCGATATATTGCCAAAACTGAAAATTTCC
CGGCAAATCGGCAACTTGCCGGAATTGAAATTTTC
CGGCAAATCGATATATTGCCAAAACTGAAAATTTCC
CGGCAAATCGGCAACTTGCCGGAATTGAAATTTTC
CGGCAAATCGATATATTGCCAAAACTGAAAATTTTC
CGGCAAATCGGCAAATTTGTGGGAACTGAAAATTTTCTGCAATATGGCAATATGCCGAAACTGAAAATTTTC
CGGCAAATCGGCAAATCGCCGGAATTGAAAATTTTC
CGCAAATCGACAATTCATCGATAACCATCATCGATAATCATCGATTGAAAATTTCTGGCAAAGCTGCAACTCGTCAATT
TGCAGAAAATTAATAATTTTC
CGGCAAATCGGTAAATTTGCCGGAATTGGAAATTTTC
Nr of selected repeats 16 Similarity 0.809524
Consensus:

CGGCAAATCGGcAaaTTGCCaaAAcTAAAAaTTtC
>Cele-UNSB01_3:11898352-11906615 Satlength=8264 Nr of Repeats=45
RepeatLength=184 seed=TACGCAGCCG
TACGCAGCCGAACGAATTATGAAAGAGTACAGTAGACTAATCATGATCAAGCGAAAAGATCCGACTCAGAATATGAACA
TATTGCAATACATCGGAGGTATATAGATTTCCGAAGACACTTTCCAATTAACCAAACGGTTCAAATTTCTAGCAAACATC
TCCTTACTTGAACACTCTTGGCCAATG
TACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAATTATGTCCGAGAAAAAGATCCTACTCAGAATATGAACAT
ATTCAAAAATATCGGAGGTATATAGATTTCCGAAGAGCCTTTCCAATTAACCAAACGGTTCAAATTTCTAGCAAACATCT
CCTTACTTGAACACTCTTGGCCAATG
TACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAATTATGTCCGAGAAAAAGATCCTACTCAGAATATGAACAT
ATTCGAATACATCAGAGGTATATAGATTTCCGAAGAGCCTTTCCAATTAACCAAACGGTTCAAATTTCTAGCAAACATCT
CCTTACTTGAACACTCTTGGCCAATG
TACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAATTATGTCCGAGAAAAAGATCCTACTCAGAATATGAACAT
ATTCGAATACATCGGAGGTATATAGATTTCCGAAGAGCCTTTCCAATTAACCAAACGGTTCAAATTTCTAGCAAACATCT
CCTTACTTGAATACTCTTGGCCAAT
TACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAATTATGTCCGAGAAAAAGATCCTACTCAGAATATGAACAT
ATTCGAATACATCGGAGGTATATAGATTTCCGAAGAGCCTTTCCAATTAACCAAACGGTTCAAATTTCTAGCAAACATCT
CCTTACTTGAATACTCTTGGCCAAT
TACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAATTATGTCCGAGAAAAAGATCCTACTCAGAATATGAACAT
ATTCGAATACATCGGAGGTATATAGATTTCCGAAGAGCCTTTCCAATTAACCAAACGGTTCAAATTTCTAGCAAACATCT
CCTTACTTGAACACTCTTGGCCAATG

TACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAATTGTGTCCGAGAAAAAGATCCTACTCAGAATATGAACAT
ATTCGAATACATCGGAGGTATATAGATTCCCGAAGAGCCTTTCCAATTAACCAAACGGTTCAAATTCTAGCAAACATCT
CCTTACTTGAACACTCTTGGCCAATG

TACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAATTGTGTCCGAGAAAAAGATCCTACTCAGAATATGAACAT
ATTCGAATACATCGGAGGTATATAGATTCCCGAAGAGCCTTTCCAATTAACCAAACGGTTCAAATTCTAGCAAACATCT
CCTTACTTGAACACTCTTGGCCAATG

Nr of selected repeats 41 Similarity 0.970891

Consensus:

TACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAATTaTGTCCGAGAAAAAGATCCTACTCAGAATATGAACAT
ATTCgAAtAcAtCGGAGGTATATAGATTCCCGAAGAgcCTTTCCAATTAACCAAACGGTTCAAATTCTAGCAAACATCT
CCTTACTTGAACACTCTTGGCCAATg

>Cele-UNSB01_3:11990778-11991299 Satlength=522 Nr of Repeats=14 RepeatLength=35
seed=CCGATTTGCC

CCGATTTGCCGAAATTTTAAATCCGACAATTTT

CCGATTTGCCGAAATTTTCAAATCCGGCAATTTT

CCGATTTGCCAGAAATTTTCAATCCGGCAATTTG

CCGATTTGCCGAAATTTTCAAATCCGGCAATTTGG

CGATTTGCCGAAATTTTCAATCCGGCAATTTG

CCGATTTGCCGAAATTTTCGATCCGGCAATTTG

CCGATTTGCCGAAATTTTCAATCCGGCAATTTGCCTTTGCCGAAATTTTCGATCCGGCAATTTG

CCGATTTGCCGAAATCTTTCAATCCGAAAATTTG

CCGATTTGCCGAAATTTTCAATCCGGCAATTTG

CCGATTTGCCAGAAATTTTCAATCCATCAATTTG

CCGATTTGCCGAAATCTTTCAATCCGAAAATTTG

CCGATTTGCCAGAAATTTTCAATCCGGCAATTTA

CCGATTTGCCTAAATCTTTATCCGGCAATTTG

CCGATTTGTGAAATCTTTCAATCCGAAAATTTG

Nr of selected repeats 10 Similarity 0.809053

Consensus:

CCGATTTGCCnGAAATTTTCAATCCGgcAAtTTg

>Cele-UNSB01_3:12003957-12004292 Satlength=336 Nr of Repeats=7 RepeatLength=11
seed=GTACTGTAGA

GTACTGTAGAG

GTACTGTAGAG

GTACTGTAGAA

GTACTGTAGAC

GTACTGTGGAA

GTGCTGTAGAAGTGCCTTAGGATTACTGTAGTTTTAAAAAAGTTGTTGTGTTTTGAAGGGAGATTGAGTTAGGGGTAGT

GTAGGAGTATGGTTGTGGAACCTTAGTA

GTACTGTAGGTGTATTGTATTGGAATTGTAGGGGTACGTTAGGGTTACTGTGTTTCTGTAGGAACACTCCTGGATTACT

CCAGTAGTGCTGTAGGGGTACCGTATTGGTACTGTATGGGTACTATATAGGAACTATAGGGGTACTGTATTGGTACCGT

AGGAGGTACTATAGG

Nr of selected repeats 5 Similarity 0.854545

Consensus:

GTACTGTaGAn

>Cele-UNSB01_3:12010851-12011440 Satlength=590 Nr of Repeats=30 RepeatLength=12
seed=GGCTTAGGCT

GGCTTAGGCTTA

GGCTTAGGTATA

GGCTTAGGCTTAGTCTTAGGCCTA

GGTTTAGGCTTA

GGCTTTGGCTTA

GGCTAAGGCTTA

GGCTCAGGCTTAGGTCTA

GGTTTAGGCTTA
GGCTCAGGCTGAATCTTA
GGCTTAGGTATA
GGCTTAGGCTTAGTCTTAGGCCTA
GGTTTAGGCTTA
GGCTTTGGCTTA
GGCTAAGGCTTA
GGCTCAGGCTTAGGTCTA
GGTTTAGGCTTA
GGCTCAGGCTGAATCTTA
GGCTTAGGTATA
GGCTTAGGCTTAGTCTTAGGCCTA
GGTTTAGGCTTA
GGCTTTGGCTTA
GGCTAAGGCTTA
GGCTCAGGCTTAGGCCTA
GGTTTAGGCTTA
GGCTCAGGCTGA
GGCTTAGGCTCA
GGCTGAGGCTTA
GGCTCAGGCTGA
GGCTTAGGCTTTAAAAAATTGTTTCCAAAACTTATTTTTAGTTGGCATACTGAAAAAATTGAATTTTTTTGTAGT
TTTTTTGTCTTTTTTTTTTTGGTTTTTTGGAGAAATTAGAATTTTTGCTTTTCGTTTTTTGGTCAAATTTTTTGCAA
CAGCCCTGTTA
GGCTTGGGCTTAGGCTTA

Nr of selected repeats 20 Similarity 0.774854

Consensus:

GGcTtAGGCTTA

>Cele-UNSB01_3:12025839-12025976 Satlength=138 Nr of Repeats=8 RepeatLength=12

seed=TAAGCCTAAG

TAAGCCTAAGACTAAGCCTATACG

TAAGCCTAAACC

TAAGCCTAAGCC

TAAGCCTGAGCC

TAAGCCTAAGCATAACCATAACCCGAAGCA

TAAGCCTAAGCC

TAAGCCTAGGCA

TAAGCCTAATCCTACCCGAAGCG

Nr of selected repeats 5 Similarity 0.822222

Consensus:

TAAGCCTaagCc

>Cele-UNSB01_3:12040777-12040867 Satlength=91 Nr of Repeats=6 RepeatLength=12

seed=CCTAAGCCTA

CCTAAGCCTAAGCCTGAGACTAAGCTCTAC

CCTAACCCTAAC

CCTAAGCCTAAG

CCTACGCCTAAG

CCTAGGCCTAAG

CCTAAGCCTAAG

Nr of selected repeats 5 Similarity 0.833333

Consensus:

CCTAagCCTAag

>Cele-UNSB01_3:12087067-12087157 Satlength=91 Nr of Repeats=4 RepeatLength=12

seed=AGCCTGAGCC

AGCCTGAGCCCG
AGCCTAAGCCTGAGCCTAGGTCTAAGCCTAAACCTAAACCTAAGACTAACCCCTA
AGCCTGAGCCTC
AGCCTGAGCCTG
Nr of selected repeats 3 Similarity 0.851852
Consensus:
AGCCTGAGCCTg
>Cele-UNSB01_3:12088649-12088899 Satlength=251 Nr of Repeats=9 RepeatLength=12
seed=TAAGCCTAAG
TAAGCCTAAGAC
TAAGCCTAAGCC
TAAGCCTAAGCC
TAAGCCTAAGCC
TAAGCCTAAGCC
TAAGCCCAAGCCCAAGCCCAAGCCTAGGGCTAATCAGTGATGGGCAGCGAACATGCTTTCTTGGCGAACGACGAATTTCG
GCAATTTGTCTATGCAGTTTTTTAAGTTTTCCAGTTTTTTTCTGAAGTTTTTTTCTGTATAATGGCG
TAAGCCTAAGCC
TAAGTCTAAGCC
TAAGCCTGAGCCTAATCC
Nr of selected repeats 7 Similarity 0.936508
Consensus:
TAAGCCTAAGCC
>Cele-UNSB01_3:12102276-12102493 Satlength=218 Nr of Repeats=6 RepeatLength=34
seed=TTGCCGAATT
TTGCCGAATTTTCCGTTTGCCGAGCTCGTCAAAC
TTGCCGAATTTGCTATTTGCCGAGCTTGTCAAAT
TTGCCGAATTTGCTATTTGCCGAGCTCGTCAAAC
TTGCCGAATTTGCCGTTTGCCGAGCTTGTCAAAT
TTGCCGAATTTGCCGTTCAATTTTGCCGTTTGTCGAGTTTCGTCAAAA
TTACCGAATTTGCCGTTTGCTAGCACGGCAGAT
Nr of selected repeats 5 Similarity 0.811765
Consensus:
TTgCCGAATTTgCcgTTTGCCgAGCtcGtCAaAt
>Cele-UNSB01_3:12120993-12121420 Satlength=428 Nr of Repeats=12 RepeatLength=35
seed=AATTGCCGGA
AATTGCCGGAACAAAACTTCCGGCAAATCGGCA
AATTGCTGGAATTGAAATTTTCCGGAAAATCGGCA
AATTGCCGGAATTGAAATTTCTGGCAAATCGGCA
AATTGCTGGAATTGAAATTTTCCGGAAAATCGGCA
AATTGCCGGAATTGAGAATTTCCGGCAAATCGTCA
AATTGCTGGAATTGAAATTTTCCGGAAATATCGGCA
AATTGCCGGAATTGAAAATTTCCGGCAAATCGGCA
AATTGCCGGAATTGAAAATTTTCCAGCACCTCGGCA
AATTGCCGGAATTGAAAATTTTCGCAAATCAACA
AATTGCCGGAATTGAAAATTTCCGGCAAATCGGTA
AATTGCCGGAATTGAAATTTCCGACAAATCGACAAACCGGCG
AATTGCCGGAATTGAAAATTTCCGGCAAATCGGCG
Nr of selected repeats 10 Similarity 0.840847
Consensus:
AATTGCCcGGAATTGAAAaTTTCCGGcAaATCGGCA
>Cele-UNSB01_3:12166501-12166666 Satlength=166 Nr of Repeats=15 RepeatLength=11
seed=ACATTTTTTTG
ACATTTTTTTGC
ACATTTTTTTGA

ACATTTTTTGT
ACATTTTTTGC
ACATTTTTTGA
ACATTTTTTGC
ACATTTTTTGA
ACATTTTTTGA
ACATTTTTTGA
ACATTTTTTGT
ACATTTTTTGC
ACATTTTTTGA
ACATTTTTTGC
ACATTTTTTGC
ACATTTTTTGC
ACATTTTTTGC
CATTTTTTGC

Nr of selected repeats 13 Similarity 0.919192

Consensus:

ACATTTTTTGN

>Cele-UNSB01_3:12168292-12168722 Satlength=431 Nr of Repeats=13 RepeatLength=34
seed=AAGTATTTTT

AAGTATTTTTGCCGGTTTTTTTGCCGAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCTAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCCGAAATTTCC
AAGTATTTTTGCCGATTTTTTTGCCGAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCCGAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCTAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCCGAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCCGAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCTAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCCGAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCCGAAATTTCC
AAGTATTTTTGCCGGTTTTTTGCTAAATTTCC
AAGTATTTTTGCCGAAATTTTC

Nr of selected repeats 12 Similarity 0.954843

Consensus:

AAGTATTTTTGCCGGTTTTTTGCCGAAATTTCC

>Cele-UNSB01_3:12227970-12228196 Satlength=227 Nr of Repeats=6 RepeatLength=35
seed=TTCCGGCAA

TTCCGGCAAATTGGCAAATTGCTGAAATTAATAAT
TTCTGGCAAATCAGCAAACCGGCAATTTGGCGCAATGAAAT
TTCTGGCAAATCACAAATTGCCGAACTAAAAA
TTCCGGCAAATTGGCAAGTTGCCGTTTTGAACAT
TTCCGGCAAATCGACAAACCGGCAATTTGTCGAAAATGAAAT
TTCCGGCAAATTGGCAAGTTGCCGTTATGGAGCAT

Nr of selected repeats 4 Similarity 0.676190

Consensus:

TTCCGGCAAATTGGCAAATTGCTGAAATTAATAAT

>Cele-UNSB01_3:12229422-12230200 Satlength=779 Nr of Repeats=21 RepeatLength=35
seed=TTCAATTCCG

TTCAATTCGGCAATTTGCCGATTTGCCAGAAAT
TTCAATTCGGCAATTTGACCAATTTCCGGAAAT
TTCAATTCGGCAATTTGGCAATTTGCCGAAAT
TTCAATTCGGCAATTTGTCGATTTGCCAGAAAT
TTCAATTCGGCAATTTGTCGATTTGCCAGAAAT
TTCAATTCGGCAATTTGCCGATTTGCCAGAAAT
TTCAATTCGGCAATTTGTCGATTTGCCAGAAAT

TTCAATTCGGACAATTTGCCGATTTGCCAGAAATT
TTCAATTCGGCAATTTGGCCAATTTTCCAGAAATT
TTCAATTCGGCAATTTGTTAATTTGCCGAAATTC
TCAATTCGGCAATTTAGCCAATTTGTCAGAAATT
TTCAATTCGGCAATTTGGCCAATTTGCCAGAAATT
TTCAATTCGGCAATTTGTTAATTTGCCGAAATTT
TTCAATTCGGACAATTTGTCGATTTGCCAGAAATT
TTCAATTCGGCAATTTGCCGATTTGCCAGAAATT
TTCAATTCGGCAATTTGTCGATTTGCCAGAAATT
TTCAATTCGGACAATTTGCCGATTTGCCAGAAATT
TTCAATTCGGCAATTTGTTAATTTGCCGAAATTT
TTCAATTCGGACAATTTGTCGATTTGCCAGAAATT
TTCAATTCGGCAATTTGCCGATTTGCCAGAAATT
TTCAATTCGGCAATTTGCCGATTTGCCAGAAATT

Nr of selected repeats 15 Similarity 0.834492

Consensus:

TTCAATTCGGCAATTTGtCgATTTGCCaGAAATT

>Cele-UNSB01_3:12305276-12305678 Satlength=403 Nr of Repeats=10 RepeatLength=40
seed=ATTCCAGAAT

ATTCCAGAATTTTTTCGAATTTTCCAGAAAGTTCTAGAAC
ATTCCAGAATTTCTTGAATTTTCCAAAAGGTTCTAGAAC
ATTCCAGAATTTCTTGAATTTTCCAAAAGGTTCTAGAAC
ATTCCAGAATTTTTTTTAAATTTTCCAGAAGGTTCTAGAAC
ATTCCAGAATTTTTTTTAAATTTTCCAGAAGGTTCTAGAAT
ATTCCAGAATTTTTTTCAAATTTTCCAGAAGGTTCTAGAAC
ATTCCAGAATTTTTTTTAAATTTTCCAGAAGGTTCTAGAAT
ATTCCAGAATTTTTTTCAAATTTTCCAGAAGGTTCTAGAAC
ATTCCAGAATTTTTTTAAAAATTTTCCAGAAGGTTCTAGAAC
ATTCCAGAATTTTTTTTAAATTTTCCAGAAGGTTCTAGAAT

Nr of selected repeats 8 Similarity 0.860714

Consensus:

ATTCCAGAATTTtTTaaAATTTTCCAgAAGGttCTAGAAc

>Cele-UNSB01_3:12308090-12308555 Satlength=466 Nr of Repeats=12 RepeatLength=35
seed=AAAATTTCCG

AAAATTTCCGGCAAATCAGCTAATTGCCAGAATTG
AAAATTTCCGGTAAATCGGCAAATAGCCGGAATTG
AAAATTTCCGGCAAATCAGCTAATTGCCAGAATTG
AAAATTTCCGGTAAATCGGCAAATAGCCGGAATTG
AAAATGTCCGGCAAATCAGCTAATTGCCAGAATTG
AAAATTTCCGGTAAATCGGCAAATGCGGGAATTG
AAAATTTCCGGCAAATCAGCTAATTGCCAGAATTG
AAAATTTCCGGAAAATCGGCGAATTGCCGGAAGTG
AAAATTTCCGGCAAATCAGCTAATTGCCAAAATTG
AAAATTTCCGGTAAATAGGCAAATGCGGGAATTGA
AAAATTTCTGGCAAATCGGCAAATGCCAAATTACCGTAAATTTAAATTTCTAACAATTTGCCAAAATTGA
AAAATTTTCGGTAAATCGGCAAATCAGCAATTTCCCAAAAATT

Nr of selected repeats 9 Similarity 0.868783

Consensus:

AAAATTTCCGGcAAATCaGctAATtGCCaGAATTG

>Cele-UNSB01_3:12309471-12309813 Satlength=343 Nr of Repeats=8 RepeatLength=35
seed=GGAATTGAAA

GGAATTGAAAATTTCCGGGAAATCGGCAAGTTGGCGGAAATTTAAATTTCCCGGAAATCGGCAAATTTGGC
GGAATTGAAAATTTCCGGCTAATTTGGCAAATTTGCCGAAATTTAAATTTCCGAGAAATCGGCAAATTTGGC
GGAATTGAAAATTTCCGGGAAATCGGCAAATTTGGC

GGAATTGAAAATTTCCGGCAAAGTGGCAAGTTGGC
GGAATTGAAAATGTCCGGCAAATCGGCAAATTGGC
GAAATTGAAAATGTCCGGCAAATCGGCAAATTGGC
GGAATTGAAAATTTCTGCAAACCGGCAAATTGCC
GGAATTGAAAATTTCCGGCAAATTGGA

Nr of selected repeats 5 Similarity 0.843810

Consensus:

GgAATTGAAAAttTCCgGcAAAtcGGCAAaTTGgC

>Cele-UNSB01_3:12312970-12313186 Satlength=217 Nr of Repeats=11 RepeatLength=20
seed=AAATAGATTG

AAATAGATTGACAGACGGAA
AAATAGATTGACAGACGGAA
AAATAGATTGACAGACGGAA
AAATAGATTGACAGACGGAA
AAATAGATTGACAGACGGAA
AAATAGATTGACAGACGGAA
AAATAGATTGTCAGACGAAA
AAATAGATTGACAGACAAAA
AAATAGATTGACAGACGGAA
AAATAGATTGACAGACGAAC
AAATAGATTGACAGACGGAA

Nr of selected repeats 7 Similarity 0.904762

Consensus:

AAATAGATTGACAGACGaAA

>Cele-UNSB01_3:12321003-12321555 Satlength=553 Nr of Repeats=10 RepeatLength=43
seed=AATTGCCGGT

AATTGCCGGTTTACCGATTGCGCGAAATTTTTATTTTCAGAC
AATTGCCGGTTTACCGATTGCGCGAAATTTTCGGTTTTTCGGCA
AACTGCCGGTTTACCGATTGCGCGAAAGTTTTTCATTTTCGGCG
AATTGCCGGTTTCGCGATTGCGCGAAATTTTCATTTTCGGCGAATAGGCGTTTTCGGATTGCGCGAATTTTTAGTT
TTCGACAAATTTTCCGTTTACCGTTTGTCTAGAAATTTTCAATTCGGACAGATAGCTGGTTTTCGGATATGCCGGAAT
TTTCATTTTCGGAC
AATTGCCGGTTTACCGATTGCGCGAAATTTTCAGTTTTTCGGCA
AATTGCCGGTTTCGACGATTGCGCGAAATTTTCATTTTCGGACA
AATTGCCGGTTTACCGATTGCGCGAAATTTTCATTTTCGGAC
AATTGCCGGTTTACCGATTGCGCGAAATTTTCATTTTCGGCG
AATTGCCGGTTTACCGATTGCGCGAAATCTCATTTTCGGCA
AGTTGCCGGTTTCCAGTAATTTTATTTTCGGCA

Nr of selected repeats 7 Similarity 0.748854

Consensus:

AATTGCCGGTTTACCGATTtGCCgGAAaATTTTCATTTTCGGCa

>Cele-UNSB01_3:12376126-12377123 Satlength=998 Nr of Repeats=30 RepeatLength=32
seed=AAATTTGTGA

AAATTTGTGAAAATTTAGATCCATTTTGCTAACAAAATGTGTGCCATTTAGGCCATTTTGTTC
AAATTTATGAAAATTTAGGCCATTTTGTCA
AAATTTGTGAAAATTTAGGCCATTTTGTCA
AAATTTGTGAAAATTTAGGCCATTTTGTCA
AAATTTGTGAAAATTTAGGCCGTTTTACTAAA
AAATTTGTGAAAATTTAGGCCATTTTGTCTA
AAATTTGTGAAAATTTAGGCCGTTTGTCTA
AAATTTGTGAAAATTTAGGCCATTTTGTCA
AAATTTGTGAAAATTTAGGCCATTTTGTTC
AAATTTGTGAAAATTCAGGCCATTTTGTCTA
AAATTTGTGAAAATTTAGGCCATTTTGTCCA

AAATTTGTGAATATTCAGGCCCATTTTGTTC
AAATTTGTGAAAATTCAGGCCCATTTTGTCTA
AAATTTGTGAAAATTTAGGCCATTATGCCAG
AAATTTGTGAAAATTTAGGCCGTTTTACTAA
AAATTTGTGAAAATTTAGGCCCATTTTGTCTA
AAATTTGTGAATATTTAGGCCGTTTTGTCTA
AAATTTGTGAAAATTTAGGCCCATTTTGGCCCCA
AAATTTGTGAATATTCAGGCCCATTTTGGCCCCA
AAATTTGTGAATATTCAGGCCCATTTTGTCTA
AAATTTGTGAAAATTTAGGCCATTATGACCAG
AAATTTGTGAAAATTTAGGCCGTTTTACTAAA
AAATTTGTGAAAATTTAGGCCCATTTTGTTC
AAATTTGTGAAAATTTAGGCCCATTTTGTCTA
AAATTTGTGAATATTTAGGCCGTTTTGTCTA
AAATTTGTGAAAATTTAGGCCCATTTTGGCCCCA
AAATTTGTGAATATTAAGGCCCATTTTGTTC
AAATTTGTGAAAATTCAGGCCCATTTTGTCTA
AAATTTGTGAAAATTTAGGCCCATTTTGTCTA
AAATTTGTGAATATTTAGGCCCATTTTGTTC

Nr of selected repeats 18 Similarity 0.874992

Consensus:

AAATTTGTGAAaATTTAGGCCCATTTTGTcTCA

>Cele-UNSB01_3:12433825-12433951 Satlength=127 Nr of Repeats=9 RepeatLength=12

seed=TAAGCCTAAG

TAAGCCTAAGCC

TAAGCCTTAGCTTAGGAT

TAAGTCTAAGCC

TAAGCATAAGCC

TAAGCCTAAGTA

TAAGCCTAAGCCTAAGTA

TAAGCCTAAGCC

TAAGCCTAAGCCTAAGAC

TGAGCCTAAGCC

Nr of selected repeats 6 Similarity 0.814815

Consensus:

TAAGCCTAAGCC

>Cele-UNSB01_3:12445241-12445717 Satlength=477 Nr of Repeats=10 RepeatLength=32

seed=ATTCAAATTT

ATTCAAATTTTCATTGGAATAATTTGGCGGGA

ATTCAAATTTTTTTAGAAAAATTTTGCCGTAACCTCCAATTTCTTCAGAAAAAAATTTTGGCGGAAATTCTCATTCTAT

AGAAAAATATTGGCTGGATATCAATTTTTTTGGAACATTTTTTTGACGGGA

ATTCAAATTTTTTTACAGATACATTTTGGCGAAA

ATTCAAATTTCTTCAGAAAAAGTGTGGCGGGG

ATTCAAATTTTTTTCTTAAAAATTTTGGCGAAA

ATTCAAATTTTGTCTTAAAAATTTTGGCGGTA

ATTCAAATTTCTACAGAAAAAAATTTGGCGGGAATTCAAGCTTCTTCAGAAAAATATTTGCGGAA

ATTCAAATTTCTTCAAAAAATTTGGTGGGA

ATTTAAATTTCTTCATAAAACATTTGCCAGAAA

ATCAAATTTCTTCGAAAAAAATTTGGCGAGAATCAAATTTCTTCAAAACATTTTGGCGGGA

Nr of selected repeats 6 Similarity 0.602694

Consensus:

ATTCAAATTTctTCagAAAAntTTGGCGaaA

>Cele-UNSB01_3:12447381-12447465 Satlength=85 Nr of Repeats=7 RepeatLength=12

seed=GGCTTAGGCT

GGCTTAGGCTTA
GGCTTAGGCTTA
GGCTTAGGCTTA
GGCTTAGGCTTA
GGCTTAGGCTTA
GGCTTAGGCTTA
GGCTTAGGCTTA
GGCTTAGGCTTT

Nr of selected repeats 7 Similarity 0.968254

Consensus:

GGCTTAGGCTTA

>Cele-UNSB01_3:12475925-12476790 Satlength=866 Nr of Repeats=62 RepeatLength=11

seed=TTTTTGACACA

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACATTGTATGCACATTTTCTGTACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTACACAT

TTTTTGACACATT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACATTGTATGCACATTTTCTGTACAT

TTTTTGACACAT

TTTTTGACACATTTTTTCAAAT

TTTTTGACACAT

TTTTTGACACATTTTCTGTACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACATTTTCTGTACAT

TTTTTGACACAT

TTTTTGACACAT

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TTTTTGACACAT

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TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACATTTTCTGTACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACAT

TTTTTGACACATTTTTTCAAAT

TTTTTGACACAT

TTTTTGACACATTTTCTGTACAT

TTTTTGACACAT

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TTTTTGACACAT

TTTTTGACACAT

TTTTTGACAT
TTTTTGACAT
TTTTTGACATTTTCTGTACAT
TTTTTGACAT
TTTTTGACAT
TTTTTGACAT
TTTTTGACAT
TTTTTGACAT
TTTTTCACAT
TTTTTGACAT
TTTTTGACAT
TTTTTGACATTGTATGCACATTTTCTGTACAT
TTTTTGACAT
TTTTTGACAT
TTTTTGACATTGTATGCACATTTTCTGTACAT
TTTTTGACAT
TTTTTGACAT
TTTTTGACAT
TTTTTCACAT
TTTTTGACATTGTATGCACATTTTCTGTACAT
Nr of selected repeats 46 Similarity 1.000000

Consensus:

TTTTTGACAT

>Cele-UNSB01_3:12492090-12492261 Satlength=172 Nr of Repeats=7 RepeatLength=19
seed=CAATTTACCA

CAATTTACCAAAAATTTGTCAATTTATCGAAAATTTAG
CAATTTACCAAAAATTTGT
CAATTTACCAAAAATTTAG
CAATTTACCAGAAATTTTACAATTTGCCAAAACCTGG
CAATTTATCAAAAATTTAG
CAATTTACCAGAACTTTGA
CAATTTACCAAAAATTTGT

Nr of selected repeats 5 Similarity 0.791667

Consensus:

CAATTTAcCAaAAaTTTgn

>Cele-UNSB01_3:12493882-12494280 Satlength=399 Nr of Repeats=13 RepeatLength=16
seed=ACGTAGGCAC

ACGTAGGCACGTAGGC
ACGCAGGCACGTAGGC
ACGTAGGCACGTAGGC
ACGTAGGCACATAGGC
ACGTAGGCACATAGGCACGCAGGT
ACGTAGGCACCAGGGCTGGGACTTTTTTGGTTTTTTTTTGTGTTGGTTTTTTTGGTATTTTGACGATTTTTCACGGTTA
GAAATAAATTCAAGCATCAAAAATTTTTTGTTTTTTTTGTGTTTTTGCATTTTCGAAAACCTTAATTTTTTTGTTTTTTGGTC
CAAATTGTTTTTTCGTCCCAGTCCTGGTAGGC
ACGTAGGCACGTAGGC
ACGTAGGCACGTAAAC
ACGTATGCACGTAGGC
ACGTAGGCACGTAGGC
ACGTAGGCACGTAGGC
ACGTAGGCACGTAGGC
ACGTAGGCACGTAGGC
ACGTAGGCACGTAGGC
ACGTAGGCACGTAGGC

Nr of selected repeats 10 Similarity 0.916667

Consensus:

ACGTAGGCACGTAGGC

>Cele-UNSB01_3:12499748-12499928 Satlength=181 Nr of Repeats=14 RepeatLength=12

seed=CTTAGACTTA

CTTAGACTTAGA

CTTAGGCTTAGGATAAGG

CTTAGGCTTAGG

CTTAGGCTTAGA

CTTAGACTTAGA

CTTAGACTTAGA

CTTAGACTTAGA

CTTAGACTTAGA

CTTAGACTTAGA

CTTAGACTTAGA

CTTAGACTTAGA

CTTAGACTTAGA

CTTATACTTAGA

CTTAGACTTAGACTTAGA

Nr of selected repeats 12 Similarity 0.929293

Consensus:

CTTAGACTTAGA

>Cele-UNSB01_3:12542724-12542833 Satlength=110 Nr of Repeats=5 RepeatLength=15

seed=CGACCTGCGA

CGACCTGCGACCTAGAGGGTTAGGTCGCATTG

CGACCTGCGACCTAG

CGACCTGCGACCTTG

CGACCTGCGACCTAG

CGACCTGCGACCTTGCGACCTAGGTCGCATTG

Nr of selected repeats 3 Similarity 0.940741

Consensus:

CGACCTGCGACCTaG

>Cele-UNSB01_3:12547936-12548181 Satlength=246 Nr of Repeats=7 RepeatLength=35

seed=AATTGCCGGA

AATTGCCGGAATTCAAAATTTCCGGCAAATCGGAA

AATTGCCGGAATTCAAAATTTCCGGCTAATCGGCA

AATTGCCGGAATTCAAAATTTCCGGCAAACCGGCA

AATTGCCGGAATTCAAAATTTCCGGCAAATCGGCA

AATTGCCGGAATTTAAAATTTCCGGCAAACCGGCA

AATTGCCGGAATTCAAAATTTCCGGCAAACCGGCA

AATTGCCGGAATTCAAAATTTCCGGCAAATGGCA

Nr of selected repeats 7 Similarity 0.912925

Consensus:

AATTGCCGGAATTCAAAATTTCCGGCAAAtCGGCA

>Cele-UNSB01_3:12593157-12594697 Satlength=1541 Nr of Repeats=44

RepeatLength=35 seed=TTGCCAGAAT

TTGCCAGAATTGAAAAATTTCCGACAAATCGGCAAG

TTGCCAGAATTAAAAATTTCCGGAAAATCGGCAAG

TTGCCAGAATTAAAAATTTCCGGTAAATCGACAAA

TTGACAGAATTGAAAAATTTCCGGCAAATCGGTAAG

TTACCAGAATTGAAAAATTTCCGGTAAATGGCAAA

TTGCCAGAATGAAATATTTCCGGGAAATCGGCAAA

TTGCCAGAATTGGAGTATTTTGAAAAATCGGCAAA

TTGCCAGAATTGAAGTATTTTGAAAAATCGGCGAA

TTGCCAGAATTGAAAAATTTCCGACAAATCGGCAAG

TTGCCAGAATTAAAAATTTCCGGAAAATCGGCAAA

TTGCCAGAATTGAAGTATTTTGGAAAATCGGCAA
TTGCCAGAATTGAAGTATTTTGGAAAATCGGCAA
TTGCCAGAAATGAAATATTCGGGAAAATCGGCAA
TTGCCAGAATTAAAAATTTCCGGAAAATCGGCAA
TTGCCAGAAATGAAATATTCGGGAAAATCGGCAA
TTGCCAGAATTGGAGTATTTTGGAAAATCGGCAA
TTGCCAGAATTGAAAATTTTCCGGAAAATCGGCAA
TTGCCAGAATTGAAAATTTCCGGTAAATTTGGCAA
TTGCCAGAATTGGAGTATTTTGGAAAATCGGCAA
TTGCCAGAATTGGAGTATTTTGGAAAATCGGCGAA
TTGCCAGAATTGAAAAATTCGGACAAATCGGCAAG
TTGCCAGAATTAAAAATTTCCGGAAAATCGGCAA
TTGCCAGAATTGAAGTATTTTGGAAAATCGGCAA
TTGCCAGAAATGAAGTATTTTGGAAAATCGGCAA
TTGCCAGAATTGAAAATTTTCCGGAAAATCGGCAA
TTGCCAGAATTGAAAATTTTCCGGAAAATCGGCGA
TTGCCAGAATTGAACATTTCCGGCAAACCGGCAA
TTGTCAGAATTGAAATATTCAGGCGAATAGGTAAA
TTGCCAGAATTGAAAATTTTCCGGAAAATCGGCGA
TTGCCAGAATTGAACATTTCCGGCAAACCGGCAA
TTGTCAGAATTGAAATATTCAGGCGAATAGGTAAA
TTGCCAGAATTGAAAATTTCCAGTAAATCGACAAA
TTGACAGAATTGAAGTATTTTGGAAAATCGGCAAG
TTGCCAGAATTGAAAATTTCCGGCAAATCGGTAAG
TTGCCAGAATTGAAAATTTCCGGCAAATCGGCAA
TTGCCAGAATTGAAAATTTCCGGTAAATTTGGCAA
TTGCCAGAAATGAAATATTCGGGAAAATCGGCAA
TTGCCAGAATTTAAAAATTTCCGGGAAAATCGGCAAG
TTGCCAGAATTGAAAATTTCCGGAAAATCGGCAA
TTGCCAGAATGGGAAAATTTCCGGAAAATCGGCAAG

Nr of selected repeats 44 Similarity 0.791362

Consensus:

TTGCCAGAATTGAAaaaTTccGGnAAATCGGCAAa

>Cele-UNSB01_3:12605711-12605849 Satlength=139 Nr of Repeats=9 RepeatLength=12

seed=TAGGCATAGG

TAGGCATAGGCA

TAGGCTTAGGCTTAGGACCAGGCT

TAGGCATAGACT

TAGGCTTAGGCTCAGGCTTAGTCT

TAGGCATAGGCA

TAGACATAGGCA

TAGGCATAGGCA

TAGGCATAGGCAAATGTT

TAGGCTTAGGCT

Nr of selected repeats 6 Similarity 0.829630

Consensus:

TAGGCATAGGCa

>Cele-UNSB01_3:12608882-12609486 Satlength=605 Nr of Repeats=14 RepeatLength=43

seed=AGCAGCCGAC

AGCAGCCGACAATTGCCGGTTGCCTTAAAATTGAAGTAAATCC

AGCAGCTGACAGCTAGCGGTTGCAGGAAAAAATTCAGTAATTTCT
AGCAGCCGTGAGTTGCCGGTTGCCGAAAAAATGCAGTAATTTCT
ACAGCCGACAGTTCTCGGTTGCCGAAAAAATGCAGTAAATCC
AGCAGCTGACAGTCAACGGTTGCCGAAAAAATGCAATAATTTCT
AGCAGACGACAGTTGCCGGTTGCCGAAAAAATGCGATGATTTA
AGCAGCCGACAGTTGCCTGTTACCGAAGAATTGCAGTAATCTC
AGCAGCCGACAGTTGCCGGTTGCCGAAAAAATGCGATGATTTA
AGCAGCCGACAGTTGCCTGTTACCGAAGAGTTGCAGTAATCTC
AGCAGCCGACAGTTGCCGGTTGCCGAAAAAATGCGATGATTTA
AGCAGCCGACAGTTGCCTGTTACCAAAGAATTGCAGTAATCTC
AGCAGCCGACAGTTGCCGGTTGCCGAAAAAATGCAGTAATCTC
AGCAGCCGACAGTTGCCGGTTGCCGAAAAAATGCAGTAACTTC
AGCAGCCGACAGTTGCCGGTTGCCTTAAAATTGCAGTAATTTCT

Nr of selected repeats 11 Similarity 0.800423

Consensus:

AGCAGCCGACAGTTGCCgGTTgCCgAAaAATTGCagTaAtTtTc

>Cele-UNSB01_3:12626974-12627042 Satlength=69 Nr of Repeats=4 RepeatLength=17
seed=TGAAAATAAT

TGAAAATAATCACGGAA
TGAAAATAATCACGGAA
TGAAAATAATCACGGAA
TGAAAATAATCACGGAA

Nr of selected repeats 4 Similarity 1.000000

Consensus:

TGAAAATAATCACGGAA

>Cele-UNSB01_3:12644803-12645326 Satlength=524 Nr of Repeats=7 RepeatLength=35
seed=TTGCCGGAAT

TTGCCGGAATTGAAAAATTTCTGGCAAATCGGCAAATTGACGAAATTAATAAATTTTCCCGTTGCCTACCCGCCTGCCTA
CAGGCATTGCATTAATAAAGGAAAAAACTAATTTTTTGCCTGTTGGTTTTCTTGGAGATTGAAATTTCCGCCAAAAT
TTTTTTGCCAAAAATTTGAAATTTCCCGCAAAAAAATTTTCAAAAACAAAAAAATTTGAAAATTTCTGGCAAATC
GGCAAT
TTGCCGGAATTAAAAATTTCCGGCAAATCAGCAAATTGGCGGAACTGAAAAATTCAGCAAATTGTCAAATTCGCGGAA
CTAAACATTTCCGGCAAATCGGCAA
TTGGCGGAATTGAAATTTCCGCCAAACCGGCAA
TTGCCGGAATTGAACATTTCTGGCAAACCGGAAAT
TTGCCGGAATTGAAACTTCTGGCAAACCGGCAA
TTGCCGGAATTGAACATTTCCGGCAAATCGGCAAT
TTGCCGGAATTGAAATTTTACAGATCGGCACTA

Nr of selected repeats 5 Similarity 0.729630

Consensus:

TTGcCGGAATTGnAaAtTTctGgCAaAcCGGcAat

>Cele-UNSB01_3:12692847-12693292 Satlength=446 Nr of Repeats=15 RepeatLength=17
seed=ATTTTTTCCG

ATTTTTTCCGCAAATAG
ATTTTTTCCGCCGGTTCG
AGTTTTTCCGCCGGTAG
ATTTTTTCCGCCGGTTCG
AGTTTTTCCGCAAGTAT
ATTTTTTCCGCAAGTAG
ATTTTTTCCGCAAGTAA
ATTTTTTCCGCCGGTTCGAGTTTTTTCGCGGAGTAG
ATTTTTTCCGCAAGTAG
ATTTTTTCCGCCGATAGATTTTTCTGCCGGTAG
ATTTTTTCCGCAAGTAG

ATTTTTCCGCCGGTTCA
ATTTTTCCGCAAGTAA
ATTTTTCCGCCGGTTCGAGTTTTTCGGCAAGTAA
ATTTTTTCGCGCTATACTCTATACGCTATACGCTATACGCTATACGCTAATTTTGAAGTTTTCAAAAAAAAAATAAATTT
TGAAAATTTTATTAGATAGAGGTAGTCAAAGAGCATTGAAGGTAGTCAATGAGCATTTATACATCAGATCTCATCTC
C
Nr of selected repeats 10 Similarity 0.687449
Consensus:
AtTTTTTCCGCaaGTag
>Cele-UNSB01_3:12700775-12700871 Satlength=97 Nr of Repeats=4 RepeatLength=24
seed=AAGCACCACC
AAGCACCACCTCCTCCGACTACAA
AAGCACCACCTCCTCCAACACTACAA
AAGCACCACCTCCTCCAACACTACAA
AAGCACCACCTCCTCCAACACTACAA
Nr of selected repeats 4 Similarity 0.972222
Consensus:
AAGCACCACCTCCTCCaACTACAA
>Cele-UNSB01_3:12712606-12713078 Satlength=473 Nr of Repeats=10 RepeatLength=35
seed=GATTTGCCGG
GATTTGCCGGAAATTTTCGATTCGGCAATTTGCC
GATTTGCCGGAAATTTTCGATTCGGCAATTTGCC
GATTTGCCGGAAATTTTAAATCCGGCAAATTTGCCGATTTGTGAGAAATTATCGATTCGGCAAATTTGTCGATTTTTCGG
AAATTTGCAATTCGGCAACTTGCC
GATTTGCCGGAAATTTTCAATTCTGGCAATTTTCC
GATTTGCCGGAAATTTGTAATCCGGCAATTTGCC
GATTTGCCGGAACTTTCAATTCGGCAATTTGCT
GATTTGCCGGAAATTTGCGTTTTCCGGCAATTTGCC
GATTTCCGGCAAGTTGCC
GATTTGCCGGAAATTTCTCAATTATGGCAATTTTCC
GATTTGCCGGAAATTTGCAATTCGGCAATTTGCCGATCTGTGAGAAATTTCAATTTCTGGCAATTTGCCGATTTGTCA
GAAATTATCGATTCGGCAATTTGCC
Nr of selected repeats 7 Similarity 0.791446
Consensus:
GATTTGCCGGAAAtTTtCaATTCcGGCAATTTgCC
>Cele-UNSB01_3:12788240-12788411 Satlength=172 Nr of Repeats=5 RepeatLength=35
seed=AATTTGAATT
AATTTGAATTTTCCGCCAAAAATCCTTTTCTGAGAT
AATTTGAATTTCCGCCAAAAAATTCGGAGAA
AATTTGAATTTCCGCCAAAAATCATTCTGAGAA
AATTTGAATTTCCGCCAAAAAATTCGGAAAA
AATTTGAATTTCCGCCAAAAATCATTCTGAGAA
Nr of selected repeats 3 Similarity 0.923810
Consensus:
AATTTGAATTTcCGGCCAAAAATCaTTTTCTGAGAA
>Cele-UNSB01_3:12788650-12788963 Satlength=314 Nr of Repeats=8 RepeatLength=35
seed=TTCAAATTTT
TTCAAATTTTATGTGAAAGACATTTTGGCGGTAAA
TTCAAATTTTCTGTGAAAGACTTTTGGCGGTAAA
TTCAAATTTTTTGTGAAAGTCATTTTGGCGGGAAA
TTCAAGTTTTCCGAGAAAATTTTTGGCGGGAAA
TTCAAATTTCTACAATAATAATTTTGGCGGGAAT
TTCAAATTTCTGAGAAAACCATTTTTCCGGGAAGTTTAATTTTTCTGTGAAAGACATTTTGGCGGGAAA
TTCAAGTTTTCACAAAAACATTTGTTGGAGGAAA

TTCAAATTTTCACAAAAAAAGTTTTGGCGGAAAT
Nr of selected repeats 5 Similarity 0.658559

Consensus:

TTCAAATTTTctgtgaAAgacaTTTTGGCGGnAAa

>Cele-UNSB01_3:12817254-12818910 Satlength=1657 Nr of Repeats=46

RepeatLength=36 seed=GATATTTTCA

GATATTTTCATGTTTCGGCAAAAATGCCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAATGCCGATTTGCCG

GATATTTTCATGTTCTGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAATGCCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTGGCAAAAAGTACCGATTTGCTA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAATGCCGATTTGCCG

GATATTTTCATGTTCTGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAATGCCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCG

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTGGCAAAAAGTACCGATTTGCTA

GATATTTTCATGTTTCGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTGGCAAAAAGTACCGATTTGCCA

GATATTTTCATGTTTGGCAAAAAGTACCGATTTGCCA

Nr of selected repeats 46 Similarity 0.952800

Consensus:

GATATTTTCATGTTCCGGCAAAAAGTACCGATTTGCCa

>Cele-UNSB01_3:12834918-12835593 Satlength=676 Nr of Repeats=18 RepeatLength=35
seed=TTTCCGGCAA

TTTCCGGCAAACCGGCAAATTGCTGGAAC TGAGCA
TTTCCGGCAAAGCGGTAAATTGCCGGAATTGAAAA
TTTCCGGCAAATCACCAAACCGGCAGTTTGCCGAAAATCAAAAT
TTTCCGGCAAATCGATAAATTGCCGGAATTGAACA
TTTCCGGCAAATCGGTAAATTGCTGGAAC TGAGCA
TTTCCGGCAAATCGGCAAATTGCCGGAATTGAACA
TTTCCGGAAAATCGGCAAACCGGCAATTTGCCGAAAATCAAAAT
TTTCCGGCAAATCGGCAAATTGTCGGAATTGAAAA
TTTCCGGCAAATCGGTAAATTGCTGGAAC TGAGCA
TTTCCGGCAAAGCGGTAAATTGCCGGAATTGAAAA
TTTCCGGCAAATCACCAAACCGGCAGTTTGCCGAAAATCAAAAT
TTTCCGGCAAATCGATAAATTGCCGGAATTGAACA
TTTCCGGCAAATCGGTAAATTGCTGGAAC TGAGCA
TTTCCGGCAAATCGGCAAATTGCCGGAATTGAAAA
TTTCCGGCAAATCACCAAACCGACAGTTTGTCGAAAATCAAAAT
TTTCCGGCAAATCGATAAATTGCCGGAATTGAACA
TTTCCGGAAAATCGGCAAACCGGCAATTTGCCGAAAATCAAAAT
TTTCCGGCAAATCGGCAAATTGTCGGAATTGAAAA

Nr of selected repeats 13 Similarity 0.878877

Consensus:

TTTCCGGCAAATCGgtAAATTGCcGGAAtTGAAcA

>Cele-UNSB01_3:12836433-12837192 Satlength=760 Nr of Repeats=21 RepeatLength=34
seed=TTTCAATTCC

TTTCAATTCCGGCATTTTACCAATTTGCCGGAAT
TTTCAATTCCGCCAATTTACCAATTTGCCGGAAGTTTCAAATTTGGCAATTTGCCGGTTTGCCGGATA
TTTCAATTCCGCCAATATAACCAATTTGCCGGAAG
TTTCAATTACGGCAATTCGCCGATTTGCTGGAAT
TTTCAATTCCGCCAATTTGCCGGTTTGCCGGAATTCATTTCCGGCATTTTACCAATTTGCCGGTAT
TTTCCATTCCGCCAACTTGCCGATTTGAGAGAAA
TTTCAATTCCGGAAATTTGCCGATTTGCCGGAAT
TTTCAATTCCGGAAT
TTTCAATTCCGCCAATTTGCCGGTTTGCTAGAAA
TTTCAATTCCGGCATTTTACCAATTTGTCGGAAG
TTTCAATTCCGCCAATATAACCAATTTGCCGGAAG
TTTCAATTCCGGAAATTTGCCGGTTTGCCGGATA
TTTCAATTCCGCCAATTTACCACTTTGCCGGAAT
TTTAAATTTCCGGCATTTTACCAATTTGCCGGAAG
TTTCAATTTCCGGCAATTTATTAATTTGCCGGAAG
TTTCAATTTCCGGCAATTTGCCGATTTGCCGGAAT
TTTCAATTCCGGAAA
TTTCAATTCCGGCATTTTACCAATTTGCCGGAAT
TTTCAATTCCGCCAATTTATCAATTTGCCGGAAGTTTAAATTTTGGCGATTTGCCGGTTTGCCGGATA
TTTCAATTCCGCCAATTTACCACTTTGCCGGAAT
TTTCAATTCCGGAAA

Nr of selected repeats 15 Similarity 0.747664

Consensus:

TTTCAATTcCGgCAaTTTaCCaATTGcCGGAAn

>Cele-UNSB01_3:12842209-12842347 Satlength=139 Nr of Repeats=11 RepeatLength=12
seed=TATACATATA

TATACATATACA
TATACATATACA

TATACATATACA
TATACATATACA
TATACATATACA
TATACATATACA
TATACATATACA
TATACATATACA
TATACATATACA
TATACATATACA
TATACATATACA
TATACATATACATATACA

Nr of selected repeats 10 Similarity 1.000000

Consensus:

TATACATATACA

>Cele-UNSB01_3:12885748-12886017 Satlength=270 Nr of Repeats=5 RepeatLength=43
seed=GGCAAATCGG

GGCAAATCGGCAAACCGGCAATTTGTCAAATATTCAAATTTCC
GGCCAATCGGCAAATCGGGAAATTTGGTGAATTGAAAATTTCCGGAAAATTTGGCAAATTTGCCGAAATTTCAATTTGCC
AAAAATGTAAATTTCCG

GGCAAATCGGCAATCCGGCAAACCTGGTGAATTGAAAATTTTCCG

GGCAAATCGGCAAACCGGGGAATTATTGGAATTGAAAATTTCC

GGCAAATCGGCAAACCGGCACTTTGCAAAAAATAAAAAATTTCT

Nr of selected repeats 3 Similarity 0.689394

Consensus:

GGCAAATCGGCAAACCGGcAaTTtgtnaAAtaTnaAAATTTCC

>Cele-UNSB01_3:12889217-12889593 Satlength=377 Nr of Repeats=11 RepeatLength=34
seed=TTTCAATTCC

TTTCAATTCCGGCAAATTTGGCGATTTACCGGAAA

TTTCAATTCCGGCAATTTGCCGACTTGCCGAAA

TTTCAATTCCGGCAATATGTTCGATTTACCAAAAT

TTTCAATTCCGGCAATATGTCAATTTACCAAAA

TTTCAATTCCGGCAATTTGCAAAATTTACCGGAAG

TTTCAGTTCCAGCATTTTGCCATTTGCCAGAAAT

TTTCAATTCCGGCAATTTGCCGATTTACCTGAAA

TTTCAATTACGGCAATTTTCCGGTTTGCCGAAAT

TTTCAATTCCGGCAATTTGCCTTTTTGCCGAAA

TTTCAATTCCGGCAAATTTGCCGATTTGCCGAAAT

TTTAATTCCGACAATTTGCCGATTTGCCGAAA

Nr of selected repeats 7 Similarity 0.788982

Consensus:

TTTCAATTCCGGCAATtTGcCgATTTaCCgAAa

>Cele-UNSB01_3:12934390-12934631 Satlength=242 Nr of Repeats=8 RepeatLength=35
seed=TTTTAATTCC

TTTTAATTCCTGCAATTTGCCGATTGTCGGAAAT

TTTTAATTCGGCAATTTGCCGATTGTCGGAAAT

TTTTATTTCCGGAAAT

TTGTAATTCGGCAATTTACCGGTTTGCCGAAAA

TTTTAATTCGGCAATTTGCCGTTTGCCGGGAAT

TTTTAATTCGGCAATTTGCCGTTTGCCGGGAAT

TTTTAATTCGCAAT

TTTTAATTCGGCAATTTGCCGTTTGCCGAAAT

Nr of selected repeats 6 Similarity 0.888254

Consensus:

TTTTAATTCGGCAATTTGCCGtTTGcCGGaAAT

>Cele-UNSB01_3:12996870-12997291 Satlength=422 Nr of Repeats=8 RepeatLength=35
seed=GGAAATTTTA

GGAAATTTTAAATTTTCGGCAATTTGCCGTTTTGCCGGAAACTTTCAATTCCGGCAACTTGCCGATTTGCTGGAAGTCTT
AAATTCTGGCATTGTTGCCAGTTTGCC
GGAAATTTTAAATTTCCGGAAAGTTTGCCGTTTTGCC
GGAAATTTTAAATTTCCGGCAATTTGCCGTTAGCC
GGAAATTTTAAATTTCTGCAATCTTCCGCTTTGCT
GGAAATTTTAAATTTCCGGCAACTTGCCGTTTTGAC
GGAAATTTTCATTTTCCGGTAATTTGCCGTTTTGCTGAAAGTTTTAAATTTCCGGCAATTTGCTGATTTGTCGAAAATTTT
CATTTTCCGGCAATCTGCCAGTTTGCT
GGAAATTTTAAATTTCCGGTAATTTGCCGTTTTGCC
GGAAATTTTAAATTTCCGGTAATTTGCCGATTTGCT
Nr of selected repeats 5 Similarity 0.820952
Consensus:

GGAAATTTTAAATTTCCGcGcAAAttgCCGgTtGcc
>Cele-UNSB01_3:13000875-13002076 Satlength=1202 Nr of Repeats=5 RepeatLength=32
seed=GACCAATCAG
GACCAATCAGCGACTCGCTCCGCCCATTTTCG
GACCAATCAGCGTCATCGAGCTCCATTTAACCCTAAATTTTATAGATTAAGATGAACGTAATAATATAGAAAAATATTC
AATTAGTTTGAATAAAATTTATTTTTTAACAATTTTATTTTCAAATAATCGAATATTTCTATATATTTCTACATTC
ATCTTCAATCTATAAAATTTGGGTCAATACGGAGCTCAAAGACGCTGATTGGTCAGAGAATGGGCGGGGCGAATCGCTG
ATTGGTCGGAGAGTTCTTAGTGATTTTCTGGTTTTTATAGAAAATTTCCGATAATTTTGGGATTTTCGATTGTTCAAAA
AAAATCCAAAATAGTCTCAAATTCAGAAAATCACAAAAAACTTTAAAAAATCGCGAAAATCAAATTTTCAGACCCC
AGACGACATTGAAACACTCGCTTCCGTAGACGAAGATGGTATTAATCTAGAAGAAGACGCATGTACAATTAATTCGAT
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GAAGACGCTGCTTGGTCTGAAATGGGCGGAGCAAGTCGCTGATTGGTCGGGGAGTTTTCCGCGATTTTTCTGAATTTGAG
ACTATTTTGGATTTTTTTTCAAACAATCGAAATCCCAAAAATTTATCGGAACTTTCTATAAAAACAGAAAATCACTAAG
AACTCTCC

GACCAATCAGCGATTCGCCCCGCCACTCTCT
Nr of selected repeats 3 Similarity 0.861111
Consensus:

GACCAATCAGCGAtTCGcCccGCCCAcTcTcT
>Cele-UNSB01_3:13002319-13002507 Satlength=189 Nr of Repeats=5 RepeatLength=38
seed=TTTTGGCGGG
TTTTGGCGGGATTTCAAATTTGAATTTTTTGAATA
TTTTGGCGGGAATTCAAATTTTAATTTTTTTGAAAATA
TTTTGGCGGGAATTCAAATTTTAATTTTTTTGAAAATA
TTTTGGCGGGAATTCAAATTTTAATTTTTTCGAAAACAT
TTTTGGCGGGAATTTAAATTTTAAATTTTTTTGAAAATA

Nr of selected repeats 3 Similarity 0.811966
Consensus:

TTTTGGCGGGAATTCAAAtTTnAaTTTTTtGAAAAtA
>Cele-UNSB01_3:13026111-13026534 Satlength=424 Nr of Repeats=13 RepeatLength=35
seed=AAATTTTGAT
AAATTTTGATTTTTGGCGATTTGCCGA
AAATTTTGATTTTTGGCGATTTGCCAG
AAATTTTGATTTTTGGCAATTATCCGATTTGCCGG
AAATTTTGATTTTTGGCGATTTGCCAG
AAATTTTGATTTTTGGCAATTATCCGATTTGCCGG
AAATTTTGAATTTTGGCAATTTTCCGATTTGCCGG

AAATTTTGATTTTTGGCAATTTGCCGAATTGCCGG
AAATTTTGATTTTTGGCAATTTGCCGAATTGCCGG
AAATTTTGATTTTTGGGGATTTGCCGG
AAATTTTGATTTTTGGCAATTTGCCCTATTTGTCCG
AAATTTTGATTTTTGGCAATTTGCCGATTTGTCCG
AAATTTTGATTTTTGGCAATTTGCCGATTTGCCGG
AAATTTTGATTTTTGGCAATTTCCGATTTGCCAA
Nr of selected repeats 9 Similarity 0.900529

Consensus:

AAATTTTGATTTTTGGCAATTTgCCGAtTTGcCGG
>Cele-UNSB01_3:13035804-13036305 Satlength=502 Nr of Repeats=16 RepeatLength=35
seed=ATTTGCCGGA

ATTTGCCGGAATTTTTGATTTTCGGCAATATACCG
ATTTGCCGGAACATTTGATTTTCTGGAATATACCG
ATTTGCCGGAATTTTTGGTTTTTCGGAA
ATTTGCCGGAATTTAGAAATTCGGCAATATGCCG
ATTTGCCGGAATTTTTGATTTTCGGCAATATGCCG
ATTTGCCGGAATTTTTGATTTTCGGCAATATACCG
ATTTGCCGGAACATTTGATTTCCGGCAATATGCCG
ATTTGCCGGAATTTTTGATTTCCGGCAATATGCCG
ATTTGCCGGAATTTTTGATTTTCGGCAATATACCG
ATTTGCCGGAACATTTGGTTTCCGGCAATATGCCG
ATTTGCCGGAATTTTTGGTTTTTCGGAA
ATTTGCCGGAATTTAGAAATTCGGCA
ATTTGCCGATTTGCCGGAATTTGATTTCCGGCAATATGCCG
ATTTGCCGGAATTTTTGGTTTTTCGGAA
ATTTGCCGGAATTTAGAAATTCGGCAATATGCCG
Nr of selected repeats 10 Similarity 0.867936

Consensus:

ATTTGCCGGAATTTtGAtTTcCGGCAATATgCCG
>Cele-UNSB01_3:13044209-13044762 Satlength=554 Nr of Repeats=5 RepeatLength=32
seed=ACCAATCAGC

ACCAATCAGCGATTTGCTCCGCCCACTTTTCGG
ACCAATCCGCTGACCGAGGCATTTGATTTGGTTTGAATTTGGGCGGAGCAGCGAATTGCTGATGCGAAATACGGGAAGTT
CTCATTTTGATGGAAATTCGCAAAATCTTTAAAAAACAATAATCTTCTCAAATTCGAAAAAATCACAAGGAAAT
CGAAGAAAATCGCGATTTTGGATTTCCCG
ACCAATCAGCGATTTGCTCCGCCCACTTTTGA
ACCAATCAGCGTTTCGAGGCATTTGATTTGGTTCAAATTTGGGCGGAGCAGCGAGTTGCTGATTTGGATTTTTTCAGTTTTTA
AATTTTTAAAGCTTTTTTTAACGGAAAAATTCGAGAAAACCATAGATTTTGGATGAGAAATGATGAAAATTTTCATGAAA
AAATGGAAAAATGATTTGGAAATTAATCAAAAAATCTTGAAAAAATTTTTTTTCAGAGAAAATGCTTCATTTTTGGCT
CTGAAACGCCTTTTTTTATTTGTGCCTCCCG
ACCAATCAGCAATTTGCTCCGCCCACTTTTGA

Nr of selected repeats 3 Similarity 0.916667

Consensus:

ACCAATCAGCgATTTGCTCCGCCCACTTTtGa
>Cele-UNSB01_3:13065987-13066581 Satlength=595 Nr of Repeats=17 RepeatLength=35
seed=AAATTCAAAT

AAATTCAAATTTATTTGAGAAATATTTTATGACGGG
AAATTCAAATTTTCTGATAAATATTTTATGGCGGT
AAATTCAAATTTATTTGCGAGATATTTTTTGGCGGA
AAATTCAAATTTATTTGAGAAATATTTTTTGGCTGG
AAATTCAAATTTTCTGAGAAATATTTTTTGGCGGG
AAATTCAAATTTTTAAGAAAAATTTTTTGGCGGG
AAATTCAAATTTTGGAGAAATATTTTTTGGCAGG

AAATTCAAATTATTTGAGAAATATTTTATGGCGGA
AAATTCAAATTATTTGCGAGATATTTTTGGCGGG
AAATTCAAATTATTTGAGAAATATTTTATGGCGGG
AAATTCAAATTTTCTGAGAAATATTTTATGGCGGG
AAATTCAAATTTTCTGAGAAATATTTTATGGCGGT
AAATTCAAATTATTTGCGAGATATTTTTGGCGGA
AAATTCAAATTATTGGAGAAATATTTTTGGCTGG
AAATTCAAATTTTCTGAGAAATATTTTATGGCGGA
AAATTCAAATTATTTGCGAGATATTTTTAGCGGG
AAATTCAAATTATTTGAGAAATATTTTATGGCGGG
Nr of selected repeats 16 Similarity 0.851746

Consensus:

AAATTCAAATTaTtTGaGAAATATTTTaTGCGGGg

>Cele-UNSB01_3:13121321-13121505 Satlength=185 Nr of Repeats=5 RepeatLength=31
seed=GATTTTTTCA

GATTTTTTCAGTGAAAATCGAAAATTTTCG

GATTTTTTCAGGGAAAACCGAAAATTTTGGAAATTTTCAGGGAATATTAACAATTTTTA

GATTTTTTCAGGGAAAACCAAAAAATTC

GATTTTTTCAGAGAAAACCTTAAAATTTGTG

GATTTTTTCAGAGAAAATTGAAAGAATTTGG

Nr of selected repeats 3 Similarity 0.659722

Consensus:

GATTTTTTCAGnGAAAAnCnaAAAAttTtcg

>Cele-UNSB01_3:13127780-13127920 Satlength=141 Nr of Repeats=4 RepeatLength=35
seed=CGGCAATTTG

CGGCAATTTGCCAAAAATGAAAATTTCCGGCAAAT

CGGCAATTTGCCAAAAATGAAAATTTCCGGCAAAT

CGGCAATTTGCCAAAAATCAAAAATTTCCGGCAAAT

CGGCAATTTGCCTAAAATCAAAAATTTCCGGCAAAC

Nr of selected repeats 4 Similarity 0.936508

Consensus:

CGGCAATTTGCCaAAAAATcAAAATTTCCGGCAAAT

>Cele-UNSB01_3:13139705-13140905 Satlength=1201 Nr of Repeats=30

RepeatLength=20 seed=TGTAGATTTA

TGTAGATTTACAAAGGTCTA

TATAGATTTACAAAGTTCTATGTAAATCTACAACGTTCTATGTGAATTTACGGAAGCCTT

TGTAGATTTACGAAATTCTA

TGTAAATTTACAAAGTTCTA

TGTGGATTTACAAAGTCTA

TGTAGATTTTCAAAGTTCTA

TGTAGATTTACAAAGGTCTA

TATAGATTTACAAAGTTCTATGTAAATCTACAACGTTCTATGTGAATTTACGGAAGCCTT

TGTAGATTTACGAAATTCTA

TGTAAATTTACAAAGTTCTA

TGTGGATTTACAAAGTCTA

TGTAGATTTTCAAAGTTCTA

TGTAGATTTACAAAGGTCTATATAAATTTACAAAGTTCTATGTAAATCTACAACGTTCTATGTGAATTTACGGAAGCCT

AC

GTAGATTTACAAAATTTGA

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TTTCAAAGGTTACACGGTAAGGGATCAGTGATCAACTTCAGAACTTCTCTCTCCTTCCATCTCTCTCAAAGTC

TAGTCACGTTCCCGTTCAGAAACCACAAAGTCATAAAATTTGAACGACCAGATTTTTTTTTTGGCGTTTGCAAACCGT

AACCATCCTTGATTCATCATGATTTTGATGATCACTATTGGAAAAATCACTTTGATCAAAAAAAATTCAAAATTGAC

GTGTTACGAACGTCTATTTTTGATTTAAAAAGTTACATGGGCAATTGGGCTTTGATCATTAAAAATGTTTTCTA

TGTAGATTTACGAAGTTGTA
TGTAGATTTACGGAGCTCCA
TGTAGATTTAAGTAGAACTACGTAGATTGACAATGTAAGAAGTTCTATGTAAATTTGCAATGTTCCA
TGTAGATTTACAAAGTTATATGTTAGTTTACAAAGTCCTG
TGTAGATTTACGAAACACTA
TGTACATTTACTGCACCTTG
TGTAAATTTACGGAGCTCAA
TGTAGATTTACGGAGCTCTG
TGTGGATTTACAAAGCTCAA
TGTAGATTTACGGAGATCTATGTTTCATTTACTAAACTCCT
TATAGATTTACAGAGCTCAA
TGTAGATTTACGGAGCTCAA
TGTAGATTTACGGAGCTCTG
TGTGGATTTACGGATCTCAA
TGTAGATTTACGGCGTTCTA

Nr of selected repeats 22 Similarity 0.674981

Consensus:

TGTAGATTTACgAgnTctA

>Cele-UNSB01_3:13143562-13144065 Satlength=504 Nr of Repeats=16 RepeatLength=19
seed=TTGGCAATTT

TTGGCAATTTACCAAAAATTTGGCAGTTGACTAAAATGTTGGCAGCTAACAAAAAAAT
TTGGCATTTGACCAAAAAT
TTGCCAATTTATCAAAAAT
TTGGCAATTTACTGAAACT
TTGGCAGTTTACCAAAAAG
TTAGCAATTTACTAAAAAT
TTGGCAATTTACTACAAAT
TTGCCAATTTACCAAAAAGATGGTAACTTTTTTAAAATTTGATCAAAAATATGGAAATCTGCTAAAAAT
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TTGGCAATTTACCAAAAAC
TTGGCAATTTACTAAAAAT
TTGCCAATTTACCAAAAAGATGGTAACTTTTTTTTTAATTTGAAAATTTGATCAAAAATTTGGTATTTTACAGAAAAT
TTGGCAATTTACTAAAAAT
TTGGCAATGTACCAAAAATGGCATTACTACAAATTTGGTAGTTTACCAAAAAGC
TTGGCAATTTACAAAAAT

Nr of selected repeats 10 Similarity 0.809747

Consensus:

TTGGCAaTTTACcAAAAAt

>Cele-UNSB01_3:13181955-13182047 Satlength=93 Nr of Repeats=5 RepeatLength=15
seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA
CGAAAAGGGGAACTGCAAAAAAGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAGATA
CGAAAAGGGGAGCAA

Nr of selected repeats 3 Similarity 0.881481

Consensus:

CGAAAAGGGGAGatA

>Cele-UNSB01_3:13182222-13182299 Satlength=78 Nr of Repeats=5 RepeatLength=15
seed=TCCCCTTTTC

TCCCCTTTTCGTATC
TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA

TCCCCTTTTTGCAGA
TCCCCTTTTTCGTTCTGC

Nr of selected repeats 4 Similarity 0.777778

Consensus:

TCCCCTTTTTcGcAga

>Cele-UNSB01_3:13188476-13189044 Satlength=569 Nr of Repeats=13 RepeatLength=35
seed=TGCCGGAATT

TGCCGGAATTGAAATTTTTCGGCAAATCGGCAAACCGGTAAAATTTAACATTTTCTCTTTTACAAGGCATAGAAATCTA
GAAAAT

TGCCGGAATTTAGAATTTTTCGACAAAGTGGCAAAT

TGCCGGAATTTAAATTTTTCGGCAAATCGGCAAAT

TGCCGGAATTTGAAAATTTTCGGCAAATCGGCAAAT

TGCCGGAATTTAGAATTTTTCAGCAATA

TGCCGGAATTTAAATTTTTCGGCAAATCGGCAAAT

TGCCGGAATTTGAAAATTTTCGGCAAATCGGCAAAT

TGCCGGAATTTAACATTTTCGGTAAATAGGCAAAT

TGCAGGAATTTAAAATTTTTCGGCAAAGCGGTAAGT

TGCCGGAATTTGAAATTTTCGGCAAATTTTCGGCAAATTTTCGGCAAATCGGCAAAT

TGCCGGAATTTAAAATTTTTCGGCAAATCGGCAAATTTGACAAATT

TGCCGGAATTTGAAAATTTCTAGCTAATCGGCAAAT

TGCCAGAATTTAGAATTTTTCGGCAAATTTGCCGAAAATCAAAATTTTCCGGTAGTTCTCAAATCGGCAAAT

Nr of selected repeats 8 Similarity 0.817687

Consensus:

TGCCGGAATTTAAAaTTTcCGGCAAAtcGGCAAAT

>Cele-UNSB01_3:13248196-13248346 Satlength=151 Nr of Repeats=9 RepeatLength=12
seed=TAAGCCTAAG

TAAGCCTAAGCC

TGAGCCTAAGCA

TAAGCCTAAGCC

TAAGCCTAAGCA

TAAGCCTAAGCC

TGAGCCTAAGCCTAAGAC

TAAACCTAAGCC

TAAACCTAAGAC

TAAGCCTGAGCCTCAGCCTAGGCTTAATCATATGACGCAGCCTAATCC

Nr of selected repeats 7 Similarity 0.830688

Consensus:

TAAgCCTAAGCc

>Cele-UNSB01_3:13289132-13289912 Satlength=781 Nr of Repeats=10 RepeatLength=78
seed=CGAAGTTGCT

CGAAGTTGCTGGATCAACGATCACAACAGGCGGATTTGTCTGCACAACCGGATCAGAAGTCGTCTGACTTGGATCTTT

CGCAGTTGCTGGTCCAGAGATCACAACAGGCGGATTTGGCGGCATAACCTGAGCAACGGTAGTGTCATTTGGTTCTTC

CGAAGTTGCTGGATCAACGATCACAACAGGCGGATTTGGCGGCATAACCTGAGCAACGGTAGTGTCATTTGGTTCTTC

CGAAGTTGCTGGATCAACGATCACAACAGGCGGATTTGGCGGCATAACCTGAGCAACGGTAGTGTTGTTTGGTTCTTC

CGAAGTTGCTGGTCCAGAGATCACAACAGGCGGATTTGGCGGCATAACCTGAGCAACGGTAGTGTCATTTGGTTCTTC

CGAAGTTGCTGGATCAACGATCACAACAGGCGGATTTGGCGGCATAACCTGAGCAACGGTAGTGTTGTTTGGTTCTTC

CGAAGTTGCTGGTCCAGAGATCACAACAGGCGGATTTGGCGGCATAACCTGAGCAACGGTAGTGTCATTTGGTTCTTC

CGAAGTTGCTGGATCAACGATCACAACAGGCGGATTTGGCGGCATAACCTGAGCAACGGTAGTGTTGTTTGGTTCTTC

CGAAGTTGCTGGTCCAGAGATCCCAACAGGCGGATTTGGCGGCATAACCTGAGCAACGGTAGTGTCATTTGGTTCTTC

GCTACCGCCC
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GCTACCTCCC
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GCTACCGTCCGCTACCAACC
GCTACCGCTCCGTTATGCC
GCTACCGCCCGCTACCAACC
GCTACCGCTCCGTTATGCC
GCTACCGCCCGCTGTCGCAT
Nr of selected repeats 101 Similarity 0.923248
Consensus :
GCTACCGCCC

>Cele-UNSB01_3:13409998-13411238 Satlength=1241 Nr of Repeats=25
RepeatLength=43 seed=CGGAAATTTT

CGGAAATTTTGGATTTTCGGTAATTTGCCGGTTTACTGGTTTGC
CGGAAATTTTCAATTCCGGCAACTTGCCAGTTTGCCGGTTTGC
CGGAAATTTTCATTTTCAAAAATTTGCCAGTTTGCTGATTTGCCGAACATCAGTTTGC
CGGAAGTTTTTCAGAGGGATTTTAATAAGACCGAAAAATTTAGAACTGTGAAAATTTTGGCAAATCGGAAAATTGCCAA
ATTGCCGATTTGC
CGGAAATTTTATTTTTCGGCAATTTGCCGGTTTGCCGATTTTC
CGGAAATTTTGGATTTTTCGAAAAATTGCCAGTTTGCCGATTTGC
CGGAAATTTTATTTTTCGACAATTTGCCGATTTGC
CGAAAATTTTCATTTTCCACAATTTGCCAGTTTGCCGATTTGC
CGGAAATTTTCAATTCCGGCAATTTGCCGATTTGCCGATTTGCAGGAAATATTTATTTTCGACAATTTGCCAGTTTGA
CGATTTGC
CGGAAATTTTATTTTTCGGCAATTTGCCGGTTTGCCGATTTTC
CGGAAATTTTGGATTTTTCGAAAAATTGCCAGTTTGCCGACTTGT
CGGAAATTTTATTTTTCGACAATTTGGCCGATTTACCGATTTGC
CGGAAATTTTGGTTTTTCAAAAATTTGCCGGTTTGTTCGATTTGC
CGGAAATTTTAAATTTCCGGCAAAGTGCCGATTTGC
CGGAAAATTTCAATTCCGGCAATTTGCCAGTTTGCCGATTTGC
CGAAAATTTTCATTTTAAAAATTTGCCGGTTTGTTCGATTTGCTAGAAAATTTTCATTTTCGACAATTTGCCGGTTTGC
CGGAAATTTTCATTCTCCACAATTTGCCAGTTTCCGATTTGC
CGGAAAGTTTCAATTCCGGCAATTTGCCGGTTTGCCAAATTTGC
CGGAAATTTTCATTTTCAAAAATTTGCCGGTTTGCCGATTTGC
CGGAAATTTTCATTTTCAAAAATTTGCCAGTTTGCCGATTTGC
CGGAAGTTTTTAGAGGGATTTTGTATAAGACCGAACAATTTACTGTGAAAATTTTGGCAAATCGGAAAATTGCCAGTTT
GCCGATTTGC
CGGAAATTTTATTTTTCGGCAATTTGCCGGTTTGCCGATTTTC
CGGAAATTTTGGATTTTTCGAAAAATTGCCAGTTTGCCGATTTGC
CGGAAATTTTATTTTTCGACAATTTGCCGATTTGC
CGAAAATTTTCAATTCCGGCAAATATCTTGTGTTGCCGGTTTTT

Nr of selected repeats 17 Similarity 0.776106
Consensus:

CGGAAATTTTnAtTTtCggcAAtTTGCCnGTTTGCCGATTTgC

>Cele-UNSB01_3:13415830-13416475 Satlength=646 Nr of Repeats=18 RepeatLength=34
seed=CGGAATTGAA

CGGAATTGAAATTTCCGGCAAATCGACAACCTTGC
CGGAATTGAAATTTCCGACAAAATCGGCAAATAT
CGGAATTGAAATTTCTGTAAACCGGCAAATCGC
CGGAATTGAAATTTCCGGCAAATCGACAACCTTGC
CGGAATTGAAATTTCCGGCAAATCGACAACCTTGC
CGGAATTGAAATTTCCGACAAAATCGGCAAATTAC
CGGAATTGAAATTTCCGGCAAATGGCAGATTAC
CGGAATTGAAATTTCCGGCAAATGGGCAAATTGC
CGGAATTGAAATTTCCGGCAAATCGACAACCTTGC
CGGAATTGAAATTTCCGGCAAATCGACAACCTTGC
CGGAATTGAAATTTCCGGCAAATCGACAACCTTGC
CGGAATTGAAATTTCCGGCAAATCGACAACCTTGC
CGGAATTGAAATTTCCGGCAAATCGACAACCTTGT
CGGAATTGAAACTTTCCGGTAAATTTGTCAGACTTGAAATTTGCCGGCAAATCGGCAAATGGT
CGGAATTGAAGTGTCCGGCAAATCGGCAAATCGGCAAATTTTC
CGGAATTTAAATTTCCGGCAAATGGGCAAATCGC
CGGAATTTAAATTTCCGGCAAATGGGCAAATTGC
CGGAATTGAAATTTCCGGCAAATCGGCAAATTGC
CGGAATTGAAATTTCCGACAAAATCGAAAAATTGC

Nr of selected repeats 15 Similarity 0.854715

Consensus :

CGGAATTGAAATTTCCcGgCAAATcGgCAAaTTgC

>Cele-UNSB01_3:13432209-13432275 Satlength=67 Nr of Repeats=5 RepeatLength=11

seed=AAAAATGTGC

AAAAATGTGCA

AAAAATGTGCAAAAATTGTGAA

AAAAATGTGCA

AAAAATGTGCA

AAAAATGTGCA

Nr of selected repeats 4 Similarity 1.000000

Consensus :

AAAAATGTGCA

>Cele-UNSB01_3:13445252-13445836 Satlength=585 Nr of Repeats=45 RepeatLength=12

seed=AGTTATATAG

AGTTATATAGTA

AGTTATATAGTA

AGTTATATAGTT

AGTTATATAGTA

AGTTATATAGTA

AGTTATATAGTT

AGTTATATAGTTAATTGTATAGTA

AGTTATATAGTT

AGTTATATAGTA

AGTTATATAGTA

AGTTATATAGTT

AGTTATATAGTT

AGTTATATAGTT

AGTTATATAGTA

AGTTGTATAGTA

AGTTATATAGTA

AGTTATATAGTA

AGTTATATAGTA

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AGTTATATAGTA

AGTTATATAGTT

AGTTATATAGTA

AGTTATATAGTA

AGTTATATAGTA

AGTTATATAGTTAATTGTATAGTA

AGTTATATAGTT

AGTTATATAGTA

AGTTATATAGTAAGTTATAGTT

AGTTATATAGTA

AGTTATTTAGTAAGTTATAGTA

AGTTATATAGTA

AGTTATATAGTT

AGTTATATAGTA

AGTTATATAGTA

Nr of selected repeats 41 Similarity 0.931707

Consensus:

AGTTATATAGTa

>Cele-UNSB01_3:13483516-13483661 Satlength=146 Nr of Repeats=5 RepeatLength=31

seed=CCAAAAATGA

CCAAAAATGACTGAAAATTGG

CCAAAAATGACTGAAATTAGTCAAAAAATTGG

CTAAAAATGACTGAAAATATTCAAAAAATTGG

CCAAAAATGACCGAAAATAGTCAAAAAATTAG

CCAAAAATGACTGAAAATAGTCAAAAAATAG

Nr of selected repeats 4 Similarity 0.863799

Consensus:

CcAAAAATGACTGAAAaTAgTCAAAAAatTaG

>Cele-UNSB01_3:13559329-13561136 Satlength=1808 Nr of Repeats=95

RepeatLength=19 seed=AAAAATAGAT

AAAAATAGATTGGCATAACGA

AAAAATAGCTTGGCATAACGA

AAAAATAGATTGGCATAACG

AAAAATAGATTGACAGACG

AAAAATAGATTGACAGACG

AAAAATAGATTGACAGACA

AAAAATAGAGTGACAGACG

AAAAATAGATTGGCAGACG

AAAAATAGATTGACAGACA

AAAAATAGATTGACAGACG

AAAAATAGATTGTTACAAG

AAAAATAGATTCTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGGTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGGTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGGTACACG

AAAAATAGATTGTTACACG

AAAAATAGATTGTTACACG

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AAAAATAGATTGGTACACG

AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGGTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGGTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGGTACACG

Nr of selected repeats 93 Similarity 0.940307

Consensus:

AAAAATAGATTGtTACACG

>Cele-UNSB01_3:13583922-13584205 Satlength=284 Nr of Repeats=8 RepeatLength=30

seed=TTTCAGGCCA

TTTCAGGCCAATTGCAGTCATTTTCGAGCCGATTTTCAGTCATTGTTGAACA

TTTCAGGCCAATTTTCGGTCAATTTTGGACA

TTTCAGGCCAATTCCGGTCATTTTGGACA

TTTCAGGCCAATTTTGGCCATTTTGGATATTTTCAGGGAAATTTCTGTTCAT

TTTCAGGCCAATTTTCAGTCATTTCTGAACA

TTTCTGGCCAATTTTCGTTCATTTTGTAGACA

TTTCAGGCCAATTTTCAGTCATTTTGGACA

TTTCAGGCCAATTTTCAGTTATTTTGTAGACA

Nr of selected repeats 5 Similarity 0.822222

Consensus:

TTTCaGGCCAATTTcnGTCAAtTttTggACA

>Cele-UNSB01_3:13762939-13765339 Satlength=2401 Nr of Repeats=60

RepeatLength=40 seed=ATTTTTCTAG

ATTTTTCTAGAAAGTTCTAGAACATTTCCAGAATTTTCCCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCCCA

ATTTTTCTAGAAAGTTGTGAAACATTTCCAGAATTTTCTCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCCCA

ATTTTTCTAGAAAGTTGTGAAACATTTCCAGAATTTTCTCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAAATTTCCCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCCCA

ATTTTTCTAGAAAGTTGTGAAACATTTCCAGAATTTTCTCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAAATTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAAATTTCTCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAAATTTCTCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACATTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAAATTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCTAGAAATTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAAATTTCCCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCTCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCTCG

ATTTTTCTAGACAGTTCTGGAACATTTCCAGAAATTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCTAGAAATTTCCCA

ATTTTTCTAGAAAGTTTCAGGAACATTTCCAAAATTTTCTCG

ATTTTTCTAGAAAGTTCTAGAAAATTCAGAAATTTCCCG
ATTTTTCTAGAAAGTTCTGGAACATTACAGAAATTTCCCG
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTCG
ATTTTTCTAGACAGTTCTGGAACATTCCAGAATTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCGGAATTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTCG
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAAATTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCG
ATTTTTCTAGAAAGTTCTGGAACATTCCAAAAATTTCCG
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTCG
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACATTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAAATTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAAATTTCCCG
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCCCA
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ATTTTTCTAGAAAGTTCTGGAACATTCCAGAAATTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCTAGAAATTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAAATTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCTCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAATTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGAAATTTCCCG
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTAGAACATTCCAGACTTTTCCCA

Nr of selected repeats 60 Similarity 0.908418

Consensus :

ATTTTTCTAGAAAGTTCTGGAACATTCCAGAatTTTCCa

>Cele-UNSB01_3:13765752-13765977 Satlength=226 Nr of Repeats=15 RepeatLength=15

seed=CCACGATGGG

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCACGGTGGGTCTCA

CCACGATGGGTCTCA

CCACGATGGGTCTCG

CCACGATGGGTCTCG

CCACGATGGGTCTCA

CCACGATGGGTCTTA

CCACGATGGGTCTCA

CCACGATGGGTCTCG

CCACGATGGGTCTCG

CCACGATGGGTCTCA

CCACGATGGGTCTCG

CCACGATGGGTCTCG

Nr of selected repeats 15 Similarity 0.930582

Consensus :

CCACGATGGGTCTCa

>Cele-UNSB01_3:13900788-13900959 Satlength=172 Nr of Repeats=7 RepeatLength=24
seed=AAGAAGGATG

AAGAAGGATGCCGAAGAGAAGAAG
AAGAAAGATGCCGAAGAGAAGAAG
AAGAAGGATGCTGAAGATGAGAAG
AAGAAGGATGCAGGAGATGAGAAG
AAGAAGGATGCTGAAGATGAGAAG
AAGAAGGATGCTGGAGATGAGAAGAAG
AAGAAGGATGCTGGAGAGAAGAAA

Nr of selected repeats 6 Similarity 0.825926

Consensus:

AAGAAGGATGCTGaAGAGaAGAAG

>Cele-UNSB01_3:14059760-14060650 Satlength=891 Nr of Repeats=57 RepeatLength=15
seed=TCGTGGTGAG

TCGTGGTGAGACCCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCCT
TCGTGGTGAGACCCCT
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACTCA
TCGTGGTGAGACCCCT
TCGTGGTGATACCCA
TCGTGGTAAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACTCA
TCGTGGTGAGACCCCT
TCGTGGTGAGACCCCT
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
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TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACTCA
TCGTGGTGAGACCCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCTTTCATGGTTAGACCCA
TCGTGGTGAGACCCCT
TCGTGCTGAGACCATTTCATGGAGAGACCCA
TCGTGGTGAGACCCCT

TCGTGGTTAGACCCA
TCGTGGTGAGATCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACTCA
TCGTGGTGAGACCCT
TCGTGGGGAGACTCT
TCGTGGTGAGACCCT
TCGTGGTTAGACCCGACCCA
TCGTGGTTAGACCCA
TCGTGGTGAGATCTT
TCGTGGTGAGCCCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACTTT
TCGTGGTGAGACCCA
TCGTGGTGAGACTTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCT

Nr of selected repeats 54 Similarity 0.868872

Consensus:

TCGTGGTGAGACCct

>Cele-UNSB01_3:14063373-14064273 Satlength=901 Nr of Repeats=60 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACTCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGAACTT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCA

TCGTGGTGAGACTCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
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TCGTGGTTAGACCCA
TCGTGGTTAGACCCA
TCGTGGTGAGATCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTTAGACCCA
TCGTGGTGAGATCTT
TCGTGGTGAGCCCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACTTT
TCGTGGTGAGACCCA
TCGTGGTGAGACTTT
TCGTGGTGAGACCCA
TCGTGGTGAGACTTT

Nr of selected repeats 60 Similarity 0.880778

Consensus:

TCGTGGTGAGACCca

>Cele-UNSB01_4:1-5637 Satlength=5637 Nr of Repeats=464 RepeatLength=12

seed=AAGCCTAAGC

AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCTAAGCTAAT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCCT
AAGCCTAAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAACCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCT
AAGCCTAAGCT

AAGCCTAAGCCT
AAGCCTAAGCCTAAGCCT

Nr of selected repeats 403 Similarity 0.920412

Consensus:

AAGCCTAAGCCT

>Cele-UNSB01_4:125359-125607 Satlength=249 Nr of Repeats=13 RepeatLength=19
seed=TGGTTGAGGC

TGGTTGAGGCTCACAATTT
TGGTTGAGGCTCTCTATTT
TGGTTGAGGCTCACAGTTT
TGGTTGAGGCTCAGGATTTT
TGGTTGAGGCTCTCTATTA
TGGTTGAGGCTCTCTATTT
TGGTTGAGGCTCTCTATTT
TGGTTGAGGCTCTCTATTT
TGGTTGAGGCTCTTTATTT
TGGTTGAGGCTCTTTATTT
TGGTTGAGGCTCACAGTTT
TGGTTGAGGCTCTCTATTT
TGGTTGAGGCTCTCTATTT
TGGTTGAGGCTCTCTATTT
TGGTTGAGGCTCTTTATTT

Nr of selected repeats 12 Similarity 0.880914

Consensus:

TGGTTGAGGCTCtctATTT

>Cele-UNSB01_4:128195-129066 Satlength=872 Nr of Repeats=28 RepeatLength=19
seed=TTGGTTGAGG

TTGGTTGAGGCTCACAATT
TTGGTTGAGGCTCAAAATT
TTGGTTGAGGCTAACAATT
TTGGTTGAGGCAAAAAATT
TTGGTTGAGGCTAAAAATT
TTGGTTGAGGCTAAAAATT
TTGGTTGAGGCTAACAATT
TTGGTTGAGGCTCTCGATG
TTGGTTGAGGCTCGCGATG
TTGGTTGAGGCTTTGATT
TTGGTTGAGGCTCTCAGGAATTT
TTGGTTGAGGCTCTCAGGATT
TTGGTTGAGGCTCTCGTT
TTGGTTGAGGCTCAGGATT
TTGGTTGAGGCTCTAGATTTTCTTTTTTTTTTGGCTCTAGATTTTTTTTTTTTTTTTTTTGGGGGGGGGGGGGGGGGGGGGGCA
GATAGCTCAGTCGGTAGTGGTGCCGCTAGCAGTCTGGAGGTCACGAGTTCAAGCCGGCCTCACCCTTAGGTTACCC
CAGCCTCTATTGGGAAGTGGAGCAATCCACGACTGGATTATCGGCCACAGTCCCGGCTAGGACGTGGCTTAAATTACA
GCCAGAGGGATCACCACCAGGAGTGTACCTGAATCCAGATCCGAGTGCATAGCACTTGAAGAACGGATCGTCCTT
TAATCCTTTAATCCTTTTTTAAAGGCTAAAAATT
TTGGTTGAGGCTAACAATT

TTGGTTGAGGCTAACAAATT
TTGGTTGAGGCTAAAAAATT
TTGGTTGAGGCTAAAAAATT
TTGGTTGAGGCTAACAAATT
TTGGTTGAGGCTCTCGATG
TTGGTTGAGGCTCTCGATG
TTGGTTGAGGCTTTAATT
TTGGTTGAGGCTCTCAGGAATTT
TTGGTTGAGGCTCTTAGGATT
TTGGTTGAGGCTCTCGTT
TTGGTTGAGGCTCAGGATT
TTGGTTGAGGCTCTAGATT

Nr of selected repeats 19 Similarity 0.809582

Consensus :

TTGGTTGAGGCTaacaATt

>Cele-UNSB01_4:129890-130903 Satlength=1014 Nr of Repeats=21 RepeatLength=22
seed=TTGGTTGAGG

TTGGTTGAGGCTCAGGATTTTGTAGTGAGGCTAGGGCGAGTTCTTGTAAAAATTCTATGAAGCCGCGAAAAAATTCGGT
CACGAACCTGAAACATGACAAAAGCGTATGCGGCGTCCGTATTGATTGGCGTCTTTATATCGACTTCTTCCACTTTCCC
GTGCTCCTCAAAAACGTGACGAATCTCTCGTTCCTTACATCCGACGGCATATTTCCGACGAAAAGCGTCCCTCGTCGCC
TCGTCGTCGTCCTGTTTTAGCCGCCACGTGGATGGTTCCTTAGTCGGGCGGCCCGATTCCCGCTTCCACTTCCGCCTT
CTCGTTTTACTGTGCGCTCCGTGTTGAGCTCGATTAATCGATCCGGAATGTATTTGCCCTCCTGATCACGTAGAATTCC
AGCTGGATCACATTGAACACGCTTGCCGAGCACTGATTTTAGACGGTCCATTAAGGTGTATCTGACCTTCCGAGCACAA
TCATTTCTCTCGAAATTCACGTAGGCTAGGCGTTCGTCTTCTTCCGGGTTTTTGACCACTTTTATCTGAAAAAATTGGT
ATAAAATTGCGGAAATCTCAGGATTTT

TTGGTTGAGGCTCAGGATTTT
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TTGGTTGAGGCTCTCAGGATTT
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TTGGTTGAGGCTCTCAGGATTT
TTGGTTGAGGCTTTCTGGATTT
TTGGTTGAGGCTCTCTGGATTT
TTGGTTGAGGCTCAGGATTT
TTGGTTGAGGCTTTCTGGATTT
TTGGTTGAGGCTCTCTGGATTT
TTGGTTGAGGCTCTCAGGATTT
TTGGTTGAGGCTTTCTGGATTT
TTGGTTGAGGCTCTCTGGATTT
TTGGTTGAGGCTCAGGATTT

Nr of selected repeats 16 Similarity 0.915152

Consensus :

TTGGTTGAGGCTcTCTGGATTT

>Cele-UNSB01_4:160082-160208 Satlength=127 Nr of Repeats=8 RepeatLength=14
seed=CCTAAGCCTA

CCTAAGCCTAAAGCCCTAAGCACAAAGGT
CCTAAGCCTAAGGT
CCTAAGCCTAAGGC
CCTAAGCCTAATGC

CCTAGGCCTAAGGC
CCTAAGCCTAAGGC
CCTAAGCCTAAGGC
CCTAAGCCTAAGGC

Nr of selected repeats 7 Similarity 0.918367

Consensus:

CCTAAGCCTAAGGC

>Cele-UNSB01_4:186112-186245 Satlength=134 Nr of Repeats=7 RepeatLength=19

seed=CCTCAACCAA

CCTCAACCAAAAATCTAGAG
CCTCAACCAAAAATTCTGAG
CCTCAACCAAAAATCGAGAG
CCTCAACCAAAAATCTAGAG
CCTCAACCAAAAATTCTGTG
CCTCAACCAAAAATCGAGAG
CCTCACCAAAAATTTTGAG

Nr of selected repeats 7 Similarity 0.826232

Consensus:

CCTCAACCAAAAATcnaGAG

>Cele-UNSB01_4:201016-202120 Satlength=1105 Nr of Repeats=53 RepeatLength=20

seed=CTCAACCAA

CTCAACCAAAAAATCATGGTAGC
CTCAACCAAAAAATCATGGTAGC
CTCAACCAAAAATTCGGGAGAGC
CTCACCAAAAAATCCAGAAAGC
CTCAACCAAAAAATCCTTAGC
CTCAACCAAAAAATCCTGAGC
CTCAACCAAAAAATCATGGTAGC
CTCAACCAAAAAATCCTGAAC
CTCAACCAAAAAATCCTGAAC
CTCAATCAAAAAATCCTGAGC
CTCAACCAAAAAATCATGGTAGC
CTCAACCAAAAAATCCTGAGC
CTCAATCAAAAAATCCTTAGC
CTCAACCAAAAAATCCTTAGC
CTCAACCAAAAAATCATGGTAGC
CTCAACGAAATATCCTGAGC
CTCAACCAAAAAATCCTGAGC
CTCAACCAAAAAATTCCTTAGC
CTCAACCAAAAAATCATGGTAGC
CTCAACCAAAAAATCCTGAGC
CTCAATCAAAAAATCCTGAGC
CTCAATCAAAAAATCATGGTAGC
CTCAACCAAAAAATCCTGAGC
CTCAATCAAAAAATCCTTAGC
CTCAACCAAAAAATCATGGTAGC
CTCAACGAAATATCCTGAGC
CTCAACCAAAAAATCCTGAGAGC
CTCAACCAAAAAATCCTGGTAGC
CTCAACCAAAAAATCCTGAGC
CTCAACCAAAAAATTCCTTAGC
CTCAACCAAAAAATCATGGTAGC
CTCAACCAAAAAATCCTGAGT
CTCAACCAAAAAATCCTGAGAGT

CTCAGCCTCAACCAAAAAATT
CTGAGCCTCAACCAAAAAATT
CTCAGCTTCAACCAAAAAATC

Nr of selected repeats 30 Similarity 0.934713

Consensus:

CTCAGCCTCAACCAAAAAATT

>Cele-UNSB01_4:236013-237239 Satlength=1227 Nr of Repeats=63 RepeatLength=18

seed=CTCAACCAAA

CTCAACCAAACTCTTAGT
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTCAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTCAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTCAGC
CTCACCCAAATTCTCAGC
CTCACCCAAATTCTCAGC
CTCAACCAAACTCTTAGT
CTCAACCAAACTCTTCAGCCTTACCCAAATTCTCAGC
CTCACCCAAATTCTCAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTCAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTAGC
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CTCAACCAAACTCTTCAGC
CTCACCCAAATTCTCAGC
CTCACCCAAATTCTCAGC
CTCAACCAAACTCTTAGT
CTCAACCAAACTCTTCAGC
CTCACCCAAATTCTCAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTCAGC
CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTAGC
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CTCAACCAAACTCTTAGC
CTCAACCAAACTCTTCAGC

CTCAACCAAACCTCTTAGC
CTCAACCAAACCTCTTAGC
CTCAACCAAACCTCTTCAGC
CTCACCCAAATTCTCAGC
CTCACCCAAATTCTCAGC
CTCAACCAAACCTCTTAGT
CTCAACCAAACCTCTTCAGCCTTACCCAAAATCTCAGC
CTCAACCAAACCTCTTTAGC
CTCAACCAAATTCTCAGC
CTCAGCCAAACCTCTTCAGCCTCACCTAACTCTTAGC
CTCAACCAAATTCTTCAGT
CTCAACCAAATTCTCAGC
CTCACCCAAATTCTCAGC
CTCAACCAAACCTCTTCAGC
CTCAACCAAACCTCTTAGC
CTCAACCAAACCTCTTAGC
CTCAACCAAATTCTCAGCCTCACCTAACTCTTCAGC

Nr of selected repeats 43 Similarity 0.898938

Consensus:

CTCAaCCAAAcTCTtAGC

>Cele-UNSB01_4:242271-242555 Satlength=285 Nr of Repeats=12 RepeatLength=22
seed=TGAGGCTCTC

TGAGGCTCTCTAGATTTTTGGC
TGAGGCTCTCTAGATTTTTGGT
TGAGGCTCTCAGGATTTTTGGT
TGAGGCTCTCTTGATTTTTGAT
TGAGGCTCACTGGATTTTTGAT
TGAGGCTCTCTGGATTTTTGGGTGAGGCTCAGAATTTTCGGT
TGAGGCTCTCTTGATTTTTGGT
TGAGGCTCTCTGGATTTTTGAT
TGAGGCTCTCTGGATTTTTGGG
TGAGGCTCTCAGGATTTTTGGT
TGAGGCTCTCTGGATTTTTGGT
TGAGGCTCTCTGGATTTTTGGT

Nr of selected repeats 11 Similarity 0.886501

Consensus:

TGAGGCTCTCTgGATTTTTGgT

>Cele-UNSB01_4:244645-245490 Satlength=846 Nr of Repeats=8 RepeatLength=18
seed=AGCCTCAACC

AGCCTCAACCAAACCTCTTACAAGGAAAGGAAGTCAATCTATCTATGCTCCAGTGCATTTTTTCGCTGACTTCTATATCA
AGTAAATGGCCTCAAAAAGGGTTCTGAGAGATTAGAAATTGTTTTTGGGGTTTTTAGGGTCTAACAAACAATGTGGGA
GTTTTTTGGAAATTTTTATTTTTTTGAAAAAATCTGAAATTTTTTCGATCCATTGGACACCAAATTTTTGGTCAAAAA
TTTTTTTTTTTTGAAAAAATCCAAAACCTATTTTTTTGTATCCGGGCATGCAAAAAGCTACATATTTCTCGAATTGAGC
CTTTTTTACAATTTTTTACAATTTTTTACAAAGGGCCCGATTGCAGTTTTTAAAAGTTGAAGAAAAAATTTTCCACT
GAAAGAATCGAACACGAGACCTTTATTTTTATTATTCCAAGCGTTTACCATTCCGCCATCAACCGTTGTTTTTTATTGTT
TTCCATGTTTGTAACCATTTTATAATGATTGAAAATCATTTTTTTGTATAAGTAAAAATGAATAAGTACGAAATAGTATTG
AAAACCTAGGAGGGCGCAGAGAAAAATTTTCAGATGGCGATTTTCAGGGGTTTCAGAGTTGAGTTCCGCCGCTGAAATTTTT
GTGGTGATCTAGTCTAAACATAAGCTTTCAAATGACATACGTCTCAATTTAAAGTCCGATACTAGATTGACTTCCTTTC
CTTGTT

AGCCTCAACCAAACCTCTC
AGCCTCAACCAAATTCTT
AGCCTCAACCAAACGCTT
AGCCTCAACCAAATTCTT
AGCCTCAACCAAACCTCTT

AGCCTCAACCAAActCTT
AGCCTCACCCAAActCTTC
Nr of selected repeats 5 Similarity 0.925926
Consensus:
AGCCTCAACCAAActCTT
>Cele-UNSB01_4:286805-287284 Satlength=480 Nr of Repeats=13 RepeatLength=37
seed=TTGGCGGGAA
TTGGCGGGAATTCAAATTTCTGAGAAAATATT
TTGGCGGGAATTCAAAATTTAATTTTTGAAACATATT
TTGGCGGGAATTCAAAATTTAATTTTTCGAAAACATT
TTGGCGGGAATTTAAAATTTAATTTTTGAAAATATT
TTGGCGGGAATTCAAATTTAATTTTTGAAAATATT
TTGGCGGGAATTCAAATTTAATTTTTGAAAATATT
TTGGCGGGAATTTAAAAGTTTTAATTTTTGAAAATATT
TTGCCGGGAATTCAAATTTTATTTTTGAAAATATT
TTGGCGGGAATTTAAAATTTAATTTTTGAAAATATT
TTGCCGGGAATTCAAATTTTATTTTTGAAAATATT
TTGGCGGGAATTCAAATTTTATTTTTGAAAATATT
TTGGCGGGAATTCAAATTTAATTTTTGAAAATATT
TTGGCGGGAATTCAAATTTTATTTTTGAAAATATT
Nr of selected repeats 9 Similarity 0.933934
Consensus:
TTGgCGGGAATTCAAAtTTTaATTTTTGAAAATATT
>Cele-UNSB01_4:287372-287852 Satlength=481 Nr of Repeats=32 RepeatLength=15
seed=TCGTGGTGAG
TCGTGGTGAGAGCTT
TCGTGGAGAGACCCT
TCTTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGAGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGTTGTGAGACCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT

TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACGCA

Nr of selected repeats 32 Similarity 0.882258

Consensus:

TCGTGGTGAGACCCa

>Cele-UNSB01_4:355820-356311 Satlength=492 Nr of Repeats=11 RepeatLength=45
seed=GAAGGATCAG

GAAGGATCAGAACATCAGGAGGTACCCATGTGATCATTTCGGCTCT
GAAAGATCAGATCATCAGGCAGAGCCTCATGTTCTTTTGGAGCT
GAAGGATCAGACCATCAGGAGGTACCCCTTACGATCCTTCTTATCT
GAAGGATCAGATCATCAGAAGGTACCCATGTGATCCTTCGGATCG
GAAGGATCAGATCATCAGGCAGAGCCTCATGTTCTTTTAGAGCT
GAAGGATCAGAACATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGGATCAGACCATCAGGAGGTACCCGTACGATCCTTCTTATCT
GAAGGATCAGAACATCAGAAGGTACCCATGTGATCCTTCGGAGCT
GAAGGTTTCAAGATCAGGAAGAGCCTCGTGATCCTTTGGAGCT
GAAGTATCAGACCATCAGGAGGTACCCCTTACGATCCTTCTTATCT
GAAGGATCAGAACATCAGAAGGTACCCATGTGATCCTTCGGAGCT

Nr of selected repeats 7 Similarity 0.826455

Consensus:

GAAGGATCAGAnCATCAGgAGGTACCCaTgtGATCCTTCggAtCT

>Cele-UNSB01_4:388221-388493 Satlength=273 Nr of Repeats=8 RepeatLength=34
seed=TTGCAGGAAA

TTGCAGGAAATTTCAATTACCGCAATTTGCCGGT
TTGCAGGAAATTTCAATTCAGCCGATTTGCCGGT
TTGCCGAAATTTCAATTCGGCAATTTGCCGGT
TTGCAGGAAATTTCAATTACGGCAATTTGCCGGT
TTGCAGGAAATTTCAATTCGCCAATTCGCCGGT
TTGCAGGAAATTTTAATTACGGAAATTTGTCCGGT
TTGCCGAAATTTCAATTCGGTCAATTTGCCAAC
TTGCAGGAAATTTCCATTCCGGCAATTTGCCGAT

Nr of selected repeats 8 Similarity 0.823529

Consensus:

TTGCaGGAAATTTCAATTCGgCAATTTGCCGgT

>Cele-UNSB01_4:391568-391630 Satlength=63 Nr of Repeats=4 RepeatLength=15
seed=TCCCCTTTTC

TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA
TCCCCTTTTTCGAGA
TCCCCTTTTCGTTCTGC

Nr of selected repeats 3 Similarity 0.762963

Consensus:

TCCCCTTTTcGcAga

>Cele-UNSB01_4:552425-552551 Satlength=127 Nr of Repeats=9 RepeatLength=12
seed=TAGGCTTAGG

TAGGCTTAGGTT
TAGGCTAAGGCT
TAGGGTTAGGCTGAGGCT
TAGTCTTAGGCC
TAGGTTTAGGCT
TAGGCTTAGGCT
TAGGCTTAAGCTCAGGTTTCAGACT
TAGGCTTAGGAT

TAGGATTAGGCT

Nr of selected repeats 7 Similarity 0.788360

Consensus:

TAGGcTTAGGcT

>Cele-UNSB01_4:600866-601084 Satlength=219 Nr of Repeats=10 RepeatLength=16

seed=AGGCATGTAG

AGGCATGTAGGCATGT

AGGCATGTAGGCATGT

AGGCATGTAGGCATGA

AGGCGTGTAGGCATGT

AGGCATGTAGGCATGT

AGCCATGTAGCAATGC

AGGCATGTAGCCATGT

AGGCACGTAGGCAGGT

ATGCATGTAGGCATGTAGACATTTTCATGTCATCAATTTAGGTTTCCAAGCTAAAACTCCTAAATCTTGGAAATGT

AGGCGTGTAGGCGTGC

Nr of selected repeats 9 Similarity 0.796296

Consensus:

AGGCaGTAGgCATGt

>Cele-UNSB01_4:634851-634943 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTTCGAGA

TCCCCTTTTCGTTCTGC

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTcGtagc

>Cele-UNSB01_4:646705-646786 Satlength=82 Nr of Repeats=4 RepeatLength=15

seed=TAAGCCTAAG

TAAGCCTAAGCCCAC

TAAGCCTAAGCCCAC

TAAGCCTAAGCCCAC

TAAGCCTAAGCCCCTTAGGCTAAGCCCATTAAGCC

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TAAGCCTAAGCCCAC

>Cele-UNSB01_4:695215-705007 Satlength=9793 Nr of Repeats=96 RepeatLength=102

seed=TGATATGTCG

TGATATGTCGAACGATTGATAGTTTGGGAATCAAGAGAATCAGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG

CATATCTTTCTCCAGTACCACCT

TGATATGTCGAACGATTGATAGTTTGGGAATCAAGAGAATCAGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG

CATATCTTTCTCCAGTACCACCT

TGATATGTCGAACGATTGATAGTTTGGGAATCAAGAGAATCAGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG

CATATCTTTCTCCAGTACCACCT

TGATATGTCGAACGATTGATAGTTTGGGAATCAAGAGAATCAGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG

CATATCTTTCTCCAGTACCACCT

TGATATGTCGAACGATTGATAGTTTGGGAATCAAGAGAATCAGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG

CATATCTTTCTCCAGTACCACCT

TGATATGTCGAACGATTGATAGTTTGGGAATCAAGAGAATCAGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG

CATATCTTTCTCCAGTACCACCT

TGATATGTCTGAACGATTGATAGTTTGGGAATCAAGAGAATCTGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG
CATATCTTTCTCCAGTACTTCCC
TGATATGTCTGAACGATTGATAGTTTGGGAATCAAGAGAATCAGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG
CATATCTTTCTCCAGTACCACCT
TGATATGTCTGAACGATTGATAGTTTGGGAATCAAGAGAATCTGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG
CATATCTTTCTCCAGTACCACCT

Nr of selected repeats 96 Similarity 0.972641

Consensus:

TGATATGTCTGAACGATTGATAGTTTGGGAATCAAGAGAATCTGTTGGACGATCAATTCATCTTTGGGTCTTGCTGCAG
CATATCTTTCTCCAGTACCACCT

>Cele-UNSB01_4:782171-782295 Satlength=125 Nr of Repeats=4 RepeatLength=31
seed=CAAAAATCGG

CAAAAATCGGGAAATTTTCACAAAAAATGT
CAAAAATCGGGAAATTTTCACAAAAAATGT
CAAAAATCGGGAAATTTTCACAAAAAATGC
CAAAAATCGGGAAATTTTCACAAAAAATGC

Nr of selected repeats 4 Similarity 0.949821

Consensus:

CAAAAATCGGGAAATTTTCACAAAAAATGc

>Cele-UNSB01_4:984710-985413 Satlength=704 Nr of Repeats=35 RepeatLength=19
seed=CAATAATTTTC

CAATAATTTTCCAAAAAAT
CAATAATTTTCATAAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCATTAATAAAAAAAT
CAATAATTTTCATAAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCATTAATAAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCATAAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCATAAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCCAAAAAAT
CAATAATTTTCCAAAAAAT
CGATAATTTCCGAAAAAAT
CAATAATTTTCCAAAAAAT

CATTAATTTTCATTTAAAAAAAT
CAATAATTTCCCAAAAAAT
CAATAATTTCCAAAAACAT
CAATAATTTCCAAAAACAT
CGATAATTTCCGAAAAAAAT
CAATAATTTCCATAAAAAAT
CAATAATTTCCCAAAAAAT
CATTAATTTTCATTTTAAAAAAAT
CAATAATTTCCCAAAAAAT
CAATAATTTCCCAAAAAATTTATTAATTTTCATTTAAAAAAAT
CAATAATTTCCCAAAAAAT
CAATAATTTCCCAAAAAAT
CAATAATTTCCCAAAAAAT
CAATAATTTCCCAAAAAAT

Nr of selected repeats 27 Similarity 0.905233

Consensus:

CAATAATTTCCcAAAAAAAT

>Cele-UNSB01_4:1076311-1076365 Satlength=55 Nr of Repeats=4 RepeatLength=12
seed=AGCCTAAGCC

AGCCTAAGCCTA
AGCCTAAGCCTA
AGCCTAATCCTT
AGACTAAGCCTAAGCCTG

Nr of selected repeats 3 Similarity 0.851852

Consensus:

AGCCTAAGCCTa

>Cele-UNSB01_4:1078257-1078305 Satlength=49 Nr of Repeats=4 RepeatLength=12
seed=AGGCTTAGGC

AGGCTTAGGCTT
AGGCTTAGGCTT
AGGCTTAGGCTT
AGGCATAGGCTC

Nr of selected repeats 4 Similarity 0.888889

Consensus:

AGGCTTAGGCTt

>Cele-UNSB01_4:1160688-1160967 Satlength=280 Nr of Repeats=7 RepeatLength=40
seed=ATTTTCTAG

ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACAATCCAGACTTTTCCCA
ATTTCTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTCG
ATTTTTCTAGAAAGTTCTGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAGAGTTCTGGAACATTCCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATCCAGACTTTTCCCA

Nr of selected repeats 6 Similarity 0.911111

Consensus:

ATTTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCA

>Cele-UNSB01_4:1160589-1161121 Satlength=533 Nr of Repeats=4 RepeatLength=35
seed=AAAATATTTT

AAAATATTTTTGAACCAGCCGCTGACCGCGCCTACGGCGCGGGCAACGACTGGCACCATTAAAAGTATTTGACACACAT
ACACTTTTCTAGAAAGTTCTCGAATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTCTAGAAAGTTCTG
GAACATTTTCTAGAAAGTTCTGGAACAATCCAGACTTTTCCCAATTTTCTAGAAAGTTCT
GGAACATTCCAGAAATTTTCTCGAATTTTCTAGAAAGTTCTGAACATTCCAGACTTTTCCCAATTTTTCTAGAGAGTTCT

GGAACATTCCAGACTTTTTCCCAATTTTTCTAGAAAGTTCTGGAACATCCCAGACTTTTTCCCAATTTTTCTAGAAAGTTC
TGGAACATTCCAGACTTTTTTCAGATTTTTCC

AAAATATTTTTTTCACAGAAAATTTAAATTTCCCTCC
AAAATATTTTTTTTCGGAAAATTTAAATTTCCCTCC
AAAATATTTTTTTTCAGAAAATTTAAATTTCCCGCC

Nr of selected repeats 3 Similarity 0.898413

Consensus:

AAAATATTTTTtCaGAAAATTTAAATTTCCCTcCC

>Cele-UNSB01_4:1161180-1161420 Satlength=241 Nr of Repeats=16 RepeatLength=15

seed=GGTCTCACCA

GGTCTCACCACGACA

GGTCTCACCACGATG

GGTCTCACCACGATG

GGTCTCACCACGACA

GGTCTCACCACGGTG

GGTATCACCACGACG

GGTCTCACCACGATG

GGTCTCACCACGATG

GGTCTCACCACGATG

GGTCTCACCACGATG

GGTCTCACCACGATG

GGTCTCACCACGATG

GGTCTCACCACGATG

GGTTTCACCACGACG

GGTCTCACCACGGTG

GGTCTCGCCACGATG

GGTCTCACCACGATG

GGTCTCGCCACGATG

Nr of selected repeats 16 Similarity 0.880741

Consensus:

GGTCTCACCACGAtG

>Cele-UNSB01_4:1160701-1161595 Satlength=895 Nr of Repeats=10 RepeatLength=40

seed=GTTCTGGAAC

GTTCTGGAACATTCCAGACTTTTTCCCAATTTTTCTAGAAA

GTTCTGGAACATTTCCAGACTTTTTCCCAATTTTTCTAGAAA

GTTCTGGAACAATCCAGACTTTTTCCCAATTTCTCTAGAAA

GTTCTGGAACATTCCAGAATTTCTCGATTTTTCTAGAAA

GTTCTGGAACATTCCAGACTTTTTCCCAATTTTTCTAGAGA

GTTCTGGAACATTTCCAGACTTTTTCCCAATTTTTCTAGAAA

GTTCTGGAACATCCCAGACTTTTTCCCAATTTTTCTAGAAA

GTTCTGGAACATTCCAGACTTTTTCCAGATTTTCCAAAATTTTTTTCACAGAAAATTTAAATTTCCCTCCAAAATATT

TTTTTTCGGAAAATTTAAATTTCCCTCCAAAATATTTTTTTTCAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCACAGA

AAATTTAAATTTCCCGCCAAAATTTTGGGTCTTACCACGGTGGGTCTCACCACGACAGGTCTCACCACGATGGGTCTCA

CCACGATGGGTCTCACCACGACAGGTCTCACCACGGTGGGTATCACCACGACGGGTCTCACCACGATGGGTCTCACCAC

GATGGGTCTCACCACGATGGGTCTCACCACGATGGGTCTCACCACGATGGGTCTCACCACGACGGGTCTCACCACGGTG

GGTCTCGCCACGATGGGTCTCACCACGATGGGTCTCGCCACGATGGGTCTCACCACGATGGGTCTCGCCACGAAGATCT

CGCAGCAACATTTTTTTAAATTTTCCAGAAG

GTTCTAGAACAATCCAGAATTTTTTCGAATTTTCCAGAAGTTCTAAAGCTTTTCAGAATTTTCCAGAAG

GTTCTGTAAACATTCTAGAATTTTCCAGAAATTTCCAGAAG

Nr of selected repeats 7 Similarity 0.844444

Consensus:

GTTCTGGAACATTCCAGAcTTTTCCCaATTTTTCTAGAAA

>Cele-UNSB01_4:1161685-1161942 Satlength=258 Nr of Repeats=8 RepeatLength=11

seed=GTACTCCTAC

GTACTCCTACAGTACCTCTACA

ATTTCCCGCCAAAATTTTTTCACTGAAAATTTGA
ATTTCCCGCCAAAATTTTTTCACTGAAAATTTGA
ATTTCCCGCCAAAATTTTTTCACTGAAAATTTGA
ATTTCCCGCCAAAATTTTTTCACTGAAAATTTGA
ATTTCCCGCCAAAATTTTTTCACTGAAAATTTGA
ATTTCCCGCCAAAATTTTTTCACTGAAAATTTAA
ATTTCCCTCCAAAATTTTTTCTCAGAAAATTTGA
ATTTCCCGCCAAAATTTTTTCTCAGAAAATTTAA
ATTTCCCGCCAAAATTTTTTCTCAGAAAATTTAA
Nr of selected repeats 18 Similarity 0.995643
Consensus:

ATTTCCCGCCAAAATTTTTTCACTGAAAATTTGA
>Cele-UNSB01_4:1359612-1359777 Satlength=166 Nr of Repeats=11 RepeatLength=15
seed=CCACGATGGG
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTTT
CCACGATGGGTCTCA
CCACGGTGGGTCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTTT
CCACGATGGGTCTCA
CCACGGTGGGTCTCG
Nr of selected repeats 11 Similarity 0.880404
Consensus:

CCACGATGGGTCTCn
>Cele-UNSB01_4:1362949-1363282 Satlength=334 Nr of Repeats=9 RepeatLength=34
seed=ATTGCCGGA
ATTGCCGGAATTGAAATTTCTGGCGA
ATTGCCGGAATTGAAATTTCCGGCAAATTGGCATATTGCTGGTTTTGAAAATTTCTAGCAAATCGACAA
ATTGCCGGAATTCAAATTCCTAGCAAATCGGCAA
ATTGCCGGAATTGAAATTTCTGGCAAATTGGCAA
ATTGCCGGAATCGAAATTTCTGGCAAATTGACAA
ATTGCCGGAATTGTAATTTCTGGCAAATTGGCAA
ATTGCCGGAATTGAAATTTCTGGCAAATCGACAT
ATTGCCGGAATTAAAATTTCTGGCAAATTGGCAA
ATTGCCGGAATTGAAATTTCTGGCAAATTGGCAA
Nr of selected repeats 7 Similarity 0.886088
Consensus:

ATTGCCGGAATTgAAATTTCTGGCAAAtGgCAA
>Cele-UNSB01_4:1370044-1370460 Satlength=417 Nr of Repeats=8 RepeatLength=12
seed=TAGGCTTAGG
TAGGCTTAGGCT
TAGGCTTAGGCG
TAGACTTAGGTT
TAGGCTTAGGTTTAGGCTTATTTTTGGGCTTATGCTTATTCT
TAGGCTTAGGCT
TAGGCTTAGGCTTAGGCTTACTTTTTTAAAAA
TAGGCTTAGGCTTGGCGTCAGTGGCGAGCGTTAGATGCTTTTTGTGCTATTACGATAATCCAGAAATAAATAATTCGGT
CATGAATTTTTTGCTTCTCAAAATCTCGAAAATTTGAATTATGAATATTTTTTAAAGTGCTCAACTGTTAC
TATGCAAAAATATGACATTTAATTCCAATTTTACATAAACATGTGCGAGTTTGAACATCTAAGTACCATTTAATATTT
TTTTCTAGTTAATTGGGCTTTTGGAGCTTGTAAAAAATATATT

TAGGCTTAGTCT

Nr of selected repeats 5 Similarity 0.822222

Consensus:

TAGgCTTAGgct

>Cele-UNSB01_4:1429332-1429629 Satlength=298 Nr of Repeats=15 RepeatLength=21

seed=AAAATTGACT

AAAATTGACTAAAATCGTCA

AAAATTGACTAGAATCGTCA

AAAATCGACTAAAAATCGTCA

AAAATTGACTAGAATCGTCA

AAAATCGACTAAAATCGTCA

AAATTTGACTAAAAATCGTCA

AAAATTGACTAAAAATCGTCA

AAAATTGACTAAAAAACGTCA

AAAATTGACTAAAAAACGTCA

AAAATTGACTAAAAATCGTTA

AAAATTGACTAAAAATCGTTA

AAAATTGACTAAAAATCGTTA

AAAATTGACTAAAAATCGTTA

AAAATTGACTCAAAAA

AAAATTGACTT

Nr of selected repeats 10 Similarity 0.908289

Consensus:

AAAATtGACTAAAAAtCGTcA

>Cele-UNSB01_4:1444044-1444098 Satlength=55 Nr of Repeats=4 RepeatLength=12

seed=CATAGGCATA

CATAGGCATAGG

CATAGGCATAGA

CATAGGCATAGG

CATAGGCATAGGCATAGG

Nr of selected repeats 3 Similarity 0.925926

Consensus:

CATAGGCATAGg

>Cele-UNSB01_4:1452742-1452796 Satlength=55 Nr of Repeats=4 RepeatLength=12

seed=TATATGTATA

TATATGTATATG

TATATGTATATG

TATATGTATATG

TATATGTATATGTATATG

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TATATGTATATG

>Cele-UNSB01_4:1454445-1454610 Satlength=166 Nr of Repeats=11 RepeatLength=15

seed=AGACCCATCG

AGACCCATCGTGAAA

AGACCCATCGTGGTG

AGACCCATCGTGGCG

AGACCCACCGTGGTG

AGACCCATCGTGGAA

AGACCCATCGTGGTG

AGACCCATCGTGGCG

AGACCCATCGTGGCG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

Nr of selected repeats 11 Similarity 0.880404

Consensus:

AGACCCATCGTGGtG

>Cele-UNSB01_4:1461281-1461373 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGTATC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGA

TCCCCTTTTCGCTCTGC

Nr of selected repeats 5 Similarity 0.840000

Consensus:

TCCCCTTTTCGtatac

>Cele-UNSB01_4:1490085-1491772 Satlength=1688 Nr of Repeats=46 RepeatLength=35

seed=AAAAAATTTT

AAAAAATTTTGTGTTGAAAAGTTAAAAAATATATATCCTTACCAGCCGATGACCGCGCCTCTGGCGCGGCCAACGACT

GGCGGAGTTTAAAATGTATAACAAATAGATGTCCTTAA

AAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGA

AAAAAATTTTAGCGGGAAATTCAAATTTTCAGTGA

AAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGA

AAAAAATTTTAGCGGGAAATTCAAATTTTCAGTGA

AAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGA

AAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGA

AAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGA

AAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGA

AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTG
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTG
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
Nr of selected repeats 30 Similarity 0.963442
Consensus:

AAAAAATTTTTGGCGGGAAATTCAAATTTTCAGTGA
>Cele-UNSB01_4:1491894-1492067 Satlength=174 Nr of Repeats=5 RepeatLength=35
seed=GAAAATTTGA
GAAAATTTGAATTTCCCGCCAATATTTCTTCATA
GAAAATTTGAATTTCCCGCCAAAATTTTTTTTCACT
GAAAATTTGAATTTCCCGCCAAAATTTTTTTTCACT
GAAAATTTGAATTTCCCGCTAAAATTTTTTTTACT
GAAAATTTGAATTTCCCGCTAAAATTTTTTTTACT
Nr of selected repeats 3 Similarity 0.949206
Consensus:

GAAAATTTGAATTTCCCGCcAAAATTTTTTTtCACT
>Cele-UNSB01_4:1492099-1492204 Satlength=106 Nr of Repeats=7 RepeatLength=15
seed=CTCACCACGA
CTCACCACGAAGGGG
CTCACCACGATGGGT
CTCACCACGAAGGGT
CTCACCACGATGAGT
CTCACCACGAAGGGT
CTCACCACGAAAGGT
CTCACCACGATGGGT
Nr of selected repeats 7 Similarity 0.873016
Consensus:

CTCACCACGAaGGGT
>Cele-UNSB01_4:1508767-1509123 Satlength=357 Nr of Repeats=5 RepeatLength=12
seed=AGGCTTAGGC
AGGCTTAGGCCTA
AGGCTTAGGCCTAATAAAAAAATCCGAATTTAATTTTTATTTTGCGAATTTTTTCATCCCAGAAAAACTGACTTTTTTCAG
GGGAAAAATCTCAGAAATTCCTGTGATTTTAGCAAAAAATCAGGTAATTTTGAGGGAAAAATTTGAATTTTTCAAAAAT
TTCCGGTAAGAAGTGCACATAATTTGTGATTTTTAAACAAATTTTGGATCAAAAAATCAACTTTTTTTGGGAAAAATTTTCA
AAAATCTGCCAATTTTGCTGAAAAAAAAGTAAAATTTTACGACTTTTTTTCCGAGAAGTTTTGGCAATTTG
AGGCTTAGGCCT
AGGCGTAGGCGT
AGGCTTAAGCTT
Nr of selected repeats 4 Similarity 0.740741
Consensus:

AGGctTAgGctt
>Cele-UNSB01_4:1530750-1530982 Satlength=233 Nr of Repeats=8 RepeatLength=29
seed=CCACCCGGGA
CCACCCGGGAGATGTCGGCTGTTCTAAAT
CCACCCGGGAGGCGTCGGCTGCTCTAAGC
CCACCCGGGAGTTGTCGGCTGCTCTATGC
CCACCCGGGAGATGTCGGCTGTTCTAAAT

CCACCCGGGAGGCGTCCGGCTGCTCTTAAAC
CCACCCGGGAGATGTCGGTTGTTCTAAAC
CCACCCGGGAGGTGTCGGCTGCTCTAAAC
CCACCCGGGAGGTGTCGGCTGCTCTAAAC

Nr of selected repeats 8 Similarity 0.850575

Consensus:

CCACCCGGGAGgtGTCGGCTGcTCTAAac

>Cele-UNSB01_4:1558589-1558964 Satlength=376 Nr of Repeats=4 RepeatLength=94

seed=TCCCATTGAT

TCCCATTGATTTGTCTACAAAGGCATCGAAAAGCACCCAATATTTGGAGAACAGAAGATTTTGAGAATTACTGCCTTC
AGAAATGGACAATTT

TCCCATTGATTTGTCTACATAGGGCATTGAAAAGCACCCAATATTTAGAGAACAGAAGATTTTGAGAATTACTGCCTTC
AGAAATTGATGATTT

TCCCATTGATTTGTCTGCAAAGAGCATCGAAAAGCACCCAATATTTAGAGAACAGAAGATTTTGAGAATTACTGCCTTC
AGAAATGGACAATTT

TCCCATTGATTTGTCTACATAGGGCATTGAAAAGCACCCAATATTTAGAGAACAGAAGATTTTGAGAATTACTGCCTTC
AGAATTGATGATTT

Nr of selected repeats 3 Similarity 0.924350

Consensus:

TCCCATTGATTTGTCTaCAaAGgGCATcGAAAAGCACCCAATATTTaGAGAACAGAAGATTTTGAGAATTACTGCCTTC
AGAAATgGACAATTT

>Cele-UNSB01_4:1580035-1580182 Satlength=148 Nr of Repeats=7 RepeatLength=21

seed=CCATAGGTGG

CCATAGGTGGAAGATCTCATG

CCATAGGTGGATGATCAGATA

CCATAGGTGGAAGATCAGATA

CCAAAGGTGGAAGCTCTTATA

CCATAGGTGGAAGCTTTTATA

CCATAGGTGGATGATCTCATA

CCATAGGTGGATGATCAGATA

Nr of selected repeats 7 Similarity 0.794407

Consensus:

CCATAGGTGGAaGaTCtnATA

>Cele-UNSB01_4:1584655-1585480 Satlength=826 Nr of Repeats=7 RepeatLength=101

seed=TTGATTTTTTC

TTGATTTTTTCGGGGGGCACTTTTGCTATCATTACTTATATATAAAAAATACTGTCCGTCTGTCCATAGTGTGTAGTCTA
CGTAGTCTTTGTAGTGTACAAAGTTTTGGCTTATGAAGGAATATTGGTTTTCGGGTTAGTGGCGGATATGGTCGGGGTA
CTGTAGGTATACGGTAGGGTACTGTAGTTTTTCGAAAAA

TTGATTTTTTCGTCTTTTGAAGGATATTGGTTTTCGGGGTAGTGGCGGATATGGTCGGGGTACTGTAGGTATACGGTAG
GGTTACTGTAGTTTTGGAAAATT

TTGATTTTTTCGTCTTATGAAGGAATATTGGTTTTCGGGGTAGTGGCGGATATGGTCGGGGTATTGTAGGTATACGGTAG
GGTTACTGTAGTTTTGGAAAATT

TTGATTTTTTCGTCTTATGAAGGAATATTGGTTTTCGGGTTAGTGGGGGGATATGGTAGGGGTACTGTAGGTATACGGTAG
GGTTACTGTAGTTTTGGAAAATT

TTGATTTTTTCGTCTTATGAAGGAATATTGGTTTTCGGGGTAGTGGCGGATATGGTCGGGGTATTGTAGGTATACGGTAG
GGTTACTGTAGTTTTGGAAAATT

TTGATTTTTTCGTCTTATGAAGGAATATTGGTTTTCGGGTTAGTGGGGGGATATGGTAGGGGTACTGTAGGTATACGGTAG
GGTTACTGTAGTTTTGGAAAAAT

TTGATTTTTTCGTCTTTTGAAGGGATATTGGTTTTCGGGTTAGTGGCGGATATGGTCGGGGTACTGTAGTAGTACTGTAA
GGGTACTGTAGGTATACGGTAGGGTACTGTAGTTTTGGAAAATT

Nr of selected repeats 5 Similarity 0.952475

Consensus:

TTGATTTTTTCGTCTTaTGAAGGaATATTGGTTTTCGGGgTAGTGGGcGGATATGGTcGGGGTAcTGTAGGTATACGGTAG
GGTTACTGTAGTTTTGGAAAAT

>Cele-UNSB01_4:1639262-1639353 Satlength=92 Nr of Repeats=6 RepeatLength=14
seed=ACTACACACT

ACTACACACTACAC
ACTACACACTACAC
ACTACACACTACAC
ACTACACACTACAC
ACTACACACTACAC
ACTACACACTACAC
ACTACACACTACAACTACAC

Nr of selected repeats 5 Similarity 1.000000

Consensus:

ACTACACACTACAC

>Cele-UNSB01_4:1643155-1643244 Satlength=90 Nr of Repeats=6 RepeatLength=12
seed=TTAGGCTTAG

TTAGGCTTAGCATTAGGATCAGTC
TTAGGCTTCGGC
TTAGGCTTAAGCTGGGC
TTAGGCTTAGGC
TTAGGCTTAGGC
TTAGGCTTAGGC
TTAGGTTTAGGC

Nr of selected repeats 4 Similarity 0.888889

Consensus:

TTAGGcTTaGGC

>Cele-UNSB01_4:1647487-1647595 Satlength=109 Nr of Repeats=9 RepeatLength=12
seed=CTTAAGCTTA

CTTAAGCTTAGA
CTTAAGCTTAGG
CTTAAGCTTAGG
CTTAAGCTTAGG
CTTAAGCTTAGG
CTTAAGCTTAGG
CTTAAGCTTAGG
CTTAAGCTTAGG
CTTAAGCTTAGG
CTTAAGCTTAGG

Nr of selected repeats 9 Similarity 0.975309

Consensus:

CTTAAGCTTAGG

>Cele-UNSB01_4:1654144-1654247 Satlength=104 Nr of Repeats=5 RepeatLength=23
seed=ATTTAATTAA

ATTTAATTAATATTT
ATTTATTTAATTAATATGT
ATTTATTTAATTAATTAATATTT
ATTTATTTAATTAATATTTATTC
ATTTAATTAATAATTATTTATTT

Nr of selected repeats 3 Similarity 0.729469

Consensus:

ATTTAtTTAATtAaTattTATTt

>Cele-UNSB01_4:1669669-1669879 Satlength=211 Nr of Repeats=6 RepeatLength=35
seed=ATTTCCGGCA

ATTTCCGGCAAATCGGCAATACGCCGTA AATTTAAA
ATTTCCGGCAAATCGGCAATATGCCAAAAATGGAT
ATTTCCGGCAAATCGGCGATTTGCCGAAAATGGCA
ATTTCCGGCAAGTCGGCAATATGCCGAAAATAAAC
ATTTCCGGCAAATCGGCAATACGCCGTA AATTTAAA
ATTTCCGGCAAATCGGCAATATGCCGAAAATGAAC

Nr of selected repeats 6 Similarity 0.819683

Consensus:

ATTTCCGGCAAATCGGCAATAtGCCGaAAATgaAa

>Cele-UNSB01_4:1695920-1696142 Satlength=223 Nr of Repeats=6 RepeatLength=37
seed=CGCCAAAATG

CGCCAAAATGTTTTCAAAAAATTAAATTTTGAATTCC
CGCCAAAATGATTCCAAAAATTAAATTTTGAATTCC
CGCCAAAATGTTTTCAAAAAATTAAATTTTGAATTCT
CGCCAAAATGTTTTCAAAAAATTAAATTTTGAATTCC
CGCCAAAATGTTTTCAAAAAATTAAATTTTGAATTCC
CGCCAAAATGTTTTCAAAAAATTAAATTTTGAATTCC
CGCCAAAATGTTTTCAAAAAATTAAATTTTGAATTCC

Nr of selected repeats 6 Similarity 0.894294

Consensus:

CGCCAAAATGTTTTCAAAAAATTAAaTTTGAATTCC

>Cele-UNSB01_4:1703835-1704045 Satlength=211 Nr of Repeats=11 RepeatLength=12
seed=CTAAGCCTAA

CTAAGCCTAAGCCTAATACTAAGTCTGAGCCTGCGC
CTAAGCATAAGCTTAAGCTTAAGT
CTAAGCCTAAGCCTCAACCTGTGCCTAAGCATTACC
CTAAGCCTAATA
CTAAGCCTAAGC
CTGAGCCTAAAC
CTAAGCCTAATA
CTAAGCCTAAGC
CTAAGCCTAAGCCTAAACCTCAACCTGTGT
CTAAGCATAAGC
CTAAGCCTGAGC

Nr of selected repeats 7 Similarity 0.777778

Consensus:

CTAAGCCTAAgc

>Cele-UNSB01_4:1729821-1729883 Satlength=63 Nr of Repeats=4 RepeatLength=15
seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGTTCTG
CGAAAAGGGGAGCAA

Nr of selected repeats 3 Similarity 0.703704

Consensus:

CgAAAAGGGGatCtg

>Cele-UNSB01_4:1755267-1755667 Satlength=401 Nr of Repeats=20 RepeatLength=20
seed=CAGAAAAATC

CAGAAAAATCAATAAATGCT
CAGAAAAATCAATAAATTCT
CAGAAAAATCAATAAATTCT
CAGAAAAATCAATAAATTCT
CAGAAAAATTCGATAAACTCT
CAGAAAAATCAATAAATTCT
CAGAAAAATCAATACATTCT
CAAAAAATTCGATAAACTCT
CAGAAAAATCAATAAATGCT
CAGAAAAATCAATAAATTCT
CAGAAAAATCAATAAATTCT
CAGAAAAATTCGATAAACTCT
CACAAAAATTCGATAAATTCT

CAGAAAATTCGATAAAGTCT
CAGAAAAGTCGATAATTTAT
CTGAAAAATCGATAAATTTT
CAGAAAAATCAATAAATTCC
CAGAAAAATCGATAAATTCC
CAGAAAAATGAATAAATTCT
CAGAAAAATCGATAAATTCC

Nr of selected repeats 20 Similarity 0.835088

Consensus:

CAGAAAaTCaATAAaTCT

>Cele-UNSB01_4:1766949-1767039 Satlength=91 Nr of Repeats=5 RepeatLength=12

seed=TAAGCCTAAG

TAAGCCTAAGCC

TAAGCCTAAGAC

TAAGCTTAAGCC

TAAGACTAAGGC

TAAGCCTAAACCTAAACCCAATCCAAAGCCTATGTTTAAGCC

Nr of selected repeats 4 Similarity 0.796296

Consensus:

TAAGccTAAGcC

>Cele-UNSB01_4:1777357-1777453 Satlength=97 Nr of Repeats=5 RepeatLength=16

seed=CACGTAGGCA

CACGTAGGCACGTAGG

CACGTAAGCACGTAGG

CACGTAGGCACGTAGG

CACGTAGGTACCCAGGCACCTATGCACATTGT

CACGTAGGCACTTAGG

Nr of selected repeats 4 Similarity 0.916667

Consensus:

CACGTAgGCACgTAGG

>Cele-UNSB01_4:1800043-1800133 Satlength=91 Nr of Repeats=7 RepeatLength=12

seed=TTAGGATTAG

TTAGGATTAGGA

TTAGGATTAGGA

TTATGATTAGGA

TTAGGATTAGGATTAGTC

TTAGGATTAGGA

TTAGGATTAGGA

TTAGGATTAGGA

Nr of selected repeats 6 Similarity 0.962963

Consensus:

TTAGGATTAGGA

>Cele-UNSB01_4:1802551-1803063 Satlength=513 Nr of Repeats=30 RepeatLength=16

seed=TAGGCACGTA

TAGGCACGTAGGCACGTAGATACC

TAGGCACGTAGTCGCCTAAGAACG

TAGGTACGTAGGCACG

TAGACACGTAGCTTCCAAGAAACC

TAGCCACGTAGGTACG

TAGGCACGTAGGCACG

TAGGTACGTAGGTACG

TAGGCACGTAGGCACG

TAGGTACGTAGGTACG

TAGGCACGTAGGCACG

TAGGCACGTAGGCACG

TAGGCACGTAGGCACG

Nr of selected repeats 3 Similarity 0.851852

Consensus:

TAAGcCTAAGCt

>Cele-UNSB01_4:1946817-1947132 Satlength=316 Nr of Repeats=8 RepeatLength=35
seed=GAAATTTTCA

GAAATTTTCAATTCCGGCAATTCGCCGATTTGACG
GAAATTTTCAATTTCAACGAATTACCGATTTGCCGAAAATGTCATTTTCAGCAAACCTGCCGATTTGCCG
GAAATTTTCAATTCCGGCAGTTTGCCGATTTGCCG
GAAATTTTCAATTCCGGCAATTTGCCGATTTGACG
GAAATTTTCAATTCCGGCAATTTGCCGATTTGCCG
GAAATTTTCAATTCCGGCAGTTTGCCGATTTGCCG
GAAATTTTCAATTCCGGCAATTTGCCAATTTGACG
GAAATTTTCAATTCCGGCAATCTGCCGATTTGACG

Nr of selected repeats 7 Similarity 0.927438

Consensus:

GAAATTTTCAATTCCGGCAaTTTGCCGATTTGaCG

>Cele-UNSB01_4:1949645-1950620 Satlength=976 Nr of Repeats=28 RepeatLength=35
seed=CATTTTCGCC

CATTTTCGCCGAATTGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGATTTGCCGAAAATTTT
CATTTTCGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGATTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTCTGAAAATTTTC
CATTTTCGCCGAATTGCCGATTTGCCGAAAATTTT
CATTTTCGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTCTGAAAATTTTC
CATTTTCGCCGAATTGCCGATTTGCCGAAAATTTT
CATTTTCGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGATTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGATTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGATTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTCTGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTCTGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTGCCGAAAATTTTC
CATTTTCGCCGAATTGCCGTTTCTGAAAATTTTC

Nr of selected repeats 22 Similarity 0.945083

Consensus:

CATTTTCGCCGAATTGCCGgTTTGCCGAAAATTTTC

>Cele-UNSB01_4:1966969-1971964 Satlength=4996 Nr of Repeats=213 RepeatLength=21
seed=GTAAATCTAC

GTAAATCTACAGTAATCCCTC
GTAAATCTACAAGAAACCCCC
GTAAATCTACAGTAATCCCTC

GTAAATCTACAGTAATCCCC
GTAAATCTACAGTAATACCCC
GTAAATTTACAGTAATACCCC
GTAAATCTACACAATGAGCCTCC
GTAAATCTACAGTAATACCTT
GTAAATCTACAGTAATCCATC
GTAAATCTACAATAAACCCCC
GTAAATCTACATAATGAGCCTCC
GTAAATCTACATTAACCTCC
GTAAATCTACAACATGCTTCC
GTAAATCTACACTAGTTCCCC
GTAAATCTACACAATCATCCCC
GTAAATCTACAATAAGCTCCC
GTAAATCTGCAGTAATACCCC
GTAAATTTACAGTAATACCCC
GTAAATCTACACAATGAGCCTCC
GTAAATCTACATTAACCCCC
GTAAATCTACAAAATGCTTCC
GTAAATCTTACAATCATCCCC
GTAAATCTACAATAAGCTCCC
GTAAATCTACAGTAATACCCC
GTAAATTTACAGTAATACCCC
GTAAATTTACAGTAATCCCC
GTAAATCTACACAAAATGCTTCC
GTAAATCTACAGTAATCCCTC
GTAAATCTACACAATGAGCCTCC
GTAAATCTACATTAACCCCC
GTAAAATCTACAAAATGCTTCC
GTAAATCTTACAATCATCCCC
GTAAATCTACAATAAGCTCCC
GTAAATCTACAGTAATACCCC
GTAAATTTACAGTAATACCCC
GTAAATTTACAGTAATCCCC
GTAAATCTACACAAAATGCTTCC
GTAAATCTACAGTAATCCCTC
GTAAATCTACACAATGAGCCTCC
GTAAATCTACATTAACCCCC
GTAAAATCTACAAAATGCTTCC
GTAAATCTTACAATCATCCCC

Nr of selected repeats 158 Similarity 0.856783

Consensus:

GTAAATCTACAGTAATnCCCC

>Cele-UNSB01_4:1985632-1987358 Satlength=1727 Nr of Repeats=15 RepeatLength=80
seed=AATTTCTCAA

AATTTCTCAATGGAGTGCATTTGCATCGGCGCGAAATTCGAATTTTCAGGCGAATTTACATAAAAAGTCCCGAAAATGC
ACAAAAAAGAGCATTTCTCGAATTTGGACATGATTACGGAGCTGCTAACGCCTAGTACAACACACCACCAACCACACGG
AAATCAACTTGTTCGAGGAAATGGACGATTCTGAAGACGATGATGAAGGTGATGGCTCGGAATTTCTAGTGGAACAGCAG
CCAGCAGCAGAGCCCCGAAGAGCCGAAAAGTGATGGAAAAATCGAAAAATTCGGCTATGGTTTCGGTTGGAGCAAGTTTG
GAGTTATTGAGAGGCTCAGAGATGAAATCGGCAAAATTTGTGGATATTTTGGAGCCCCGAAAATGTGGAAATTGAGAAAAG
AGCCGACAAAATTGATGGAATTCGATTGGGAAAACTTTGATGAAGGCAGATATTTGTAAGAAATCGAATTTCCCGCCAAA
AATCACTCAGAAATTGCGCTCCATTGAGTAAATGCGTGAAAAATAAAATTTCCGACATTTTTGTGTTCAGTAGAGCAC
AGTTGCAACGCAAAATTTGTTCATTTTTAAATTTGAAATCTCGAAAACTCGA
AATTTCTCAATAGCGCGCTTGCAACATCCGAACGGCGCGAAATTTGAGTTTTTGCCATAAAAATAACGAAAATCGGC
A
AATTTCTCAATAGGGCGCGCTTGCAACATTTAGTCAGCGCTAAATTTGAATTTTTGGCTATAAAAATAACAAAACTAAC
T
AATTTCTCAATAGGGCACGCTTGCAACATCTGAACGGCGCGAAATTTGAGTTTTTGCCATAAAAATAACGAAAATCGGC
A
AATTTCTCAATAGGGCGCGCTTGCAACATTTAGTCAGCGCTAAATTTGAATTTTTGGCTATAAAAATAACAAAACTAAC
T
AATTTCTCAATAGGGCACGCTTGCAACATCTGAACGGCGCGAAATTTGAATTTTTTGCCATAAAAATAACGAAAATCGGC
A
AATTTCTCAATAGGGCGCGCTTGCAACATTTAGTCAGCGCTAAATTTGAATTTTTGGCTATAAAAATAACAAAACTAAC
T
AATTTCTCAATAGGGCACGCTTGCAACATCTGAACGGCGCGAAATTTGAATTTTTTGCCATAAAAATAACGAAAATCGGC
A
AATTTCTCAATAGGGCGCGCTTGCAACATTTAGTCAGCGCTAAATTTGAATTTTTGGCTATAAAAATAACAAAACTAAC
T
AATTTCTCAATAGGGCACGCTTGCAACATCTGAACGGCGCGAAATTTGAATTTTTTGCCATAAAAATAACGAAAATCGGC
A
AATTTCTCAATAGGGCGCGCTTGCAACATTTAGTCAGCGCTAAATTTGAATTTTTGGCTATAAAAATAACAAAACTAAC
T
AATTTCTCAATAGGGCACGCTTGCAACATCTGAACGGCGCGAAATTTAAATTTTTGGTCATAAAAATAACGAAAATCGGC
A
AATTTCTCAATAGGGCACGCTTGCAACATCTGAACGGCGCGAAATTTAAATTTTTGGTCATAAAAATAACGAAAATCGGC
A
AATTTCTCAATAGGGCACGCTTGCAACATTTAGTCAGCGCTAAATTTGAATTTTTGGCTATAAAAATAACAAAACTAAC
T
AATTTCTCAATAGGGCACGCTTGCAACATCTGAACGGCGCGAAATTTAAATTTTTGGTCATAAAAATAACGAAAATCGGC
A
AATTTCTCAATAGGGCACGCTTGCAACATCTGAACGGCGCGAAATTTGAATTTTTTGCCATAAAAATAACGAAAATCGGC
A

Nr of selected repeats 14 Similarity 0.854212

Consensus:

AATTTCTCAATAGGGCGCGCTTGCAACATcTgaaCgGCGCgAAATTTGAATTTTTGGCcATAAAAATAACgAAAActaaC
t

>Cele-UNSB01_4:2119001-2119076 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGAT

GGGTCTCGCCACGAT

GGGTCTCACCACGAC

GGGTCTCACCCTGT

GGGTCTCGCCACGAT

Nr of selected repeats 5 Similarity 0.840000

Consensus:

GGGTCTCaCCACgat

>Cele-UNSB01_4:2158460-2158710 Satlength=251 Nr of Repeats=6 RepeatLength=40

seed=TTCCAGAATT

TTCCAGAATTTTCACGAATTTTCTCGAATTTTCCAGAAGGTTCTAGAACA

TTCCAGAATTTTCTCGAATATTTCCAGAAGCTTCTAGAACA

TTCCAGAATTTTCTTGAACCTTCCAGAAGGTTCTAGAACA
TTCCAGAATTTTCTCGAATTTTTCAGAAGGTTCTAGAGCT
TTCCAGAATTTTCTCGAACCTTCCAGAAGGTTCTAGAACA
TTCCAGAATTTTCTCGAATTTTTCAGAAGGTTCTAGAGCT
Nr of selected repeats 5 Similarity 0.866667

Consensus:

TTCCAGAAtTTTCTcGAAttTTcCAGAAGgTTCTAGAAcCa

>Cele-UNSB01_4:2158825-2158968 Satlength=144 Nr of Repeats=5 RepeatLength=11

seed=CTACAGTACC

CTACAGTACCT

CTACAGTACTA

CTACAGTACCCCGCCATATCCCACCCTAACCCCAAACCTATATCTTCAAAGACAAAACTCATTTTTTCGTAAACT

ACAGTAATTCTACAATACTC

CTACAGTACCT

CTACAGTACTA

Nr of selected repeats 4 Similarity 0.796296

Consensus:

CTACAGTAcCTa

>Cele-UNSB01_4:2163715-2164250 Satlength=536 Nr of Repeats=8 RepeatLength=43

seed=TTGCCGAAA

TTGCCGAAATGTTTAGAGAGATTTTTGAATGACGGAAACACTTAAAACGTGCTTTTTTGAATCTTTATCCCGTTT

TTAAAAAAGATATTTTCATAGAATTTATTGACTTTTAAAGATCATTATAGGATGCGTACAATTTTGCCGATTAAATT

GAAATTTGAAATTTCCAAAAAAATGTGCAAGAACAATTTGCCAAAAAATTTTCGGCGAATCGGGAATTTCCGTTT

GCCGAA

TTGCCGAAATTTTCAATCGCGCATTTTGCCGGTTTGCTCAT

TTGCCGAAATTTTCAATTCCGGCACTTTGCCGATTTGCTGT

TTGCCGAAATTTTCAATTCCGGTTTTTTTTCCGGA

TTGCCGAAATTTTCAATCCCGGCATTTTGCCGGTTTGCCGGA

TTGCCGAAATATTCAATCCCGGCATTTTGCCGGTTTGCCGAT

TTGCCGAAATTTTCAATCCCTGCATTTTGCCGGTTTGCCGAT

TTGCCGAAATTTTCAATCCCGCATTTTGCCGGTTTGCCGAT

Nr of selected repeats 5 Similarity 0.868148

Consensus:

TTGCCGAAAttTTCAATccCgGCATTTTGCCGGTTTGCCgAt

>Cele-UNSB01_4:2179058-2179920 Satlength=863 Nr of Repeats=38 RepeatLength=21

seed=GATTTACGGG

GATTTACGGGAGTCAAATGTA

GATTTACGGGATTACTGTGGA

GATTTACGGGATGAAAATGTG

GATTTACGGGAGCACTGTGTA

GATTTACGGGACGAACATGTG

GATTTACGGAGTGAACATGTG

GATTTACGGGGTGAACATGTA

GATTTACGGCGTAAACTTGTG

GATTTACGGGATGAAAATGTGAATTTACCGGATGAACATGTA

GATTTACGGGAGCACTATGTAGATTTACAAGGTGAACATGTG

GATGTACGGGAGCACTATGTA

GATTTACAGGGTGAACATGTA

GATTTACGGGGTGAACATGTA

ATTTACGGGAGCACTATGTAGATTTACAAGGTGAACATGTG

GATGTACGGGAGCACTATGTA

GATTTACAGGGTGAACATGTA

GATTTACGGGGTGAACATGTA

ATTTACGGGAGCACTATGTA

GATTTACGGGGTGAAAATGTG
GATTTACGGGGTGAAAATGTG
GATTTACGGGGTGAACTGTG
GATTTACGGGGTGAGCAAGTG
GATTTACGGGAGAACTATGTA
GATTTACGGGGTGAAAATGTG
GATTTACGGGATGAACATGTA
GATTTACGGGATGAACTTGTG
GATTTACGGGGTGAACTGTG
GATTTACGGGGTGAGCAAGTG
GATTTACGGGAGCACTATGTA
GATTTACAGGGTGAAAATGTG
GATTTACGGGATGAAAATGTG
GATTTACGGGATGAACATGTA
GATTTACGGGATGGAAAATGTG
GATTTACGGGATGAACATGTA
GATTTACGGGAGCACTATGTA
GATTTACAGGGTGAACTGTG
GATTTACAGGGTGAACTGTG
GATTTACAGGGTGAACTGTG

Nr of selected repeats 31 Similarity 0.686520

Consensus:

GATTTACgGGgtGAAcATGTg

>Cele-UNSB01_4:2205280-2205605 Satlength=326 Nr of Repeats=13 RepeatLength=21
seed=AAAATAGCTT

AAAATAGCTTAAAATTGATTA
AAAATAGCTGAAAATTCACTA
AAACTAGCTTAAAATAGACGA
AAAATAGCTTTAAAATTCACT
AAAATAGCTTAAAATTGACTG
AAAATAGCTTAACTTGACTGAACATTCAAAA
AAAATAGCTTAAAATTTAAGAAAATTGTCTGAAAGTAGCTGAAAATAGACTA
AAAATAGCTTAAAATTGACTG
AAAATAGCTGAAAATTCACTA
AAACTAGCTTAAAATAGACTA
AAAATAGCTTAAAATTCACT
AAAATAGCTTTAAAATTGACTG
AAAATAGCTTAACTTGACTGAAAATTCACT

Nr of selected repeats 9 Similarity 0.765993

Consensus:

AAAaTAGCTtAAAATtgACTa

>Cele-UNSB01_4:2267683-2267908 Satlength=226 Nr of Repeats=15 RepeatLength=15
seed=CGATGGGTCT

CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCACCT
CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCACCT
CGATGGGTCTCACCA
CGATGGGTCTCGCCA

CGATGGGTCTTTCCA
CGATGGGTCTCACCA
CGATGGGTCTCGCCA
CGATGGGTTTCGCCA

Nr of selected repeats 15 Similarity 0.914497

Consensus:

CGATGGGTCTCaCCA

>Cele-UNSB01_4:2268162-2268293 Satlength=132 Nr of Repeats=4 RepeatLength=11

seed=GTACTCCTAC

GTACTCCTACA

GTACTCCTACAGTACAACAGTACCCCGACCATATCCCACTACTAACCCCAAATCTATATCTCTTCAAAGACTAAAACA

CAATTTTTTCTAAACTACA

GTAATCCTACC

GTACTCCTACA

Nr of selected repeats 3 Similarity 0.838384

Consensus:

GTAcTCCTACa

>Cele-UNSB01_4:2419217-2421562 Satlength=2346 Nr of Repeats=23 RepeatLength=70

seed=AAAAATCGAT

AAAAATCGATAAGTTCGCCGAAAATTTGAACTTGGCGCTGTTTTATCGATGGAGCGCATTTTTAACGGCGAAAGATTGA
ATTTTCCGCC

AAAAATCGATGTTTTGAAGTTTTTCTCAATAGAGCGCACTTTCAACAGCGAGAAAATTTGAATTTTCCACC

AAAAATCGATTTTTTAAAAGTTTTTCTCAATAGAGCGCACTTTCAACAGCGAAAAAATTTGAATTTTCCACC

AAAAATCGATTTTTTAAAAGTTTTTCTCAATAGAGCGCACTTTCAACAGCGAAAAAATTTGAATTTTCCACC

AAAAATCGATTTTTTAAAAGTTGTTCTCAATAGAGCGCATTTTTCTACAGCGAAAAAATTTGATTTTTCGTC

AAAAATCGATGTTTTGCTTTTTTCCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCTACC

AAAAATCGATTTTTTAAAAGTTTTTCTCAATAGAGCGCACTTTCTACAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATTTTTTAAAAGTTTTTCTCAATAGAGCGCACTTTCAACAGTGAAAAAATTTGAATTTTCCGCT

AAAAATCGATGTTTTGCTTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCA

AAAAATCGATGTTTTGAAGTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATTTTTTGAAGTTTTTCTCAACAGAGCGCGATTACACCAGCGAAAAAATTTGAATTTTCCGCA

AAAAATCGATGTTTTGAAGTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATGTTTTGAAGTTTTTCTCAACAGAGCGCGATTACACCAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCC

AAAAATCGATTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTTCAACAGCGAAAAAATTTGAATTTTCCGCC

AAAAACCGATTTTTCTATTTAAATTTTTTCCAGAAAATTCGCCCTCCAAACCGGCCGAACCTACGTGATGGCAACCATC

AAAAATCGCC

AAAAATCGTCCGGCTCAATGGCTCCGTTGCGAGATTATCGATTTTTTGGCGAACGCCAACGTGGCTCTTCGCTACGTGGA

TCTGGGAACACGTGGCATCCTGAAGCTCAAAAATTTGCACCGAATGCACATTGAGCACACAAAATCGCGCCGGCTTGC

ATTGAAATTGGCCGATTTCTCGACGACGATTTATCGATGGCCGACAGCGAAATGGAGTGGGAATACACATTTTTGGCGTG

AAATTGTACCCTATGACGTGCCGATCGTTGTGCGACCCGATATGGGTGAGAAATTTACGGATTTCTCTCGGAAAAGCG

ACAAAATGCAATTTTTGCATGTTCTGTGCGCTCCATTGATAATTTTACCCGAAATCACAGAATTTTACCAAACTTC

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AAATTTCTCTGCGGAACAATTCGATCGATTTTTCAGGGGAAAATGCGCTCCATAGCTAATTCGCGCGAATTTTCGTC

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AAAAATCAATAATTTTCCAATCATTTTCAGAATTCCTGGAAACCGGCAAACTGCAATTTCTCGCAGATTCGGGTGCGCCGGC

GACGAAGACGACGAAAATTTGCTCGATAAAAATCCCGTCCCGTCCCGTTTTTCACTGAACGATCCGACGATTTACGTA

CCCAGAAAGAGGATGATGATGATGGAAATGTTAGCGACGATAAGGATAGCGGATGATTTTATTGATTTTTTTCGATTTTC

TCCCGTGAAAAATTGCAAAA

Nr of selected repeats 14 Similarity 0.884668

Consensus:

AAAAATCGATtTTTTgAAGTTTTTCTCAATAGAGCGCAtTTTCAaCAGCGAAAAAaTTGAATTTTcCgCc

>Cele-UNSB01_4:2422782-2423615 Satlength=834 Nr of Repeats=8 RepeatLength=104
seed=CCTGCGAAAG

CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGGGTTATC
GGTGAATTTTTGGGATCTGCCAGGGA
CCTGCGAAAGCAAATCTCTGGCCTGACGGAGGGCCAGCTAACTCTCTCCCTTAAGCCTTCGGGTGCTTCCTGGGTTATC
GGTGAATTTTTGGGTCTGTCAGGGT
CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGGGTTATC
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CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGGGTTATC
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CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGGGTTATC
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CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGGGTTATC
GGTGAATTTTTGGGTCTGTCAGGGT
CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGGGTTATC
GGTGAATTTTTGGGTCTGTCAGGGT
CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGGGTTATC
GGTGAATTTTTGGGTCTGTCAGGGT

Nr of selected repeats 7 Similarity 0.985348

Consensus:

CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGGGTTATC
GGTGAATTTTTGGGTCTGTCAGGGT

>Cele-UNSB01_4:2456640-2457356 Satlength=717 Nr of Repeats=5 RepeatLength=144
seed=TTCTAGGCCA

TTCTAGGCCACCAATTGGAAAATCATCATAAATTGGCTTAAAATCCAGATTTTTGGAGTCTGGTACCTGCAACATGTTGC
CCTGTAGTTTTTCTACAAGTTAGGATATATTAATTTTTGGTGGCCTAAAAGTCCAAATTATGGAT
TTCTAGGCCACCAATTGGAAAATCATCATAAATTGGCTTAAAATCCAGATTTTTGGAGTCTGGTAACTGCAACATGTTGC
CCTGTAGTTTTTCTACAAGTTAGGATATATTAATTTTTGGTGGCCTAAAAGTCCAAATTATGGAT
TTCTAGGCCACCAATTGGAAAATCATCATAAATTGGCTTAAAATCCAGATTTTTGGAGTCTGGTAACTGCAACATGTTGC
CCTGTAGTTTTTCTACAAGTTAGGATATATTAATTTTTGGTGGCCGAGAAGTCCGAATTTTGGAT
TTCTAGGCCAACCAATTGCAAAATCATCATAAATTGGCTTAAAATCCAGATTTTTGGAGTCCGGTAACTGCAACATGTTGC
CCTGTAGTTTTTCTACAAGTTAGGATATATTAATTTTTGGTGGTCTAGAAACTCAAAACTGGGAA
TTCTAGGCCACCAACTTGTAATCGTAGATCTCGGCTTAAAATCAAAGTTTTTTGAAATGTAAAAATTGCACCATGTTG
CCCGAAATTTGCTCTAGAAACAGCGTTAATTTTCAATGGCCTAGAAAAGTCAAAACTGGGAT

Nr of selected repeats 4 Similarity 0.915326

Consensus:

TTCTAGGCCAcCAATTgGAAAATCATCATAAATTGGCTTAAAATCCAGATTTTTGGAGTcTGGTAaCTGCAACATGTTGC
CCTGTAGTTTTTCTACAAGTTAGGATATATTaATTTTTGGTGGcCtAaAAgTCcaAAatTatGGAT

>Cele-UNSB01_4:2599504-2602273 Satlength=2770 Nr of Repeats=17 RepeatLength=164
seed=CTTTTTTCTT

CTTTTTTCTTTTAAAAAACTATTCAGCATAGTCATATTTATCAAAAAAATTATTTTTTTAAAGATTATTTTTTAAGAAAT
TCAGAAAATGCATCTAAAGCTTCTTTTCAAAAATTCAAAAGTACCGAAAAATCATATAAAGTGCTT
CTTTTTTCTTTTATAAAACTGTTTAGCATAGTCGAATATAACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGAAAAATCATAAAA
GTGCTT
CTTTTTTCTTTTATAAACTGTTTAGCATAGTCAAATATAACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGAAAAATCATATAAA
GTGCTT
CTTTTTTCTTTTATAAACTGTTTAGCATAGTCGAATATAACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGAAAAATCATAAAA
GTGCTT

CTTTTTTCTTTTATAACACTGTTTAGCATAGTCAAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATATAAA
GTGCTT
CTTTTTTCTTTTATAAACTGTTTAGCATAGTCGAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATAAAA
GTGCTT
CTTTTTTCTTTTATAACACTGTTTAGCATAGTCAAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATAAAA
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CTTTTTTCTTTTATAACACTGTTTAGCATAGTCAAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATAAAA
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CTTTTTTCTTTTATAACACTGTTTAGCATAGTCAAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATAAAA
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GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATAAAA
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CTTTTTTCTTTTATAACACTGTTTAGCATAGTCAAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAA
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GTGCTT
CTTTTTTCTTTTATAAACTGTTTAGCATAGTCGAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATAAAA
GTGCTT
CTTTTTTCTTTTATAACACTGTTTAGCATAGTCAAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATATGAA
GTGCTT

Nr of selected repeats 16 Similarity 0.982520

Consensus :

CTTTTTTCTTTTATAAAcACTGTTTAGCATAGTCaAATATACCAGAAAATACCAAACAAAGTATGCTATCTTGTACGAAA
GATTATTTTAAAAAATTCAGAAAATGCATCTAAAGCGGTTTTTTTTTCAAAAATTCAAAAGTACCGGAAAATCATAaAAA
GTGCTT

>Cele-UNSB01_4:2676914-2677180 Satlength=267 Nr of Repeats=11 RepeatLength=19

seed=CGCCAAGTAT

CGCCAAGTATCGAGAAAAG

CGCCAAGTGTCCGAAAATA

CGCCAAGGATCGAGAAATGCGCCAAGGCTCCAGAAATG

CGTCAAGTATCAAGAAAAG

CGCCAAGTATCGTGAAAAGCACCTAGGCGCCAGAAATG

CGTCAAGTATCGAGAAAAG

CGCCAAGTATCCAAAAATG

CGCCAAGTATCGTGAAAAT

CGCCAAGTATCCAAAAATGCGCCATGTTTCGCGAAAAG

CGCTAAGTATCCAAAAATA

CGCCAAGTATCGAGAAAAAG

Nr of selected repeats 8 Similarity 0.694345

Consensus:

CGcCAAGTATCgagAAAAg

>Cele-UNSB01_4:2701520-2702341 Satlength=822 Nr of Repeats=4 RepeatLength=175

seed=AACTTGTGAC

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AACTTTGTGAATCTAGTTTTTGAAAAAATTTAAAATTTGTGGCAATTTTCACCGATTTTTCGTGAATTTCCGAGCTAAAA

TTGAAAAATTCATTGTG

AACTTGTGACGGTGGGTATGGATTTTATGCACATATTTTGTTTGAAATAGTCTACCAAGTAAACTGGTGAAGTTTCAAA

AACTTTGTGGATCTAGTTTTTGAAAAAAGTTCAAATTTGCGCCAATTTTGACCAATTTTGGTGGTTTTCTGAGCTAAAA

TTGAAAAGTTGGGAATG

AACTTGTGACGGTGGGTATGGATTTTTTTTACATAATTCGTTCTAAATAGTCTACCGAGGAAACTGGTAAAGTTTCAAG

AGCTTTGTGGCCCTAGTTTTTCGAAAAAAGTTCCAAAATGTGCCAATTTTGACCAATTTTGGTGGTTTTCTGAGCTAAAA

TTGAAAAGTTGGGAATG

AACTTGTGACGGTGGGTATGGATTTTTTTTACATAATTCGTTCTAAATAGTCTACCGAGGAAACTGGTAAAGTTTCAAG

ACTTTGTGGCCCTAGTTTTTCGAAAAAAGTTCCAAAATGTGCTAATTTTTCACGCATTTCTGTAATAATTGCCTAATAAAT

CAAATTTCCATTTTTATTTAGGAAAATAATCGTTTTTTAATGTGATATATTTATTTAAAAGCAATTTTTCGTTTCATATT

CTGTTTTGTTTTGATCGAATTTTAGTGGTTTTTCGGAGCAAAAATAGAAAAATTCATATG

Nr of selected repeats 3 Similarity 0.715980

Consensus:

AACTTGTGACGGTGGGTATggaATTTTaTgcacaTAatTtGTTcgAAatagTctAccnaGtaAAcTGGTgAAGTTTCAaA

AaCTTTGTGgatCTAGTTTTtGAAAAAAGTTcaAAatTgTgCcaATTTgACCAaTTTgGTGgtTTTTctGAGCTAAAA

TTGAAAAGTTgggAaTG

>Cele-UNSB01_4:2721172-2721362 Satlength=191 Nr of Repeats=5 RepeatLength=40

seed=GAATTTTCCA

GAATTTTCCAGAAAGTTCTAGAAAAATCCAGAATTTTTTC

GAATTTTCCAGAAAGTTCTAGAACATTCCAGAATTTTTTC

GAATTTTCCAGAAATTTCTAGAAAAATCCAGAACGTTTTTC

GAATTTTCCAGAAAGTTCTGGAATATGCCAGATTTTTCTC

GAATTTTCCAGAACGTTCTAGAACATTCCA

Nr of selected repeats 4 Similarity 0.822222

Consensus:

GAATTTTcCAGAAagTTCTaGAAaATtCCAGAattTTtTC

>Cele-UNSB01_4:2728247-2729274 Satlength=1028 Nr of Repeats=42 RepeatLength=21

seed=TTTGGATTTT

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TTTGGATTTTTTGGCTTAAAACTGGATTTGTAGGCTTAAAA

TTTCGGATTTTTTAGGCTTAAAA

TTTAGATTTTTTAAGCTTAAAA

TTTGGATTTTTTGGCTTAAAACTGGATTTGTAGGCTTAAAA

TTTCGGATTTTTTAGGCTTAAAA

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TTTGGATTTTTTAGGCTTTAAA

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TTTGGATTTTTTAGGCTTAAAA

TTTGGATTTTTTGGCTTAAAAATTTGGATTTGGAAGCTTAAAA

TTTGGATTTTTTAGGCTTAAAG

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TTTGCATTTTTAAGCCTAAAA
TTTGGATTTTGAAGCTTAAAA
TTTGGATTTCTAAGCTTAAAA
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TTTGGATTTTTAGGCTTAAAG
TTTGGATTTTTAAGCTTAAAA
TTTGCATTTTTAAGCCTAAAA
TTTGGATTTTGAAGCTTAAAA
TTTGGATTTCTAAGCTTAAAA
TTTGGATTTTTAGGCTTAAAAATTGAATTTCTAGGCTTCAA
TTTGGATTTTTAGGCTTGAAA
TTTGGATTTTTAAGCTTAAAA

Nr of selected repeats 35 Similarity 0.859037

Consensus:

TTTGGATTTTTAgGCTTaAAA

>Cele-UNSB01_4:2780831-2781210 Satlength=380 Nr of Repeats=12 RepeatLength=11
seed=TACTGTAGGA

TACTGTAGGAG

TACTGTAGGATTACTGTAGTTTGGGAAAAATTGACTTTTTGTCTTATGAAGGAATATTGGTTTGGAGTTAGTGGAGGGA
TATGGTCGGGG

TACTGTAGAGA

TACTGTAGGAG

TACTGTAGGAT

TACTGTAGGATTACTGTAGTTTGGAAAAAATTGACGTTTCGTCTTTTGAAGGAATATTGGTTTGGAGATTAGTGATGGGA
TATGGACGGG

TACTGTAGTAG

TACTGTAGAGG

TACTGTAGGAG

TACTGTAGGATTACTGTAGTTTGGGAAAAAATTGACTTTTCATCTTTTGAAGGAATATTAGTTTGGGGTTAGTGGAGGGA
TATGGTCGGGG

TACTGTAGTAGTACAATAGAGA

TACTGTAGGAG

Nr of selected repeats 8 Similarity 0.787698

Consensus:

TACTGTAGgAG

>Cele-UNSB01_4:2843789-2844131 Satlength=343 Nr of Repeats=4 RepeatLength=87
seed=TGAAGTCGTA

TGAAGTCGTAGGATTTGTGACTGGTGTCTTTGCACTCTGTGGAGAAGACGTAGCTTCATCCGTTGTCTCATTCTTTGG
TT

TGAAGTCGTAGGATTCTGTGTAGCGACTGGTGTGCGTTGTTACTCTGTGAAGGGGACGTGGCTTCTTCTGTTGAGTCAGGC
TTCTGAGG
TGAAGTCGTAGGCTTCAGTGTGGTGGTTGGTGTGCGTTGTCGTAGGTGGAGAAGACGTAGCTTCATCCGTTGTCTCATT
TTCTGGTT
TGAAGTCGTAGGATTCTGTGTGGTACTGATGTCGTTTCATTCTGTGAAGGGGACGTGGCTTCTTCCGTTGTGCTATGC
TTCTCGGG

Nr of selected repeats 3 Similarity 0.685393

Consensus:

TGAAGTCGTAGGaTTcTGTGTgGtGacTGgTGTGCGTTgtanTctGTGaAGggGACGTgGCTTcTCCgTTGtgcAtgC
TTCTnnGG

>Cele-UNSB01_4:2889237-2889839 Satlength=603 Nr of Repeats=7 RepeatLength=35
seed=TTTTCAATTC

TTTTCAATTCAGGAATTTGACGGTTTGTGATTTGCCGAAATTTTTTTTCGGCAAATTACCGGTTTGCCGAAAGTCA
ATTTGCCGGAAGTTTTAGAGGTTTTTTTTATAAGACGGAAACACTTGAAACAGTGCTTTTTGATTTTTTTTCCGTAT
TTTTTTAGATACTTTCATAGAAAATTCCTACTTTTCAAATAAGTGTAGGAACATTTCATAGGATGCATAAAATTTTACC
GATTAATTTGAAATTTCTGAAACTTCCAAAACAAATGTGCAAATCTGCAATTTGCCGAAAACCGGCAAACCTCGGCAAAT
CTGCAATTCGCGACTTGCCAGTCTGCCTGAAA
TTTTCAATTCGCGCAATTTGCCGATTTGCCAATTTGCCTGAAAATTTTAAATCCGGAAATTTGCCGTTTTGCCTGCAT
TTTTCAATTCAGCAATTTGCAGTTTTGCCTGAAT
TTTTCAATTCGCGCAATTTGCAGTTTTGCCTGAAT
TTTTCAATTCAGCAATTTCCGATTTGCCTGAAT
TCTTCAATTCGCGCAACTCGCAATTTGCTTGAAT
TTTTCAATTCAGCAATTTGCAGATTTGCCTGTAT

Nr of selected repeats 5 Similarity 0.801905

Consensus:

TtTTCAATTCaaGCAAtTtgCagaTTTGCCtGaAT

>Cele-UNSB01_4:2892401-2892617 Satlength=217 Nr of Repeats=5 RepeatLength=24
seed=GCTTCTGGAG

GCTTCTGGAGCTACCGGTTACCCG
GCTTCTGGAGCCACAGGTTATCCA
GTTTCTGGAGCCACAGGTTATCCTGTCTCTGGGGCTACCGGCTATCCAGCCTCTTCCATGACCGACTCACCG
GCTTCTGGAGCTACAGACTATCCA
GCCTCTGGAGCCACAGGATATCCAGCCTCGGGAGCCACCGGTTATCCGGCTTCTTCTATGACGGACTCACCG

Nr of selected repeats 3 Similarity 0.777778

Consensus:

GCTTCTGGAGCtACaGgtTAtCCa

>Cele-UNSB01_4:2898426-2898868 Satlength=443 Nr of Repeats=12 RepeatLength=19
seed=ACCTAGGCAT

ACCTAGGCATAAATTAGGC
ACCTATGCATAAAGCAGGC
ACCTAGGCATTATTAGGC
ACCTATGCATGAATTAGGC
ACCTAGGCATAAGATAGGC
ACCTAGGCATAATTTAGGCACCGATGCATGAGGTAGGC
ACCTGGGCATAAAGTAGGC
ACCTAGGCATAAGTTAGGTACATAGTCATAAGCTAGGCACCGATACAAAAGTACGCATATAGGCTTAAAGTAGGCACA
TAGGAATCTAGGTTTAAAGATAGGTACCTACGCACAAGTTAGGCTCATAGGCATAAGGTAGGCACGTAGGCACGTGGGTA
TAAGATACGC
ACCTAGACATAAAGGTAGGTATCTAGTCATAAGGTAGGCACAAAAAC
ACCTAGGCATAAATTAGGCACCGATGCATAAGGTAGGC
ATCTAGGCATAAAGCAGGC
ACCTAGGCATAAAGGTAGGT

Nr of selected repeats 8 Similarity 0.751880

Consensus:

ACCTAgGCATaAagtAGGC

>Cele-UNSB01_4:2909681-2910188 Satlength=508 Nr of Repeats=14 RepeatLength=35
seed=ATTCCGGCAA

ATTCCGGCAATTTGCCGATTTGCCGAAAATTTTCA
ATTCCGGCAAATTACCGATTTGCCGAAAATTTTCA
ATTCCCTGCAATTTGCCGATTTGCCGAATATTTTCA
ATTCCGGCAATTTGCCGATTTGCCGAAAAGTTCA
ATTCCGGGCAATTTGTTCGATTTGCCGAAGCTGTTCA
ATTCCGGCAATTTGTTCGATTTGCCTAAAATTTTCA
ATTCCGGCAATTTCCGAAACTGTTAA
ATTCCGGCAAATTTGCCGATTTGCCGAAAATTTTCA
ATTCCGGCAATTTGCTGATTTTCGAAAATTTTAA
ATTCCGGGCAATTTGCCAATTTGCCGAAACTGTTAA
ATTCCGGCAATTTGCCGATTTGCCGAAAAGTTCA
ATTCCGGGCAATTTGTTCGATTTTCGAAACTGTTAA
ATTCCGGCAATTTGCCAATTTGCCGAAAATTTTCA
ATTCCGGCAAATTTGCCGATTTGCCGAAAATATTCAATATCGGCAATTTTCGAAAATTTTTTT

Nr of selected repeats 11 Similarity 0.820606

Consensus:

ATTCCGGCAATTTGcCGATTTGCCGAAAaTtTTcA

>Cele-UNSB01_4:2933784-2933839 Satlength=56 Nr of Repeats=5 RepeatLength=11
seed=TTGTTTACAAG

TTGTTTACAAG
TTGTTTACAAG
TTGTTTACAAG
TTGTTTACAAG
TTGTTTACAAG

Nr of selected repeats 5 Similarity 1.000000

Consensus:

TTGTTTACAAG

>Cele-UNSB01_4:2990271-2990613 Satlength=343 Nr of Repeats=19 RepeatLength=16
seed=TAGGCATGTA

TAGGCATGTAGACATGTAGGTTTG
TAGGCATGTAGGAATG
TAGGCATATAGGTGTG
TAGGCATGTAGGCATG
TAGGTATGTAGGCATA
TAGGCATGTAGGCATGTAGGCATTCGGCTTG
TAGGCATTTAGGCATG
TAGGCATGTAGGCATG
TAGGAATGTAGGCATG
TAGCCATGTAGCCATG
TAGGCATGTAAGCATG
TAGGCATGCAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGCCATGTAGCCATG
TAGGCATGTAGCCATG
TAGGCATGTAGGCATGTAGGCATTCGGCTTG

Nr of selected repeats 16 Similarity 0.859028

Consensus:

TAGGCATGTAGGCATG

>Cele-UNSB01_4:3002005-3002220 Satlength=216 Nr of Repeats=4 RepeatLength=43
seed=TTTGCCGGAA
TTTGCCGGAATTTAAAAATTTCTGGCAAACCTGGCAAACCGGTAAGTTGCCGCAATTGAAAATTTCCGGCAAATCGATAAA
TCGGCTA
TTTGCCGGAATTGAAAACCTACCGGCAAATCTGCAAACCTGGAAA
TTTGCCGGAATTTAAAAATTTCTGTAAATCTGCAAACCGGCAG
TTTGCCGGAATTTAAAAATTTCTGGCAATTTGGCAAACCGGCAG
Nr of selected repeats 3 Similarity 0.739899
Consensus:
TTTGCCGGAATTGAAAATtTcCtGnaAATcTGCAAACcGGcAg

>Cele-UNSB01_4:3004201-3004345 Satlength=145 Nr of Repeats=6 RepeatLength=24
seed=GCGGCCGACA
GCGGCCGACACTTTGCGGGTTGCT
GCGGCCGACACCTTACGGGTTGTA
GCGGCCGACACCTTACGGGTTGTT
GCGGCCGACACGTTACGGGTTGTA
GCGGCCGACACCTTACGGGTTGTA
GCGGCCGACACTTTGCAGGTTGTT
Nr of selected repeats 6 Similarity 0.855556
Consensus:
GCGGCCGACACcTTaCGGGTTGta

>Cele-UNSB01_4:3018891-3018971 Satlength=81 Nr of Repeats=4 RepeatLength=16
seed=AGGTAGGAAG
AGGTAGGAAGGAAGGT
AGATAGGAAGGTAGGA
AGGTAGGTAGGTATGT
AGGTAGGTAGGTAGGAAGGCAGGTAGGTACGC
Nr of selected repeats 3 Similarity 0.722222
Consensus:
AGgTAGGaAGGtAgGt

>Cele-UNSB01_4:3087838-3087930 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=CGAAAAGGGG
CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAGTTA
CGAAAAGGGGAGCAA
Nr of selected repeats 5 Similarity 0.760000
Consensus:
CgAAAAGGGGAgcta

>Cele-UNSB01_4:3088105-3088197 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCTTTTC
TCCCCTTTTCGTTGC
TCCCCTTTTCGTATC
TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA
TCCCCTTTTCGCAGA
TCCCCTTTTCGTTCTGC
Nr of selected repeats 5 Similarity 0.768889
Consensus:
TCCCCTTTTcGtagc

>Cele-UNSB01_4:3090317-3090467 Satlength=151 Nr of Repeats=8 RepeatLength=15
seed=CACGATGGGT

CACGATGGGTCTCGG
CACGATGGGTCTCAT
CACGATGGATCTCAC
CACGATGGGTCTCAC
CACGATGGGTTCACAC
CACGATGGGTCTCGC
CACGATGGATCTCAC
CACGATGGGTCTCACCGGATGGGCCTCACCACGAAGGCTCACAC

Nr of selected repeats 7 Similarity 0.843386

Consensus:

CACGATGGgTCTCac

>Cele-UNSB01_4:3135501-3135649 Satlength=149 Nr of Repeats=4 RepeatLength=37
seed=TGGCGGGAAT

TGGCGGGAATTCAAATTTTAATTTTCCGAAAACATTT
TGGCGGGAATTCAAATTTCAATTTTGTAGAACTCATTT
TGGCGGGAATTCAAATTTTAATTTTCCGAAAACATTC
TGGCGGGAATTCAAATGTTAATTTTCCGAAAACATTT

Nr of selected repeats 4 Similarity 0.867868

Consensus:

TGGCGGGAATTCAAATtTtAATTTTccGAAaaCATTT

>Cele-UNSB01_4:3176916-3177039 Satlength=124 Nr of Repeats=7 RepeatLength=12
seed=TAGGCTTAGG

TAGGCTTAGGCT

TAGGCGTAGGCA

TAGGCTTAGGCT

TAGGCTTAGGCATATGCA

TAGGCATAGGAATATACATAGGCATCCAAGGCCTTGATCCAGCCC

TAGACTTAGGTT

TAGGCTTAAGTT

Nr of selected repeats 5 Similarity 0.755556

Consensus:

TAGgCtTAgGct

>Cele-UNSB01_4:3192518-3194426 Satlength=1909 Nr of Repeats=53 RepeatLength=35
seed=CGGCAATTTG

CGGCAATTTGCCGATTTGCCGAAATTTTCAGTTC
CAGCAATTTGCCGATTTGCCGAAATTTTCAGTTC
CGGCAATTTGCCTATTTGCCGAAATGTTTAATTT
CGGCAATTTGTCTATTTGCCGAAATGTTCAATTC
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Nr of selected repeats 43 Similarity 0.870738

Consensus:

CGGCAATTTGCCnATTTGCCGGAATgTTcAATTC

>Cele-UNSB01_4:3222029-3222419 Satlength=391 Nr of Repeats=5 RepeatLength=16

seed=TACATGCCTA

TACATGCCTACATGCC

TACATGCCTACATGCC

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TACATGCCTATATGCC

TACATGCCTACATGCC

Nr of selected repeats 4 Similarity 0.958333

Consensus:

TACATGCCTAcATGCC

>Cele-UNSB01_4:3226485-3226669 Satlength=185 Nr of Repeats=11 RepeatLength=16

seed=CATGCCTACA

CATGCCTACACGCCTA

CATGCCTACATACATA

CATGCCTACATGCCTG
CATGCCTACATTCCCTA
CATTCCCTACATGCCTG
CATGCCTACATGTCTG
CATGCCTACATGCCTA
CATGCCTACATGCCTA
CATGCCCACATGTCTA
CATGCTTACATGCCTA
CATGCCTACATGCCTATATGCATA
Nr of selected repeats 10 Similarity 0.816667
Consensus:

CATGCCTACATgcCTa
>Cele-UNSB01_4:3230422-3232144 Satlength=1723 Nr of Repeats=67 RepeatLength=16
seed=ATGCCTACAT
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Nr of selected repeats 46 Similarity 0.819565

Consensus:

ATGCCTAcATGcCTAc

>Cele-UNSB01_4:3232737-3232899 Satlength=163 Nr of Repeats=6 RepeatLength=18

seed=CCTTCGCCTA

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CCTTCGCCTACCTGCATG

CCTTCGCCTACCTACGTG

CTTTCGCCTACATGTGTG

CCTTCGCCTACCTACGTA

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Nr of selected repeats 4 Similarity 0.765432

Consensus:

CcTTCGCCTACcTAcgTg

>Cele-UNSB01_4:3243719-3271867 Satlength=28149 Nr of Repeats=1487

RepeatLength=19 seed=CCTCACTCAA

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Nr of selected repeats 1365 Similarity 0.827742

Consensus:

CCTCACTCAAAaTcTgAG

>Cele-UNSB01_4:3274030-3274126 Satlength=97 Nr of Repeats=6 RepeatLength=16
seed=AGGCATGTAG

AGGCATGTAGGCATGT
AGGCATGTAGGCATGC
AGGCATGTAGGCATGT
AGGCATGTAGACATGT
AGGAATGTAGGCATGT
AGGCATGTAGACATAT

Nr of selected repeats 6 Similarity 0.872222

Consensus:

AGGCATGTAGgCATGT

>Cele-UNSB01_4:3353341-3353481 Satlength=141 Nr of Repeats=5 RepeatLength=33
seed=CGGCATATGC

CGGCATATGCCGTGAATTTTAAAAATCGGCATAA
CGGCATATGCCGTGAATTTTAAAAATCGGCATAA
CGGCATGTGCCATGAATTTTAAAAATCGGCATAA
CGGCATATGCCGCTCCAAAAAC
CGGCATTATGCCGGCAT

Nr of selected repeats 3 Similarity 0.946128

Consensus:

CGGCATaTGCCgTGAATTTTAAAAATCGGCATAA

>Cele-UNSB01_4:3371888-3372867 Satlength=980 Nr of Repeats=27 RepeatLength=35
seed=AATCGGCAAG

AATCGGCAAGTTGCCGGAATTGAAATTTCCGGGA
AATCGGCAAGTTACCGAAATTGAAAATTTCCGGCA
AATCGGCAAGTTACCGGAATTGAAAATTACCGGCA
AATCGGCAAGTTACAGGAATTGAAAGCTTCAGGCA

AATCGGCAAGTTACAGGAATTGAAAGCTTCAGGCA
AATCGGCAAGTTACAGGAATTGAAAGCTTCAGGCA
AATCGGCAAGTTGCCGGAATTGAAAATTTCCGGCA
AATCAGCAAGTTACAGAAATTGAAAGCTTCAGGCA
AATCGGCAAGTTGCCGGAATTGAAAATTTCCGGCA
AATCGGCAAGTTACCGAAATTGAAAATTTCCGGCA
AATTGGCAAGCTGCCGGAATTGAAAATTTACCGGCA
AATCGGCAAGTTACCGGAATTGAAAATTTCCGGCG
AATCGGCAAGTTACCGGAATTGAAAATTTCCGGTG
AATTGGCAAGTTGCCGGAATTGAAAATTTCCGGCG
AATCGGCAAGTTACCGAAATTGAAAATTTCCGGCA
AATCGGCAAGTTACCGGAATTGAAAATTTACCGGCA
AATCGGCAAGTTACAGGAATTGAAAATTTCCAGGCA
AATCGGCAAGTTACCAGAATTGAAAATTTCCGGCAAATTGACAAGTTACCGGAATTGAAAATTTCCGGCA
AATCGGCAAGTTGCCGGAATTGAAAATTTCCGGGA
AATCGGCAAGTTACCGGAATTGAAAGCTTCAGGCT
AATCGGCAAGCTGCCGGAATTGAAAATAACCGGCA
AATCGGCAAGTTACCGAAATTGAAAATTTCCGGCA
AATCGGCAAGTTACCGAAATTGAAAATTTCCGGGA
AATCGGCAAGTTACCGAAATTGAAGATTTCCGGCA
AATCGGCAAGTTACCGAAATTGAAGATTTCCGGCA
AATCGGCAAGTTACCGAAATTGAAAATTTCCGGGA
AATCGGCAAGTTACCGAAATTGAAGATTTCCGGCA

Nr of selected repeats 25 Similarity 0.852698

Consensus :

AATCGGCAAGTTaCcGgAATTGAAAatTTCcGGCA

>Cele-UNSB01_4:3428944-3430273 Satlength=1330 Nr of Repeats=24 RepeatLength=45
seed=TCTGATCCTT

TCTGATCCTTAAGCTCCGAAGGATCACAGGGGGTACCTCCTGATGA
TCTGATCCTTCAGCTCCAAAGGATCAGAAGGGTACCTCCTGGTGA
TCTGATCCTTAAGCTCCGAAGGATCACAGGGGGTACCTCCTGGTGA
TCTGATCCTTCAGCTTCAAAGGATCATAAGGGTACCTCCTGGTGA
TCTGATCCTTCAGCTTCAAAGGATCAGAAGGGTACCTCCTGGTGA
TCTGATCCTTAAGCTCCGAAGGATCACAGGGGGTACCTCCTGGTGA
TCTGATCCTTCAGCTTCAAAGGATCATAAGGGTACCTCCTGGTGA
TCTGATCCTTCAGCTTCAAAGGATCAGAAGGGTACCTCCTGGTGA
TCTGATCCTTCAGCTCCGAAGGATCAGAAGGGTACCTCCTGATGA
TCTGATCCTTCAGCTTCAAAGGATCATAAGGGGTATAAATGCAATAAAATCAAGCAAAGTTGATACAGGTCCAGGTTCCG
AACTTTGTCTGACAAACTTTTTTTTACTTTGACGGACAGTCCTGAATACACCTATTGAACATTTCTAATAGTCCATAGG
ATTCCATTTACCATGCTTTATATCAGTTTTCCGGTAATTTTTGTTTTGTCCGCTAAGATACTTTGTACCCAAAAGTTTG
TCATCACGGAGAATTGATCAACTTTGCTTGATTTATTGCTTTTATAACCCCT
TATGATCCTTTGAAGCTGAAGGATCAGATCACCAGGAGATAACCCCC
TGTGATCCTTTGAAGCTGAAGGATCAGATCATCAGGAGATAACCCCC
TGTGATCCTTTGAAGCTGAAGGATCAGATCATCAGGAGGTACCCT
TCTGATCCTTCGGAGCTGAAGGATCAGATCACCAGGAGGTACCCT
TCTGATCCTTTGAAGCTGAAGGACCAGATCACCAGGAGGTACCCT
TATGATCCTTTGAAGCTGAAGGATCAGATCACCAGGAGGTACCCC
TGTGATCCTTCGGAGCTTAAAGATCAGATCACCAGGAGGTACCCT
TATGATCCTTTGAAGCTGAAGGATCAGATCATCAGGAGGTACCCT
TCTGATCCTTTGAAGCTGAAGGATCAGATCATCAGGAGGTACCCT
TCTGATCCTTTGAAGCTGAAGGATCAGGTACCAGGAGGTACCCT
TCTGATCCTTCGGAGCTGAAGGATCAGATCATCAGGAGGTACCCT
TCTGATCCTTTGAAGCTGAAGGATCAGATCATCAGGAGGTACCCT

TCTGATCCTTTGAAGCTGAAGGATCAGATCATCAGGAGGTACCCT

Nr of selected repeats 17 Similarity 0.598811

Consensus:

TCTGATCCTTcgnAGCTgAAGGATCAGatcAncAGGagGTACCCT

>Cele-UNSB01_4:3517707-3518097 Satlength=391 Nr of Repeats=27 RepeatLength=12

seed=TAAGCCTAAG

TAAGCCTAAGCT

TAAGCCTAAGAT

TAAGCCTAAGCCTAAGAT

TAAGCCTAAGCC

TAAGCTTAAGCC

TAAGCCTAAGCCTAAGAA

TAAGCCTAAACC

TAAGCCTATGCC

TATGCCTAAGCC

TAAGCCTAAGTCTTAGCCTTGGCT

TAAGCCTAAGCCAGAGCTTAAGCTCAAGCCAAAAT

TAAGCCTAAGCC

TAAGCCTCAGCCTAGGTC

TAAGCCTAGGTC

TAAGCCTAAGCT

TAAGCCTAAAAGCTAGGCCAAAGCC

Nr of selected repeats 21 Similarity 0.808059

Consensus:

TAAGCCTAAGCT

>Cele-UNSB01_4:3630301-3630781 Satlength=481 Nr of Repeats=28 RepeatLength=16

seed=TGCCTACATG

TGCCTACATGCCTTCA

TGCCTACATGCCACA

TGCCTACATGCCTACA

TGCCTACTTGCCAACA

TGCCTACATGCCACA

TGCCTACATGCCTACA

TGCCTACATGCCTACA

TGCCTACATGCCTACA

TGCCTACATGCCTACA

TGCCTACATGTCTACA

TGCCTACATGCCTACA

TGCCTACATGCCTACA

TGCCTACATGCCTACA

TGCCTACATGCCTATA

TGCATACATGTTTGCATTTCCTTCA

TGCCTACATGCCTACA

TGCCTACATGACCACA
TGCCTACATGCCTACA
TGCCTACTTGCCAACA
TGCCTACATGCCCACA
TGCCTACATGCCTACA
TGCCTACATGCCTACA
TGCCTACATGCCTACA
TGCCTATATGCATACATGTTTGCA
TGCCTTCATGCCTACA
TGCCTACATGCCTTCAT
TCCTACATGTCTACA
TGCCTACATGCATACATGTTTGCATGCCTACA

Nr of selected repeats 23 Similarity 0.914032

Consensus:

TGCCTACATGCCTACA

>Cele-UNSB01_4:3670951-3671065 Satlength=115 Nr of Repeats=7 RepeatLength=12
seed=TTAGGCTTAG

TTAGGCTTAGGCATAGGCTCAGGCTTTGGCTCAGGA
TTAGGCTTAGGCTTAAAC
TTAGGATTAGGA
TTAGGCTTAGGC
TTAGGATTAGGC
TTAGGCTTAGGA
TTAGGCTTAGGA

Nr of selected repeats 5 Similarity 0.866667

Consensus:

TTAGGCTTAGGA

>Cele-UNSB01_4:3714325-3715225 Satlength=901 Nr of Repeats=15 RepeatLength=21
seed=TGTAGATTTA

TGTAGATTTATGGGAACCTGC
TGTAGATTTATAAAAACCTGGTGTGCATTTACGGGCATATATTGTGAACTAATGGGAACCTAATCCGGATTTAAGCAA
TCTGG
TGTAGATTTACGGGGCCTACTATACATTTACAGAAGTATAT
TGTAGATATACGGGAATCTTG
TGTAGATTTTCGTGAATAGTGAGTTGTGATCCAACAACCTTTCAATTTTCAAAAAATCGGGCGTCAAAGTACTCAAGCAC
CTGCAAATAGAAAAACCCAGCTGACGCTTAATACTCCCCGTATCAGAGAGCAAATGCATCAGATACAGTAAGGAGGG
GTACACATGTGGATCTCACATGTGAAAAGTTCAGCAGATTTCATGTGAATTATGTGTTTTTTTTTTGTTGCGGTTTCAGTT
TTTTTTTTCAGCGCGCGCCCGAAATAAATGTGATGCGACACACAGCGGGCCGACAAAGGAGAAAGCCCCCGCCGGC
GTAATTTGGATGAAATTAGTGGTGTATGGAAGGATTGAGATGGGAGATTATATGATTAATGTTGTTAAACACAAACT
TGCTGGTGAGGATGGTATGATTTTGGGGGAGAGAGAGAAAATCGGATTTTTTGAAGGATGATGTAGGATGACGGAGTGA
TAACAGTGATACGGTACTTGTTTTTGGTTTTGGAAATTGTTGGGTTAG
TGTGGATTTACGGGAGGCATTG
TGTAGATTTACGGAAGCCTAG
TGTAGAATTACGGGAGCATAG
TGTATATTTACGGGAGTCTAT
TGTAGAATTACGGGAGCATAG
TGTAGATTTATGCGAGTATAT
TGTAGATTTACGGGAGCATAG
TGTAGATCTACGGGAGGCTAT
TGTAGATTTACGGGAGGTATTG
TGTAGATTTACGAGAGTCTAT

Nr of selected repeats 10 Similarity 0.670875

Consensus:

TGTAGATTTAcGgGAgccTan

>Cele-UNSB01_4:3733029-3733089 Satlength=61 Nr of Repeats=4 RepeatLength=15
seed=TCGTGGTGAG
TCGTGGTGAGACCCA
TCGTGGTGAGACCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCT

Nr of selected repeats 4 Similarity 0.940741

Consensus:

TCGTGGTGAGACCCa

>Cele-UNSB01_4:3733495-3734015 Satlength=521 Nr of Repeats=15 RepeatLength=40
seed=TTTCTAGAAA

TTTCTAGAAAATTCGAGAAAATTCGGGATTGGTCCAGAAT

TTTCTAGAAAA

TTCTAGAAAAGTTGTGGAATGGTCCAGAAT

TTTCTAGAAAATTCGGGAAAATCTGGAATATTCCAGAAC

TTTCTAGAAAATTCGAGAAAATGTCTGCAATGTTCTAGAAC

TTTCTAGAAAATTCGAGAAAATTCGGGAATGGTCCAGAAT

TTTCTAGAAAATTCGAGAAAATTCGGGAATGGTCCAGAAT

TTTCTAGAAAATTCGGTAAAATCTGGAATATTCCAGAAC

TTTCTAGAAAATTCGGGAAAAGTCGGCAATGTTCTAGAAC

TTTCTAGAAAATTCGAGAAAATTCGGGAATGGTCCAGAAT

TTTCTAGAAAA

TTCTAGAAAAGTTCTGGAATGGTCCAGAAG

TTTCTAGAAAAGTTCTGAGAAAATTCGGGAATGGTCCAGAAT

TTTCTAGAAAATTCGAGAAAAGTTCTGGAATGGTCCAGAAT

TTTCTAGAAAATTTGGGAAAATCTGGAATATTCCAGAAC

Nr of selected repeats 11 Similarity 0.820606

Consensus:

TTTCTAGAAAATTCGaGAAAATTCnGGAATggTCCAGAAT

>Cele-UNSB01_4:3758727-3758973 Satlength=247 Nr of Repeats=6 RepeatLength=41

seed=AAATTTTAA

AAATTTTAACTAGAAGTGGGCGAAAATCATTCAAAAATTC

AAATTTTAACTAAAAGTGGGCGAAAATCATTCAAAAATTC

AAATTTTAACTAAAAGTGGGCGAAAATCATTCAAAAATTC

AAATTTTAAACGAGAAGTGGGCGAAAATCATTCAAAAATTC

AAATTTTAAACGAGAAGTGGGCGAAAATCATTCAAAAATTC

AAATTTTAAACGAGAAGTGGGCGAAAATCATTCAAAAATTC

Nr of selected repeats 6 Similarity 0.945799

Consensus:

AAATTTTAAACgAgAAGTGGGCGAAAATCATTCAAAAATTC

>Cele-UNSB01_4:3817232-3817391 Satlength=160 Nr of Repeats=5 RepeatLength=21

seed=TAGTTTGTAG

TAGTTTGTAGTGTGCAGTGTG

TAGTTTGTAGATTGCAGTTCAAAAAACCAATCAAAAATATTAGAGAAATGGAAATTATTTCAAGTTTTTGCTAATA

TTGC

AGTTTGTAGTTTG

TAGTTTATAGTTCACAGTTTA

TAGTTTATAGTTTGTACTTTG

Nr of selected repeats 3 Similarity 0.661376

Consensus:

TAGTTTaTAGTttgcAgTtTg

>Cele-UNSB01_4:3888107-3888300 Satlength=194 Nr of Repeats=12 RepeatLength=16

seed=TAGGCATGTA

TAGGCATGTA

TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGAATG
TAGGCATGTAGGCATG
TAGGAATGTAGACATGTAGGGATG

Nr of selected repeats 9 Similarity 0.981481

Consensus:

TAGGCATGTAGGCATG

>Cele-UNSB01_4:3896416-3896737 Satlength=322 Nr of Repeats=5 RepeatLength=18
seed=ATTAGTATTG

ATTAGTATTGCCCTCGGAGACCTTCCGAAA

ATTAGTATTGCCCTACCT

ATTAGTCTTGCACTCTCTAATAGTCTTGCGTTAACTTTTTTGTATTGCAAACCCGTCTCGCTAATTTTCAGGATTTCAAC
AACAAATTTTTGCCTATTTTGCACAGTTTTTCACATCATTTCTACGAGATTGAAGTTTTTGAACCTTATATGAAAATCAAA
TTTTCTGAATTTTTACATATGATTCGAGTTTTTTCCAGGAAAAAACTAGTAAGCGCAAAGTCAGAAAATGTTCTGAAA

ATTAGTATTGCACTCCTT

ATTAGTCTTGCACTCCTT

Nr of selected repeats 3 Similarity 0.802469

Consensus:

ATTAGTaATTGCaCTcCcT

>Cele-UNSB01_4:4053946-4054647 Satlength=702 Nr of Repeats=6 RepeatLength=12
seed=TAAGCCTAAG

TAAGCCTAAGTC

TAAGCCTATGCC

TAAACCTAAGCC

TAAGCCTCAGTC

TAAGCCTATGCCTAAACC

TAAACCTAAGCCTAAGCTAAAGCCTGATATCTATTTTTTCAGTCCCATTACCTGTGGAGGCCACTTTACCGCCCAGGCC
TACATCCAATCCTTTGTCTCTCCCGGCTACCCAAAGACCTTTGCAAATGGCGCCGAATGTGTGTGGACTGTGGAATCTA
CGCCAGGACAAGTGGTTTCTTTGATTGTGAGTTTTTTAATTTTTTTTGAATGTACTGGGTATGGGTATTATTATTTTA
GATGAAAAGCGGCAAAACATGGGGATAAATTCAAAGAAAAATGAAAATTTTCAGCAGAAATTTGTTTTTATCCGGTAAAAA
ACCGGATTTAACAACAACCTCTTTGTTTTATAAGAATTTTCATTTGTTCCACAACATTAATTAACATTAATTAACATT
AGTTCTCGTTAGGACCTTCACACACCTTCGCAAGACCATTTTCATAAGCACGGATGTTGAAATCGATGGAATGTCTGAA
AATTAATAATAACTAAATCGTTTTAGCGAACAATCTAACTTACTCTCCAAATGTCCATACATTGGTTTTTTTCGTTAGGT
CGTAGGCATCGATCCATTCTTCGGCAGTGCAATTATGGTGGAGTACGTAGGCAAACCTCGTAGTGCTGAGTTTAGGATA
GTT

Nr of selected repeats 4 Similarity 0.759259

Consensus:

TAAgCCTaaGcC

>Cele-UNSB01_4:4229494-4229583 Satlength=90 Nr of Repeats=7 RepeatLength=12
seed=GTTGCGTGTC

GTTGCGTGTCGC

GTTGCGTGTCGC

GTTGCGTGTCGC

GTTGCGTGTCGTCGC

GTTGCGTGTCGC

GTTGCGTGTCGA

GTTGCGTGTCGC

Nr of selected repeats 6 Similarity 0.962963

Consensus:

GTTGCGTGTGCGC

>Cele-UNSB01_4:4229497-4230359 Satlength=863 Nr of Repeats=71 RepeatLength=12

seed=GCGTGTGCGCG

GCGTGTGCGCGTT

GCGTGTGCGCGTT

GCGTGTGCGCGTT

GCGTGTGCGTGTGCGCGTT

GCGTGTGCGCGTT

GCGTGTGCGAGTT

GCGTGTGCGCGTT

GCGTGTGCGGTCGAGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GCGTGTGCGCGTT

GCGTGTGCGCGTC

GAGTGTGCGCGTC

GCGTGTGCGCGTT

GCGTGTGCGCGTC

GCGTGTGCGCGTC

GCGTGTGCGCGTT

GCGTGTGCGCGTT

GCGTGTGCGCGTT

GCGTGTGCGCGTT

GCGTGTGCGCGTT

GCGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GAGTGTGCGCGTC

GCGTGTGCGCGTT

GCGTGTGCGCGAT

GCGTGTGCGGTT
GCGTGTGCGGTT

Nr of selected repeats 69 Similarity 0.901298

Consensus:

GCGTGTGCGGTT

>Cele-UNSB01_4:4261575-4261676 Satlength=102 Nr of Repeats=6 RepeatLength=17

seed=GATGCCCCCT

GATGCCCCCTCTGAACG

GATGCCCCCTCTGAACG

GATGCCCCCTACGAACAA

ATGCCCCCTTTGACCTA

ATGCCCCCTTAGAACGC

GATGCCCCCTCTCTC

Nr of selected repeats 4 Similarity 0.722222

Consensus:

gATGCCCCCTctGAaCgn

>Cele-UNSB01_4:4368763-4369020 Satlength=258 Nr of Repeats=5 RepeatLength=11

seed=GTAAGTAGG

GTAAGTAGG

GTAAGTAGGTATACGGTAGGGTTACTGTAGTTTGGAAAAATTGAGTTTTTTGTCTACAGAAGAGGTATTGGGTTGGGA

GTTGGTGGGAGATAATGCCAAGCTACTGTAGTG

GTAAGTAGG

GTAAGTAGGTATACGGTAGGGTTACCGTAGTTTGGAAAAATTGAGTTTTTTGTCTACAGAAGAGGTATTGGGTTGGGA

GTTGGTGGGAGATAATGCCAAGCTACTGTAGTG

GTAAGTAGG

Nr of selected repeats 3 Similarity 1.000000

Consensus:

GTAAGTAGG

>Cele-UNSB01_4:4388126-4388633 Satlength=508 Nr of Repeats=13 RepeatLength=11

seed=CTACAGTACT

CTACAGTACTC

CTACAGTACTA

CTACAGTACTTGGACATTATCCCCAGCAACTCCAACCCAAAACCTCTTCTGTAGACAAAACTCAATTTTTCCAGA

CTACAGTAACCTACCGTATGC

CTACAGTACTC
CTACAGTACTA
CTACAGTACCTTGACATTATCCCCCAGCAACTCCCAACCCAATACCTCTTCTGTAGACAAAACTCAATTTTTCCCAA
CTACAGTAACCCTACCGTATAC
CTACAGTTCTC
CTACAATACTA
CTACAGTACCTTGACATTATCCCCCCCACCAACTCCCAACCCAATACCTCTTCTGTAGACAAAACTCAATTTTTCTTA
AACTACAGTAACCCTACCGTATAC
CTACAGTACTC
CTACAGTACTA
CTACAGTACCTTGACATTATCCCCCTACCCACTCCCAACCCAATACCTCTTCTGTAGACAAAAACCCAATTTTTCCCA
AACTACAGTAACCCTACCGTATAC
CTACAGTACTC

Nr of selected repeats 9 Similarity 0.878788

Consensus:

CTACAGTACTc

>Cele-UNSB01_4:4398109-4398181 Satlength=73 Nr of Repeats=4 RepeatLength=18
seed=TTTTTTGATA

TTTTTTGATAATTCTTGT
TTTTTTGATAATTCTTGA
TTTTTTGATAATTCTTGA
TTTTTTGATAATTCTTGA

Nr of selected repeats 4 Similarity 0.962963

Consensus:

TTTTTTGATAATTCTTGa

>Cele-UNSB01_4:4418485-4418703 Satlength=219 Nr of Repeats=5 RepeatLength=35
seed=TTCCGGCAAA

TTCCGGCAAATCGACAATTTGCCGAAAAACAGAGT
TTCCGGCAAATCGGCATATTAGCAAATTTGCCGGAATTGAAA
TTCCTGGCAAACCGGCAATTTGGGTTTGCACTTTTCTTATTGGAAATTTCAATTTTTGAAAAT
TTCAGGCAAATCGGCAAATTTGCCGGAATTGAATAC
TTCCGGCAAATCGACAATTTGCCGAAAATCAGAGT

Nr of selected repeats 3 Similarity 0.675676

Consensus:

TTcCGCAAATCGaCAAtTtGCCGaaAAAtcaGAgT

>Cele-UNSB01_4:4464716-4464793 Satlength=78 Nr of Repeats=5 RepeatLength=15
seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAGCAA

Nr of selected repeats 4 Similarity 0.748148

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_4:4479166-4488089 Satlength=8924 Nr of Repeats=327 RepeatLength=26
seed=GTCTAACTTT

GTCTAACTTTAAACAATTAATCTACCGTTCTAACATTTGAAAATTAATCTACCGTTCTAACTCTTAAAAATCTACAAGA
AGATCTTTTCTTGCCTTGAAGCGCAAAGAAAAGAAAAGGACTATTTAGACTTAGGCACATACTAGGATTTCCCAACT
GGAATAAAATATTGGAAATCCTTATGACACACCGGCGGTATGGCGCGGCTTAAGCCTAAATAGCCACTTTTATCAAAT
ACATTTGAGCGAGGCGGTTGTAAACTATTCTTTTAGCAAAAATTAATACTTTTAACTTTTAAATTT
AAAAATCGGAACGGTATTTAATACTTTGGAAATTCATCTACTG
GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATG

GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATGGTCTATAACTTTGAAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCTAATG
GTATAACTTTGAAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGAAATTCATCAACTG
GTCTAACTTTGGAAATTCATCTAATG
GTCTAACTTTGGAAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGAAAATTCATCTAATG
GTCTAACTTTGGGAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG
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GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG
GTATAACTTTGAAAATTCATCTAATG
GTCTAACTTTGGGAATTCATCAACTG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG
GTCTAACTTTGGGAATTCATCTAATG

Nr of selected repeats 305 Similarity 0.965297

Consensus:

GTCTAACTTTGGAAATTCATCTAATG

>Cele-UNSB01_4:4525521-4525683 Satlength=163 Nr of Repeats=12 RepeatLength=12
seed=GCCTAAGCCT

GCCTAAGCCTAA

GCCTAAGACTAC

GCCTACGCCTAA

GCTTAAGCCTCC

GCCTAAGCCTCC

GCATAAGCCTAAGCCTAACATAAGTTTAA

GCCTAAGCCTAC

GCTTAAGCCTAC

GCCTAACCTTA

GCCTAAGGCTAA

GCCTAAGCCTAC

GCCCAAGCCTAA

Nr of selected repeats 11 Similarity 0.751515

Consensus:

GCCTAAGCCTac

>Cele-UNSB01_4:4598852-4599551 Satlength=700 Nr of Repeats=6 RepeatLength=11
seed=GCAGTAGGCA

GCAGTAGGCAG

GCAGTAGGAAG

GCAGTAGGCAA

GCAGTAGGCAA

GCAGTAGGCAG

GCAGTAGGCAAGCGGTGGGCAGTCAGAAGGCAGGCTGTAGGGAAATGCACTTGACGAAAATAGCTTACCCACAGATCC
ATGCGTAATTTGTGATTTTATCTTGATGTAGTATAATGGCAGTGAGAATCGCAAAAATGCGGGCAAACAACGGAGGAAC
AAATCCAACCCAGAAGAGGAGTGTGTTGTTTAAATTTGAATAATTCCTTCAAAAAATTAATTTTGTATCTCTAGATAATT
GAAAAGAAAACTCACAACCGCTTGAGGTCTCTTTTGTGAACACTCTCGAAACGTTTTTCCATCAACATTTTGCCTGA
ATCTCTGTTCCCTCAAGAGGATGGACAACAAGTAGTAAGAAAGTAGGACAAGCTTAATGATGCCGACGATGAGAAATGAA
AGACGGGTTTACTTGTTCATATTGGGGAAAAACAGAGGAGGAGTGGATTCAAAGATTACTACAAATGTTTCCAAATT
GACTCATTCAATTTGGTGTAAAAGTTATTGCTAAATGTAGTACGGGGTGTCAACACCCTGATATTATTATAAATGTAAAC
ATTTACGGGGAAAGAAGCTATAATTTGGGAAATGTGCAGCCGACAAATTCCTGGTTCACAAATAGTCATCATCAGAAGC
TGTCGCAGGCAG

Nr of selected repeats 5 Similarity 0.878788

Consensus:

GCAGTAGGcAg

>Cele-UNSB01_4:4620647-4621153 Satlength=507 Nr of Repeats=13 RepeatLength=11
seed=CTACAGTACT

CTACAGTACTC

CTACAGTACTA

CTACAGTACCTTGACATTATCCCCCAGCAACTCCAACCCAAAACCTCTTCTGTAGACAAAACTCAATTTTTCCAGA

CTACAGTAACCCTACCGTATGC

CTACAGTACTC

CTACAGTACTA

CTACAGTACCTTGACATTATCCCCCAGCAACTCCAACCCAATACCTCTTCTGTAGACAAAACTCAATTTTTCCAAA

CTACAGTAACCCTACCGTATAC

CTACAGTTCTC

CTACAATACTA

CTACAGTACCTTGACATTATCCCCCAGCAACTCCAACCCAATACCTCTTCTGTAGACAAAACTCAATTTTTCTAA

ACTACAGTAACCCTACCGTATAC

CTACAGTACTC

CTACAGTACTA
CTACAGTACCTTGACATTATCCCCCCCACCCACTCCCAACCCAATACATCTTCTGTAGACAAAAACCCAATTTTTTCCCA
AACTACAGTAACCTACCGTATAC
CTACAGTACTC
Nr of selected repeats 9 Similarity 0.878788
Consensus:
CTACAGTACTc
>Cele-UNSB01_4:4665165-4665209 Satlength=45 Nr of Repeats=4 RepeatLength=11
seed=TGACAACTTTT
TGACAACTTTG
TGACAACTTTG
TGACAACTTTG
TGACAACTTTG
Nr of selected repeats 4 Similarity 1.000000
Consensus:
TGACAACTTTG
>Cele-UNSB01_4:4768182-4768259 Satlength=78 Nr of Repeats=5 RepeatLength=15
seed=CGAAAAGGGG
CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAGATA
Nr of selected repeats 4 Similarity 0.777778
Consensus:
CgAAAAGGGGAgTa
>Cele-UNSB01_4:4768434-4768526 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCTTTTC
TCCCCTTTTCGTTGC
TCCCCTTTTCGTATC
TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA
TCCCCTTTTGCAGA
TCCCCTTTTCGTTCTGC
Nr of selected repeats 5 Similarity 0.768889
Consensus:
TCCCCTTTTcGtagc
>Cele-UNSB01_4:4858228-4858874 Satlength=647 Nr of Repeats=17 RepeatLength=35
seed=TTGCCGAAA
TTGCCGAAATTTTGGTTTCCAGCAAGTTGCCGAA
TTGCCGAAATTTTGGTTTCCAGTTGCCTAT
TTGCCGAAATTTTGGTTTCCAGTTGCCTATTTGGCAGAAATTTTGGTTTCCGGCAAGTTCCGAT
TTGCCGAAATTTTGGTTTCCGGCAATTTGCCTATTTGCCGGATATTTTGGTTTCCAGCAAGTTGCCGAA
TTGCCGAAATTTTGGTTTCCGGCAAGTTTCCGAT
TTGCCGAAATTTAGGTCTCCGGCAAGTTACCTAT
TTGCCGAAATTTTGGTTTCCGGCAAGTTTCCGAT
TTGCCGAAATTTTGGTTTCCGGCAATTTGCCGAT
TTGCCGAAATTTTGGTTTCCGGCAAGTTTCCGAT
TTGCCGAAATTTTGGTCTCCGGCAAGTTGCCTAT
TTGCCGAAATTTTGGTTTCCGGCAAGTTTCCGAT
TTGCCGAAATTTTGGTCTCCGACAAGTTGCCGAT
TTGCCGAAATTTTGGTTTCCGCAAGTTTCCGAT
TTGCCGAAATTTTAGTCTCCGGCAAGTTTCCGAT
TTGCCGAAATTTTGGTCTCCGGCAAGTTGCCGAT

TTTTTCAGAAAATTAAAAATTTCCCTCCAAAATATTT
TTTTTCAGAAAATTTAAATTTCTCTCCAAAATATTT
TTTTTCAGAAAATTTAAATTTCCCTCCAAAATATTT
TTTTTCAGAAAATTTAAATTTCCCTCCAAAATATTT
Nr of selected repeats 13 Similarity 0.973626

Consensus:

TTTTTCAGAAAATTaAAAATTTCCCTCCAAAATATTT

>Cele-UNSB01_4:4987504-4988044 Satlength=541 Nr of Repeats=32 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGAC

GGGTCTCACCACGAT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGATGGGCCTCGCCGCGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGATGGGCCTCGCCGCGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGATGGGCCTCGCCGCGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCGCCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGATGGGCCTCGCCGCGAT

GGGTCTCACCACGGT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

Nr of selected repeats 28 Similarity 0.940506

Consensus:

GGGTCTCACCACGaT

>Cele-UNSB01_4:4988071-4988281 Satlength=211 Nr of Repeats=14 RepeatLength=15

seed=ACCCATCGTG

ACCCATCGTGGTGAG

ACCCATCGTGGCGAG

ACCCATCGTGGTGAG

ACCCATCGTGGTGAG

ACCCATCGTGGCGAG

ACCCATCGTGGTGAG

ACCCATCGTGGTGAG

ACCCATCGTGGAAAT

ACCCATCGTGGTGAG
ACCCACCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCACCGTGGTGAG

Nr of selected repeats 14 Similarity 0.916972

Consensus:

ACCCATCGTGGtGAG

>Cele-UNSB01_4:4987504-4989222 Satlength=1719 Nr of Repeats=80 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGAC

GGGTCTCACCACGAT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGATGGGCCTCGCCGCGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGATGGGCCTCGCCGCGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGATGGGCCTCGCCGCGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCGCCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGATGGGCCTCGCCGCGAT

GGGTCTCACCACGGT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGATGGGCGTGAAAGACCCATCGTGGTGAGACCCATCGTGGCGAGACCCATCGTGGTGAGACCCATC

GTGGTGAGACCCATCGTGGCGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGAAATACCCATCGTGG

TGAGACCCACCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCACCGTGGTGAG

ACCCATCGTGGTGACAGAAAAATTTAAATTTCCCTCCAAAATATTTTTTTTCAGAAAAATTTAAATTTCCCTCCAAAATAT

TTTTTCAGAAAAATTTAAATTTCCGCGCAAATATTTTTTCACAGAAAAATTTAAATTTCCGCGCAAATTT

GGGTCTCACCACGAC

GGGTCTCACCACGAT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT
GGGTCTCACCACGGT
GGGTCTCACCACGATGGGCCTCGCCGCGAT
GGGTCTCACCACGGT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGGT
GGGTCTCACCACGATGGGCCTCGCCGCGAT
GGGTCTCACCACGGT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGATGGGCCTCGCCGCGAT
GGGTCTCACCACGGT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCGCCACGAT
GGGTCTCACCACGGT
GGGTCTCACCACGATGGGCCTCGCCGCGAT
GGGTCTCACCACGGT
GGGTCTCACCTCGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGGT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGGT
GGGTCTCACCACGATGGGTATTTCCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCGCCACGAT
GGGTCTCACCACGAT
GGGTCTCGCCACGAT
GGGTCTCACCACGATGGGTCTTTCCACGAT
Nr of selected repeats 69 Similarity 0.943090

Consensus:

GGGTCTCACCACGaT

>Cele-UNSB01_4:4990413-4990623 Satlength=211 Nr of Repeats=6 RepeatLength=35
seed=AATATTTTTT

AATATTTTTTTTCAGAAAATTTAAATTTCCCTCCAA
AATATTTTTTTTCAGAAAATTTAAATTTCCCTCCAA
AATATTTTTTTTCAGAAAATTTAAATTTCCCTCCAA
AATATTTTTTTTCAGAAAATTTAAATTTCTCTCCAA
AATATTTTTTTTCAGAAAATTTAAATTTCCCTCCAA
AATATTTTTTTTCAGAAAATTTAAATTTCCCTCCAA

Nr of selected repeats 6 Similarity 0.964444

Consensus:

AATATTTTTTTTCAGAAAATTaAAATTTCCCTCCAA

>Cele-UNSB01_4:4990696-4991348 Satlength=653 Nr of Repeats=40 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGAC

GGGTCTCACCACGAT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGATGGGCTCGCCGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCCCACGAT

GGGTCTCACCACGT

GGTCTCACCACGATGGGCCTCGCCGAT

GGGTCTCACCACGGT

GGGTCTCACCCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCACCACGATGGGTATTTCCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCGCCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCGCCACGAT

GGGTCTCACCACGATGGGTCTTTCCACGAT

Nr of selected repeats 33 Similarity 0.951515

Consensus:

GGGTCTCACCACGAT

>Cele-UNSB01_4:5061085-5061475 Satlength=391 Nr of Repeats=8 RepeatLength=39

seed=CCAAGTGGAG

CCAAGTGGAGCCAGCACTATGACTGCTGTCCGAGGAGCA

CCAAGTGGAGCCAGCCCTATGACGGCCTTTGGAGGAGCA

CCAAGTGGAGCCAGCACAATGACCGCTGTCCGCGGAGCA

CCAAGTGGAGCCAGCACTATGACGGCCGTTGGAGGAGCA

CCAAGTGGAGCGAGCACAATGACCGCTGTTGGTGGAGCA

CCAAGTGGAGCAAGCACCATGACCGCCGTCGGAGGAGCC

CCAACCGGAGCAAGTACAATGACCGCTGTTGGTGGAGTC
CCAACTGGAGCGTCTACAATGACTGCTATCGGAGGAGCCCCATCTGGTGCTTCCACTATGACCGCTGTGGGAGGTGCTC
CGAGAGGAGCTTCAACCATGACTGCTGTCGGTGGAGCA

Nr of selected repeats 7 Similarity 0.784921

Consensus:

CCAACTGGAGCcAGCACnATGACcGcTtGGaGGAGCa

>Cele-UNSB01_4:5124505-5124705 Satlength=201 Nr of Repeats=12 RepeatLength=16

seed=CTACGTGCCT

CTACGTGCCTACGTGC

CTACGTGTCTACGTGC

CTACGTGCCTACGTGC

CTACGTGCCTACGTGC

CTACGTGCCTACGTGC

CTACGTGCCTACGTGC

CTACGTGCCTACGTGC

CTACGTGCCTACGTGC

CTACGTGCCTACGTGC

CTACGTGCCTACGTGC

CTACGTGCCTACGTGC

CTACGTTCCTACGTGCCTACGTGC

Nr of selected repeats 11 Similarity 0.969697

Consensus:

CTACGTGCCTACGTGC

>Cele-UNSB01_4:5337721-5338093 Satlength=373 Nr of Repeats=18 RepeatLength=12

seed=AGAAGGAGGA

AGAAGGAGGAGA

AGAAAGAGGAGA

AGAAGGAGGAGAAGGAGGATAA

AAAGGAGGAGA

AGAAGGAGGAAA

AGAAGGAAGACGATAAGAAAAGATGAGAAAAAGGATGAGAAAAAGGATGAAAAGGAAGAAGATAAGAAGAGTGAAGATA

AGAAGGAGGATGAAAAAGAAAAAGATGACGATA

AGAAGGAAGACA

AGAAGGATGATAAGAAGAGTGATAATAAGGATGATAAAGATGATGAGAAGAAAGAAGAGAAGAAAGATGATAAAGAGGA

AA

AGAAGGAGGAAA

AGAAGGAGGAAA

AGAAGGAGGAAA

AGAAGGAGGAAA

AGAAGGAGGAAA

AGAAGGAGGAGGAAA

AGAAGGAAGAGA

AGAAAGAGGAAA

Nr of selected repeats 11 Similarity 0.864646

Consensus:

AGAAGGAGGAaA

>Cele-UNSB01_4:5363528-5363903 Satlength=376 Nr of Repeats=15 RepeatLength=25

seed=TTTACTCTCT

TTTACTCTCTGTCTTCACAGTATAT

TTTACTCTCTTGCTTCACAGAATAA

TTTACTCTCTGGCTTCACAGAATAT

TTTACTCACTGGCTTCACAGAATAT

TTTACTCTCTGGCTTCACAGTATAT

TTTACTCTCTGGCTTCAGAGTATAT

TTTACTCTCTGGCTTCACAGAATAA
TTTACTCTCTGGCTTCACAGTATAT
TTTACTCTCTGGCTTCACAGTACAT
TTTACTCTCTGGCTTCACAGAATAA
TTTACTCTCTGGCTTCACAATATAT
TTTACTCTCTGGCTTCACAGAATAA
TTTACTCTCTGGCTTCACAGAATAA
TTTACTCTCTGGATTACAGTATAT
TTTACTCTCTGGCTTCACAGTACAT

Nr of selected repeats 15 Similarity 0.890286

Consensus:

TTTACTCTCTGGCTTCACAGtATAt

>Cele-UNSB01_4:5366596-5366788 Satlength=193 Nr of Repeats=10 RepeatLength=12
seed=TCCTCTTTCT

TCCTCTTTCTTTTCATCCTTCTTTTCTTCCTTCTTTTCTTCCTTATTCTCATCGTTTTTC
TCCTCTTTCTTC
TCCTCTTTCTTC
TCCTCTTTTTTC
TCCTCTTTCTTC
TCCTCTTTCTTC
TCTTCTTTCTTC
TCTTCTTTCTTTGCTTCCTTTTGTTCATCCTTTTTG
TCTTCTTTCTTT
TCCTCTTTCTTC

Nr of selected repeats 8 Similarity 0.896825

Consensus:

TCcTCTTTCTTC

>Cele-UNSB01_4:5521070-5521205 Satlength=136 Nr of Repeats=9 RepeatLength=15
seed=CCACGATGGG

CCACGATGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCAA
CACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGCCTCG
CCACGATGAGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA

Nr of selected repeats 7 Similarity 0.898413

Consensus:

CCACGATGGGTCTCa

>Cele-UNSB01_4:5529418-5534698 Satlength=5281 Nr of Repeats=110 RepeatLength=48
seed=TTGCCCGTAA

TTGCCCGTAATTTATATTTTTCTGAAGATGAGCAATTCAATTTTTGAT
TTGCCCGTAATTTATATTTTTCTGAAGATGAGCAATTCAATTTTTGAT
TTGCCCGTAATTTATATTTTTCTGAAGATGAACAATTCAATTTTTGAT
TTGCCCGTAATTTATATTTTTCTGAAGATGAACAATTCAATTTTTGAT
TTGCCCGTAATTTATATTTTTCTGAAGATGAACAATTCAATTTTTGAT
TTGCCCGTAATTTATATTTTTCTGAAGATGAGCAATTCAATTTTTAAA
TTGCCCGTAATTTACATTTTTCTGAAGATGAGCAATTCAATTTTTGAT
TTGCCCGTAATTTATATTTTTCTGAAGATGAGCAATTCAATTTTTGAT
TTGCCCGTAATTTATATTTTTCTGAAGATGAGCAATTCAATTTTTAAA
TTGCCCGTAATTTACATTTTTCTGAAGATGAGCAATTCAATTTTTGAT
TTGCCCGTAATTTATATTTTTCTGAAGATGAACAATTCAATTTTTGAT

TCCACTGACCA

Nr of selected repeats 5 Similarity 0.951515

Consensus:

TCCACTGACCa

>Cele-UNSB01_4:5945791-5945941 Satlength=151 Nr of Repeats=6 RepeatLength=25

seed=CCAGAGAGTA

CCAGAGAGTAAAGTATACTGGGAAG

CCAGAGAGTAAAATATACTGGGAAG

CCAGAGAGTAAAATATACTGGGAAA

CCAGAGAGTAAAATATAGTGGGAAA

CCAGAGAGTAAAAAATAGTGGGATA

CCAGAGAGTAAAATATAGTGGGATA

Nr of selected repeats 6 Similarity 0.875556

Consensus:

CCAGAGAGTAAAATATAcTGGGAaa

>Cele-UNSB01_4:6076861-6077186 Satlength=326 Nr of Repeats=6 RepeatLength=55

seed=AAGAGTCCCC

AAGAGTCCCCGTACAAATGAAAGGTTTTAAGGATTGGATACCTAGGGTT

AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCTAGGGTT

AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCTAGGGTT

AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCTAGGGTT

AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCTAGGGTT

AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCTAGGGTT

AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCTAGGGTT

Nr of selected repeats 4 Similarity 1.000000

Consensus:

AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCTAGGGTT

>Cele-UNSB01_4:6158202-6158352 Satlength=151 Nr of Repeats=6 RepeatLength=25

seed=TTTACTCTCT

TTTACTCTCTGGCTTCACAGAATAA

TTTACTCTCTGGCTTCACAGTATAT

TTTACTCTCTGGCTTCACAGTATAA

TTTACTCTCTGGTTTTACAGTATAT

TTTACTCTCTGGCTTCACAGAATAA

TTTACTCTCTGGCTTCACAGAATAT

Nr of selected repeats 6 Similarity 0.882667

Consensus:

TTTACTCTCTGGCTTCACAGaATAa

>Cele-UNSB01_4:6277867-6278002 Satlength=136 Nr of Repeats=7 RepeatLength=19

seed=ATTGACAGAC

ATTGACAGACGAAAAAATAG

ATTGACAGACGAAAAAATAG

ATTGACAGACGAAAAAATAG

ATTGACAGACGAAAAAATAG

ATTGACAGACGAAAAAATAG

ATTGACAGACGAAAAAATAT

ATTGACAGACGAAAAAATAG

Nr of selected repeats 5 Similarity 0.971930

Consensus:

ATTGACAGACGAAAAATAg

>Cele-UNSB01_4:6359332-6359386 Satlength=55 Nr of Repeats=4 RepeatLength=13

seed=TTTCATTTGT

TTTCATTTGTTATTG

TTTCATTTGTAAT

TTTCATTTGTAGT

TTTCATTTGTAAT

Nr of selected repeats 3 Similarity 0.931624

Consensus:

TTTCATTTGTAaT

>Cele-UNSB01_4:6425603-6430447 Satlength=4845 Nr of Repeats=192 RepeatLength=25

seed=TTAGAGTAAA

TTAGAGTAAATAAAATTGGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGGAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATGTATTGGCAGAACA
TTAGAGTAAATATATTGGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGGAGAACA
TTAGAGTAAATAAAATTGGCAGAACA
TTAGAGTAAATATATTGGCAGAACA
TTAGAGTAAATAAAATTAGCAGGATG
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAATAAAATAAAATTAGGAGAACA
TTAGAGTCAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTGGCAGAACA
TTAGAGTAAATAAAATTGGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
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TTAGAGTAAATGTATTGGCAGAACA
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TTAGAGTAAATAAAATTAGCAGAACA
TTAGAATAAAATAAAATTAGGAGAACA
TTAGAGTAAATAAAATTGGCAGAACA
TTAGAGTAAATATATTGGCAGAACA
TTAGAGTAAATAAAATTAGCAGGATG
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAATAAAATAAAATTAGGAGAACA
TTAGAGTAAATATATTGGCAGAACA

TTAGAGTAAATAAAATTAGCAGAACA
TTAGAATAAATAAAATTAGGAGAACA
TTAGAGTAAATAAAATTGGCAGAACA
TTAGAGTAAATATATTGGCAGAACA
TTAGAGTAAATATATTGGCAGAACA
TTAGAGTAAATAAAATTAGCAGGATG
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGGAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATAAAATTAGCAGAACA
TTAGAGTAAATATATTGGCAGAACA
TTAGAGTCAATAAAATTAGCAGAACA
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Nr of selected repeats 177 Similarity 0.908867

Consensus:

TTAGAGTAAATAAAATTAGCAGAACA

>Cele-UNSB01_4:6539759-6539908 Satlength=150 Nr of Repeats=10 RepeatLength=12
seed=CAGAATATAT

CAGAATATATTC
CAGAATATATTC
CAGAATATATTT
CAGAATATATTC
CAGAATATATTTTCAGATATTC
CAGAATATATTT
CAGAATATATTC
CAAAATATATTC
CAGAATATATTTTCAGATATTC
CAGAATATATTTCAAATGTATTC

Nr of selected repeats 7 Similarity 0.915344

Consensus:

CAGAATATATTC

>Cele-UNSB01_4:6669007-6669090 Satlength=84 Nr of Repeats=4 RepeatLength=22
seed=AAGCGGTAAC

AAGCGGTAACGTTCGTCTATATA
AAGCGGTAACGTTCGTCTATATA
AAGCGGTAACGTTCGTCTATATA
AAGCGGTAACGTTATAT

Nr of selected repeats 3 Similarity 1.000000

Consensus:

AAGCGGTAACGTTCGTCTATATA

>Cele-UNSB01_4:6734929-6735237 Satlength=309 Nr of Repeats=9 RepeatLength=31
seed=CCCGCCAAAA

CCCGCCAAAAATTTTTTGAAAAAATTTAATT
CCCGCCAAAAATTTTTTGAAAAAATTTGAATT
CCCGCCAAAAATTTTTTGAAAGAAATTCGGATT
CCCGCCAAAAATTTTTTGAAAAAATTTGAATT
CCCGCCAAAAATTTTTTGAAAAAATTTAAATT
CCCGCCAAAAATTTTTTGAAAAAATTTGAATT
CCCGCCAAAAATTTTTTGAAAAAATTTAAATTCCCGCGTAAATTTTTTGAAAAAATTTGAATT
CCCGCCAAAAATGTTTTGAAAAAATTTAAATT
CCCGCCAAAAATTTTTTAAAAAATTTGAATT

Nr of selected repeats 7 Similarity 0.897593

Consensus:

CCCGCCAAAAATTTTTTGAAAAAATTTgAATT

>Cele-UNSB01_4:6945378-6946401 Satlength=1024 Nr of Repeats=11 RepeatLength=93
seed=TGCTTCTCGT

TGCTTCTCGTCCACCACCACCACCGAAGGGAAGTGAAGTCCACCACCACCACCAACTGGAGAACCACAGGATCTT
TCTGGAGAAGGTAA
TGCTTCTCGTCCACCACCACCACCGAAGGGAAGTGAAGTCCACCACCACCACCAACTGGAGAACCACAGGATCTT
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TGCTTCTCGTCCACCACCACCACCGAAGGGAAGTGAAGTCCACCACCACCACCAACTGGAGAACCACAGGATCTT
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Nr of selected repeats 11 Similarity 0.961942

Consensus:

TGCTTCTCGTCCACCACCACCGAAGGGAAGTGAAGTCCACCACCACCACCAACTGGAGAACCACAGGATCTT
TCTggAGAAGGTAA

>Cele-UNSB01_4:7151737-7153750 Satlength=2014 Nr of Repeats=178 RepeatLength=11
seed=TGACAACCTC

TGACAACCTCG

TGACAACTTCA
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GACAACTTCG
TGGCAACTTCG
TGACAACTTCGG
GACAACTTCG
TAACAACCTTCGTGAAAACCTCA
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TGACAACTTTG
TGACAACGTCA
TGATAACTTCGG
GACAACTTCGG
GACAACTTCG
TGACAACTTCG
TGACAACTTCG
TGACAACTTCA
TGACAACTTTG

Nr of selected repeats 131 Similarity 0.801993

Consensus:

TGACAACTTCg

>Cele-UNSB01_4:7464716-7464914 Satlength=199 Nr of Repeats=5 RepeatLength=40
seed=TCCAGAATTT

TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTCCCGATTTTCTAGAAAGTTCTGGAACAC
TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTTCGAAATTTCCAGAAGATTCTAGATT

Nr of selected repeats 4 Similarity 0.966667

Consensus:

TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACat

>Cele-UNSB01_4:7464933-7465143 Satlength=211 Nr of Repeats=6 RepeatLength=35
seed=CAGAAAATTT

CAGAAAATTTAAATTTCCCGCCAAAATATTTTTCT
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTCA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTCT
CAGAAAATTTAAATTTCCCTCAAAATATTTTTTT
CAGAAAATTTAAATTTCCCTCAAAATATTTTTTT
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTCA

Nr of selected repeats 6 Similarity 0.926349

Consensus:

CAGAAAATTTAAATTTCCCGC AAAATATTTTTct

>Cele-UNSB01_4:7464716-7465331 Satlength=616 Nr of Repeats=6 RepeatLength=40
seed=TCCAGAATTT

TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTCCCGATTTTCTAGAAAGTTCTGGAACAC
TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTTTCGAAATTTCCAGAAGATTCTAGATT
TCCAGAATTTTAGAATTTTCAGAAAATTTAAATTTCCCGCCAAAATATTTTTCTCAGAAAATTTAAATTTCCCGCCAAA
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TTAAATTTCCCGTCAAAATTTGGGTCTTACCACGATGGGTCTCACCACGACGGGTCTCACCACGATGGGTCTCACCTC
GATGGGTCTCACCACGATGGGTCTCACCACGATGGGTCTCGCCACGAAGATCTCGCAGCAACATTTTTTTATTTTTGAT
TTTTCAGAAGGTTCTAGAATAA

Nr of selected repeats 4 Similarity 0.966667

Consensus:

TCCAGAATTTTctCGATTTTCTAGAAAGTTCTGGAACat
>Cele-UNSB01_4:7715733-7715854 Satlength=122 Nr of Repeats=6 RepeatLength=17
seed=CTCATTGCCT
CTCATTGCCTACCCTTG
CTCATTGACTACCCTTG
CTCTTTGCCTACCTCTTT
CTCATTGACTACCTGTG
CTCATTGCCTTCCTGTT
CTCATTGCCTACTTGTTCGTTGACTACCTTTT
Nr of selected repeats 4 Similarity 0.764706
Consensus:
CTCATTGaCTaCCcgTg

>Cele-UNSB01_4:7767635-7768760 Satlength=1126 Nr of Repeats=25 RepeatLength=45
seed=AGCACCA
AGCACCAATCAGGCGGACCACCAGGACCATTTGATCCATCAGG
AGCACCAATCAGGCGGACCACCAGGACTATTTGATCCATCAGG
AGCACCAATCAGGCGGACCACCAGGACCATTTGGTCCATCAGG
AGCACCAATCAGGCGGACCACCAGGACCATTTAATCCATCAGA
AGCACCAATCAGGCGGACCAACAGGACCATTTGATCCTTCAGG
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AGCACCAATCAGGCGGACCACCAGGACCATTTGATCCTTCAGG
Nr of selected repeats 25 Similarity 0.965432
Consensus:

AGCACCAATCAGGCGGACCACCAGGACCATTTgATCCaTCAGG
>Cele-UNSB01_4:8048486-8048578 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=CGAAAAGGGG
CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAGATA
CGAAAAGGGGAGCAA
Nr of selected repeats 5 Similarity 0.768889
Consensus:
CgAAAAGGGGAgcta

>Cele-UNSB01_4:8048753-8048845 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCTTTTC
TCCCCTTTTCGTTGC
TCCCCTTTTCGTATC
TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA
TCCCCTTTTTCGAGA
TCCCCTTTTCGTTCTGC

Nr of selected repeats 5 Similarity 0.768889

Consensus:

TCCCCTTTTcGtagc

>Cele-UNSB01_4:8107145-8107415 Satlength=271 Nr of Repeats=18 RepeatLength=15

seed=CTCACCACGA
CTCACCACGAAGGGT
CTCACCACGATGGGT
CTCGCCACGATGGGT
CTCGCCACGATGGGT
CTCGCCACGATGGGT
CTCACCACGAAGGGT
CTCACCACGATGGGT
CTCATCACGAAGGGT
CTCACCACGATGGGT
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CTCATCACGAAGGGT
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CTCACCACGATGGGT
CTCACCACGATGGGT

Nr of selected repeats 18 Similarity 0.902977

Consensus:

CTCACCACGA^tGGGT

>Cele-UNSB01_4:8289359-8289627 Satlength=269 Nr of Repeats=6 RepeatLength=45

seed=TCTGATCCTT
TCTGATCCTTCAGCTCCGAAGGATCGTAAGGGTACCTCCTGATGG
TCTGATCCTTCAGCTCCAAAGGATCACGAGGCTCTTCCTGATGT
TCTGATCCTTCAGCTCCGAAGGATCACATGGGCACCTTCTGATGA
TCTGATCCTTCAGATAAGAAGGATCGTAAGGGTGCCTCCTGATGG
TCTGATCCTTCAGCTCCGAAGGATCGTAAGGGTACCTCCTGATGG
TCTGATCCTTCAGCTCCAAAGGATCACGAGGCTCTTCCTGATGT

Nr of selected repeats 4 Similarity 0.851852

Consensus:

TCTGATCCTTCAGcTccGAAGGATCgtAaGGGtaCCTcCTGATGg

>Cele-UNSB01_4:8500583-8501255 Satlength=673 Nr of Repeats=21 RepeatLength=32

seed=TTTTACAGAA
TTTTACAGAAATTTTGAATTCCCGCCACAAT
TTTTACAGAAATTTTGAATTCCCGCCAAAAT
TTTTACAGAAAACCTTGAATTCCCGTTAAAAT
TTTTACAGAAATTTTGAATTCCCGCCAAAAT
TTTTACAGAAAATGTGAATTCCCGCCAAAAT
TTTTACAGAAAATTTTGAATTCCCGCCAAAAT
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TTTTCACAGAAAATTTGAATTCCCGCCAAAAT
TTTTCACAGAAAATTTGAATTCCCGCCAAAAT
TTTTCACAGAAAATTTGAATTCCCGCTAAAAA
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TTTTCACAGAAAATTTGAATTCCCGCCAAAAT
TTTTCACAGAAAATTTGAATTCCCGCCAAAAT
TTTTCACAGAAAATTTGAATTCCCGTTAAAAA
TTTTCACAGAAAATTTGAATTCCCGCCAAAAT
TTTTCACAGATATTTGAATTCTCGCCAAAAGT

Nr of selected repeats 21 Similarity 0.903571

Consensus:

TTTTCACAGAAAAtTtTGAATTCCCGCCAAAAT

>Cele-UNSB01_4:8501471-8501871 Satlength=401 Nr of Repeats=10 RepeatLength=40
seed=AGAAGGTTCT

AGAAGGTTCTGGAACATTCCAGCATTTTCTCAAATTTTCC
AGAAGGTTCTGGAACATTCCAGAAATTTTCTCAAATTTTCC
AGAAGGTTCTGGAACATTCCAGAAATTTTCTCGGATTTTCC
AGAAGGTTCTGAAACATTCCAGAAATTTTCTCAAATTTTCC
AGAAGGTTCTGGAACATTCCAGAAATTTTCTCAAATTTTCC
AGAAGGTTCTGGAACATTCCAGAAATTTTCTCGGATTTTCC
AGAAGGTTCTGGAACATTCCAGAAATTTTCTCAAATTTTCC
AGAAGGTTCTGGAACATTCCAGAAATTTTCTCGGATTTTCC
AGAAGGTTCTGGAACATTCCAGAAATTTTCTCGAATTTTCC

Nr of selected repeats 10 Similarity 0.953333

Consensus:

AGAAGGTTCTGGAACATTCCAGAAATTTTCTCaaATTTTCC

>Cele-UNSB01_4:8501476-8504168 Satlength=2693 Nr of Repeats=54 RepeatLength=40
seed=GTTCTGGAAC

GTTCTGGAACATTCCAGCATTTTCTCAAATTTTCCAGAAG
GTTCTGGAACATTCCAGAAATTTTCTCAAATTTTCCAGAAG
GTTCTGGAACATTCCAGAAATTTTCTCGGATTTTCCAGAAG
GTTCTGAAACATTCCAGAAATTTTCTCAAATTTTCCAGAAG
GTTCTGGAACATTCCAGAAATTTTCTCAAATTTTCCAGAAG
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GTAATCCTACAGTACTCCTACAGTACCTCTACAGTACAACCTACAGTACCCCAACCATATCCCGACACTAACCCCAAAGC
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GTTCTGGAACATTCCAGAATTTTCCCGATTTTTCTAGAAA
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Nr of selected repeats 51 Similarity 0.884078

Consensus :

GTTCTGGAACaTTCCAGAATTTTctCgAtTTTTCTAGAAa

>Cele-UNSB01_4:8504239-8504449 Satlength=211 Nr of Repeats=6 RepeatLength=35

seed=GAAAATTTAA

GAAAATTTAAATTTCCCGCCAAAATATTTTTCTCA
GAAAATTTAAATTTCCACCAAATATTTTTTTCA
GAAAATTTAAATTTCCCTCCAAATTTTTTTCTCC
GAAAATTTAAATTTCCCTCCAAATATTTTTTTCA
GAAAATTTAAATTTCCCTCCAAATATTTTTTTCA
GAAAATTTAAATTTCCCGCCAAAATATTTTTCACA

Nr of selected repeats 6 Similarity 0.898413

Consensus :

GAAAATTTAAATTTCCCTCCAAAATATTTTTcTCA

>Cele-UNSB01_4:8504495-8505035 Satlength=541 Nr of Repeats=35 RepeatLength=15

seed=TCTCACCACG

TCTCACCACGACGGG

TCTCACCACGATGGG

TCTCACCACGATGGA

TCTCACCACGATGGG

Nr of selected repeats 34 Similarity 0.956744

Consensus:

TCTCACCACGATGGG

>Cele-UNSB01_4:8600392-8600896 Satlength=505 Nr of Repeats=13 RepeatLength=11

seed=CTACAGTACT

CTACAGTACTC

CTACAGTACTA

CTACAGTACCTTGACATTATCCCCCAGCAACTCCCAACCCAATACCTCTTCTGTAGACAAAACTCAATTTTTCTTAA

ACTACAGTAACCTACCGTGTAT

CTACAGTACTT

CTACAGTACTA

CTACAGTACCTTGACATTATCCCCCAGCAACTCCCAACCCAATACCTCTTCTGTAGACAAAACTCAATTTTTCTTAA

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CTACAGTACCA

CTACAGTACCTTGACATTATCCCTCACCAACTCCCAACCCAAAACCTCTTCTGTAGACAAAACTCAATTTTTCCCAA

CTACAGTAACCCTACCGTATAC

CTACAGTACTC

Nr of selected repeats 9 Similarity 0.865320

Consensus:

CTACAGTACTn

>Cele-UNSB01_4:8607400-8623699 Satlength=16300 Nr of Repeats=831

RepeatLength=20 seed=ATACGATATA

ATACGATATAGCTATAAACG

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Nr of selected repeats 721 Similarity 0.881205

Consensus:

ATACGATATAGCTaTttACG

>Cele-UNSB01_4:8831351-8831453 Satlength=103 Nr of Repeats=6 RepeatLength=17

seed=TTCATTCCGT

TTCATTCCGTGATTATT

TTCATTCCGTGATTATT

TTCATTCCGTGATTATT

TTCATTCCGTGATTATT

TTCATTCCGTGATTATT

TTCATTCCGTGATTATT

Nr of selected repeats 6 Similarity 1.000000

Consensus:

TTCATTCCGTGATTATT

>Cele-UNSB01_4:9041393-9041548 Satlength=156 Nr of Repeats=8 RepeatLength=17

seed=AGGCAATGAG

AGGCAATGAGAAAGAGT

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AGGCAATGAGAAAGAGT

AGGCAATGAGAAAAGGTAGTCAACGAGCAACAAGTG

GGCAATGAGAACAGGA

AGGCAATGAGCACAGGT
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AGGCAAAGAGCAAGGGT
Nr of selected repeats 5 Similarity 0.781482
Consensus:
AGGCAAtGAGaAAGaGT
>Cele-UNSB01_4:9095021-9107795 Satlength=12775 Nr of Repeats=451
RepeatLength=27 seed=ATAGTGGGAA
ATAGTGGGAAGCCACAGAGAGTAAATA
ATAGTGGGAAGCCACAAAGAGAGTAGAAGTAAATATTGTGAAGCCAAGAAGAAATAAGGGGCCAGAGAGTAAATAATAG
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ATACATTGTGGGGATTTCCCACTATGTCGATACATTGTAAGGATTTCCCACTATGTCGATACATTGTGGGGATTTTCGAC
Nr of selected repeats 334 Similarity 0.885216

Consensus:

ATAGTGGGAAGCCACAGAGAGTAaAAT

>Cele-UNSB01_4:9125039-9126314 Satlength=1276 Nr of Repeats=76 RepeatLength=15

seed=CTCACCACGA

CTCACCACGATGGGT

CTCACCACGAAGGGT

CTCACCACGATGGGC

CTCACCACGAAGGGT

CTCACCACGAAGGGT

CTCACCACGATGGGT

CTCACCACGATGGGT

CTCACCACGATGGGT

CTCACCACGAAAGGTCTCGCCACAATGGGT

CTCACCACGATGGGT

CTCACCACGAAAGGTCTCAATACGAAGGGT

CTCACCACGAAGGGT

CTCACCACGATGGGT

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CTCACCACGATGGGT

CTCACCACGATGGGT

Nr of selected repeats 55 Similarity 0.889240

Consensus:

CTCACCACGAtGGGT

>Cele-UNSB01_4:9469814-9470654 Satlength=841 Nr of Repeats=56 RepeatLength=15

seed=ACGATGGGTC

ACGATGGGTCTCACC

ACGATGGGTCTCACC

ACGATGGGTCTCACC

ACGATGGGTCTCACC

ACGATGGGTCTCGCC

ACGATGGGTCTCGCC

ACGATGGGTCTCGCT

ACGATGGGTCTCACC

ACGATGGGTCTTTCC

ACGATGGGTCTCACC

ACGGTGGGTCTCGGC

ACGATGGGTCTCACC

ACGATGGGTCTCACC

ACGATGGGTCTTTCC

ACGATGGGTCTCACC

ACGGTGGGTCTCGCC

ACGATGGGTCTCGCC

ACGATGGGTCTCGCC

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ACGACGGGTCTCACC
ACGATGGGTCTCACC
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ACGATGGGTCTTTCC
ACGATGGGTCTCACC
ACGGTGGGTCTCGCC

Nr of selected repeats 56 Similarity 0.902684

Consensus:

ACGATGGGTCTCnCC

>Cele-UNSB01_4:9470711-9470851 Satlength=141 Nr of Repeats=5 RepeatLength=30
seed=AATTTTCCAG

AATTTTCCAGAAGGTTCTAGAACAATCCAGAATTTTTTCG

AATTTTCCAGAAGGTTCTGGAACATTCCAG

AATTTTCTAG

AATTTTCCAGAAGGTTCTAAAGCTTTTCAG

AATTTTCCAGAAGGTTCTGGAACATTCTAG

Nr of selected repeats 3 Similarity 0.822222

Consensus:

AATTTTCCAGAAGGTTCTggAaCaTtccAG

>Cele-UNSB01_4:9470964-9471243 Satlength=280 Nr of Repeats=10 RepeatLength=11
seed=GTACTCCTAC

GTACTCCTACC

GTACTCCTACA

GTACTCCTACAGTACTATTACAGTACCCCGACCATATCCACTACTAACC GCAAACCTATATCTCTTCAAAGACAAAA

ACACAATTTTTTCATAAACTACA

GTAATCCTACC

GTACTCCTACA

GTACTCCTACA

GTACTCCTACA

GTACTACTACAGTACCCCGACCATATCCCACTACTAACCTCAAACCTATATCTCTTCAAAGACAAAAACACAATTTTT

CCCAAACCTACA

GTAATCCTACC

GTACTCCTACA

Nr of selected repeats 8 Similarity 0.883117

Consensus:

GTAcTCCTACa

>Cele-UNSB01_4:9493015-9493149 Satlength=135 Nr of Repeats=4 RepeatLength=11
seed=CCCTACAGTA

CCCTACAGTAC

CCCTACAGTACTACTACAGTACCTTGACATTATCCATCACCAACTCCCAACGCAATATCCCTTCAAAGCTGAACAACC

AAAATTTCTAAACTACAGTAA

CCCTACAGTAA

CCCTACAGTAC

Nr of selected repeats 3 Similarity 0.919192

Consensus:

CCCTACAGTAc

>Cele-UNSB01_4:9825630-9825857 Satlength=228 Nr of Repeats=5 RepeatLength=45
seed=GGGTACCTCC

GGGTACCTCCTGATGATCTGATCCTTCAGCTTCAAAGGATCAGAA

GGGTACCTCCTGGTGATCTGATCCTTAAGCTCCGAAGGATCACAGG

GGGTACCTCCTGGTGATCTGATCCTTCAGCTCCGAAAGATCAGAA
GGGTACCTCCTGGTGATCTGATCCTTAAGCTCCGAAGGATCACAGG
GGGTACCTCCTGGTGATCTGATCCTTCAGCTCCGAAAGATCAGAA

Nr of selected repeats 3 Similarity 0.920988

Consensus:

GGGTACCTCCTGgTGATCTGATCCTTCAGCTcCgAAaGATCAGAA

>Cele-UNSB01_4:10086561-10087053 Satlength=493 Nr of Repeats=10 RepeatLength=11
seed=TACTGTAGGG

TACTGTAGGGT

TACTGTAGGGTTACTGTAGTTTAGGAAATTTTGATTTTTTCAGCTTTTGAAGGGATATTGCGTTGGGAGTTGGTGATGGA

TAATGTCAAGGTACTGTAGTAGTACTGTCTGGTG

TACTGTAGGGTTACTGTAGTTTAGGAAATTTTGATTTTTTCAGCTTATGAATGGATATTGCGTTGGGAGTTGGTGATGGA

TAATGTCAAGGTACTGTAGTAG

TACTGTAGGGG

TACTGTAGGGT

TACTGTAGGGTTACTGTAGTTTGGCAAATTTTGATTTTTTCAGCTTTTGAAGGGATATTGGGTTGGGAGTTGGTGATGAA

TAATGTCAAGGTACTGTAGTAG

TACTGTAGGGG

TACTGTAGGGT

TACTGTAGGGT

TACTATAGGGTTACTGTAGTTTAGGAAATTTTGATTTTTTCAGCTTTTGAAGGGATATTGCGTTGGGAGTTGGTGATGGA

TAATGTCAAGGTACTGTAGTAGTACTGTAGTAG

Nr of selected repeats 6 Similarity 0.935354

Consensus:

TACTGTAGGGT

>Cele-UNSB01_4:10323949-10324337 Satlength=389 Nr of Repeats=26 RepeatLength=15

seed=GACCCATCGT

GACCCATCGTGACGA

GACCCATCGTGGTGA

GACCCATCGTGGTGA

GACCCATCGTGGTGA

GACCCATCGTGGTGA

GACCCATCGTGGTAA

GACCCATCGTGGTGA

GACCCATCGTGGCGA

GACCCATCGTGACGA

GACCCATCGTGGTGA

GACCCATCGTGGTGA

GACCCATCGTGGTGA

GACCCATCGTGACGA

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GACCCATCGTGGTGA

GACCCATCGTGACGA

GACCCATCGTGGTGA

GACCCATCGTGGT

GACCCATCGTGGTGA

GACCCGTCGTGCTGA

GACCCATCGTGGTGA

GACCCGTCGTGCTGA

GACCCATCGTGGTGA

GACCAATCGTGGTGA

Nr of selected repeats 25 Similarity 0.898074

Consensus :

GACCCATCGTGgtGA

>Cele-UNSB01_4:10324370-10326780 Satlength=2411 Nr of Repeats=67

RepeatLength=35 seed=GAAATTCAAA

GAAATTCAAATTTTCAGTGAAAAAATTTTGGCGG
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GAAATTCAAATTTTCAGTGAAAAAATTTTAGCGG
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ATTGTTACACGAAAAATAG

Nr of selected repeats 20 Similarity 0.967867

Consensus:

ATTGTTACACGAAAAATAG

>Cele-UNSB01_4:11013752-11031328 Satlength=17577 Nr of Repeats=392

RepeatLength=45 seed=TCCTGGTGAT

TCCTGGTGATCTGATCCTTAAGCTCCGAAGGATCAGAAGGGTACC
TCCTGGTGATGTGATCCTTAAGCTCCGAAGGATCACAGGGGTACC
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Nr of selected repeats 347 Similarity 0.928761
Consensus :

TCCTGGTGATCTGATCCTTaAGCTcCgAAGGATCAgAaGGGTACC
>Cele-UNSB01_4:11032975-11034460 Satlength=1486 Nr of Repeats=33
RepeatLength=45 seed=TCACCAGGAG
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TCACCAGGAGGTACCCTTGTGATCCTTCGGAGCTGAAGGATCAGA
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Nr of selected repeats 33 Similarity 0.911616

Consensus:

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RepeatLength=26 seed=G TTCACCAAA

G TTCACCAAAATTTAGTGACTCTGGCC

G TTCACCAAAATTTAGTGACTCTGGCC

G TTCACCAAAAATAGTGACTCTGGCC

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G TTCACCAAAATTTAGTGACTCTGGCC

G TTCACCAAAATTTAGGCC

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Nr of selected repeats 331 Similarity 0.919481

Consensus:

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>Cele-UNSB01_4:11083607-11084360 Satlength=754 Nr of Repeats=4 RepeatLength=11
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TTTGAATATA

TTTGAATATA

TTTGAATATA

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TTTGAATATA

>Cele-UNSB01_4:11084695-11084799 Satlength=105 Nr of Repeats=4 RepeatLength=26
seed=CCAGAGTCAC

CCAGAGTCACTATGTTTGGTGAAGT

CCAGAGTCACAATTTTTTGGTGAACAA

CCAGAGTCACTATTTTTAGTGAAGT

CCAGAGTCACTATTTTTAGTGAAGT

Nr of selected repeats 4 Similarity 0.863248

Consensus :

CCAGAGTCACtATtTTTaGTGAActg

>Cele-UNSB01_4:11101964-11102048 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=AAATCTAATC

AAATCTAATCCAATGTGGAAC

AAATCTAATCCAATATGGCCG

AAATCTAATCCAATATGGAAC

AAATCTAATCAAATATGGTCG

Nr of selected repeats 4 Similarity 0.777778

Consensus :

AAATCTAATCcAAATaTGGaaCg

>Cele-UNSB01_4:11132963-11135728 Satlength=2766 Nr of Repeats=35
RepeatLength=79 seed=GAAACTAAAA

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GAAACTAAAAACCTAATGAGACCCCAGAATACTGCCGGTATTCTGTCAGGACTCATTAGGTAGAGAGGAGACTTCACAGAA

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Nr of selected repeats 35 Similarity 0.918347

Consensus :

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>Cele-UNSB01_4:11180885-11199179 Satlength=18295 Nr of Repeats=470

RepeatLength=39 seed=TTTATGAAAA

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Nr of selected repeats 322 Similarity 0.947627

Consensus:

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>Cele-UNSB01_4:11742877-11743140 Satlength=264 Nr of Repeats=13 RepeatLength=17
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Nr of selected repeats 10 Similarity 0.809259

Consensus:

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>Cele-UNSB01_4:12149712-12149981 Satlength=270 Nr of Repeats=10 RepeatLength=11
seed=GTACTGTAGG

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TACTGTAGGATTACTGTAGTTTTGGAAAAATTGACTTTTTGTCTTTTGAAGTGATATTGGTTTGAGGTTAGTGGTGGGA
TATGGTCGGG
GTACTGTAGTA
GTACTGTAGTA
GTACTGTAGGA
GTACTGTAGGATTACTGTATTTTTGAAAAAATTGGTTTTTCGTCTTTTGAAGTGATATTGCTTTTGGGTTAGTGTCCG
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GTACTGTAGTT
GTACTGTAGAG
GTACTGTAGGA

Nr of selected repeats 7 Similarity 0.832612

Consensus:

GTACTGTAGna

>Cele-UNSB01_4:12150067-12150386 Satlength=320 Nr of Repeats=8 RepeatLength=40
seed=TCCAGAACT

TCCAGAACCTTCTGGAAAAATTCGAGAAAAATCTGGAATGT
TCCAGAACCTTCTGGAAATCCGAGAAAAATCTGGAATGT
TCCAGAACCTTCTGGAAAAATTCGAGAAAAATCTGGAATGT
TCCAGAACCTTCTGGAAAAATCCGAGAAAAATCTGGAATGT
TCCAGAACCTTCTGGAAAAATTTGAGAAAAATGCTGGAATGT
TCCAGAACCTTCTGGAAAAATTTGTAAAAATCTGGAATGT
TCCAGAACCTTCTGGAAAAATTCGAGAAAAATCTGGAATGT
TCCAGAACCTTCTGGAAAAATTTGAGAAAAATGCTGGAATGT

Nr of selected repeats 7 Similarity 0.946032

Consensus:

TCCAGAACCTTCTGGAAAATTCGAGAAAATtCTGGAATGT

>Cele-UNSB01_4:12150586-12159522 Satlength=8937 Nr of Repeats=274

RepeatLength=32 seed=CGGGAATTCA

CGGGAATTCAAATTTTCTGTGAAAAATTTTGG

CGGGAATTCAAATTTTCTGTGAAAAATTTTGG

CGGGAATTCAAATTTTCTTTGAAAAATTTGGG

CGGGAATTCAAATTTTGTGAAAAATTTTGG

CGGGAATTCAAATTTTCTGTGAAAAATTTTGG

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CGGGAATTCAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAGAAATTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTCTTTGAAAAATTTGGG

Nr of selected repeats 262 Similarity 0.923743

Consensus:

CGGGAATTCAAaTTTCTGTGAAAAATTTTGG

>Cele-UNSB01_4:12289740-12290350 Satlength=611 Nr of Repeats=8 RepeatLength=35
seed=AAATTTGAAT

AAATTTGAATTTCCCGTCAAAATCTTTTTCTCAGA

AAATTTGAATTTCCCGCCTAAAAATTTTTCTTGG

AAATTTGAATTTCCCGCCTAAAAATTTTTCTCATAAATTTGAAGTTCTCGCCCATATTTTTAAGGGTCCCACCACGAT

GGGTCTCGCCAGTTCGAGGTGGTACTTAAGCTAACAAAAAGTTTCTCAGA

AAATTTGAATTTCCCGCCTAAAAATTTTTCTCAGAAATTTGAGTTTTCGGTCAAAATTTATGGGTCTCACCACGAATG

TTCCAGAATTTTTTTCGAATTTCCAGAAGTTCTGGAATTTCCAGAAGTTCTGGAATTTCCAGAAGTTCTGGAA

CATTCCAGAATTTTCTCGAATTTCCAGAAGTTCTAGAATTTATAGAATTTTCTGGAATTTTCCAGATGATTCCAAA

CCAAAATTGAAATTTCCCGCCTAAAAATTTTTCTCAGA

AAATTTGAATTTCCCTCAAAAAATTTTTTTACTGA

AAATTTGAATTTCCCTGCTAAAAATTTTTTTCACTGA

AAATTTGAATTTCCCGCCTAAAAATTTTTTTCACTGA

AAATTTGAATTTCCCGCCTAAAAATTTTTTTCACTTA

Nr of selected repeats 5 Similarity 0.847619

Consensus:

AAATTTGAATTTCCcgccAAAAAttTTTTTcaCtgA

>Cele-UNSB01_4:12303349-12310067 Satlength=6719 Nr of Repeats=128

RepeatLength=59 seed=TCCATAATTC

TCCATAATTCCTCAGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAATCCATATTT

TCCATAATTCCTCAGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTAATAT

TCCATAATTCCTCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

TCCATAATTCCTCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

TCCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

TCCATAATTCCTCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

TCCATAATTCCTCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

TCCATAATTCCTCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

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TCCATAATTCCTCAGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

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TCCATAATTCCTCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

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TCCATAATTCCTCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

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TCCATAATTCCTCATAATTCCTCGTTTTAAAAATTTTGGAAACCAGTGAAGTCTTGATAT

Nr of selected repeats 5 Similarity 0.991667

Consensus:

GGTTGATTTGCGGCACTCTACAGATAGTGGATCTGCTTCTTACCAATCTTCCCGTTACCGCCACGCACTtAAGCTCCAA
ACTATTTTATTTTTTTTG

>Cele-UNSB01_4:12476016-12476336 Satlength=321 Nr of Repeats=18 RepeatLength=16

seed=GTGCCTACGT

GTGCCTACGTGCCTAC

GTGCCTACGTGCCTAC

GTGTCTACGTGCCTAC

GTGCCTACGTGCCTAC

GTTCCCTACGTGCCTGC

GTGCCTGCGTGCCTACGTACCTTC

GTGCCTACGTGCCTACGTACCTTC

GTGCCTACGTGCCTAC

GTGCCTATGTGCCTAC

GTGCCTACGTGCCTAC

GTCCCTACGTTCCCTAC

GTGCCTACGTGCCTAC

GTGCCTACGTGCCTACGCGCTAT

GTGCCTACGTGCCTAT

GTGCCTACGTCCCTAC

GTTCCCTACGTGCCTAC

GTGCCTACGTGCCTACGCGCTAT

GTGCCTACGTGCCTAT

Nr of selected repeats 14 Similarity 0.887363

Consensus:

GTgCCTACGTGCCTAC

>Cele-UNSB01_4:12649750-12649885 Satlength=136 Nr of Repeats=5 RepeatLength=27

seed=ACAATAAAGT

ACAATAAAGTACTATGTATTACCGTAT

ACAATAAAGTACTATGTATTACCGTAT

ACAATAAAGTACTATGTATTACCGTAT

ACAATAAAGTACTATGTATTACCGTAT

ACAATAAAGTACTATGTATTACCGTAT

Nr of selected repeats 5 Similarity 1.000000

Consensus:

ACAATAAAGTACTATGTATTACCGTAT

>Cele-UNSB01_4:12734217-12734312 Satlength=96 Nr of Repeats=5 RepeatLength=19

seed=AAAAATAGAT

AAAAATAGATTGGCAGACG

AAAAATAGATTGACAGACG

AAAAATAGATTGACAGACG

AAAAATAGATTGACAGACG

AAAAATAGATTGACAGACG

Nr of selected repeats 5 Similarity 0.971930

Consensus:

AAAAATAGATTGaCAGACG

>Cele-UNSB01_4:12770724-12770816 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA

CGAAAAGGGGATCTG

CAAAAAGGGGATCTG

CGAAAAGGGGAGATA

CGAAAAGGGGAGATA

CGAAAAGGGGAGCAA

Nr of selected repeats 5 Similarity 0.768889

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_4:12770991-12771083 Satlength=93 Nr of Repeats=5 RepeatLength=15

seed=TCCCCTTTTC

TCCCCTTTTCGTTGC

TCCCCTTTTCGTATC

TCCCCTTTTCGTATC

TCCCCTTTTCGCAGATTCCCCTTTTGCAGA

TCCCCTTTTCGTTCTGC

Nr of selected repeats 3 Similarity 0.881481

Consensus:

TCCCCTTTTCGTatC

>Cele-UNSB01_4:12787287-12803219 Satlength=15933 Nr of Repeats=166

RepeatLength=96 seed=GTTCCCATAA

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GTGAAGCTTCTGGTAAT

GTTCCCATAAATTGGGTTAGCTACCTCTCATAAGTAAGTAGTATGGGACTGAAAAGATACTAAATGAGCTTATTCTAAGG
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GTGAAGCTTCTGGTAAT
GTTCCATAATTGGGTTAAATACCACTCATAAGTAAGTAGTATGGGACTGAAAAGATACTAAATGAGCTTATTCTAAGG
ATGAAGCTTCTGGTAAT

Nr of selected repeats 162 Similarity 0.969395

Consensus:

GTTCCATAATTGGGtTAaaTACCaCTCATAAGTAAGTAGTATGGGACTGAAAAGATACTAAATGAGCTTATTCTAAGG
GTGAAGCTTCTGGTAAT

>Cele-UNSB01_4:12842983-12843155 Satlength=173 Nr of Repeats=5 RepeatLength=35
seed=AAACCGGCAA

AAACCGGCAATTTAAAAAATGCCGGAAGTTTTGA
AAACCGGCAATTGCCGAAATGCGGAAAATCTCG
AAACCGGCAATTGCCGATATTGCCGAAAATCTTAA
AAACCGGCAATTGCCGTAATTGCCGAAAATTCACA
AAACCGGCAATTGCCAATTGCCGAAAATTCACA

Nr of selected repeats 3 Similarity 0.759259

Consensus:

AAACCGGCAATTGCCGaaATTGCCgAaAAAtTctca

>Cele-UNSB01_4:12895275-12902336 Satlength=7062 Nr of Repeats=272
RepeatLength=26 seed=CATTGCGGCG

CATTGCGGCGGATTTTTGAAAAATGG
CATTGCGGCGGATTTTTGAAAAATGA
CATTGCGGCGGATTTTCAAAAAATGA
CATTGCGGCGGATTTTTGAAAAATGA
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CTAGTACCTGTGAAAATTGGAACTCGACACAAAAACCTCTCTAGCGCGGCTTAAATTTACTTTCCCTGGCCCACAAACTT
ACCAATAATA

Nr of selected repeats 12 Similarity 0.993146

Consensus:

TTTTTAAAAAATCTAGAATCCAAATCTATCAAAACATTTCCGGAATTCGATAATTTTTATTTTTGTTTTTTGAGCCTA
CTAGTACCTGTGAAAATTGGAACTCGACACAAAAACCTCTCTAGCGCGGCTTAAATTTACTTTCCCTGGCCCACAAACTT
ACCAATAATA

>Cele-UNSB01_4:13187743-13188346 Satlength=604 Nr of Repeats=12 RepeatLength=12
seed=GCTTGGGTTT

GCTTGGGTTTAG

GCTTGTGTTTAGGATTGGATTCAG

GCTTGGGTTTAGTTTTTTGTGCTTGCCTACCACATATTTAGTTAATTTTAGCAGAAGCTCTGGTTTTTCATTTAGGCTT
GCTTTTGCCAAGCAAATATGCCAATTTTCCCTCGAGTCTACATACTATGCTAATTGGAAAATTTTTCAAAAAGTAACTTT
GCGTGAACCCAAAATAAACTTACACGGTCAATCCAGTGGTATGAAATAAAAATAAATGCTTTGTTCAATTATTTTA
TTACTTTCAATTCCTTCACTTTTGCACATTTTCTGTTAACCCTCTCACAATCAGGAATCCAATGCCAGATAAGTTATTT
GTACACAATTAAGCTTCAATAAGAGAGAATTTCTCAGGTTTAATCTTAG

GCTAGGTTTTAGGTTGCTATAGGATTTTAGATTTGCTATGGGCTTAAGCTTTTGTATTGATTGGTGTAGGCTAAGGT
TCAAGATAGGTTGGATTTAGGCTTGAG

GCTTGGGTTTAG

GCTTGGGTTTAA

GTTTGGGTTTAG

GCTTGGGTTTAA

GCTTGGGTTTAG

GCTTGGGTTTAG

GCTTGGGTTTAG

GCTTGGGTTTAG

Nr of selected repeats 9 Similarity 0.907407

Consensus:

GCTTGGGTTTAG

>Cele-UNSB01_4:13187743-13188478 Satlength=736 Nr of Repeats=17 RepeatLength=12
seed=GCTTGGGTTT

GCTTGGGTTTAG

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TTTACTCTCTGGCTTCACACTATAT
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TTTACTCTCTGGCTTCACACTATCT
TTTACTCTCTGGCTTCACAGAATAT
TTTACTCTCTGGCTTCACACTATAT
TTTACTCTCTGGCTTCACAGAATAT
TTTACTCTCTGGCTTCACACTATCT
TTTACTCTCTGGCTTCACAGAATAT
TTTACTCTCTGGCTTCACACTATAT
TTTACTCTCTGGCTTCACACTATCT
TTTACTCTCTGGCTTCACAGAATAT
TTTACTCTCTGGCTTCACACTATCT
TTTACTCTCTGGCTTCACAGAATAT
TTTACTCTCTGGCTTCACACTATCT
TTTACTCTCTGGCTTCACAGAATAT
TTTACTCCCTGGCTTCACCATGTTT
TTTACTCTCTGGCTTCACACTATAT

Nr of selected repeats 131 Similarity 0.786650

Consensus:

TTTACTCTCTGGCTTCACAgAATAT

>Cele-UNSB01_4:13614335-13614410 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=CACAGGAGGC

CACAGGAGGCTGGGA

CACAGGAGGCTGGGA

CACAGGAGGCTGGGA

CACAGGAGGCTGGGA

CACAGGAGGCTGGGA

Nr of selected repeats 5 Similarity 1.000000

Consensus:

CACAGGAGGCTGGGA

>Cele-UNSB01_4:13645449-13645792 Satlength=344 Nr of Repeats=22 RepeatLength=15

seed=ACCCATCGTG

ACCCATCGTGGCGAG

ACCCACCGTGGTGAG

ACCCGTCGTGGTGAG

ACTCATCGTGGCGAG

ACCCATCGTGGTGAG

ACTCATCGTGGTGAG

ACCCATCGTGGCGAG

ACCCATCGTGGTGAG

ACCCATCGTGGTGAG

ACCCATCGTGGTGAT

ACCCATCGTGGCGAG

ACCCATCGTGGTGAG

ACCCATCGTGGCGAG

ACCCATCGTGGTGAG

ACCCATCGTGGCGAG

ACCCATCGTGGTGAT

ACCCATCGTGGCGAG
 ACCCATCGTGGTGAT
 ACCATCGTGGCGAG
 ACCCATCGTGGTGAG
 ACCCATCGTGGCGAG
 ACCCACCGTGGTGAGACCCGTCATGGTGAG
 Nr of selected repeats 19 Similarity 0.894997
 Consensus:

ACCCATCGTGGtGAG
 >Cele-UNSB01_4:13645884-13646555 Satlength=672 Nr of Repeats=18 RepeatLength=35
 seed=GAAATTTAAA

GAAATTTAAATTTTCTGAGAAAAATATTTTGGCGGGAATTTTAAATTTTCTGAGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGAAAAAAAAATTATTTTGGCGG
 GAAATTTAAATTTTCTGAAAAAAAAATTATTTTGGCGG
 GAAATTTAAATTTTCTGAGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGAGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGAGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGAGAAAAATATTTTGGGAGA
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGAGAAAAATATTTTGGGAGA
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGAGAAAAATATTTTGGGAGA
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGAGAAAAATATTTTGGGAGA
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
 Nr of selected repeats 15 Similarity 0.948481

Consensus:
 GAAATTTAAATTTTCTGtGAAAAATATTTTGGCGG
 >Cele-UNSB01_4:13646609-13646697 Satlength=89 Nr of Repeats=4 RepeatLength=23
 seed=AATATTTATT

AATATTTATTTATTTATTTAATA
 AATATTTATTTATTTATTTAATA
 AATATTTATTTATTTATTTAATT
 AATATTTATTTATTTATTT
 Nr of selected repeats 3 Similarity 0.961353
 Consensus:

AATATTTATTTATTTATTTAATa
 >Cele-UNSB01_4:13645885-13647427 Satlength=1543 Nr of Repeats=25
 RepeatLength=35 seed=AAATTTAAAT
 AAATTTAAATTTTCTGAGAAAAATATTTTGGCGGGAATTTTAAATTTTCTGAGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGAAAAAAAAATTATTTTGGCGGG
 AAATTTAAATTTTCTGAAAAAAAAATTATTTTGGCGGG
 AAATTTAAATTTTCTGAGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGAGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGAGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGAGAAAAATATTTTGGCGGG
 AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG

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AAATTTAAATTTTCTGAGAAAAATATTTTGGAGAG
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AAATTTAAATTTTCTGTGAAAAATATTTTGGCGGG
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AAATTTAAATTTTCTGAAAAATCCAAAATCTGG
AAATCTAAATTAATTAATTAATATTTATTTATTTATTTAATAAATATTTATTTATTTATTTAATAAATATTTATTTATT
TATTTAATTAATATTTATTTATTTATTTAATATTTATTTATTTATTTAATTAACCAGCCGCTGACCGCGCTACGGCGC
GGCAACGACTGGCACCATTAAAAGTATTTTGACACACATACACTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGG
AACACTCCAGAATTTTCCCGATTTTCTAGAAAGTTCTGGAACATTCCAGTATTTTCTCGATTTTCTAGAAAGTTCTG
GAACATTCCAGTATTTTCTCGATTTTCTAGAAAGTTCTGGAACATTCCAGTATTTTCTCGATTTTCTAGAAAGTTCT
GGAACATTCCAGTATTTTCTCGATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTCTAGAAAGTTCT
TGGAACATTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACATTCCAAAATTTTCTCGATTTTCTAGAAAGTT
CTGGAACATTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACATTCCGGAACATTCCGAGAATTTTCTGAAATTTCCAGAAGAT
TTTAGATTTCCAGAATTTTAGAATTTTCCAGA
AAATTTAAATTAACCCGCCAAAATATTTTTCACAGA
AAATTTAAATTTCCCTCCAAAATATTTTTCAGA
AAATTTCAAATTTCCCGCCAAAATATTTTTCACAGA
AAATTTAAATTTCCCGCCAAAATATTTTTCACAGA
AAATTTAAATTTCCCGCCAAAATATTTTCTCAGA

Nr of selected repeats 19 Similarity 0.791694

Consensus:

AAATTTAAATTTtCtGtgaAAAATATTTTggcggG

>Cele-UNSB01_4:13647491-13647701 Satlength=211 Nr of Repeats=14 RepeatLength=15

seed=CCACGATGGG

CCACGATGGGTCTCA

CCACGATGGGTCTCG

CCACGATGGGTCTCT

CCACGATGGGTCTCT

CCACGATGGGTCTCA

CCACGGTGGGTCTCG

CCACGGTGGGTCTCA

CCACGATGGGTCTCA

CCACGATGGGTCTCG

CCACGATGGGTCTCT

CCACGATGGGTCTCT

CCACGATGGGTCTCT

CCACGATGGGTCTTT

CCACGATGGGTCTCA

Nr of selected repeats 14 Similarity 0.902320

Consensus:

CCACGATGGGTCTCn

>Cele-UNSB01_4:13646820-13647869 Satlength=1050 Nr of Repeats=12

RepeatLength=40 seed=GTTCTGGAAC

GTTCTGGAACACTCCAGAATTTTCCCGATTTTCTAGAAA

GTTCTGGAACATTCCAGTATTTTCTCGATTTTCTAGAAA

GTTCTGGAACATTCCAGTATTTTCTCGATTTTCTAGAAA

GTTCTGGAACATTCCAGTATTTTCTCGATTTTCTAGAAA

GTTCTGGAACATTCCAGTATTTTCTCGATTTTCTAGAAA

GTTCTGGAACATTCCAGAATTTTCTCGATTTTCTAGAAA

GTTCTGGAACATTCCAAAATTTTCTCGATTTTCTAGAAA

GTTCTGGAACATTCCAAAATTTTCTCGATTTTCTAGAAA

GTTCTGGAACATTTCGAGAATTTTTTCGATTTTTCTAGAAA
GTTCTGGAACATTTCGAGAATTTTTTCGAAATTTCCAGAAGATTTTAGATTTCCAGAATTTTAGAATTTTCAGAAAATTT
AAATTACCCGCCAAAATATTTTTTCACAGAAAATTTAAATTTCCCTCCAAAATATTTTTTTTCAGAAAATTTCAAATTTCCC
GCCAAAATATTTTTTCACAGAAAATTTAAATTTCCCGCAAATATTTTTTCACAGAAAATTTAAATTTCCCGCCAAAATAT
TTTTCTCAGAAAATTTAAATTTCCCGCCAAAATTTGGGTCTTACCACGGTGGGTCTTACCACGACGGGTCTCACCACG
ATGGGTCTCACCACGATGGGTCTCGCCACGATGGGTCTCTCCACGATGGGTCTCTCCACGATGGGTCTCACCACGGTGG
GTCTCGCCACGGTGGGTCTCACCACGATGGGTCTCACCACGATGGGTCTCGCCACGATGGGTCTCTCCACGATGGGTCT
CTCCACGATGGGTCTCTCCACGATGGGTCTTTCCACGATGGGTCTCACCACGATGGGTCTCGCCACGAAGATCTCGCAG
CAACATTTTTTAAATTTTCCAGAAG

GTTTTGGAACATTCCAGAATTTTCTAGAATTTTCCAGAAGTTCTAAAGCTTTTCAGCATTTTCCAGAAG
GTTCTGGAACATTCTAGAAAATTTCCAGAATTTCCAGAAG

Nr of selected repeats 10 Similarity 0.891111

Consensus:

GTTCTGGAACATTCCAGaATTTTCTCGATTTTTCTAGAAA

>Cele-UNSB01_4:13647739-13648797 Satlength=1059 Nr of Repeats=13

RepeatLength=27 seed=TTTTTAAAT

TTTTTAAATTTTCCAGAAGGTTTTGGAACATTCCAGAATTTTCTAGAATTTTCCAGAAGGTTCTAAAGCTTTTCCAGCA
TTTTCCAGAAGGTTCTGGAACATTCTAGAAAATTTCCAGAATTTCCAGAAGGTTCTGGAACATTTCCAGAATTTTCCCGA
AGTTTTCAAATTTCCCTTCCAAAGACAAAACACAATTTTTTCCAAACTACAGTAATCTACCCTACTCCTACAGTACTA
CTACAGTACCCCGCCATATCCCCCTACTAACCCCAAATAATATCCCTCCAACAGCCGAAAACGCCTGCCTTTGTAAG
CTATGACGTCACTTCTTAAACAAACGGACACTATTTTTTTATATATAGGTAATGATAAGACAAAAGTCAATTTTTTCCCA
AACTACAGTAATCTTACAGTACTCCTACAGTACCTCTACAGTATTACTACAGTACCCGTCCATATCCCACCACTAATCT
CAAACCAATATTTCTTCAAAGACAAAACGTCAATTTTTTCCAAACTACAGTAATCTACCCTACTACTACAGTACCCCG
TCCATATCCCCCTACTAACCCCAAATAATATCCCTCCAACAGCCGAAAACGCCTGCCTTTATAAGCTATGACGTCACA
GACTACAAACTACGGAACAAACGGAATTATTTTTTTATATATAGGTAATGATATTTATTTATTTAATTAATATTTATTT
ATTTATTTAATTAATATTTATTTATTTATTTAAT

TTTTTAAACTTCTAAC

TTTTTAAATTCATATACCGTTCTAAC

TATTTAAATTCATATACCATTTCTAAT

TTTTTGAAATTCACATACCGTTCTAAC

TTTTCAAATTCATATACCGTTCTAAC

TTTTTAAATTCATGTACCATTTCTAAT

TTTTTGAAATTCATGTACCGTTCTAAC

TTTTTAAATTCATATACCGTTCTAAC

TTTTTAAATTCATATACCGTTCTAAC

TTTTTAAATTCATGTACCATTTCTAAT

TTTTTAAATTCATATACCGTTCTAAC

TTTTTAAATTCATATACCGTTCTAAC

Nr of selected repeats 11 Similarity 0.892256

Consensus:

TTTTTAAATTCATaTACCgTTCTAAC

>Cele-UNSB01_4:13661650-13661868 Satlength=219 Nr of Repeats=6 RepeatLength=31

seed=AATTCAAATT

AATTCAAATTTCTTCAAAAAATTTGGCGGG

AATTCAAATTTCTTCAAAAAATTTGGCGGG

AATTCAAATTTCTTCAAAAAATTTGGCGGG

AATTCAAATTTCTTCAAAAAATTTGGCGGG

AATTCAAATTTCTTCAAAAAATTTGGCGGGAATCCGAATTTCTTCAAAAAATTTGGCGGG

AATTCAAATTTATTTAAAAATTTAAGCCAAA

Nr of selected repeats 4 Similarity 0.942652

Consensus:

AATTCAAATTTccTCAAAAAATTTGGCGGG

>Cele-UNSB01_4:13730774-13730818 Satlength=45 Nr of Repeats=4 RepeatLength=11

seed=CACATTTTTT

CACATTTTTTTG
CACATTTTTTTC
CACATTTTTTTG
CACATTTTTTTC

Nr of selected repeats 4 Similarity 0.919192

Consensus:

CACATTTTTTc

>Cele-UNSB01_4:13731432-13732897 Satlength=1466 Nr of Repeats=8

RepeatLength=164 seed=AAAATTCAAA

AAAATTCAAATGATTTGAAAATGAAAGAGCCCGAAACCGAAGAAATTGTATCTCTTGATTTTTATAATTTTTTTCACGGA
ACTTTTTGTGCATTTTTTGTCTCAGCAAGTGGATGTAGATTGCACAATTTTTTGTATCTTGCAATTAATAAAAAAATGTAATG
TCTTTATTCTATATTTACTCTAATGTTCTGCCATTATGAGTAAATATAAAACTCTTCAGCATAGTCAAAAATACCAG
AAAATGACAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTAAAAATTGATAAAAAATAAATAAAAGCTGATTTTT
TCA

AAAATTCAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTATTTTCATAAACTCTTCAGCATAGTCAAAAATACC
AGAAAATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTAAAAATTGATAAAAAATATAAAAAGCTGATTT
TTTTCT

AAAATTCAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTATTTTCATAAACTCTTCAGCATAGTCAAAAATACC
AGAAAATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTAAAAATTGATAAAAAATATAAAAAGCTGATTT
TTTTCA

Nr of selected repeats 5 Similarity 1.000000

Consensus:

AAAATTCAAAGTATGGGAAAATCATATGGAGTCATTCTTTTTTATTTTCATAAACTCTTCAGCATAGTCAAAAATACC
AGAAAATGCCAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTTAAAAATTGATAAAAAATATAAAAAGCTGATTT
TTTTCA

>Cele-UNSB01_4:13759189-13759529 Satlength=341 Nr of Repeats=30 RepeatLength=11
seed=GCACATTTTTT

GCACATTTTTTA

GCACATTTTTCT

GCACATTTTTTA

GCACATTTTTG

GCACATTTTTTA

GCACATTTTTTGA

CACATTTTTG

GCACATTTTTT

GCACATTTTTG

GCACATTTTTTATTGCGTTTTTA

GCACATTTTTG

GCACGTTTTTG

GCACATTTTCAA
CACATTTTGG
GCACATTTTFT
GCACATTTTAA
GCACATTTTAA
CACATTTTAA
GCACATTTTAA
GCACAATTTTG
GCACATTTTAA
GCACATTTCTA
GCACATTTTGG
GCACATTTCTA
GCACTTTTGG
GCACATTTTGG
GCACATTATTA
GCACGTTTTTA
GCACATTTCTA
GCACATTTTGG

Nr of selected repeats 22 Similarity 0.772787

Consensus:

GCACATTTTAA

>Cele-UNSB01_4:13851511-13852113 Satlength=603 Nr of Repeats=12 RepeatLength=40
seed=AAAATTCTGG

AAAATTCTGGAAAGCTCTAGAACCTTTTGAAAAATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAAGTTTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAAATTCGAA
AAAATTCTGGAATGTTCTAGAAGCCCCTGAAAAATTCGAG
AAAATTCTGGAATGTTCTAGAAGCTTCTAAAAATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAATATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAATATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAATATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAATATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGAAAAATTCGAAA
AAAATTCTTGAATTTTCTAGAACCTTCTGAAAAATTCGTG
AAAATTCTGGAATGTTGTGGTGAGACCTTGCTGAGACCCATTGTGGTGAGACCTGAGACCCATTGTGGTGAGACCCCTT
A

AAAATTTGGCGGGAAATTCAAAATTTATGAGAACATTGTTTTGAGGGAAATTCAGTTTTCTGTGAAACTATTTTTGT
TTTAGTACCTTCTGGAAGTTTCAAGAAGCTGAAAAATTTGGGG

Nr of selected repeats 9 Similarity 0.870370

Consensus:

AAAATTCTGGAATGTTCTAGAAcCTTCTGgAAaATTCGAG

>Cele-UNSB01_4:13917663-13921092 Satlength=3430 Nr of Repeats=37

RepeatLength=93 seed=AGGGCCGCGAG

AGGGCCGCGAGGCCCAATTAGGTGCAGAAATATTGGACATTCGTTAAGCCTATTCTAAGCCGAACAACCAAGTTTG
AGGGCCGCGAGGCCCGAACACTCTCTGAAACTGTGGGCCAGCTTTAATCCTGTTCCAAGCAGATTGTTCTTCGCTCAAGC
CTACCAACCAGGTTTG
AGGGCCGCGAGGCCCGAACACTCTTGGAAACTGGGCTGGCTTTAATCCTATTCCAAGCAGATTGTTATTCACTCAAGCCT
ATCAACCAAGTTTG
AGGGCCGCGAGGCCCGAATAGTCTTGGAAACTGGGCTGGCTATAATCCTATTCCAAGCAGGTTGTTATTCACTCAAGCCT
ATCAACCAAGTTTG
AGGGCCGCGAGGCCCGAATAGTCTTGGAAACTGGGCTGGCTATAATCCTATTCCAAGCAGGTTGTTATTCACTCAAGCCT
ATCAACCAAGTTTG
AGGGCCGCGAGACCCGAATAGTCTTGGAAACTGGGCTGGCTATAATCCTATTCCAAGCAGGTTGTTTTTCACTCAAGCAT
ATCAACCAAGTTTG

AGGGCCGCAGGCCCAAATAGTCTTGAAACTGGGCTGGCTATAATCCTATTCCAAGCAGGTTGTTATTCCTCAAGCCT
ATCAACCAAGTTTG
AGGGCCGCAGGCCCAAATAGTCTTGAAACTGGGCTGGCTATAATCCTATTCCAAGCAGGTTGTTATTCCTCAAGCCT
ATCAACCAAGTTTG
AGGGCCGCAGGCCCAAATAGTCTTGAAACTGGGCTGGCTATAATCCTATTCCAAGCAGGTTGTTATTCCTCAAGCCT
ATCAACCAAGTTTG
AGGGCCGCAGGCCCAAATAGTCTTGAAACTGGGCTGGCTATAATCCTATTCCAAGCAGGTTGTTATTCCTCAAGCCT
ATCAACCAAGTTTG

Nr of selected repeats 33 Similarity 0.954220

Consensus:

AGGGCCGCAGGCCCAAATAGTCTTGAAACTGGGCTGGCTATAATCCTATTCCAAGCAGGTTGTTATTCCTCAAGCCT
ATCAACCAAGTTTG

>Cele-UNSB01_4:14030114-14030248 Satlength=135 Nr of Repeats=6 RepeatLength=11
seed=AGTACTGTAG

AGTACTGTAGG

AGTACTGTAGG

AGTACGGTAGG

ATTACTGTAGTTTGGGAAAAATTGTGTTTTTGTCTTTTGAAGAGATATAGGTTTGGGGTTAGTAGTGGGATATGGTCGG
G

GTACTGTAGT

AGTACTGTAGG

Nr of selected repeats 4 Similarity 0.939394

Consensus:

AGTACTGTAGG

>Cele-UNSB01_4:14030460-14031210 Satlength=751 Nr of Repeats=45 RepeatLength=15
seed=CCCATCGTGG

CCCATCGTGGTGAGA

CCCATCGTGGCGAGA

CCCATCGTGGTGAGA

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTTGCGAGACCAACCGTGGTGAGA

CCCGTCGTGGTGAGA

CCCATCGTGGTGAGG

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTTGCGAGACCAACCGTGGTGAGA

CCCGTCGTGGTGAGA

CCCATCGTGGTGAGG

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTTGCGAGACCAACCGTGGTGAGA

CCCGTCGTGGTGAGA

CCCATCGTGGTGAGG

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTGGTGAGG

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTGGTGAGA

CCCATCGTGGTGAGG

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTGGTGAGA
CCCATCGTGGCGAGA
CCCATCGTGGCGAGA
CCCATCGTTGCGAGACCAACCGTGGTGAGA
CCCGTCGTGGTGAGA
CCCATCGTGGTGAGG
CCCATCGTGGCGAGA
CCCATCGTGGCGAGA
CCCATCGTGGTGAGA
CCCATCGTGGCGAGG
CCCATCGTGGCGAGA
CCCATCGTGGCGAGA
CCCATCGTGGTGAGA
CCCATCGTGGAAAGA
CCCATCGTGGCGAGACCAACCGTGGTGAGA
CCCGTCGTGGTGAGA
CCCATCGTGGTGAGA

Nr of selected repeats 40 Similarity 0.901766

Consensus:

CCCATCGTGGcGAGA

>Cele-UNSB01_4:14031556-14031756 Satlength=201 Nr of Repeats=5 RepeatLength=40
seed=AATGTTCCAG

AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGG
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGG
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGG
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGA
AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTTG

Nr of selected repeats 5 Similarity 0.973333

Consensus:

AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTgg

>Cele-UNSB01_4:14046078-14046558 Satlength=481 Nr of Repeats=12 RepeatLength=40
seed=CAGAACCTTC

CAGAACCTTCTAGAAAAATCCGAGAAAATTCTGGAATGTTT
CAAAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGTTT
CAGAACCTTCTGGAAAATTTGAGAAAATTTCTGGAATGTTT
CAGAACCTTCTGGAAAATTTGAGAAAATTTCTGGAATGTTT

Nr of selected repeats 12 Similarity 0.914646

Consensus:

CAGAACCTTCTGGAAAATtCAGAAAATTTCTGGAATGTTT

>Cele-UNSB01_4:14046107-14046777 Satlength=671 Nr of Repeats=11 RepeatLength=40
seed=CTGGAATGTT

CTGGAATGTTCCAAAACCTTCTGGAAAATTTGAGAAAATG
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATT
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATT
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATT
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATT
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATT

CTGGAATGTTCCAGAACCTTCTGGAAACTTTGAAAAAATCCGGAATGCTCCAGAACCTTCTAGAAAATTCGAGAAAAT
T

CTGGAATGTTCCAGAACCTTCTGGAAAATCCGAGAAAATG
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATT
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATT
CTGGAATGTTTCCAGAACCTTCTGGAAAATTCGAGAAAATT
CTGGAATGTTCCAGAACCTTCTGAAAAATGAAAAATTTTGGCGGGAATTCAAAATTTCTGTGAAAAATTGTGGCGGGAA
TTCAAATTTCTGTGAAAAATTTTGGCGGGAATTCAAAATTTCTGTGAAAAATTTTAGCGGGAATTCAAAATTTCTGT
GAAAAATTTTGGCGGGAATTCAAAATTTCTGTGAAAAATTTTGGCGGGAATTCAAAATTTCTGTGAAAAATT

Nr of selected repeats 9 Similarity 0.940741

Consensus:

CTGGAATGTTCCAGAACCTTCTGGAAAATttGAGAAAATt

>Cele-UNSB01_4:14068578-14068998 Satlength=421 Nr of Repeats=24 RepeatLength=15

seed=ACGATGGGTC

ACGATGGGTCTCACC

ACGATGGGTCTCGCC

ACGATGGGTCTCACC

ACGATGGGTCTCGCC

ACGACGGGTCTCACC

ACGATGGGTCTCGCC

ACGATGGGTCTCACC

ACGATGGGTCTCACC

ACGACGGGTCTCACC

ACGATGGGTCTTACC

ACGATGGGTCTCATC

ACGACGGGTCTCACC

ACGGTGGGTCTCGCAACGATGAGTATCACCACGACGAGTCTCACC

ACGATGGGTCTCACC

ACGATGGGTCTCGCCACGACGGGTATCGCC

ACGATGGGTCTCACTACGGTGGGTATCGCA

ACGATGGGTCTCACC

ACGATGGGTCTCGCC

ACGATGGGTCTCACC

ACGATGGGTCTCACC

ACGATGGGTCTCGCC

ACGACGGGTCTCACC

ACGATGGGTCTCGCC

ACGATGGGTCTCACC

Nr of selected repeats 21 Similarity 0.916191

Consensus:

ACGATGGGTCTCaCC

>Cele-UNSB01_4:14093954-14094851 Satlength=898 Nr of Repeats=32 RepeatLength=32

seed=CGACCTGCGA

CGACCTGCGACCTG

CGACCTAGCGACCTAGGTCGCTTTG

CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

CGACCTGCGATCTAGCGACCTGGGTCGCTTTG

CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

CGACCTGCGATCTAGCGACCTGGGTCGCTTTG

CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

CGACCTGCGATCTAG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGATCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAG
CGACCTGCGACCTAG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGATCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAG
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CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

Nr of selected repeats 24 Similarity 0.987923

Consensus:

CGACCTGCGACCTAGCGACCTGGGTCGCTTTG

>Cele-UNSB01_4:14106561-14106695 Satlength=135 Nr of Repeats=6 RepeatLength=11
seed=AGTACTGTAG

AGTACTGTAGG

AGTACTGTAGG

AGTACGGTAGG

ATTACTGTAGTTTTGGGAAAAAATTGTGTTTTTTGTCTTTTGAAGAGATATAGGTTTGGGGTTAGTAGTGAATATGGTCGG
G

GTACTGTAGT

AGTACTGTAGG

Nr of selected repeats 4 Similarity 0.939394

Consensus:

AGTACTGTAGG

>Cele-UNSB01_4:14106973-14107062 Satlength=90 Nr of Repeats=6 RepeatLength=15

seed=ACCCATCGTG

ACCCATCGTGGCGAG

ACCCATCGTGGTGAG

ACCCATCGTGAAAA

ACCCATCGTGGTGAG

ACCCATCGTGGCGAG

ACCCATCGTGGTGAG

Nr of selected repeats 5 Similarity 0.946667

Consensus:

ACCCATCGTGGtGAG

>Cele-UNSB01_4:14107092-14108860 Satlength=1769 Nr of Repeats=51

RepeatLength=35 seed=GGGAAATTTA

GGGAAATTTAAATTTTCTGAAAAAATATTTTGGC

GGGAAATTTAAATTTTCTGAAAAAATATTTTGGC

GGGAAATTTAAATTTTCTGTGAAAAAATATTTTGGG

GGGAAATTTAAATTTTCTGTGAAAAAATATTTTGGG

GGGAAATTTAAATTTTCTGTGAAAAAATATTTTGGG

Consensus :

GGGAAATTTAAATTTTCTGTgAAAAATATTTTGGC

>Cele-UNSB01_4:14107093-14113320 Satlength=6228 Nr of Repeats=160

RepeatLength=35 seed=GGAAATTTAA

GGAAATTTAAATTTTCTGAAAAAATATTTTGGCG

GGAAATTTAAATTTTCTGAAAAAATATTTTGGCG

GGAAATTTAAATTTTCTGTGAAAAAATATTTTGGAG

GGAAATTTAAATTTTCTGTGAAAAAATATTTTGGAG

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GGAAATTTAAATTTTCTGTGAAAAATATTTTGGCG
GGAAATTTAAATTTTCTGTGAAAAATATTTTGGAG
GGAAATTTAAATTTTCTGTGAAAAATATTTTGGCG
Nr of selected repeats 111 Similarity 0.941169

Consensus:

GGAAATTTAAATTTTCTGtgAAAAATATTTTGGcG

>Cele-UNSB01_4:14154469-14154585 Satlength=117 Nr of Repeats=4 RepeatLength=29
seed=TACATTGCAA

TACATTGCAAGATTTTCTTACTCTGTAGG
TACATTGCAAGATTTTCTTACTATGTAGG
TACATTGCAAGATCTTCTTACTATGTAGG
TACATTGCAAGATCTTCTTACTATGTAGG

Nr of selected repeats 4 Similarity 0.946360

Consensus:

TACATTGCAAGATcTTCTTACTaTGTAGG

>Cele-UNSB01_4:14405343-14406331 Satlength=989 Nr of Repeats=13 RepeatLength=76
seed=AATGCTAGAG

AATGCTAGAGGACACTCATTTCGACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTCGGTGTCTTTGTGCATGCTCG
AATGCTAGAGGACACTCCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTCGGTGTCTTTGTGCATGCTCG
AATGCTAGAGGACACTCCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTCGGTGTCTTTGTGCATGCTCG
AATGCTAGAGGACACTCCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTCGGTGTCTTTGTGCATGCTCG
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AATGCTAGAGGACACTCCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTCGGTGTCTTTGTGCATGCTCG
AATGCTAGAGGACACTCCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTCGGTGTCTTTGTGCATGCTCA

Nr of selected repeats 13 Similarity 0.967611

Consensus:

AATGCTAGAGGACAcTCCTTTGCACGAAaGGAAGTGGGAGAGACTGTGGAGTTGTCGGTGTCTTTGTGCATGCTCg

>Cele-UNSB01_4:14407623-14408822 Satlength=1200 Nr of Repeats=70

RepeatLength=14 seed=GCTATGCGCT

GCTATGCGCTGTTC
GCTATGCGCTGTTA
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GCCATGCGCTGTAC
GCTATGCGCTGTAT
GCAATGCGCTATGCGCTGTTA
GCTATGCGCTGTAC
GCCATGCGCTGTAC
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GCAATGCGCTATGCGCTGTTA
GCTGTGCGCTGTAC
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GCTATGCGCTGTAT
GCAATGCGCTATGCGCTGTTA
GCTATGCGCTGTAC
GCCATGCGCTGTACGATATGA
GCTATGCGCTATGCGCTGTACGCTGTAC

Nr of selected repeats 52 Similarity 0.786869

Consensus:

GcTATGCGCTGTAc

>Cele-UNSB01_4:14408867-14409192 Satlength=326 Nr of Repeats=13 RepeatLength=25
seed=TAATGCCAAT

TAATGCCAATTTATAGAATCTGCCA
TAATGCCAATTTATAGAATCTGCCG
TAATGCCAATTTATAGAATCTGCCA
TAATGCCAATTTATAGAATCTGCCG
TAATGCCAATTCATAGAATCTGCCA
TAATGCCAATTTATAGAATCTGCCG
TAATGCCAATTTATAGAATCTGCCG
TAATGCCAATTTTTAGAATCTGCCA
TAATGCCAATTTATAGAATCTGCCG
TAATGCCAATTTATAGAATCTGCCG
TAATGCCAATTTATAGAATCTGCCA
TAATGCCAATTTATAGAATCTGCCG
TAATGCCAATTTTTAGAATCTGCCA

Nr of selected repeats 13 Similarity 0.948034

Consensus:

TAATGCCAATTTATAGAATCTGCCg

>Cele-UNSB01_4:14409220-14409304 Satlength=85 Nr of Repeats=6 RepeatLength=14
seed=AGCGTATAGC

AGCGTATAGCGTAT
AGCGTATAGCGTAT
AGCGTATAGCGTAT
AGCGTATAGCGTAT
AGCGTATAGCGTAT
AGCGTATAGCGTAT

Nr of selected repeats 6 Similarity 1.000000

Consensus:

AGCGTATAGCGTAT

>Cele-UNSB01_4:14410457-14414735 Satlength=4279 Nr of Repeats=57
RepeatLength=76 seed=TCGTGCAAAG

TCGTGCAAAGGAGTGTCTCTAGCATTTCGAGCATGCACAAAGACACCGACAACCTCCACAGTCTCTCCCACTTCCCT
TCGTGCAAAGGAGTGTCTCTAGCATTTCGAGCATGCACAAAGACACCGACAACCTCCACAGTCTCTCCCACTTCTTT
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Nr of selected repeats 134 Similarity 0.914962

Consensus:

CTCACCACGAaGGGT

>Cele-UNSB01_4:14618655-14620445 Satlength=1791 Nr of Repeats=7

RepeatLength=200 seed=GAAAAAGTGA

GAAAAAGTGACATTTTCAAATGAAAATTAACAACAAAAAATCAATAAATAGCAACACAAAACAAGGAAAAAAGAAAA
ATAAAGCGAAATAGGTGGAAATCCTAAAAATGCGACTATTTTTGAGAGCGCGCACCAGACTAATGTTACCGTGAACCTT
TTGTGTGCGGTACACTTTTGCCTACCGTACCCGCGGCAAATATGTGTTTCTCGGCAATTTTCATTGGGTTTTCTGTAAAA
TTCAAGATTTTATGGCTAATTTTCGGAATTTACAAGGAAAAATGTTTTATTTGAAAAAATTTGCAATTTTCGAAA
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TGCAAGTCTGCAAATTGAATGGTGTGCGCTTTGACGTTTGCCAAAAAACGTTACACTTCCAACAAAAATTTAATTT
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AATTTCTGGCTTCAAACCTAACTTTTTTTTAAATTTCCCGTAGCCATTTTGTAGCAAATTTTATGTTCTTTTCTTCAAGATTTAA
AAACAGAATTTCAAATAATTTTGAACCGCCAAGTTCAAGCA

CAACTACCACAACCTACCGTAC

Nr of selected repeats 36 Similarity 0.943361

Consensus:

CAACTACCACAACCTACCGTAc

>Cele-UNSB01_4:14648431-14648725 Satlength=295 Nr of Repeats=13 RepeatLength=21
seed=ACTACCGTAC

ACTACCGTACCAACTACCACA

ACTACCGTACCAACTACCACA

ACTACCGCACCAACTACCACA

ACTACCGTACCAACTACCACA

ACTACCGTACCAACTACCACA

ACTACCGTACCAACTACTACA

ACTACCGTACCAACTACCACA

ACTACCGTACCAACTACCACAACCACCGTAACAACTACCACA

ACTACGGTACCAACAACCACG

ACTACCGTACCAACTACCACG

ACTACCGTACCTACTACCACG

ACTACCGTACCTACTACCACG

ACTACCGTACCAACTACAACG

Nr of selected repeats 12 Similarity 0.895142

Consensus:

ACTACCGTACCAACTACCACa

>Cele-UNSB01_4:14678240-14678405 Satlength=166 Nr of Repeats=11 RepeatLength=15
seed=GACCCATCGT

GACCCATCGTGGCGA

GACCTATCGTGGCGA

GACCCATCGTGGTGA

GACCCATCGTGGAAA

GACCCATCGTGGTGA

GACCCATCGTGGCGC

GACCCATCGTGGCGA

GACCCATCGTGGCGA

GACCCATCGTGTTGA

GACCCATCGTGGTGA

GACCCATCGTGGTGA

Nr of selected repeats 11 Similarity 0.878788

Consensus:

GACCCATCGTGGnGA

>Cele-UNSB01_4:14678232-14682258 Satlength=4027 Nr of Repeats=80
RepeatLength=15 seed=CGTGGTGAGA

CGTGGTGAGACCCAT

CGTGGCGAGACCTAT

CGTGGCGAGACCCAT

CGTGGTGAGACCCATCGTGGAAAAGACCCAT

CGTGGTGAGACCCATCGTGGCGGACCCAT

CGTGGCGAGACCCAT

CGTGGCGAGACCCAT

CGTGTTGAGACCCAT

CGTGGTGAGACCCAT

CGTGGTGAGACCCAT

CGTGGTGAGACCCGT

CGTGGTGAGACCCAC

CGTGGTAAGACCCAAAATTTTGGCGGAAATTTAAATTTTCTGAGAAAAATATTTTGGCGGAAATTTAAATTTTCTGT
GAAAATGTTTTTGGCGGAAATTTAAATTTTCTGAGAAAAATATTTTGGCGGAAATTTAAATTTTCTGTGAAAATGT

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CGTGGTGAGACCCAT
CGTGGTGAGACCCGT
Nr of selected repeats 64 Similarity 0.890917
Consensus :
CGTGGTGAGACCCat
>Cele-UNSB01_4:14942266-14942426 Satlength=161 Nr of Repeats=5 RepeatLength=40
seed=TTTTCTAGAA
TTTTCTAGAAAATTTCTGGACCATTCAGAACTTTCTCGGA
TTTTCTAGAAAATTTCTGGACCATTCGGAA
TTTTCTCGAA
TTTTCTAGAAAGTTCTAGAACATTGCCGATTTTCCCGAT

TTTTCTAGAAAGTTCTGGAATATTCCAGAATTTTCCCGAA

Nr of selected repeats 3 Similarity 0.755556

Consensus:

TTTTCTAGAAAgTTCTgGAacATTcCaGAatTTTCcCGaa

>Cele-UNSB01_4:15002663-15002793 Satlength=131 Nr of Repeats=5 RepeatLength=26

seed=TGGTTAGAGT

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TGGTTAGAGTCATATTTTAGGTGAA

TGGTTAGAGTCATTATTTTAGGTGAA

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TGGTTAGAGTCATTATTTTAGGTGAA

Nr of selected repeats 5 Similarity 0.958974

Consensus:

TGGTTAGAGTCATTaTTTTAGGTGAA

>Cele-UNSB01_4:15255716-15255837 Satlength=122 Nr of Repeats=9 RepeatLength=11

seed=TGTGCAAAAA

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TGTGCAAAAAA

TGTGTAAAAAA

TGTGCAAAAAAAGCTCTAAAAA

TGTGTAAAAAA

TGTGCAAAATAT

TGTGCAAAAAAT

TGTGCAAAAAAAGCTCTAAAAA

TGTGCAAAAAAT

Nr of selected repeats 7 Similarity 0.838384

Consensus:

TGTGcAAAAAt

>Cele-UNSB01_4:15280499-15283896 Satlength=3398 Nr of Repeats=88

RepeatLength=40 seed=AGAAAGTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTCCCGACTTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTTCTCGATTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTTCTCGATTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTCCCGATTTTCT

AGAAAGTTCTGGAACATTACAGAAAGTTTCCAGATTTTCT

AGAAAGTTTGGAAACATTCCAGAAATTTTCTCGATTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTCCCGACTTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTTCTCGATTTTCT

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AGAAAGTTCTGGAACATTACAGAAATTTCCAGATTTTCT

AGAAAGTTTGGAAACATTCCAGAAATTTTCTCGATTTTCT

AGAAAGTTCTGGAACATTCCAAAAATTTCCCGATTTTCT

AGAAAGTTCTGGAACATTCTAGACTTTTCCCAATTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTTCTCGATTTTCT

AGAAAGTTCTGGAACATTACAGAAATTTCCAGATTTTCT

AGAAAGTTTGGAAACATTCCAGAAATTTTCTCGATTTTCT

AGAAAGTTCTGGAACATTCCAAAAATTTCCCGATTTTCT

AGAAAGTTCTGGTACATTCTAGACTTTCCCAATTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTTCTCGATTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTCCCGATTTTCT

AGAAAGTTCTGGAACATTCCAGAAATTTTCTCGATTTTCT

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AGAAAGTTCTGGAACATTCCAGAAATGTCCCGATTTTTCT
AGAAAGTTCTGGAACATTCCAGAAATTTCCCAATTTTTCT
Nr of selected repeats 79 Similarity 0.897220

Consensus:

AGAAAGTTCTGGAACATTcCAGAAtTTTCcCGATTTTTCT

>Cele-UNSB01_4:15284214-15284904 Satlength=691 Nr of Repeats=39 RepeatLength=15
seed=GGTCTCACCA

GGTCTCACCAACGACGGGTCTCGTCACGATG
GGTCTCACCAACGATG
GGTCTCGCCACGATG
GGTCTCACCAACGATG
GGTCTCGCCACGATG
GGTCTCACCAACGAAG
GGTCTCACCAACGAAG
GGTCTCGCCACGAAGGGTCTCGTCACGATG
GGTCTCACCAACGATG
GGTCTCGCCACGATG
GGTCTCACCAACGATG
GGTCTCGCCACGATG
GGTCTCACCAACGAAG
GGTCTCACCAACGAAG
GGTCTCGCCACGAAG
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GGTCTCACCAACGAAGGATCTTACCACGAAG
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GGTCTCACCAACGAAGGATCTTACCACGAAG
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GGTCTCACCAACGAAG
GGTCTCGCCACGAAG
GGTCTCACCAACGAAG
GGTCTCATCACGAAG
GGTCTCACCAACGAAGGATCTTACCACGAAG

Nr of selected repeats 32 Similarity 0.917921

Consensus:

GGTCTCaCCACGAaG

>Cele-UNSB01_4:15313385-15313490 Satlength=106 Nr of Repeats=7 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGAA

GGGTCTCACCACGAT

GGGTCTCACCACGAA

GGGTCTCACCACGAT

GGGTCTCACCACGAA

GGGTCTCACCACGAA

GGGTCTCACCACGAT

Nr of selected repeats 7 Similarity 0.949206

Consensus:

GGGTCTCACCACGAa

>Cele-UNSB01_4:15313710-15313830 Satlength=121 Nr of Repeats=8 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGACCCA

TCGTGGTGAGAACCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

Nr of selected repeats 8 Similarity 0.930159

Consensus:

TCGTGGTGAGACCCa

>Cele-UNSB01_4:15399620-15399800 Satlength=181 Nr of Repeats=11 RepeatLength=15

seed=GAGACCCATC

GAGACCCATCGTGGC

GAGACCCATCGTGGC

GAGACCCATCGTGGC

GAGACCCATCGTGGT

GAGACCCGTCGTGGC

GAGACCCATCGTGAT

GAGACCCATCGTGGT

GAGACCCATCGTGGC

GAGACCCATCGTGGT

GAGACCCATCGTGGC

GAGACCCACCGTGGTAAGACCCGTCGTGGT

Nr of selected repeats 10 Similarity 0.917037

Consensus:

GAGACCCATCGTGGc

>Cele-UNSB01_4:15399887-15400027 Satlength=141 Nr of Repeats=4 RepeatLength=35

seed=AAATTTTCTG

AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTT

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AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTT

AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTG

Nr of selected repeats 4 Similarity 0.904762

Consensus:

AAATTTTCTGTGAAAAaTATTTTgGcGGGAAATt

>Cele-UNSB01_4:15400092-15400412 Satlength=321 Nr of Repeats=8 RepeatLength=40
seed=GAATGTTCCA

GAATGTTCCAGAACTTTCTAGAACAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATCTGGAAAATTCTG
GAATGTTCCAGAACTTTCTAAAAAAATCGAGAAAATTCTG
GAATGTTCCAGAACTTTCTAGAAAAATGGGAAAATTCTG
GAATGTTCCAGAACTTTCTAAAAAAATCGAGAAAATTCTG
GAATGTTCCAGCACTTTCTAGAAAAATGGGAAAATTCTG

Nr of selected repeats 8 Similarity 0.897619

Consensus:

GAATGTTCCAGAACTTTCTAgAAAAATcGaGAAAaTTCTG

>Cele-UNSB01_4:15421750-15421870 Satlength=121 Nr of Repeats=8 RepeatLength=15
seed=GGTGAGACCC

GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGT
GGTGAGACCCATCGT
GGTGAGACCCTTCGC

Nr of selected repeats 8 Similarity 0.926984

Consensus:

GGTGAGACCCaTCGT

>Cele-UNSB01_4:15421887-15425906 Satlength=4020 Nr of Repeats=116
RepeatLength=34 seed=TGGCGGGAAA

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TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT
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TCCCCTTTTCGCAGA
TCCCCTTTTTCGCAGA
TCCCCTTTTTCGTTCTGC
Nr of selected repeats 4 Similarity 0.748148
Consensus:
TCCCCTTTTcGcaga
>Cele-UNSB01_4:15436315-15436698 Satlength=384 Nr of Repeats=11 RepeatLength=35
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Nr of selected repeats 7 Similarity 0.941950
Consensus:
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>Cele-UNSB01_4:15436367-15437145 Satlength=779 Nr of Repeats=9 RepeatLength=35
seed=GTAAAAAATA
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Nr of selected repeats 7 Similarity 0.929252
Consensus:
GTaAAAAATATTTTGGcGGGAAATTCAAATTTTTTA
>Cele-UNSB01_4:15460070-15462017 Satlength=1948 Nr of Repeats=10
RepeatLength=168 seed=AAAAACAAA
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Nr of selected repeats 7 Similarity 0.956160

Consensus:

AAAAACAAAAATAAAAAATTTTGGAAATGTTGGGAGAATTTTTATAGATTTGGATTCTAGATTTTTTAACAAATATTTTTGG
TAAGTTTCTGGACCTAGATATCAATTTTCAGATGCGCTAGAGGGGTTTTTGTcTTGAATTccAaTTTcaACAGaTATAT
ACAGGCACAA

>Cele-UNSB01_4:15460844-15462434 Satlength=1591 Nr of Repeats=9

RepeatLength=168 seed=AACAAAAATA

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GGCACAATA
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C

Nr of selected repeats 7 Similarity 0.956160

Consensus:

AACAAAAATAAAAAATTTTGGAAATgTTGGGAGAATTTTATAGATTTGGATTCTAGATTTTAAACAAATATTTTGGTAA
GTTTCTGGACCTAGATATCAATTTTCAGATGCGCTAGAGGGGTTTTTGTcTTGAATTccAaTTTcaACAGaTATATACA
GGCACAAAA

>Cele-UNSB01_4:15529257-15530020 Satlength=764 Nr of Repeats=4 RepeatLength=14

seed=TTGTAGTTTG

TTGTAGTTTGTAGT

TTGTAATTTGTAGT

TTGTAGTTTGTAGT

TTATAGTTTGGACCTTTGGTTTATCCTGTGATGAATACGCAGCCGACATAAAACCAAAGTCTGCGTTGAGCACGCCTAATT
TTTTTTGGTTGAGTACAAGACCGTGAGTACTGTAGGATTACTGTATAGATATTCATGGAAAACGGTAAATATCACTATT
TTCAGGTTTTCTCAACAAACTTCAAGTCTCAGAAGTATCAGACGACGGATGTTTGTACGAAATCTTTGCGCCAAAAAT
CAGCCAAATAGTTATTTGGCGGCCGGTCCGCCATCAGTTTTTACTGAAATCCATACCTACTGACCAGTTTTGTAAGTT
TTTGATAGTTATCCGCTTCCATTTTTTCTTAGTTTTTCTAGAGATTCTATCCGGTTTTCAACGGGGCCAACAAATCGATT
ATTTCTCCCAATTTGGTATGCAATGTGGAGATGATCAGGACTGGTATATAACCAAATCCCTGGAATGGTAGATATTTG
GAATTTAAATAGTTTAAAGGAAATGATTAACACATTTTTTTGAATTGAAGGTTGACTTGAGTCCCGGAGCAAATGAGCA
GAAAGTCAATGGAATATGTGGAATGGGATGGGTTATCGCTTCAGAATCACCGAGATGCAATGTTTTGTGCCACTGGGA
TGATGAGCATATTAACATTTTTTCAAATGCAAATTCATATCGATTGAAGCTAAAAATTCGAATAAACTAATTTTA
ACACACTACA

Nr of selected repeats 3 Similarity 0.936508

Consensus:

TTGTAGTTTGTAGT

>Cele-UNSB01_4:15554617-15554707 Satlength=91 Nr of Repeats=6 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGAACCA

TCGTGGTGGGACCTT

TCGTGGTGAGACCCA

TCGTGGTGAGACCTT

TCGTGGTGAGACCCA

TCGTGGTGAGACCTT

Nr of selected repeats 6 Similarity 0.887407

Consensus:

TCGTGGTGAGACCCa

>Cele-UNSB01_4:15554734-15555678 Satlength=945 Nr of Repeats=27 RepeatLength=35

seed=GAAATTCAAA

GAAATTCAAATTTTAAAGTAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTGAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTGAAAAAAATTTTAGCAG
GAAATTCAAATTTTTCAGTGAAAAAAATTTGGGCGG
GAAATTCAAATTTTTCAGTGAAAAAAATTTTAGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTGGCGA
GAAATTCAAATTTTTCAGTGAAAAAAATTTTAGCGG
GAAATTCAAATTTTTCAGTGAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTGAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTGAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTGAAAAAAATTTTAGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTAGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTAGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTAGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTAAAAAAATTTTAGCGG

GAAATTCAAATTTTCAGTAAAAAAAAATTTTGGCGG
GAAATTCAAATTTTCAGTGAAAAAAAAATTTTGGCGG
GAAATTCAAATTTTTCAGTAAAAAAAAATTTTGGCGG
GAAATTCAAATTTTCAGTGAAAAAAAAATTTTGGCGG
GAAATTCAAATTTTCAGTGAAAAAAAAATTTGGGCGG
GAAATTCAAATTTTCAGTGAAAAAAAAATTTGGGCGG

Nr of selected repeats 18 Similarity 0.936508

Consensus:

GAAATTCAAATTTTCAGTgAAAAAAAAATTTTgGCGG

>Cele-UNSB01_4:15607346-15608026 Satlength=681 Nr of Repeats=17 RepeatLength=40
seed=GAACATTCCA

GAACATTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTG
GAACATTCCAGAATTTTCTCAATTTTCTAGAAAGTTCTT
GAACATTCCAGACTTTTCCCAATTTTCTAGAAAGTTCTG
GAACATTCCAGAATTTTCTCAATTTTCTAGAAAGTTCTT
GAACATTCCAGACTTTTCCCAATTTTCTAGAAAGTTCTG
GAACATTCCAGAAATTTCCCGATTTTCTAGAAAGTTCTG
GAACATTCCAGAATTTTCTCAATTTTCTAGAAAGTTCTT
GAACATTCCAGACTTTTCCCAATTTTCTAGAAAGTTCTG
GAACATTCCAGAATTTTTCGATTTTCTAGAAAGTTCTG
GAACATTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTT
GAACATTCCAGAAATTTCCCGATTTTCTAGAAAGTTCTG
GAACATTCCAGACTTTTCCCAATTTTCTAGAAAGTTCTG
GAACATTCCAGACTTTTCCCAATTTTCTAGAAAGTTCTG
GAACATTCCAGACTTTTCCCAATTTTCTAGAAAGTTCTG
GAACATTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTT
GAACATTCCAGAAATTTCCCGATTTTCTAGAAAGTTCTG
GAACATTCCAGACTTTTCCCAATTTTCTAGAAAGTTCTG

Nr of selected repeats 17 Similarity 0.919608

Consensus:

GAACATTCCAGAAATTTTCCcCaATTTTCTAGAAAGTTCTg

>Cele-UNSB01_4:15608407-15609476 Satlength=1070 Nr of Repeats=51
RepeatLength=15 seed=CCACGATGGG

CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTTT
CCACGATGGGTCTCA
CCACGGTGGGTCTCG
CCACGATGGGTCTCG
CCACGATTGGTCTCGCCACGAAGATCTCGCAGCAACATTTTTTTAATTTTCCAGAAGGTTCTAGAACAATCCAGAATTT
TTTTCGAATTTTCCAGAAGGTTCTGGAACATTTCCAGAATTTTCTAGAATTTTCCAGAACCTTATTTCCCGCCAAAATATT
TTTCACAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCTCAGAAAATTTAAATTTCCCGCCAAAATTTTGGGTCTTA
CCACGGTGGGTCTCA
CCACGACGGGTCTCA
CCACGATGGGTCTCT

CCACGATGGGTCTCA
CCATGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGAAGGGTCTCG
CCACGATGGGTCTCG
CCACGAAGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCACCACGAAGATCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCACCACGAAGATCTCT
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCACCACGAAGATCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCACCACGAAGATCTCTCCACGAAGATCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCACCACGAAGATCTCT
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCG

Nr of selected repeats 44 Similarity 0.911299

Consensus:

CCACGATGGGTCTCa

>Cele-UNSB01_4:15642758-15643070 Satlength=313 Nr of Repeats=12 RepeatLength=26

seed=CAGAGTCACT

CAGAGTCACTAAATTTGGTGAACGGC
CAGAGTCACTATTTTTGGTGAACGGC
CAGAGTCACTATTTTTGGTGAACGGC
CAGAGTCACTAAATTTGGTGAACGGC
CAGAGTCACTATTTCTGGTGAACGGC
CAGAGTCACTATTTTTGGTGAACGGC
CAGAGTCACTATTTTTGGTGAACGGT
CAGAGTCACTATTTTTGGTGATCGGC
CAGAGTCACTATTTTTGGTGAACGGC
CAGAGTCACTATTTTTGGTGAACGGC
CAGAGTCACTATTTTTGGTGAACGGC
CAGAGTCACTATTTTTGGTGAACGGC

Nr of selected repeats 12 Similarity 0.943279

Consensus:

CAGAGTCACTATTTTTGGTGAACGGC

>Cele-UNSB01_4:15644313-15644403 Satlength=91 Nr of Repeats=8 RepeatLength=10

seed=TGTTATGATA

TGTTATGATAA

GTTATGATAG

TGTTATGTTATGATA

TGTTATGATA

TGTTATGTTA

TGTTATGTTA

TGTTATGTTATGAG

GTTATGATAG

Nr of selected repeats 5 Similarity 0.763636

Consensus:

tGTTATGaTA

>Cele-UNSB01_4:15744856-15746870 Satlength=2015 Nr of Repeats=12

RepeatLength=168 seed=GAATTCGGGA

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATTGAAAGTTTGTGGACCAGGAAAGTA

AAATTTAGCCGCGCTAAAGAGGTTTTTGTGTCGAGTTCCAATTTTACAGTTATATACTGGCACAAAAAACAAAAATA
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTGGTTTTTTTTTAAATATTATTGAAAGTTTGTGGACCAGGAAAGT

AAATTTAAGCCGCGCTAAAGAGGTTTTTGTGTCGAGTTCCAATTTTACAGGTTACTAGTAGGCGCAAAAAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAGAGGTTTTTGTGTCGAGTTCCAATTTTATAGGTTACTAGTAGGCGCAAAAAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAAAAGTTTTTGTGTCGAGTTACAATTTTACAGGTTACTAGTAGGCGCAAAAAAACAAAAATA
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAGAGGTTTTTGTGTCGAGTTCCAATTTTACAGGTTACTAGTAGGCGCAAAAAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAGAGGTTTTTGTGTCGAGTTACAATTTTACAGGTTACTAGTAGGCACAAAGAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAAAAGTTTTTGTGTCGAGTTACAATTTTACAGGTTACTAGTAGGCACAAAGAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAAAAGTTTTTGTGTCGAGTTACAATTTTACAGGTTACTAGTAGGCACAAAGAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAAAAGTTTTTGTGTCGAGTTACAATTTTACAGGTTACTAGTAGGCACAAAGAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAAAAGTTTTTGTGTCGAGTTACAATTTTACAGGTTACTAGTAGGCGCAAAAAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAAAAGTTTTTGTGTCGAGTTACAATTTTACAGGTTACTAGTAGGCGCAAAAAAACAAAAAT
AAAATTATG

GAATTCGGGAAATGTTTGATAGATTTGGATTCTAGATTTTTTAAAAATATTATAGGTGAGTTTTTGGGACAGGAAAGT

AACTTTAAGCCGCGCTAGAAAAGTTTTTGTGTCGAGTTACAATTTTACAGGTTACTAGTAGGCGCAAAAAAACAAAAAT
AAAATTATG

GGACTAGGGACTGG
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GGACTAGGGACTAGGGACTGAACTTGCAAAC
GGACTAGGGACTGCGCTTAAGATACCGAAAACCCCTGAATTTTCAGGACGACTGTCTCTCCAAAATCAAACGCTCTAG
GGACTAGGGACTGG
GGACTAGGGACTAG
GGACTAGGGACTAGGGACTGAACTTGCAAAC

Nr of selected repeats 112 Similarity 0.896439

Consensus:

GGACTAGGGACTAG

>Cele-UNSB01_4:15883454-15883531 Satlength=78 Nr of Repeats=6 RepeatLength=11

seed=TGCACATTTT

TGCACATTTT

TGCACATTTT

TGCACATTTTTCGCTCATT

TGCTCATT

TGCACATTTT

TGCACATTTT

Nr of selected repeats 5 Similarity 0.903030

Consensus:

TGCaCATTt

>Cele-UNSB01_4:15943206-15943656 Satlength=451 Nr of Repeats=14 RepeatLength=32
seed=TTGAATTCCC

TTGAATTCCTCCGCAAAAATTTTTCAAAGAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAC
TTGAATTCCTCGTTATAATTTTTCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCAAAGAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAC
TTGAATTCCTCGTTATAATTTTTCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAT
TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAT

Nr of selected repeats 13 Similarity 0.905983

Consensus:

TTGAATTCCTCCGCAAAAATTTTTCACAGAAAAT

>Cele-UNSB01_4:15944034-15944234 Satlength=201 Nr of Repeats=5 RepeatLength=40
seed=ATTTTCCAGA

ATTTTCCAGAAGGTTCTGGAACATTCCAGAATTTTCTCAA
ATTTTCCAGAAGGTTCTGGAACATTCCAGCATTTTCTCAA
ATTTTCCAGAAGGTTCTGGAACATTCCAGAATTTTCTCGG
ATTTTCCAGAAGGTTCTGGAACATTACAGACTTTTCTCGG
ATTTTCCAGAAGGTTCTGGAACATTCCAGAATTTTCTCAA

Nr of selected repeats 5 Similarity 0.920000

Consensus:

ATTTTCCAGAAGGTTCTGGAACATTcCAGaaTTTTCTCaa

>Cele-UNSB01_4:16000310-16000589 Satlength=280 Nr of Repeats=6 RepeatLength=40
seed=GATTTTTCTA

GATTTTTCTAGAAAAAATCTGGAACATTCCAGAATTTTTTC
GATTTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC
GATTTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTT
GATTTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCCC
GATTTTTCTACAAAGTTCTGGAACGTTCCAGAATTTTCCC
GATTTTTCTAGAAAGTTCTTGAACATTCCAGAATTTTTTCGAAATTTCCAGAAGATTCTAGATTTCCAGAATTTTCCC

Nr of selected repeats 4 Similarity 0.911111

Consensus:

GATTTTTCTAGAAAGTTCTGGAACaTTcCAGAATTTTCCc

>Cele-UNSB01_4:15999976-16000920 Satlength=945 Nr of Repeats=8 RepeatLength=35
seed=AAAATTTAAA

AAAATTTAAAAAAACCGTTTTCAAACCTCTACATTCAAAGTTGAAAGGCAAAACAATTATTGACTTCATAGTGATTTT
TTTTTAATTATTAATAAAAAAATATGTTTGAATTTATTTAAAAAGGCATAAAATTCAAAACCTGCCAAAAAATCTGATGAAC
TGAATTTAATAACTTCGAGAGAAAAAAAACAGTTTTTTTTTTTCGAGAATAAGCAAAATGGAAAGTTTCTGAAAGTTATCG
AATTATTTAATAACCAGCCGCTGACCGCGCCTACGGCGGGCAACGACTGGCACCATTAAGTATTTGACACACATA
CACTTCCAGAATTTTCTCGATTTTTCTAGAAAAAATCTGGAACATTCCAGAATTTTTCGATTTTTCTAGAAAGTTCTG
GAACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTTGATTTTTCTAGAAAGTTCT
GGAACATTTCAGAATTTTCCGATTTTTCTACAAAGTTCTGGAACGTTCCAGAATTTTCCCGATTTTTCTAGAAAGTTCT
TTGAACATTTCGAGAATTTTTCGAAATTTCCAGAAGATTCTAGATTTCCAGAATTTTCCCGATTTTTCTACAAAGTTCT
GGAACATTTCGAGAATTTTTCGAAATTTCCAGAAGATTCTAGATTTCCAGAATTTTAGAATTTTCAG
AAAATTTAAATTTCCCGCAAAAATTTTTTCTCAG
AAAATTTAAATTTCCCGCAAAAATTTTTTCTCAG
AAAATTTAAATTTCCCTCCAAAATTTTTTCTCCG

AAAATTTAAATTACCCGCCAAAATATTTTTCTCAG
AAAATTTAAATTTCCCACCAAAAATATTTTTTTCAG
AAAATTTAAATTTCCCTCCAAAATATTTTTTTCAG
AAAATTTAAATTTCCCACCAAAAATATTTTTTCACAG
Nr of selected repeats 7 Similarity 0.883900

Consensus:

AAAATTTAAATTTCCnCCAAAATATTTTTcTCAG

>Cele-UNSB01_4:16000962-16001082 Satlength=121 Nr of Repeats=8 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGAC

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCTCGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAC

Nr of selected repeats 8 Similarity 0.939683

Consensus:

GGGTCTCACCACGAt

>Cele-UNSB01_4:16000985-16001240 Satlength=256 Nr of Repeats=17 RepeatLength=15

seed=CCACGATGGG

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCTCGATGGGTCTCA

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCACGACGGGTCTCA

CCACGGTGGGTCTCG

CCACGATGGGCCTCG

CCACGATGGGTCTCG

CCACGATGGGTCTCG

CCACGATGGGTCTCG

CCACGATGGGTTTCA

CCACGATAGGTCTTT

CCACGATGGGTCTCA

CCACGATGGGTCTCG

CCACGATGGGTCTCG

Nr of selected repeats 17 Similarity 0.875163

Consensus:

CCACGATGGGTCTCa

>Cele-UNSB01_4:16001468-16002088 Satlength=621 Nr of Repeats=19 RepeatLength=11

seed=GTACTCCTAC

GTACTCCTACA

GTACTCCTACA

GTACTACTACAGTACCCCGACCATATTGCACTACTAATCGCAAACCTATATCTCTTCAAAGACAAAAACACAATTTTT
CATAAACTACA

GTAATCCTACCGTACA

GTACTCCTACA

GTACTACTACAGTACCCCGACCATATCCCACTAATAACTCAAACCTATATCTCTTCAAAGACAAAAACTCAATTTTT
CCTAAACTACA

GTAATCCTACC

GTACTCCTACA

GTACTCCTACA
GTACTACTACAGTACCCCGACCATATCCCACCTAATAACTCCAAACCTATATCTCTTCAAAGACTAAAACACAATTTTT
CCTAAACTACA
GTAATCCTACC
GTACTCCTACA
GTACTCCTACAGTATTACTACGGTACCCCGACCATATCCCACCTAATAACTCCAAACCTATATCTCTTCAAAGACTAAA
ACACAATTTTTCTAAACTACA
GTAATCCTACC
GTACTCCTACA
GTACTCCTACA
GTACTACTACAGTACCCCGACCATATCCCACCTAATAACTCCAAACCTATATCTCTTCAAAGACTAAAACACAATTTTT
CCTAAACTACA
GTAATCCTACC
GTACTCCTACA

Nr of selected repeats 13 Similarity 0.888112

Consensus:

GTAcTCCTACa

>Cele-UNSB01_4:16010822-16011211 Satlength=390 Nr of Repeats=5 RepeatLength=42
seed=GCTCGGCAAA

GCTCGGCAAATTTGAAATTTGCCGCACACGTCAAAAATTTTACAGTACAATTTGACTAAAATTATTGATTTTTTTCGA
CAAAAATTTAGTAAAATGACACAAAATTGAGTTAGTTTTATGCTTAAGCAGACATACTACACGGAACCTAATTCAGAAAC
CAGATGTGTGTTAAGAATTCGGTAGTTTTGGTGTTCAAAAAACATCAAAAATTATCAAAATTTTCCGAGTTTGCTGA
GCTCGGCAAATTTGCCGAATTTGCCGT

GCTCGGCAAATATTGAAAAAAGAGATTTGCCGAATTTGCCGT

GCTCGGCAAATATTGAAAAAAGAGATTTGCCGAATTTGCCGT

GCTCGGCAAATATTGAAAAAAGAGATTTGCCGAATTTGCCGA

Nr of selected repeats 3 Similarity 0.957672

Consensus:

GCTCGGCAAATATTGAAAAAAGAGATTTGCCGaATTTGCCGT

>Cele-UNSB01_4:16019565-16019814 Satlength=250 Nr of Repeats=6 RepeatLength=31
seed=TCGACAGAAG

TCGACAGAAGCTGCCGGTCTTCACACTTTCTTGACACACGCTGTGAGATCTCACAAAATTTT

TCGACAGAAGCTGTGATCATCAGACTTTCC

TCGACAGAAGCTGTGGATATCACATTTTCTCGGCAAAGCTGCCGAAACTCACACTTTCTG

TCGACAGAAGCTGTGGATATCACATTTCCC

TCGGCAGAAGCTGCCGAACTCACACTTTCT

TCGACAGAAGCTGTGGAACTTACAATTTCT

Nr of selected repeats 4 Similarity 0.665825

Consensus:

TCGaCaGAAGCTGtCgGAaaTcAcAcTTTCc

>Cele-UNSB01_4:16061332-16061647 Satlength=316 Nr of Repeats=21 RepeatLength=15
seed=CCCATCGTGG

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTGGCGAGA

CCCATCGTGGCGAGG

CCCATCGTGGTGAGA

CCCATCGTGGCGAGA

CCCACCGTGGTGAGA

CCCGTCGTGGTGAGA

CCCATCGTGGTGAGA

CCCATCGTGGTGAGA

CCCGTCGTGGTGAGA

CCCATCGTGGTGAGA

CCCATCGTGGTGAGA
CCCATCGTGGTGAGA
CCCATCGTGGTGAGA
CCCATCGTGGTGAGA
CCCATCGTGGTGAGA
CCCATCGTGGTGAGA
CCCATCGTGGTGAAA
CCCATCGTTGTGAGA

Nr of selected repeats 21 Similarity 0.916191

Consensus:

CCCATCGTGGtGAGA

>Cele-UNSB01_4:16061680-16061959 Satlength=280 Nr of Repeats=8 RepeatLength=35
seed=AATTTAAATT

AATTTAAATTTTCTGTGAAAAATATTTTGGCGGGA
AATTTAAATTTTCTGTGAAAAATATTTTGGCGGGA
AATTTAAATTTTCTGAAAAAATATTTTGGAGGGA
AATTTAAATTTTCTGAAAAAATATTTTGGAGGGA
AATTTAAATTTTCTGAAAAAATATTTTGGAGGGA
AATTTAAATTTTCTGAAAAAATATTTTGGCGGGA
AATTTAAATTTTCTGTGAAAAATATTTTGGCGGGT
AATTTAAATTTTCTGAGAAAAAATTTTGGAGGGA

Nr of selected repeats 7 Similarity 0.896599

Consensus:

AATTTAAATTTTCTGngAAAAAtATTTTGGcGGGA

>Cele-UNSB01_4:16061215-16062273 Satlength=1059 Nr of Repeats=8 RepeatLength=40
seed=GTTCCAGAAC

GTTCCAGAACCTTCTGGGAATTTCTGGAAAATTTCTAGAAT
GTTCCAGAACCTTCTGGAAAATTTCTGAAAAGCTTTAAAACCTTCTGGAAAATTTCTAGAAAATCCAAAAAGAAAGACC
CATCGTGGCGAGACCCATCGTGGCGAGACCCATCGTGGCGAGACCCATCGTGGCGAGGCCATCGTGGTGAGACCCATC
GTGGCGAGACCCACCGTGGTGAGACCCGTCTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCGTCTGG
TGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAG
ACCCATCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAGACCCATCGTGGTGAAACCCATCGTTGTGAGACCC
ATCGTGGTGAGACCCAAAATTTTGGCGGGAAATTTAAATTTTCTGTGAAAAATATTTTGGCGGGAAATTTAAATTTTCT
GTGAAAAATATTTTGGCGGGAAATTTAAATTTTCTGAAAAAATATTTTGGAGGGAAATTTAAATTTTCTGAAAAA
TTTTGGAGGGAAATTTAAATTTTCTGAAAAAATTTTGGAGGGAAATTTAAATTTTCTGAAAAAATATTTTGGCGG
GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGGGTAATTTAAATTTTCTGAGAAAAAATTTTGGAGGGAAATTTAA
ATTTTCTGAAAAATTTCTAAAATCTGAAATCTAGAATCTTCTGAAATTTCTGAAAAATTTCTCGAAT
GTTCCAGAACCTTCTAGAAAAATCGAGAAAATTTCTGGAGT
GTTCCAGAACCTTCTAGAAAAATCGGTAATAATTTCTGGAAT
GTTCCAGAACCTTCTATAAAAAATGGGAAAAGTATGGAGT
GTTCCAGAACCTTCTAGAAAAATCGAGAAAATTTGTGGAAC
GTTCCAGAACCTTCTAGAAAAATCGAGAAAATTTCTGGAAC
GTTCCAGAACCTTCTAGAAAAATCGGTAATAATTTCTGGAAT

Nr of selected repeats 7 Similarity 0.814286

Consensus:

GTTCCAGAACtTTCTAGAAAAATCGggAAAATtTcTGGAAAt

>Cele-UNSB01_4:16077133-16078206 Satlength=1074 Nr of Repeats=16
RepeatLength=37 seed=CGGGAATTCA

CGGGAATTCAAATTTTAATTTTCTAAAACATTTTGG
CGGGAATTCAATTGTTAATTTTTCGAAATCATTTCGG
CGGGAATTCAAATTTTAATTTTCCGAAAAGATTTTGG
CGGGAATTCAAATTTTAATTTTCTAAAACATTTTGG
CGGGAATTCAAATTTTAATTTTCCGAAAAGATTTTGG

AGAAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCT
AGAAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCT
AGAAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCT
AGAAAGTTCTGGAACATTCCAAAATTTTCTCGATTTTTCT
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CGCCACGATGGGTCTCACCACGATGGGCCTCGCCACGATGGGTCTCGCCACGATGGGTCTCGCCACGATGGGTCTCGCC
ACGATGGGTTTACCACGAAGGGTCTCTCCACGCCACGAAGATCTCGCAGCAACATTTTTTTAAATTTTCC
AGAAGTTCTAGAGCAATCCAGAATTTTCTCGATTTTTCT

Nr of selected repeats 328 Similarity 0.988340

Consensus:

AGAAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCT

>Cele-UNSB01_4:16219937-16221099 Satlength=1163 Nr of Repeats=29

RepeatLength=35 seed=TTCCGCCAA

TTCCGCCAAAATTTTCAAAGAAAATTTGAA

TTCCGCCAAAATTTATTTTCTTATAAATTTTGAAG

TTCCCGCCCATATTTTTAAAGGTCTCACCACGATGGGTCTCGCCAGTTCAGGTGGTACTTAAGCTAACAAAAAGTTTC
TCAGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCACTGAAAATTTGAAT
TTCCCGCCAAAAATGTTTTTCACTGAAAATTTGAAA
TTCCCGCCAAAAATGTTTTTCACTGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCACTGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCTCAGAAAATTTGAAT
TTCCCGCCGAAAATTTTTTCTCAGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCTCACAGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCACTGAAAATTTGAAT
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TTCCCGCCAAAAATTTTTTCTCAGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCACTGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCTCACAGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCACTGAAAATTTGAAT
TTCCCGCCAAAAATGTTTTTCACTGAAAATTTGGAAT
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TTCCCGCCAAAAATTTTTTCTCACAGAAAATTTGAAT
TTCCCGCCAAAAATTTTTTCACTGAAAATTTGGAAT
Nr of selected repeats 20 Similarity 0.896341
Consensus:
TTCCCGCCAAAAAtTTTTTcaCtGAAAATTTGAAT
>Cele-UNSB01_4:16220033-16221319 Satlength=1287 Nr of Repeats=15
RepeatLength=15 seed=CACGATGGGT
CACGATGGGTCTCGCCAGTTCAGGTGGTACTTAAGCTAACAAAAAGTTTCTCAGAAAATTTGAATTTCCCGCCAAAAA
TTTTTCACTGAAAATTTGAATTTCCCGCCAAAAATGTTTTTCACTGAAAATTTGAAATTTCCCGCCAAAAATGTTTTTCACT
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GAATTTCCCGCCGAAAATTTTTTCTCAGAAAATTTGAATTTCCCGCCAAAAATTTTTTCTCACAGAAAATTTGAATTTCCC
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CACGATGGGTCTCGT
CACGATGGGTCTCAC
CACGATGGGTCTCAC
CACGAAGGTCTCAC
CACGATGGGTCTCAC

CACGATGGGTCTCGT
CACAATGGGTCTCAC
CACGATGGGTCTCAC
CACGATGGGTCTCCC
CACGATGGGTCTCAC
CACGATGGGTCTCAC
CACGACGGGTCTTTC
CACGATGGGTCTTAC

Nr of selected repeats 13 Similarity 0.863248

Consensus:

CACGATGGGTCTCaC

>Cele-UNSB01_4:16343642-16344390 Satlength=749 Nr of Repeats=18 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGA

GTACTGTAGGTATACGGTAGGGTTACTTTTAGTTTTGGGAAAAATTGAGTTTTTGTACACAGAAGAGTTATTGGGTTGGAA
GTTGCTGGGGGATAATGTCAAG

GTACTGTAGTA

GTACTGTAGGA

GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTAGGAAAAATTGAGTTTTTGTCTACAGAAGAGGTATTGGGTTGGGAG
TTGCTGGGGGATAATGTCAAG

GTACTGTAGTA

GTACTGTAGGA

GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTTGTCTACAGAAGTGGTATTGGGTTGGGA
GTTGGTGAGGGATAATGTCAAGGTACAGTAGTG

GTACTGTAGGA

GTACTGCAGGTATACGGTAGGGTTACTGTAGTTTAGGAAAAATTGAGTTTTTGTCTACAGAAGAGGTATTGGGTTGGGA
GTTGCTGGGGGATAATGTCAAG

GTACTGTAGTG

GTACTGTAGGA

GTACTGTAGGTATACGGTAGGGTTACTGTAGTTCAGGAAAAATTGAGTTTTTGTCTACAGAAGAGGTATTGGGTTGGGA
GTTGTTGGGGGATAATGTCAAG

GTACTGTAGTA

GCACTGTAGGA

GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTTGTCTACAGAAGAGGTATTGGGTTGGGA
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GTACTGTAGTG

GTACTGTAGGA

Nr of selected repeats 12 Similarity 0.878788

Consensus:

GTACTGTAGgA

>Cele-UNSB01_4:16376935-16378753 Satlength=1819 Nr of Repeats=17

RepeatLength=15 seed=GGGTCTCACC

GGGTCTCACCACGAATATTCAGAAATTTTTTTCGAATTTTCCAGAAGGTTCTGGAACCTTCCAGAAGGTTCTAGAACAT
TATAGAATTTTCTGGAATTTTCCAGATGATTCAAAACCAAATTTGAAATTTCCCGCCAAAACCTTTTTCTCAGAAAATT
TGAATTTCCCTTCAAAAATTTTTTCTCAGAAAATTTGAATTTCCCTCCAAAATTTTTTCTACTGAAAATTTGAATTT
CCCGCCAAAATTTTTTCTACTGAAAATTTGAATTTCCCGCCAAAATTTTTTCTCAGAAATGTTGAGTTTTCGGCCAAA
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GGGTCTCACCACGAATATTCAGAAATTTTTTTCGAATTTTCCAGAAGGTTCTGGAACCTTCCAGAAGGTTCTAGAACAT
TATAGAATTTTCTGGAATTTTCCAGATGATTCAAAACCAAATTTGAAATTTCCCGCCAAAACCTTTTTCTCAGAAAATT
TGAATTTCCCTTCAAAAATTTTTTCTACTGAAAATTTGAATTTCCCGCCAAAATTTTTTCTACTGAAAATTTGAATTTCC
CGCCAAAATTTTTTCTCAGAAATGTTGAGTTTTCGGCCAAAATTTAT

GGGTCTCACCACGAATATTCAGAAATTTTTTTCGAATTTTCCAGCAGGTTCTGGAACCTTCCAGAAGGTTCTAGAACAT
TATAGAATTTTCTGGAATTTTCCAGATGATTCAAAACCAAATTTGAAATTTCCCGCCAAAACCTTTTTCTCAGAAAATT
TGAATTTCCCTTCAAAAATTTTTTCTCAGAAAATTTGAATTTCCCTCCAAAATTTTTTCTACTGAAAATTTGAATTT

CCCGCCAAATTTTTTTTCTACTGAAAATTTGAATTTCCCGCCAAAAATTTTTTCTCAGAAATGTTGAGTTTTTCGGCCAAA
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GGGTCTCACCACGAATATTTCCAGAATTTTTTTCGAATTTTTCCAGAAGGTTCTGGAACTTTCCAGAAGGTTCTAGAACAT
TATAGAATTTTTCTGGAATTTTTCCAGATGATTCCAAAACCAAATTTGAAATTTCCCGCCAAAACCTTTTTTCTCAGAAAATT
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GGGTCTCACCACGAATATTTCCAGAATTTTTTTCGAATTTTTCCAGAAGGTTCTGGAACTTTCCAGAAGGTTCTAGAACAT
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GGGTCTCACCACGAA

GGGTCTCACCACGAT

GGGTCTCACCACGAA

GGGTCTCACCACGAT

GGGTCTCACCACGAA

GGGTCTCACCACGAT

GGGTCTCACCACGAA

GGGTCTCACCACGAT

GGGTCTCACCACGAA

GGGTCTCACCACGAT

GGGTCTCACCACGAA

GGGTCTCACCACGAT

Nr of selected repeats 11 Similarity 0.935354

Consensus:

GGGTCTCACCACGAA

>Cele-UNSB01_4:16402456-16402561 Satlength=106 Nr of Repeats=7 RepeatLength=15

seed=GTGGTGAGAC

GTGGTGAGACCCATC

GTGGTGAGACCCTTC

GTGGTGAGACCCTTC

GTGGTGAGACCCATC

GTGGTGAGACCCTTA

GTGGTGAGACACATC

GTGGTGAGACCCTTC

Nr of selected repeats 7 Similarity 0.898413

Consensus:

GTGGTGAGACCCTTC

>Cele-UNSB01_4:16472875-16473271 Satlength=397 Nr of Repeats=25 RepeatLength=15

seed=TCTCACCACG

TCTCACCACGAAGTG

TCACACCACGAAAGG

TCTCACCACGATGGGTC

TCTCACCACGATGGA

TCTCACCACGAAGTG

TCTCACCACGAAAGG

TCTCACCACGATGCG

TCTCACCACGAAAGG

TCTCACCACGCTGGG

TCTCACCACGAAAGG

TCTCACCACGATGGGTC

TCTCACCACGATGGA

TCTCACCACGAAGTG

TCACACCACGAAAGG
TCTCACCACGATGGGTC
TCTCACCACGATGGA
TCTCACCACGAAAGG
TCTCACTACGATGGG
TCTCACCACGATGGG
TCTCACCACGAAGGG
TCTCACCACGATGGG
TCTCACCACGAAAGG
TCTCACCACGATGGGTCTTACCCCGATGGG
TATCACCACGAAGGG
TCTCACCACGAAGGG

Nr of selected repeats 21 Similarity 0.820106

Consensus:

TCTCACCACGAagGG

>Cele-UNSB01_4:16493225-16495520 Satlength=2296 Nr of Repeats=119

RepeatLength=19 seed=AAATAGATTG

AAATAGATTGTTACACGGA
AAATAGATTGTTACACGGA
AAATAGATTGTTACACGGA
AAATAGATTGTTACACGGA
AAATAGATTGTTACACGGA
AAATAGATTGTTACACGAA
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AAATAGATTGTTACACGAA
AAATAGATTGTTACACGAA
AAATAGATTGTTACACGGAT
AAATAGATTGTTACACGAAA
AAATAGATTGTTACACGGA
AAATAGATTGTTACACGGAA
AAATAGATTGTTACACGAA
AAATAGATTGCTACACGGA
AAATAGATTGTTACACGAA
AAATAGATTGTTACACGGA
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AAATAGATTGCTACACGGA
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AAATAGATTGTTACACGAA
AAATAAATTGCTACACGGA
AAATAGATTGTTACACGAA
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AAATAGATTGTTACACGAAA
AAATAGATTGTTACACGGA
AAATAGATTGTTACACGGA
AAATAGATTGTTACACGGA
AAATAGATTGTTACACGAA

Nr of selected repeats 85 Similarity 0.941540

Consensus:

AAATAGATTGTTACACGgA

>Cele-UNSB01_4:16653889-16654239 Satlength=351 Nr of Repeats=10 RepeatLength=35
seed=CAAATCGGCA

CAAATCGGCAAATTGCCGAAAATTGTAAAGTTCCGG
CAAATCGGCAATATGCCAAAAATGAAAATTTCCGG
CAAATCGGCAATATGCCAAAATGAAAATATCTGG
CAAATCGGCAATATGTCAAAAATGAAAATTTCTGG
CAAATCGGCAATATGCCAAAATGAAAATTTTCGGC
CAATCGGCAAATTGCAAAAATGGAAAATTTCCG
CAAATCGGTAATCTGTGAGAAATGAAAATTTCCGG
CAAATCGGCAATATGCCGAAAATGAAAATTTCCGA
CAAATCGGCAATATGTCAAAAATGAAAATGCTG
CAAATCGGCAATATGCCAAAATGAAAATTTCCGG

Nr of selected repeats 8 Similarity 0.824490

Consensus:

CAAATCGGCAATaTGcCaAAAATGAAAATTTCCgG

>Cele-UNSB01_4:16658516-16659248 Satlength=733 Nr of Repeats=21 RepeatLength=35
seed=TTTGGCATAT

TTTGGCATATTGCTGATTTGCCGAAAATTTCAAC
TTTGGTATATTGCCGGTTTGCCAGATATTTCAAT
TTTGGCATATTGCCGGATTGCTGAAAATTTCAAT
TTTGGCATATTGCCGATTTGCCGAAAATTTCAAC
TTTGGTATATTGCCGGTTTGCCGAAAATTTCAAC
TTTGGTATATTGCCGGTTTGCCGAAAATTTCAAT

TTTGGCATATTGCCGATTTGCCGGAAAAATTTCAAC
TTTGGTATATTGCCGGTTTGGCCGGAAAAATTTCAAT
TTTGGCATATTGCCGATTTGCCGGAAAAATTTCAAC
TTTGGCATATTGCTGATCTGCCGGAAAGTTTTCAAT
TTTGGCATATTGCCGATTTGCCGGAAAAATTTCAAT
TTTGGCATATTGCCGATTTACCGGAAAAATTTCAAT
TTTGGCATATTTCCGATTTGCCGGAAAAATTTCAAT
TTTGGCATATTGCCCATTTGCCGGAAAAATTTCAAT
TTTGGCATATTGCTGATTTTCCGGAAAAATTTCAAC
TTTGGCATATTGCCGATTTGCCGGAAAAATTTCAAT
TTTGGCATATTGCCGGATTGCTGGAAATTTTCAAT
TTTGGCATATTGCTGATTTGCCGGAAACTTCAAT
TTTGGCATGTTGCCGATTTGCCGGAAAAATTTTCAAT
TTTGGCATATTGCCGATTTTCCGGAAAAATTTTCAAC
TTTGGCATATTGCTGATTTGCCGGAAAAATTTCAAT

Nr of selected repeats 16 Similarity 0.860000

Consensus:

TTTGGcATATTGCCGaTTTGGCCGGAAAAaTTTCAAT

>Cele-UNSB01_4:16659843-16660088 Satlength=246 Nr of Repeats=7 RepeatLength=35

seed=GCAAATCGGC

GCAAATCGGCAAAATGTCCGAATTGAAATTTTCCG
GCAAATCGGCAAAATGGCCGAATTGAAATTTCCA
GCAAATCGGCAATATGCCAAAATTAACATTTCCG
GCAAATCGGCAATATGTCAAAATTGAAACTTTCCG
GCAAATCGGCAATATGCCAAAGTTGAAATTTCCG
GCAAATCGGCAATATGCCAAAGTTGAAATTTCCG
GCAAATCGGCAATATGCCAAAATTAATAATTTCCG

Nr of selected repeats 7 Similarity 0.842177

Consensus:

GCAAATCGGCAAtATGcCaaAaTTgAAAaTTTCCG

>Cele-UNSB01_4:16675153-16675373 Satlength=221 Nr of Repeats=8 RepeatLength=20

seed=TTTTAGTGAA

TTTTAGTGAAAATTTGAGAT
TTTTAGTGAAAATTTGAGAT
TTTTAGTGAAAATTTGAGAT
TTTTAGTGAAAATTTAAGATTTTTATGGAAAATTTGAGAT
TTTTAGTGAAAATTTGAGAT
TTTTAGTGAAAATTTGAGAT
TTTTAGTGAAAATTTAGTTT
TTTAAGTGAAAATCTGGGATTTTACTTGAAAAATCGTGAAAAAACCTGAAAATTGAGC

Nr of selected repeats 5 Similarity 1.000000

Consensus:

TTTTAGTGAAAATTTGAGAT

>Cele-UNSB01_4:16678025-16678676 Satlength=652 Nr of Repeats=13 RepeatLength=50

seed=GGGCGTGTTT

GGGCGTGTTTTACATGCCCCGCCCATGAAATGGAAGTTTCCACCGAAAT
GGGCGTGTTTTACATGCCCCGCCACAAAATTGATGTTTCCACCAAAAT
GGGCGTGTTTTACATGTCCCGCCACAAAATTGATGTTTCCACCAAAAT
GGGCGTGTTTTACATGCCCCGCCATAAAAATTGATGTACCACCAAAAAG
GGGCGTGTTTTACATGCCCCGCCATAAAAATTGATGTACCACCAAAAAT
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GGGCGTGTTTTACAAGCCCCGTCCATAAAAATTGATGTACCACCAAAAAG
GGGCGTGTTTTACATGCCCCGCCATAAAAATGGATGTTTCCACCAAAAAT
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GGGCGTGTTTTTTACATGCCCCGCCATAAAAATTGATGTTTCCACTAAAAAT
GGGCGTGTTTTTTACAAGCCCCGCCACAAAATTGATGTTTCCACTAAAAAT
GGGCGTGTTTTTTACAAGCCCCGCCATAAAAATTGATGTTTCCACTAAAAAT
GGGCGTGTTTTTTACAAGCCCCGCCACAAAATTGATGTTTCCACTAAAAAT

Nr of selected repeats 10 Similarity 0.897482

Consensus:

GGGCGTGTTTTTcACAtGCCCCGCCAcAAAAttGATGTtCCACcAAAAT

>Cele-UNSB01_4:16708641-16708839 Satlength=199 Nr of Repeats=5 RepeatLength=40
seed=TTCCAGAATT

TTCCAGAATTTTCTCGATTTTCTAAAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACG
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA

Nr of selected repeats 4 Similarity 0.966667

Consensus:

TTCCAGAATTTTCTCGATTTTCTAgAAAGTTCTGGAACa

>Cele-UNSB01_4:16709008-16709188 Satlength=181 Nr of Repeats=10 RepeatLength=15
seed=TGGGTCTCAC

TGGGTCTCACCACGA
TGGGTCTCACCACGA
TGGGTCTCACCACGA
TGGGTCTCACCACGA
TGGGTCTCACCACGA
TGGGTCTCACCACGG
TGGGTCTCGCCACGA

TGGGTCTCACCACGATGGGCCTCGCCACAA

TGGGTCTCGCCACGA

TGGGTCTCACGACGATTGGTCTCGCCACGA

TGGGTCTCACTTCGA

Nr of selected repeats 8 Similarity 0.895238

Consensus:

TGGGTCTCaCCACGA

>Cele-UNSB01_4:16721546-16722348 Satlength=803 Nr of Repeats=4 RepeatLength=37
seed=ATTCAAATTT

ATTCAAATTTCCGTATGTCAGAATAGCGGTAAATTCAAAGAAATTACGCAAGTTTTTGGGGTATGTGTACTTGAACATA
CGCACACACAGATTATTGCGTTACCACATTAGGACCACGGGGTATAATGAGTTGGGGGTGTGGCCTTGTGGCCGTG
GAGGTGAAAAACCCCTTTTGATCATCATTACTTCTGATGTGAAAAGTAAATTTTATACCACACTATTTATATAACATA
ACAACGTATTCTGAAATATCGAAAAATTAATAAAAAAGTAAAAGCAGTAAATTGCACAATAAATTGAAATTGCACGAAAA
ATGGAAATAAAAAATAATATGCAAGCAACTTATACTGTTTTAGTTAAAATTTAAATATGAAAATTTATTGGGAATACAGTA
TTCTAAGTGTTTACAGATCAAAACAGTTTTATGTGAGAAAAATAGACAAAATAGAGTGTTTTTTGTAAACATGTTGTTTT
TGTCTGCAGGAAATAAAAGTTACTTTTTTTGATTCCACTTTTCTAAAAAGAATAGAAAATATGCAAAAAAAAAATACAAA
AGAAAAGTGTCAATTCCTTATCATCATATCATATCGTACACTATATATGAAAGAAAAATCGTCTGTTTGTCCCGTCCTTAA
ACTCGGCAGCGACAGCGATCGAGGTCGGCGATGGACATCGCATATAATTTTGGCGGGA

ATTCAAATTTTAATTTTTTTGAAAATATTTTTGACGGGA

ATTCAAATTTTAATTTTTTTGAAAATACTTTGGCGGGA

ATTCAAATTTTAATTTTTTTGAAAATACTTTGGCGGGA

Nr of selected repeats 3 Similarity 0.951952

Consensus:

ATTCAAATTTTAATTTTTTTGAAAATAcTTTGgCGGGA

>Cele-UNSB01_4:16741502-16741626 Satlength=125 Nr of Repeats=5 RepeatLength=21
seed=TTCAAGCCTT

TTCAAGCCTTTTAAAGACCAAGCTAAAGCCTATTTAGACCAAT

TTCAAGCCTTTTTCAGACCAAT

TTCAAGCCTTTTTCAGACCAAT

TTCAAGCCTTTAGACCAAC
TTCAAGTCTTTTCAGGCCAAT
Nr of selected repeats 3 Similarity 0.915344
Consensus:
TTCAAGcCTTTTCAGaCCAAT
>Cele-UNSB01_4:16762223-16763229 Satlength=1007 Nr of Repeats=39
RepeatLength=11 seed=CTACAGTACT
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTACTCCGACCATATCCCACCACTAACCCCAAACCCATATCTCTCCAAAAGACAAAAACTCATTMTTTCCTAAA
CTACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTATCCCGACCATATCCCACCACTAACCCCAAACCTATATCTCTTCAAAAAGACAAAAACTCATTMTTTCCTAAA
CTACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCCGGCCATATTCCTACTAACCCCAAACCTATATCTCTCCAAAAGACAAAAACTCATTMTTTCCTAAA
CTACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTACTCCGACCATATCCCACCACTAACCCCAAACCTATATCTCTCCAAAAGACAAAAACTCATTMTTTCCTAAA
CTACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTATCCCGACCATATCCCACCACTAACCCCAAACCTATATCTCTTCAAAAAGACAAAAACTCATTMTTTCCTAAA
ATACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTACTCCGACCATATCCCACCACTAACCCCAAACCTATATCTCTCCAAAAGACAAAAACTCATTMTTTCCTAAA
CTACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTATCCCGACCATATCCCACCACTAACCCCAAACCTATATCTCTTCAAGAGACAAAAACTCATTMTTTCCTAAA
ATACAGTAATC
CTACAGTACTC
CTACAGTACCT
CTACAGTACTA
CTACAGTACTCCGACCATATCCCACCACTAACCCCAAACCTATATCTCTTCAAAAAGACAAAAACTCATTMTTTCCTAAA
CTACAGTAATC
CTACAGTACTCCTACAGTACCT
Nr of selected repeats 30 Similarity 0.778225
Consensus:
CTACAGTAcTn
>Cele-UNSB01_4:16773369-16773770 Satlength=402 Nr of Repeats=28 RepeatLength=11
seed=CCCCTACAGT
CCCCTACAGTAT

```
CCCCACAGTA
CCCCTACAGAAAACCTAGAGTACGGTTACAGTACCTCTGTAGTACCTCTAATGTA
CCCCTACAGTA
CCCCTACAGTAC
CTCCTACAGTA
CCCCTACAGTAC
CCCCTACAGTA
CCCCTGCAGTA
CCCCTACAGTG
CCCCTACAGTA
CCCTTACAGTAAATCTAAAGTATCTCTACAGTA
CCCCTACAGTG
CCCCTACAGAA
CCCCTACAGTA
CCCCTACAGTGCCCATACAATA
CCACTACAGTA
CCCCTACAGTAC
CCCCTACAGTA
CCCCTACAGTA
CCCCTACAGTAC
CCCCTACAGTA
CCCCTACAGTA
CCCCTACAGTAC
CCCCTACAGTA
CCCCTACAGTA
CCCCTACAGTAC
CCCCTACAGTA
CCCCTACTGTA
CCCCTACAGTATGGCTACAGTA
```

Nr of selected repeats 17 Similarity 0.887701

Consensus:

CCCCTACAGTA
>Cele-UNSB01_4:16899632-16900079 Satlength=448 Nr of Repeats=15 RepeatLength=30
seed=AAAATCAAAA

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AAAATCAAAAATTAGATGAATTTTCGAATA
AAAATCAAAAATTAGATGAATTTTCGATTA
AAAATCAAAAATGGGTGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCGATTA
AAAATCAAAAATGGGTGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCGATTA
AAAATCAAAAATGGGTGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCGATTA
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AAAATCAAAAATTAGATGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCCATTC
AAAATCAAAAATTAGCTGAATTTTCGATTA
AAAATCAAAAATTAGATGAATTTTCCAATC
AAAATCAAAAATTAGCTAAATTTTCGATTA
```

Nr of selected repeats 12 Similarity 0.938721

Consensus:

AAAATCAAAAATTAGATGAATTTTCGATTA
>Cele-UNSB01_4:16926190-16926350 Satlength=161 Nr of Repeats=4 RepeatLength=40
seed=TTCCAGAATT
TTCCAGAATTTTCCCAGATTTTCTAGAAAGTTCTGGAACG
TTCCAGAATTTTCCCAGATTTTCTAGAAAGTTCTGGAACG

TTCCAGAATTTTCCCGACTTTTCTAGAAAGTTCTGGAACG
TTCCAGAATTTTCCCGATTTTCTAGAAAGTTCTGGAGCA
Nr of selected repeats 4 Similarity 0.950000
Consensus:

TTCCAGAATTTTCCCGAtTTTCTAGAAAGTTCTGGAaCg
>Cele-UNSB01_4:16926416-16926623 Satlength=208 Nr of Repeats=6 RepeatLength=35
seed=TTGAATTTCC

TTGAATTTCCCGCCAAAATATTTTCTCAGAAAAT
TTGAATTTCCCGCCTAAATGTTTTCACATAAAAAT
TTGAATTTCCCGCCAAAATATTTTTCACAGAAAAT
TTGAATTTCCCGCCAAAATATTTCTCACAAAATAAT
TTGAATTTCCCTGCCACGATTTTTCACAAAATAAT
TTGAATTTCCCGCCAAAATATTTTCTCAGAAAAT

Nr of selected repeats 4 Similarity 0.917460
Consensus:

TTGAATTTCCCGCCAAAATATTTtTCaCagAAAAT
>Cele-UNSB01_4:16931676-16932199 Satlength=524 Nr of Repeats=4 RepeatLength=150
seed=TTGAGGGCCG

TTGAGGGCCGAGGCCCGAATACACAAAAGTATTGGACAGCCGTTAAGCCTATACTGAGCCCAAAAACCTCGAG
TTGAGGGCCGCAGTCCCGAATACACGAAGAAGTGTGGAGATCCGTCAAGCCTATTCTAAGCATAATAATTCAGTTCGA
GTGTCGCAAGCCCAAATAGACGCAGAAGCGTTGGACAACCTTTTAGGCCTATTCTGAGCCCAATAATTCATG
TTGAGGGCCGCAGTCCCGAATACACGAAGAAGTGTGGAGATCCGTCAAGCCTATTCTAAGCATAATAATTCAGTTCGA
GTGTCGCAAGCCCAAATAGACGCAGAAGCGTTGGACAACCTTTTAGGCCTATTCTGAGCCCAATAATTCATG
TTGAGGGCCGCAGGCCCGAATACACATAGAAGCGTTGGACAACCTGTTAAGCCTATTCTTAGCATAATAATTCAGTTCGA
GTGTCGCAAGCCCAAATAGACGCAGAAGCGTTGGACAACCTTTTAGGCCTATTCTAAGCCCAATAATTCATG

Nr of selected repeats 3 Similarity 0.940741
Consensus:

TTGAGGGCCGCAGtCCCGAATACACGgaAGAAGtGTTGGAgAtCcGTcAAGCCTATTCTaAGCATAATAATTCAGTTCGA
GTGTCGCAAGCCCAAATAGACGCAGAAGCGTTGGACAACCTTTTAGGCCTATTCTgAGCCCAATAATTCATG
>Cele-UNSB01_4:17138861-17138981 Satlength=121 Nr of Repeats=8 RepeatLength=15
seed=TCGTGGTGAG

TCGTGGTGAGAACCA
TCGTGGTGAGACCCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCCT

Nr of selected repeats 8 Similarity 0.866667
Consensus:

TCGTGGTGaGACCCa
>Cele-UNSB01_4:17168442-17168576 Satlength=135 Nr of Repeats=6 RepeatLength=11
seed=AGTACTGTAG

AGTACTGTAGG
AGTACTGTAGG
AGTACGGTAGG
ATTACTGTAGTTTAGGAAAATGAGTTTTTGTCTTTTGAAGAGATATAGGTTTGGGGTTATTAGTGGGATATGGTCGG
G
GTACTGTAGT
AGTACTGTAGG

Nr of selected repeats 4 Similarity 0.939394
Consensus:

AGTACTGTAGG

>Cele-UNSB01_4:17168764-17168899 Satlength=136 Nr of Repeats=9 RepeatLength=15
seed=TCGTGGTGAG
TCGTGGTGAGACCCG
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA

Nr of selected repeats 9 Similarity 0.980247

Consensus:

TCGTGGTGAGACCCA

>Cele-UNSB01_4:17168941-17169150 Satlength=210 Nr of Repeats=6 RepeatLength=35
seed=GAAATTTAAA

GAAATTTAAATTTTCTGTGAAAAATATTTTGGCGG
GAAATTTAAATTTTCTGTGAAAAATGTTTTGGCGG
GAAATTTAAATTTTCTGTAAAAAATATTTTGGAGG
GAAATTTAAATTTTCTGAAAAAATATTTTGGAGG
GAAATTTAAATTTTCTGAAAAAATATTTTGGAGG
GAAATTTAAATTTTCTGAGAAAAATATTTTGGCGG

Nr of selected repeats 5 Similarity 0.900952

Consensus:

GAAATTTaAATTTTCTGtgAAAAATaTTTTGGcGG

>Cele-UNSB01_4:17169175-17169333 Satlength=159 Nr of Repeats=4 RepeatLength=40
seed=AAAATTCTGG

AAAATTCTGGAATCTAGAATCTTCTGGAAATTTCGAA
AACATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGAG
AAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGAG
AAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGAG

Nr of selected repeats 3 Similarity 0.977778

Consensus:

AAaATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGAG

>Cele-UNSB01_4:17223540-17224619 Satlength=1080 Nr of Repeats=56
RepeatLength=19 seed=AAAAATAGAT

AAAAATAGATTGCTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTCCACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTCCACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACG
AAAAATAGATTGTTCCACG
AAAAATAGATTGTTACACGA
AAAAATAGATTGCTACACGA
AAAAATAGATTGCTACACGA
AAAAATAGATTGTTACACG
AAAAATAGATTGCTACACG

AAAAAATAGATTGTTACACG
 AAAAAATAGATTGTTCCACG
 AAAAAATAGATTGTTACACG
 AAAAAATAGATTGTTACACG
 AAAAAATAGATTGTTACACG
 AAAAAATAGATTGTTACACG
 AAAAAATAGATTGTTACACGA
 AAAAAATAGATTGCTACACGA
 AAAAAATAGATTGCTACACGA
 AAAAAATAGATTGTTACACG
 AAAAAATAGATTGCTACACG
 AAAAAATAGATTGTTACACG
 AAAAAATAGATTGTTACACG
 AAAAAATAGATTGTTCCACG
 AAAAAATAGATTGTTACACGA
 AAAAAATAGATTGCTACACGA
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 AAAAAATAGATTGCTACACG
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 AAAAAATAGATTGCTACACGA
 AAAAAATAGATTGCTACACGA
 AAAAAATAGATTGCTACACGA
 AAAAAATAGATTGTTACACG
 AAAAAATAGATTGCTACACG
 AAAAAATAGATTGTTACACG

Nr of selected repeats 41 Similarity 0.957039

Consensus:

AAAAATAGATTGTTACACG

>Cele-UNSB01_4:17319515-17323871 Satlength=4357 Nr of Repeats=66

RepeatLength=66 seed=CAATCAACC

CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTATCAAATTTTTAAAAATTTTAAAGAAAACA
 CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTATCAAATTTTTGAAATTTTAAAGAAAACA
 CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTATCAAATTTTTGAAATTTTAAAGAAAACA
 CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTATCAAATTTTTGAAATTTTAAAGAAAACA
 CAAATCAACCTATTTAGTTGACAATGTTTTCTTTATCAAATTTTTGAAATTTTAAAGAAAACA
 CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTATCAAATTTTTGAAATTTTAAAGAAAACA
 CAAATCAACCTATTTAGTTGACAATGTTTTCTTTATCAAATTTTTGAAATTTTAAAGAAAACA
 CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTATCAAATTTTTTAAATTTTAAAGAAAACA
 CAAATCAACCTATTTAGTTGACAATGGTTTTCTTTATCAAATTTTTGAAATTTTAAAGAAAACA
 CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTATCAAATTTTTTAAATTTTAAAGAAAACA
 CAAATCAACCTATTTAGTTGACAATGGTTTTCTTTATCAAATTTTTGAAATTTTAAAGAAAACA

CAAATCAACCTATTcAGTTGACAATGGTTTTCTTTTATCAAACCTTTTTAAAATTTTAAAGAAAACA

Nr of selected repeats 66 Similarity 0.958428

Consensus:

CAAATCAACCTATTcAGTTGACAATGGTTTTCTTTTAtCAAATTTTTnAAATTTTAAAGAAAACA

>Cele-UNSB01_4:17337235-17337502 Satlength=268 Nr of Repeats=10 RepeatLength=11
seed=CCTACAGTAC

CCTACAGTACT

CCTACAGTACCT

CTACAGTACTA

CTACAGTACCCCAACCATATCCCCTACTAACCAGCAAACCTATATTCCCTCAAAGACGAAGACACAGTTTTTCCTAAA
CTACAGTAAT

CCTACAGTACT

CCTAAAGTACC

CCTACAGTACTA

CTACAGTACCCCGACCATATCCCCTACTAACCCCAAACCTTTATCTCTTCAAAGACAAAACCTCAATTTTTCTGAAT
TACAGAAAT

CCTACAGCACT

CCTAAAGTACA

Nr of selected repeats 6 Similarity 0.716667

Consensus:

CCTAcAGTACT

>Cele-UNSB01_4:17389165-17390089 Satlength=925 Nr of Repeats=21 RepeatLength=44
seed=GATTGATGGC

GATTGATGGCCGAAAGGCTGTTTTCTGAGCATTGTTGTATTTTCG

GATTGATGGCCGAAAGGCTGTTTTCTGAGCATTGTAGATTTTTTCG

GATTGATGGCCGAAAGGCTGTTTTCTGAGCATTGTTGTATTTTCG

GATTGATGGCCGAAAGGCTGTTTTCTGAGCATTGTAGATTTTTTCG

Nr of selected repeats 21 Similarity 0.961328

Consensus:

GATTGATGGCCGAAAGGCTGTTTTCTGAGCATTGTAGATTTTTTCG

>Cele-UNSB01_4:17395956-17396303 Satlength=348 Nr of Repeats=5 RepeatLength=18
seed=GCACTCCCTA

GCACTCCCTATTAGTATTGCCCTCGGAGACCTTCCGAAAATTAGTATG

GCACTCCCTATTAGTCTT

GCACTCTCTAATAGCCTTGCGTTTACTCTTTTTTATTGCAGGCCCGTCTTGTTAACTTCAGGATTTCAACGAAAAAAT

TGCCTATTTTGCAACAGTTTTTCACAACATTTCTACGAGATTGAAGTTTTTGAACCTTATATGTTACAATTTAAATCAAA

TTTTCTGAATTTTTACATAAGATTCGAGCTTTTTTCAGAAAAACTAGTAAGCTCAAAGTCAGAAAAATGTTCTGAAAAT
TAGTATT
GCACTCCCTAATAGTCTT
GCACTCCCTAATAGTCTT
Nr of selected repeats 3 Similarity 0.950617
Consensus:
GCACTCCCTAaTAGTCTT
>Cele-UNSB01_4:17401416-17402316 Satlength=901 Nr of Repeats=60 RepeatLength=15
seed=ACCCATCGTG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCACCGTGGTGAG
ACCCATCGCGGTGAG
ACCCACCGTGGTGAG
ACCCGTCGTGGTGAG
ACCCATCGTGGCGAG
ACCCATCGTGGCGAG
ACTCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCACCGTGGTGAG
ACCCGTCGTGGTGAG
ACCCATCGTGGTAAG
ACCCACCGTGGTGAT
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGATGAG
ACCCATCGTGGTGAG
ACCCGTCGTGGCGAG
ACCCACCGTGGTGAG
ACCCGTCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGATGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCACCGTGGTGAG
ACCCGTCGTGGTGAG
ACCCATCGTGGTAAG
ACCCACCGTGGTGAT
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGATGAG
ACCCATCGTGGTGAG
ACCCGTCGTGGCGAG
ACCCATCGTGGTGAG
ACCCGTCGTGGCGAG
ACCCATCGTGGTGAG
ACCCGTCGTGGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCGTCGTGGCGAG
ACCCATCGTGGTGAG
ACCCGTCGTGGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCACCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCACCGTGGTGAG

ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCACCGTGGTGAG
ACCCGTCGTGGTGAG
ACCCATCGTGGTAAG
ACCCATCGTGGTGAG
ACCCATCGTGGTAAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCACCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCATCGTGGTGAG

Nr of selected repeats 60 Similarity 0.889768

Consensus:

ACCCATCGTGGtGAG

>Cele-UNSB01_4:17402400-17402610 Satlength=211 Nr of Repeats=6 RepeatLength=35

seed=AAATTTTCTG

AAATTTTCTGAGAAAAATATTTTGGCGGGAAATTT
AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTT
AAATTTTCTGAGAAAAATCTTTTGGCAGGAAATTT
AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTT
AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTT
AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTG

Nr of selected repeats 6 Similarity 0.928889

Consensus:

AAATTTTCTGtGAAAAATATTTTGGCGGGAAATTT

>Cele-UNSB01_4:17408961-17409411 Satlength=451 Nr of Repeats=28 RepeatLength=15

seed=TCTCACCACG

TCTCACCACGAAGTG
TCTCACCACGAAAGG
TCTCACCACGATGCG
TCTCACCACGATGCG
TCTCACCACGATAAG
TCTCACCACGATGGG
TCTCTCCACGAAAGG
TCTCACCACGCTGGG
TCTCACCACGATGGG
TCTCACCACGATGGG
TCTCACCACGATGGGC
CTCACCACGATGGGCCTCTCCACGAAAGG
TCTCACCACGAAAGG
TCTCACCACGATGGG
TCTCACCACGATGGG
TCTCACTACGAAAGG
TCTCACCACGATGGGTCTCTCCACAAAAGG
TCTCACCACGATGGG
TCTCACCACGAAAGG
TCTCACCACGATGGG
TCTCACCCCGATGGG
TCTCACCACGAAAGG
TCTCACCACGATGGG

TCTCACCCCGATGGG
TCTCACACGAAGGG
TCTCACACGGTGGG
TCTCACACGATGGG
TCTCACACGATGGT

Nr of selected repeats 25 Similarity 0.847111

Consensus:

TCTCACACGAtgGG

>Cele-UNSB01_4:17408894-17409724 Satlength=831 Nr of Repeats=9 RepeatLength=37
seed=ATTCCCGCCA

ATTCGCGCCAAAATATTTCCAAAAATTTAAATTTTA

ATTCGCGCCAAATATGTTTCACTACGATGGGTCTCACACGAAGTGTCTCACACGAAAGGTCTCACACGATGCGTCTC
ACCACGATGCGTCTCACACGATAAGTCTCACACGATGGGTCTCTCCACGAAAGGTCTCACACGCTGGGTCTACCA
CGATGGGTCTCACACGATGGGTCTCACACGATGGGCCTCACACGATGGGCCTCTCCACGAAAGGTCTCACACGAA
AGGTCTCACACGATGGGTCTCACACGATGGGTCTCACTACGAAAGGTCTCACACGATGGGTCTCTCCACAAAAGGT
CTCACACGATGGGTCTCACACGAAAGGTCTCACACGATGGGTCTCACCCGATGGGTCTCACACGAAAGGTCTCA
CCACGATGGGTCTCACCCGATGGGTCTCACACGAAGGTCTCACACGATGGGTCTCACACGATGGGTCTCACAC
GATGGTTCTCACACGATGGGTCTCGACACGAAGTTCTTTTTCTCAGAAATTTTAA

ATTCCAGCCAAAATGTTTTGAAAAATTTAAATTTTGA

ATTCGCGCCAAAATATTTTCAAAAAATTTAACTTTTAA

ATTCGCGCCAAAATATTTTCAAAAAATTTAAATTTTGA

ATTCGCGCCAAAATATTTTCAAAAAATTTAAATTTTGA

ATTCGCGCCAAAATATTTTCAAAAAATTTAAATTTTAA

ATTCGCGCCAAAATGTTTTGAAAAATTTAAATTTTGA

ATTCACGCCAAAATGATTTCTAAGAAAATTTCAAATTTGA

Nr of selected repeats 6 Similarity 0.896697

Consensus:

ATTCGCGCCAAAATaTTTTCaAAAAATTTAAaTTTgA

>Cele-UNSB01_4:17523613-17523740 Satlength=128 Nr of Repeats=4 RepeatLength=32
seed=GAAGAAATTT

GAAGAAATTTGAATTTGCACCAAAAATTTTTCT

GAACAAATTTGAAATCCACCAAAAATTTTCA

GAAGAAATTTGAATTTCCCGCTAAAATTTTTCT

GAAGAAATTTGAGTTTGCACCAAAAATTTTTCT

Nr of selected repeats 3 Similarity 0.861111

Consensus:

GAAGAAATTTGAaTTTgCaCcAAAATTTTTCT

>Cele-UNSB01_4:17545983-17546043 Satlength=61 Nr of Repeats=4 RepeatLength=15
seed=GTAGATCTTG

GTAGATCTTGTTTTG

GTAGATCTTGAAAAT

GTAGATCTTGTTTTG

GTGGATCTTGTTTTC

Nr of selected repeats 4 Similarity 0.675347

Consensus:

GTaGATCTTGtttTg

>Cele-UNSB01_4:17584126-17584294 Satlength=169 Nr of Repeats=7 RepeatLength=24
seed=TCAACAACAA

TCAACAACAACAGGAGAAGCTTCT

TCAACAACAACAGGAGAAGCTTCT

TCAACAACAACAGGAGAAGCTTCT

TCAACAACAACAGGAGAAGCTTCT

TCAACAACAACAGGAGAAGCTTCT

TCAACAACAACAGGAGAAGCTTCT

TCAACAACAACAGGAGAAGCTTCT

Nr of selected repeats 7 Similarity 1.000000

Consensus:

TCAACAACAACAGGAGAAGCTTCT

>Cele-UNSB01_4:17606143-17606220 Satlength=78 Nr of Repeats=5 RepeatLength=15

seed=TTCCCCTTTT

TTCCCCTTTTTCGTAT

TTCCCCTTTTGTAA

TTCCCCTTTTTCGTAT

TTCCCCTTTTTCGCAT

TTCCCCTTTTTCGTTTCAG

Nr of selected repeats 4 Similarity 0.866667

Consensus:

TTCCCCTTTTcGtAt

>Cele-UNSB01_4:17753355-17753780 Satlength=426 Nr of Repeats=17 RepeatLength=25

seed=AGCCAGAGAG

AGCCAGAGAGTAAAAAATACGGTGA

AGCCAGAGAGTAAAAATAAACTGTGA

AGCCAGAGAGTAAAAATAAACTGTGT

AGCCAGAGAGTAAAAAATACGGTGA

AGCCAGAGAGTAAAAATAAACTGTGA

AGCCAGAGAGTAAAAATATACGGTGA

AGCCAGAGAGTAAAAATATACGGTGA

AGCCAGAGAGTAAAAATATATGGTGA

AGCCAGAGAGTAAAAATATACGGTGA

AGCCAGAGAGTAAAAATATATGGTGA

AGCCAGAGAGTAAAAATAAAATTTGTGA

AGCCAGAGAGTAAAAAATACGGTGA

AGCCAGAGAGTAAAAATAAACTGTGT

AGCCAGAGAGTAAAAAATACGGTGA

AGCCAGAGAGTAAAAATAAACTGTGA

AGCCAGAGAGTAAAAATATACGGTGA

AGCCAGAGAGTAAAAATAAACTGTGG

Nr of selected repeats 17 Similarity 0.890980

Consensus:

AGCCAGAGAGTAAAAAtAtAcGtGA

>Cele-UNSB01_4:17753798-17754998 Satlength=1201 Nr of Repeats=48

RepeatLength=25 seed=ACTCTCTGGC

ACTCTCTGGCTTCACCATATATTTT

ACTCTCTGGCTTCACCGTATATTTT

ACTCTCTGGCTTCACCATATATTTT

ACTCTCTGGCTTCACAGTTTATTTT

ACTCTCTGGCTTCACCGTATTTTTT

ACTCTCTGGCTTCACAGTTTATTTT

ACTATCTGGCTTCACCATATATTTT

ACTCTCTGGCTTCACCGTATTTTTT

ACTCTCTGGCTTCACCATATATTTT

ACTCTCTGGCTTCACCGTATTTTTT

ACTCTCTGGCTTCACAGTTTATTTT

ACTCTCTGGCTTCGCCGTATTTTTT

ACTCTCTGGCTTCACCGTATTTTTA

ACTCTCTGGCTTCACCGTATATTTT

ACTCTCTGGCTTCACCGTATATTTT

ACTCTCTGGCTTCACCATATATTTT

TTAGGCTTAGGCTTAGGC

Nr of selected repeats 305 Similarity 1.000000

Consensus:

TTAGGCTTAGGC

>Cele-UNSB01_5:4-5075 Satlength=5072 Nr of Repeats=419 RepeatLength=12

seed=AAGCCTAAGC

AAGCCTAAGCCT

AAAAGGAGAACGACG
AAAAGGAGAACAACG
AAAAGGAGAACAACC
AAAAGGAGAACGACG

Nr of selected repeats 6 Similarity 0.822222

Consensus:

AAAAGGAGAAcnACG

>Cele-UNSB01_5:105684-105774 Satlength=91 Nr of Repeats=6 RepeatLength=15

seed=TTCTCCTTTT

TTCTCCTTTTCGTCTG

TTCTCCTTTTGGTTG

TTCTCCTTTTCGTCTG

TTCTCCTTTTCGTCTG

TTCTCGTTTTCGTAA

TTCTCCTTTTCGAAA

Nr of selected repeats 6 Similarity 0.792593

Consensus:

TTCTCCTTTTCGTng

>Cele-UNSB01_5:328030-329092 Satlength=1063 Nr of Repeats=6 RepeatLength=175

seed=AAATTTGGG

AAATTTGGGTTCACTCTTTTACTAGACAGTGATTGTTGCATTGTAGGATTCGGTGGACTTGTCCAACAACCTTACTTT

GGCATGAGTTTAAATAAAAAGGTTTACCATGAACTGAATCAATTTAAAATAAAAAACCTCGAGAACGAAAACATCCTCAG

TAATTTCAATCCTGTTC

AAATTTGGGTTCACTCTTTTACTAGACAGTGATTGTTGCATTGTAGGATTCGGTGGACTTGTCCAACAACCTTATTTT

GGCATGAGTTTAAATGAAAAGTGTATAATGAACTGGATCAATTTAAAATAAAAAACCTCGAGAATGAAAACATCCTCAG

TAATTTCAATCCTGTTC

AAATTTGGGTTCACTCTTTTACTAGACAGTGATTGTTGCATTGTAGGTTTTCGGTGGACTTGTCCAACAACCTTACTTT

GGCATGAGTTTAAATAAAAAGGTTTACCATGAACTGAATCAATTCAAAATAAAAAACCTCGAGAATGAAAACATCTCCAG

TTGCCTCAATCATGTTC

AAATTTGGGTTCACTCTTTTACTAGACAGTGATTGTTGCATTGTAGGATTCGGTGGACTTGTCCAACAACCTTAATTT

GGCATGCGTTTAAATAAAAAGGTTTACCATGAACTGAAACAAATTGGGAAATTTGGGAAAACCTGCGAGAACCAAAATAT

TAATTTCAATCCTGTTC

AAATTTGGGTTCACTCTTTTACTAGACAGTGATTGTTGCATTGTAGGATTTGGTGGACTTATCCAACAACCTTACTTT

GGCATGAGTTTAAATAAAAAGTGTTTACCATGAACTGAAACAAATTGGGAAATTTGGGAAAACCTGCGAGAACCAAAATAT

CTCCAGTTAAAAAAAACAGTTA

AAATTTGGGTTCACTCTTATTACTTTACAGTGATTGTTACATTGTAGATTCTGTGGACTTGTCCAACCTGTCTACGACG

GCATGAGTTTAGTAAAAAGTATTACCATGAACTGAAACAAATTGGGAAATTTGTGAAAACCTGCGAGAATCAAATATC

TCCAGTTTAAATAAAAACAGTTC

Nr of selected repeats 4 Similarity 0.911111

Consensus:

AAATTTGGGTTCACTCTTTTtACTAGACAGTGATTGTTGCATTGTAGGaTTCGGTGGACTTGTCCAACAACCTTAcTTT

GGCATGaGTTTAAATaAAAAGgtTTTAccATGAACTGaaTCAATTcAAAATAAAAAACcTCGAGAAtGAAAaCATCctCAG

TaattTCAATCCTGTTC

>Cele-UNSB01_5:345871-345991 Satlength=121 Nr of Repeats=7 RepeatLength=16

seed=CATGCCTACA

CATGCCTACATGCCTA

CATACCTACATGCCTA

CATGCCTACATGCCTA

CATGCCTACATGCCTA

CATGCCTACATGCCTA

CATGCCTACAGGTTTACATACATA

CATGCCTACATGCCTA

Nr of selected repeats 6 Similarity 0.972222

Consensus:

CATGCCTACATGCCTA

>Cele-UNSB01_5:353635-353859 Satlength=225 Nr of Repeats=14 RepeatLength=16

seed=GGCATGTAGG
GGCATGTAGGCATGTA
GGCATGTAGGCATGTA
GGCATGTAGGCATGTA
GGCATGTAGGCATGTA
GGCATGTAGGCATGTA
GGCGTGTAGGCATGTA
GGCATATAGGTATGTA
GGCATGTAGGCATGCA
GGCATGTAGGCATGTA
GGCATGTAGGCATGTA
GGCATGTTGGCATGTA
GGTATGTAGGCATGTA
GGCATGTAGGCATGTA
GGCATGTAGGCATGTA
GGCATGTAGGCATGTA

Nr of selected repeats 14 Similarity 0.928571

Consensus:

GGCATGTAGGCATGTA

>Cele-UNSB01_5:376477-376531 Satlength=55 Nr of Repeats=4 RepeatLength=12

seed=AGGCTTAGGC
AGGCTTAGGCTA
AGGCTTAGGCTA
AGGCTTAGGCTA
AGGCTTAGACCTAGGGTT

Nr of selected repeats 3 Similarity 1.000000

Consensus:

AGGCTTAGGCTA

>Cele-UNSB01_5:786342-786547 Satlength=206 Nr of Repeats=6 RepeatLength=34

seed=CAATTTGCCG
CAATTTGCCGGTTTGTCCGAAATTTCGAATCCGG
CAATTTGCCGATTTACCCGAAATTTGATTCGG
CAATTTGCCGGTTTGCCGAAAAATTCATTTTAG
CAATCTGCCGATTTGCCGAAATTTCAATTCGG
CAATTTGCCGGTTTGCCGAAATTTAAATTTCCG
CAATTTGCCGATTTGCCGAAATTTCAATTTCCG

Nr of selected repeats 5 Similarity 0.788235

Consensus:

CAATTTGCCGgTTTgcCgGAAAtTTcaAtTtcgg

>Cele-UNSB01_5:786696-786877 Satlength=182 Nr of Repeats=5 RepeatLength=35

seed=TTTCCGGCAA
TTTCCGGCAAACCGGCGAATTGCCGGAATTGAAAA
TTTCCGGTAAATCGGCCAATTGCTGGAATCGAAT
TTTCCGGTAAATCGGCCAATTGCCGGAATTGAAGA
TTTCCGGCAAACCGGCAAATTTCCGAAATTTGAAGA
TTTCCGGCAAATCGGCCAAACCGGCAAATGCGGAGTTGAAA

Nr of selected repeats 3 Similarity 0.834921

Consensus:

TTTCCGGcAAAcCGGcNAATTgCCGgAATTGAAGa

>Cele-UNSB01_5:788141-788221 Satlength=81 Nr of Repeats=5 RepeatLength=16

seed=CTACATGCCT
CTACATGCCTACATGC
CTACATGCCTACATGC

CTACATTCCTACATGC
CTACATGCCTACATGC
CTACATGTCTACATGC

Nr of selected repeats 5 Similarity 0.933333

Consensus:

CTACATgcCTACATGC

>Cele-UNSB01_5:788660-789185 Satlength=526 Nr of Repeats=12 RepeatLength=16

seed=AGGCATGTAG

AGGCATGTAGGCATGT

AGGTATGTAGGCATGT

AGGCATGTAGGCATGT

AGGCATGTAGGCATAT

AGGCATGTAGGCATGTAGGTACCAGGGAATTTTTTCATCAAATTTTCAATTTTCAGCCATCACCGCCCATCTTGCCAAGT

TCGCCGAAGGAACCGGAAAATCAGTTGCCACAATTTTGAACGCCAAGTACGAGGGAGCCGGTACTACCTCATCATCAC

TGCAGACTTCTCTGCTGAAAACCGAAAAGCTGGAAGTGTGAAGGGAAAATTTTTCAGATCTGGAAGAAGGAAGGCGAC

AGACACCTGGTTTTCCACGATGAATTTGAAATTAATCCATAGAAATTTGGGAACTTTTTTGTCTGATAACAATTATTGT

AATAAATTTTTTATTCTGAATTTTCCTCTCGTCTCTCGTA

AGCATGTAGGCATGT

AGGCATGTAGGCATGT

AGGCATGTAGGCATGT

AGACATGTAGGTATGT

AGGCATGTGT

AGGCATGTAGGCATGT

AGGCACGTAGGCATGT

Nr of selected repeats 9 Similarity 0.907407

Consensus:

AGGCATGTAGGCATGT

>Cele-UNSB01_5:790113-790281 Satlength=169 Nr of Repeats=10 RepeatLength=16

seed=AGGCATGTAG

AGGCATGTAGGCATGT

AGGCATGTAGGCATGT

AGGCATGTAGGCATGT

AGGCATGTAGGCATGT

AGGCATGTAGGCATGT

AGACATGTAGGCATGT

AGGCATGTAGGCATGT

AGGCATGTAGGCATGT

AGGCATGTAGGCAATT

AGGCATTTAGGCAATTAGGCATTT

Nr of selected repeats 9 Similarity 0.944444

Consensus:

AGGCATGTAGGCATGT

>Cele-UNSB01_5:853469-853759 Satlength=291 Nr of Repeats=23 RepeatLength=10

seed=GGCGTCAGCG

GGCGTCAGCGAGCTTCAGCGGGCATCACCAA

GGCGTCAGCGGGCGTCAGCA

GGCGTCAGCGGGATTTCAGTG

GGCGTCAGCG

GGCGGCAGCG

GGCGGCAGCG

GGCGTCAGCGGAAGTCAGCGGGAGTTAGCA

GGCGTCAGCG

GGCGTCGGCG

GGCGTCAGCG

GGCGTCGGCG
GGCGTCGGCG
GGCGTCAGCG
GGCGTCAGTG
GGCGTCAGCG
GGCGTCAGCG
GGCGTTAGCG
GGCGTCGGCG
GGCGTCAGCG
GGCGTCAGCG
GGCGTCAGCG
GGCGTCAGCG
GGCGTCAGCGGGCGTCAGCG

Nr of selected repeats 17 Similarity 0.888235

Consensus:

GGCGTCaGCG

>Cele-UNSB01_5:896085-896285 Satlength=201 Nr of Repeats=12 RepeatLength=16

seed=ATGCCTACAT
ATGCCTACATGCCTAA
ATGCCTAGATGCCTAG
ATGCCTACATGCCTAC
ATGCCTCCATGCCTACATGCCTAC

Nr of selected repeats 11 Similarity 0.956061

Consensus:

ATGCCTACATGCCTAC

>Cele-UNSB01_5:915117-915271 Satlength=155 Nr of Repeats=7 RepeatLength=20

seed=CCTACCCCAG
CCTACCCCAGGCTGACCTAG
CCTACCCCAGGCTGACCTAG
CCTACCCCAGGCTGACCTAG
CCTACCCCAGGCAGGCCTAT
CCTACCCCAGGCAGGCCTAA
CCTACCCCAGGCAGACCTAGTCTACCCTAGGCAA
CCTACCCCAGGCAGGCCTAA

Nr of selected repeats 6 Similarity 0.871111

Consensus:

CCTACCCCAGGCaGaCCTAg

>Cele-UNSB01_5:915226-915380 Satlength=155 Nr of Repeats=8 RepeatLength=20

seed=GGCAGACCTA
GGCAGACCTAGTCTACCCTA
GGCAACCTACCCCA
GGCAGGCCTAACCTACCCCA
GGCAGGCCTAACCTACCATA
GGCAGACCTAGTCTACCATA
GGCAGACCTAGTCTACCATA
GGCAGACCTAGTCCACCCTG
GGCAGACCTAGTCTACCCTA

Nr of selected repeats 7 Similarity 0.809524

Consensus:

GGCAGaCCTAgtCTACCcTA

>Cele-UNSB01_5:978655-978943 Satlength=289 Nr of Repeats=7 RepeatLength=35
seed=TGCCGATTTG

TGCCGATTTGCCAGAAATTTTCAATTCGGCAATTTGCAGGCTTCCCGGAAATTTTCAATTTCTCAAAT
TGCCGATTTGCCGAAATGTTCAATTTTCGAGAATT
TGCCGATTTGCCGAAATGTTCAATTTTCGAGAATT
TGCCGATTTGCCGAAAGTTTTTAATTTTCGGCAATT
TGCCGATTTGCCGAAATGTTCAATTTTCGAGAATT
TGCCGACTTGCCGAAATTTGTTCAATTTTCGGCAATT
TGCCGATTTGCCGAAATTTCAATTTTCACCAATTTGCTGATC

Nr of selected repeats 5 Similarity 0.809524

Consensus:

TGCCGatTTGCCGAAaTgtTcAtTtTCGagAAtT

>Cele-UNSB01_5:1026357-1026873 Satlength=517 Nr of Repeats=9 RepeatLength=35
seed=GCATTTGCCG

GCATTTGCCGATTTTCAAATTTCCGACAGTTCCGGCATTTTCGGGGTTTTGGAATTTTCGGCAATTCCA
GCATTTGCCGGTTTTCGAAATTTTCGGCAATTTTCG
GAATTTGCCGGTTTTTGAATTTCCGGCAATTACGGTATTTACTGGTTTTTGGGCACTTTCAGCAATTTTCG
GCATTTGCCGATTTTAAAAATTTCTGGCAATTCCA
GCATTTGCCGATTTTAAAAATTTCTGGCAATTCCA
GCATTTGCCGATTTTAAAAATTTCTGGCAATTCCA
GCATTTGCCGATTTTAAAAATTTCTGGCAATTCCA
GCATTTGCCGGTTTTCGAAATTTTGGCATTATG
GAATTTGCCGGTTTTTGAATTTTCGGCAATTCCTGTAATTACTGGTTTTTGGGCACTGTCAGAAATTTCTGACAATTGCC
GGATTCGAAATTTTCGGTAATTAACGGTTTTCGGGAAGTTCCGGCACATCCGGAATATGCCGGTTTTTGGGAATTTTCGG
CGATTTTCG

Nr of selected repeats 6 Similarity 0.817143

Consensus:

GCATTTGCCGaTTTttaAAATTTcTGGCAATTcCa

>Cele-UNSB01_5:1035824-1036308 Satlength=485 Nr of Repeats=20 RepeatLength=22
seed=ACAGTACTCC

ACAGTACTCCCACAGTACCACT
ACAGTACTCCTACAGTACCACT
ACAGTACTCCTACAGTACCACT
ACAGTACTCCTACAGCACTATA
ACAGTACTCCTACAGTACCACT
ACAGTACTCCTACAGTAGCACT
ACAGTACTCCTACAGTACCACT
ACAGTACTCCTACAGTACCACT
ACAGTACTCCTACAGCACTATG
ACAGTACTCCTACATTACCGCT
ACAGTACTCCAACAGTGTCAGTCAATACTCCTACAGTACCACT
ACAGTACTCCTACAGTACCACT
ACAGTACTCCTACAGCACTATA
ACAGTACTCCTACAGTACCACTT
CAGTACTCCTACAGTACCACT
ACAGTACTCCTACAGCACTATG
ACAGTACTCCTACATGACCGCT
ACAGTACTCCAACAGTGTCAGT
ACAATACTCCTACAGTACCACTTCACTACTCCTACCGTACCACT
ACAGTACTCCTACAGCACTATA

Nr of selected repeats 16 Similarity 0.776630

Consensus :

ACAGTACTCCTACAGtACcAnT

>Cele-UNSB01_5:1038307-1038528 Satlength=222 Nr of Repeats=11 RepeatLength=13

seed=GCCTATGGCC

GCCTATGGCCTACGCCTATGACTTAC

GCCTATGGCAAAC

GCCTATGGCCTCC

GCCTATGGCCTACGCCTACGGTCTAC

GCCTATGGCCTACGCCTATTACCTACGCCTATTACCTAA

GCCTATGGCCTACGCCTATAGCAACCGTCTTTGACCAAT

GCCTATGGCCTAC

GCCTATGGCCTAC

GCCTATGGCCTAC

GCCTATGGCCTAC

GCCTATGGCCTAC

Nr of selected repeats 7 Similarity 0.912088

Consensus :

GCCTATGGCCTAC

>Cele-UNSB01_5:1039029-1039263 Satlength=235 Nr of Repeats=18 RepeatLength=13

seed=CGTAGGCCAT

CGTAGGCCATATA

CGTAGGCCATATA

CGTAGGCCATAGG

CGTAGGCCATAGG

CGTAGGCCATAGG

CGTAGGCCACAGG

CGTAGGCCACAGG

CGTAGGCCATATA

CGTAGGCCATATA

CGTAGGCCATAGG

CGTAGGCCATAGG

CGTAGGCCATAGG

CGTAGGCCACAGG

CGTAGGCCATAGG

CGTAGGCCATAGG

CGTAGGCCATAGG

CGTAGGCCATAGG

CGTAGGCCATAGG

Nr of selected repeats 18 Similarity 0.894754

Consensus :

CGTAGGCCATAgg

>Cele-UNSB01_5:1057921-1058017 Satlength=97 Nr of Repeats=6 RepeatLength=18

seed=AAGCCTAAGC

AAGCCTAAGCCTATGCCA

AAGCCTAAGCCT

AAGCCTAAGTCTAAATCT

AAGCCTAAGCCAAACCT

AGGCCTAAGCCC

AAGCCTAAGCATGAGCCT

Nr of selected repeats 4 Similarity 0.691358

Consensus :

AAGCCTAAGcctaaacCt

>Cele-UNSB01_5:1115366-1136806 Satlength=21441 Nr of Repeats=722

RepeatLength=27 seed=TCTGTGGCTT

TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATTTTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACAC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATTTTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTCTCCAAAATAATTTCCAAGTTTTTAATGATTTGTTGCATATTGAAAAAACA
TTTTTCGGGTTTTTTGAAATGAATATCGTAGCTACAGAAACGGTAATACACTCTTCTGAAAATACAAAAAATTTGCAAT
TTTTTATAGCTAGGGCACTTTTTGTCTGCCCAAATATAGGCAACCAAAAATAATTTCCAAGTTTTTAATGATTTGTTGCA
TATTGAAAAACATTTTTTGGGTTTTTTGAAATGAATATCATAGCTATAGAAACGGTAGTATTTTTACTC
TCTGTGGCTTCACAGTATATTTTACAC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACTC
TCTGTGGCTTCCCACTATATTTTACTC
TCTGTGGCTTCACAGTATATTTTACAC

GGCTTAGGCTTA
GGCTGAGGCTTAGGCTGA
GGCCTAGGCTTA
Nr of selected repeats 7 Similarity 0.814815
Consensus:
GGCTTAGGCTtA
>Cele-UNSB01_5:1174135-1174237 Satlength=103 Nr of Repeats=5 RepeatLength=12
seed=CTAAGCCTAA
CTAAGCCTAAGC
CTGAGCCTAAGC
CTAAGCCTAAGA
CTAAGCCTAATAGTAAGCCTGAGTCTGAGCTTACGCGTAAGA
CTAAGCCTAAGCCCAAGCCTAGGC
Nr of selected repeats 3 Similarity 0.851852
Consensus:
CTaAGCCTAAGc
>Cele-UNSB01_5:1229040-1229117 Satlength=78 Nr of Repeats=5 RepeatLength=15
seed=CGAAAAGGGG
CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAGCAA
Nr of selected repeats 4 Similarity 0.748148
Consensus:
CgAAAAGGGGAgcta
>Cele-UNSB01_5:1229292-1229367 Satlength=76 Nr of Repeats=5 RepeatLength=15
seed=TCCCCTTTTC
TCCCCTTTTCGTTGC
TCCCCTTTTCGTATC
TCCCCTTTTCGTATC
TCCCCTTTTCGCAGA
TCCCCTTTTTCGAGA
Nr of selected repeats 5 Similarity 0.768889
Consensus:
TCCCCTTTTcGtagc
>Cele-UNSB01_5:1233778-1237846 Satlength=4069 Nr of Repeats=22 RepeatLength=185
seed=AATATAAACA
AATATAAACATACACGAATTTGTCTGATGTATAAAGATTCCCAGACACTTTCCAATTACCCAAATTGTTTCATATTCT
AAATGAGATTCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAGTT
ATGTCCGAGCAAAAAGATCCGATTCAG
AATATAAACATATTTGAATTTGACGGATGTATAAAGATTCCCAGACACTTTCCAATTACCCAAATTGTTTCATATTCT
AAATGAGATTCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAGTT
ATGTCCGAGCAAAAAGATCCGATTCAG
AATATAAACATATTTGAATTTGACGGATGTATAAAGATTCCCAGACACTTTCCAATTACCCAAATTGTTTCATATTCT
AAATGAAAATCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAGTT
ATGTCCGAGCAAAAAGATCCGATTCAG
AATATAAACATATTTGAATTTGACGATGTATAAAGATTCCCAGACACTTTCCAATTACCCAAATTGTTTCATATTCTAAA
TGAAAATCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAGTTATG
TCCGAGCAAAAAGATCCGATTCAG
AATATAAACATATTTGAATTTGACGGATGTATAAAGATTCCCAGACACTTTCCAATTACCCAAATTGTTTCATATTCTA
AATGAAAATCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGTGAATACAGAACACCAGTTAT
GTCCGAGCAAAAAGATCCGATTCAG

AATATAAACATATTTGAATTTGACgGATGTATAAAGATTCCCgAAGACACTTTCCAATTACCCAAATTGTTTCATATTCT
AAATGAgAtTCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCgAACGTATCATAAGTGAATACAGAACCAGTT
ATGTCCGAGCAAAAAGATCCGATTCAG

>Cele-UNSB01_5:1262246-1262294 Satlength=49 Nr of Repeats=4 RepeatLength=12
seed=AAGCCTAAGC

AAGCCTAAGCTT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCT

Nr of selected repeats 4 Similarity 0.944444

Consensus:

AAGCCTAAGCcT

>Cele-UNSB01_5:1265623-1265875 Satlength=253 Nr of Repeats=19 RepeatLength=12
seed=AAGCCTAAGC

AAGCCTAAGCCT
AAGCTTAAGCCT
AAGCCCAAGCGT
AAGCCTAAGCTT
AAGCCTAAGACTAAATCTA
AACCTAAGCAC
AAGCGTAAGCCT
AAGCCTACGCCTAAGCCTAAAATA

AACCTAAGCCC
AAGCGTAAGCCT
AAGCCTAAGCCT
ACGCCTAAGCCC

AATCCTAAGCTTAAGTAT

AAGCCTAAGTCT
AAGCCTAACCT
AAGCCTAGGCCT
AAGCCTAAGCCT
AAGCCTAAGCCA
AAGCCTAAGCCC

Nr of selected repeats 14 Similarity 0.804640

Consensus:

AAGCcTAAGCct

>Cele-UNSB01_5:1271695-1271973 Satlength=279 Nr of Repeats=15 RepeatLength=12
seed=CTAAGCCTAA

CTAAGCCTAAGCCCAAGCCTAGGG

CTAGGCCTAAAC
CTAAGCCTAAGT
CTAAGCCTAAGC
CTAAGTCTAAGC
CTAAGCCTAAGC

CTAAGCCTAAAAGC

CTAAGCCTAAAA

CTAAGCATAAGC

CTAAGCCTTAGATTAAGCCTACACCAAAGCCTATGCTCACGCTCGCCACTGACGCCAAGCTTAAGCCTGAGCCTACAC

CTAAGCCTAAGC

CTAAGCCTAAGCCTAAAA

CTAAGCCTAAGC

CTAAGCCTTAGAT

TAAGCCTAAGCTTAGGTCTAAGC

Nr of selected repeats 9 Similarity 0.836420

Consensus:

CTAAGCCTAAgc

>Cele-UNSB01_5:1274939-1275298 Satlength=360 Nr of Repeats=10 RepeatLength=35
seed=GAAATTTTCA

GAAATTTTCAATTCCGGCAAATTGCCTAATTGCCA
GAAATTTTCAATTTCCGGCAAATTGCCAAATTGCCA
GAAATTTTCAATTCCGGAAAATTACCAAATTGCCA
GAAATTTTCAATTCCGGCAAATTGCCAAATTGCCA
GAAATTTTCAATTCCGGCAATTTGCCGAATTGTTG
GAAATTTTCAATTCCGGCAAATGCCAAATTGCCG
GAAATTTTCAATTCCGGCAAGTTGCCGAATTGTCG
GAAATTTTCATTTTCGACAGATTGCCGCATCGGCCT
GAATTTTTCATTTTCGGCAAATTGGCGATTTGCCG
GAAATGTTTCATTTTCGGCCAATTGCCGTTTGGCGATTTACCG

Nr of selected repeats 8 Similarity 0.842177

Consensus:

GAAATTTTCAATTCCGGCAAaTTGCCaAATTGcCa

>Cele-UNSB01_5:1278621-1278717 Satlength=97 Nr of Repeats=7 RepeatLength=12
seed=CTTAGGCTTA

CTTAGGCTTAGG
CTTAGGCTTAGT
CTTAGGCTTAGG
CTTAGGCCTAGG
CTTAGTCTTAGG
CTTAGGCTTAGAATTAGCTTTTGG
CTTAGGCTTAAA

Nr of selected repeats 6 Similarity 0.822222

Consensus:

CTTAGGCTTAGg

>Cele-UNSB01_5:1284626-1284947 Satlength=322 Nr of Repeats=10 RepeatLength=11
seed=TACCTACTAG

TACCTACTAGA
TACCTACTGGA
TACCTACTAGATACC
TACCTACTATG
TACCTACTAGAGATTATCACACCAACTACTTAGTCTAGTGATAAATAAATTGTTGGTTATAAATTCAGTGCAAATTTTT
ATAACTGTTAATGTAAAAATTCCTCGAATTTAGTTGTTAGAGATATAGAATGTATTAGTGGTTTTGAGCACTTTATGGA
AGCATTAAAATGGAAGCGTTTGGTTTTTTTAAGGAGCATGTATG
TACCTACTAGA
TGCCTACTAGG
TACCTACTAGA
TACCTACTGGA
TACCTACTAGATACCTACCTACTATG

Nr of selected repeats 6 Similarity 0.789899

Consensus:

TACCTACTaGa

>Cele-UNSB01_5:1289399-1289474 Satlength=76 Nr of Repeats=5 RepeatLength=15
seed=TCGTGGTGAG

TCGTGGTGAGACCCA
TCGTGGTGAGACCCT
TCGTGGTGAGACCCT
TCGTGGTGAGACCAA
TCGTGGTGAGACCCT

Nr of selected repeats 5 Similarity 0.911111

Consensus :

TCGTGGTGAGACCct

>Cele-UNSB01_5:1289402-1291686 Satlength=2285 Nr of Repeats=44 RepeatLength=15

seed=TTGGTGAGACC

TTGGTGAGACCATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCAATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCATCGTTGGTCAAATTTTCAGTGAACAATTTTGGCGGGAAATTCAAATTTTCAGTAAAAAATTTTGGC

GGGAAATTCAAATTTTCAGTGAAAAAATTTTGGCGGGAAATTCAAATTTTAAGTGAAAAAATTTTGGCGGGAAATTC

AAATTTTCAGTAAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGAAAAAATTTTGGCGGGAAATTCAAATTTTCAG

TGTAAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGAAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGTAAAAA

ATTTTGGCGGGAAATTCAAATTTTCTGTGAAAAAATTTTGGCGGGAAATTCAAATTTTCAGTGAAAAACAATTTTGGC

GGAAATTCAAATTTTCAGTAAAAATCGAGAAATGTCTGCAATGTTCCAGAAATTTCTAGAAAAATTCAGAAAAATTCG

GAATGGTCCAGAATTTCTAGAAAAATTCAGAAATGTTCTGGAATAATTTTCCACATCTTACAGTGGTTAGAAATCAA

CAATCATTAATATATATAAAAAAATACAGTTCGTCTGTCCGGAGTTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACG

TCACGCCCAAATTTTCAGTGAGAAATAGTGGGCGTGGCACCCCTTCG

TTGGTGAGACCATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCAATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCAATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCAATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCATCGTTGGTCAAATTTTCAGTGAACAATTTTGGCGGGAAATTCAAATTTTCAGTAAAAAATTTTGG

CGGAAATTCAAATTTTCAGTGAAAAACAATTTTGGCGGAAATTCAAATTTTCAGTAAAAATCGAGAAATGTCTGCAA

TGTTCCAGAAGTTTCTAGAAAAATTCAGAAAAATTCGGAATGGTCCAGAATTTTCTAGAAAAATTCAGAAATGTTCTGGA

ATAATTTTCCACATCTTACAGTGGTTAGAAATCAACAATCATTAATATATATAAAAAAATACAGTTCGTCTGTCCG

GAGTTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGTACGCCCAAATTTTCAGTGAGAAATAGTGGGCGTGGCACCCCT

CG

TTGGTGAGACCATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCAATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCAATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCAATCG

TTGGTGAGACCCTTCG

TTGGTGAGACCCTTCG

TTGGTGAGACCATCGTTGGTCAAATTTTCAGTGAACAATTTTGGCGGGAAATTCAAATTTTCAGTAAAAAATTTTGG

CGGAAATTCAAATTTTCAGTGAAAAACAATTTTGGCGGAAATTCAAATTTTCAGTAAAAATCGAGAAATGTCTGCAA

TGTTCCAGAAGTTTCTAGAAAAATTCAGAAAAATTCGGAATGGTCCAGAATTTTCTAGAAAAATTCAGAAAAATTCGGA

ATGGTCCAGAATTTTCTGAAAAATTCAGAAATGTTCTGGAATGGTCCAGAATTTTCTAGAAAAATTCGGGAAACTCTGG

AATATTCAGAACTTTCTAGAAAAATCGAGAAATGTCTGCAATGTTCCAGAAATTTCTAGAAAAATTCAGAAAAATTCG

GAATGGTCCAGAATTTTCTAGAAAAATTCGGGAAATTCAGAAATAATTTTCCACATCTTACAGTGGTTAGAAATCAA

CAATCATTAACATATATAAAAAAATACAGTTCGTCTGTCCGGAGTTTGTAGTCTATGTAGTCTTTGTAGTCTGTGACGT
CACGCCCAAATTTTCAGTGAGAATAGTGGGCGTGGCACCCCTTCG
TGGTGAGACCCATCG
TGGTGAGACCCTTCG
TGGTGAGACCCTTCG
TGGTGAGACCAATCG
TGGTGAGACCTTTTCG
TGGTGAGACCCTTCG
TGGTGAGACCAATCG
TGGTGAGACCTTTTCG
TGGTGAGACCCTTCG
TGGTGAGACCAATCG
TGGTGAGACCCTTCG
TGGTGAGACCCTTCA

Nr of selected repeats 41 Similarity 0.901138

Consensus :

TGGTGAGACCtTCG

>Cele-UNSB01_5:1289520-1292435 Satlength=2916 Nr of Repeats=32 RepeatLength=35
seed=GCGGGAAATT

GCGGGAAATTCAAATTTTCAGTAAAAAATTTTG
GCGGGAAATTCAAATTTTCAGTGAAAAAATTTTG
GCGGGAAATTCAAATTTTAAGTGAAAAAATTTTG
GCGGGAAATTCAAATTTTCAGTAAAAAATTTTG
GCGGGAAATTCAAATTTTCAGTGAAAAAATTTTG
GCGGGAAATTCAAATTTTCAGTGAAAAAATTTTG
GCGGGAAATTCAAATTTTCAGTGAAAAAATTTTG
GCGGGAAATTCAAATTTTCAGTGAAAAAATTTTG
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GCGGGAAATTCAAATTTTCAGTAAAAACAATTTTG
GCGGAAAATTTCAAATTTCTGAGAAAAATCGAGAAATGTCTGCAATGTTCCAGAAGTTTCTAGAAAATTCGAGAAAATTC
CGGAATGGTCCAGAATTTTCTAGAAAATTCAGAAAAGTTCTGGAATAATTTTTTCCACATCTTACAGTGGTTAGAAATC
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ACCTTTTCGTGGTGAGACCCTTCGTGGTGAGACCAATCGTGGTGAGACCCTTCGTGGTGAGACCCTTCGTGGTGAGACC
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GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTTA
GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTTA
GCGGGAAATTCAAATTTGTCAGTGAAAAAAAAATTTTG
GCGGGAAATTCAAATTTCTGTGAAAAAAAAATTTTG

Nr of selected repeats 20 Similarity 0.939850

Consensus:

GCGGGAAATTCAAATTTTCAGTgAAAAAAAAATTTG

>Cele-UNSB01_5:1308044-1308391 Satlength=348 Nr of Repeats=8 RepeatLength=35

seed=AATTCTGGCA

AATTCTGGCAAATTGCCGATTTGCCGAAAATTTTC
AATTCTGGCAAATTACCGATTTGCCGAAAATTTTC
AATTCTGGCAAATTGCCGATTTGCCGAAAATTTTC
AATTCTGTCAAATTACCGATTTTCCGGAAGTTCTC
AATTCTGGCAAATTACCGATTTGCCGAAAATTTTA
AATTCTGGCAAATTGCCGATTTAAGTTTAGGAAATGTGCCGATTTGCCGAAAATTTTCGATTCCGGCAA
TTTTCCGATTTCCGAAAATTTTA
AATTCTGGCAAATTGCCGATTTGCCGAAAATTTTC
AATTCTGGCAAATTACCGATTTGCCGAAAATTTTC

Nr of selected repeats 7 Similarity 0.902041

Consensus:

AATTCTGGCAAATTaCCGATTTGCCGgAAAATTTTC

>Cele-UNSB01_5:1308547-1312321 Satlength=3775 Nr of Repeats=192 RepeatLength=20

seed=AAAATAGATT

AAAATAGATTGTTACACGA
AAAATAGATTGTTACACGA
AAAATAGATTGCTACACGA
AAAATAGATTGTTACACGA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA
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AAAATAGATTGTTACACGA
AAAATAGATTGTTACACGAA
AAAATAGATTGTTACACGAA

Nr of selected repeats 127 Similarity 0.995817

Consensus:

AAAATAGATTGTTACACGAA

>Cele-UNSB01_5:1343973-1344069 Satlength=97 Nr of Repeats=7 RepeatLength=12
seed=AGGCTTAGGC

AGGCTTAGGCTC
AGGCTTAGGCTC
AGGCTTAGGCTC
AGGCTTAGGCTC
AGGCTTAGGCTC
AGGCTTAGGCTC
AGGCTTAGGCTCAGGCTTAGATCTA
AGCTTAGGCTT

Nr of selected repeats 5 Similarity 1.000000

Consensus:

AGGCTTAGGCTC

>Cele-UNSB01_5:1379498-1379672 Satlength=175 Nr of Repeats=13 RepeatLength=12
seed=CTAAGCCTAA

CTAAGCCTAAGC
CTAAGCCTAAGC
CTAAGCCTAAGG
CTAAGCCTAAGC
CTAAGCCTAAGA
CTAAGCCTAAGC
CTAAGCCTATTCTAATC
CTCAGCCTAAGTTTAAAGCTTAAAC
CTAAGCCTCAGC
CTAAGCCTAAAG
CGAAGCCTAAGC
CTGAGCCTAAGC
CTAAGTCTAAGC

Nr of selected repeats 11 Similarity 0.826263

Consensus:

CTAAGCCTAAGc

>Cele-UNSB01_5:1390382-1390822 Satlength=441 Nr of Repeats=9 RepeatLength=40
seed=AATGTTCTAG

AATGTTCTAGAACCTCCTGGAAATTTGAGAAAATTCTGA
AATGTTCTAGACCCTTCTGGACAACTCGTGAAAATTCTGA
AATGTTCTAGATTTTTCCGAAAATTCGAGAAAATTTTG
AATGTTCTAGGGCGTATTGGAAAGTTCAAAAAAAAAATTCTGGAATATTTGGAACCTTCTGGAAAATTCGAGAAAATTCT
GG

AATGTTCTAGAACCTTCTGGAAAATTTGAGAAAATTCTGC
AATGATCTAGAACCAACTGGAAACCTCAAAAAATTCTTGAGTGTCTTGAACCTTCCGGAAAATTCGAGGAAGTTCTG
G
AATGTTCTACAACATTCTGGGAAATTCGAAAAATTCTGG
AATGTTCTAGAACCTTCTGGAAACCTCTAGAAAATTCTGA
AATGTTCTAGAACCTCTAGGAAAAAATGAGAGAATTTTGG
Nr of selected repeats 6 Similarity 0.738753
Consensus:
AATGTTCTAGAACCTtCTGGAAAatTcGAGAAAATTCTGa
>Cele-UNSB01_5:1393460-1393720 Satlength=261 Nr of Repeats=6 RepeatLength=40
seed=CTAGAACATT
CTAGAACATTCTAGAATTTTCTCGAGCATTCCAGAATTTTCTCAAACCTTCTAGAAGGTT
CTAGAACCTTCCAGAATTTTCTCAAACCTTCTAGAAGGTT
CTAGAACATTCCAGAATTTTCTCGAATTTTCCAGAAGGTC
CTAGAACATTCCAGAATTTTTTCTGAATTTTCTGAAACCGTT
CTTGAACATTCCAGAATTTTCTTAGAATTTTCCAAAATTT
CTAGAACATTTCCAGAAATTTCTTGAGTTTTCCAGAAAGTT
Nr of selected repeats 5 Similarity 0.712195
Consensus:
CTaGAACaTTcCAGAAatTTTcTcgAatTTTCCAgAangTt
>Cele-UNSB01_5:1406535-1406737 Satlength=203 Nr of Repeats=6 RepeatLength=34
seed=AAATTCAAAT
AAATTCAAATTTTTTGGAGAAAACATTTTGGCGGG
AAATTCAAATTTCTGACAAAGAATTTTAGCGGA
AAATTCAAATTTCTGAGAAATAAATTTGACGGA
AAATTCAAATTTCTAAGAAAAAATTTTGGCGGA
AAATTCAAATTTCTGAGAAATTTATTTTGGTGGG
AAATTCAAATTTTTGAAAAATAATTTTGGCGGG
Nr of selected repeats 5 Similarity 0.823529
Consensus:
AAATTCAAATTTTcTgAgAAAataAtTTTGgcGGg
>Cele-UNSB01_5:1415140-1415840 Satlength=701 Nr of Repeats=21 RepeatLength=35
seed=ATTTTCAATT
ATTTTCAATTTGTTATATTAACGATTTGCCGGAA
ATTTTCAATTCCAGCAATTTGCCGATTTTCTTGAA
ATTTTAAATTCCGTACCTTGTCATTTGCTAGAA
ATTTTCAATTCCGGCA
ATTTGTCAATTTGCCGGAA
ATTTTAAATTCCCGTAGTTTGCCGATTTGCCAGAA
ATTTTGAATTCCGTTTATTAACGATTTGCAGGAA
ATTTTCAATTCCGGCAATGTGCCAATTTGCCGGAC
ATTTTCAATTTGTTATATTAACGATTTGCCGGAA
ATTTTCAATTCCGGCAATTTGCCAATTTCCCGAA
ATTTTCAATTCCAGCAATTTGCCGATTTTCTTGAA
ATTTTCAATTCCGGCAACTTGTCATTTGCTAGAA
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ATTTGTCAATTTGTCCGGAA
ATTTTAAATTCCCGTAGTTTGCCGATTTGCCAGAA
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ATTTTCAATTCCGTTATATTAACGATTTGCCGGAA
ATTTTCAATTCCGGCAATGTGCTGATTTGCCGGAA
ATTTCCAATTCCGACAATTTGCCGATTTGCCGGGA
ATTTTCAATTCCAGCAATTTGTCATTTTGCCGGAA
ATTTTCAATTTCAACAATTTGCCGATTTTCTGTGAA

Nr of selected repeats 15 Similarity 0.700680

Consensus:

ATTTTcAATTcCggcAatTTgcCgATTTgCcnGAA

>Cele-UNSB01_5:1423918-1424416 Satlength=499 Nr of Repeats=9 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATTTGCCGATTTTCGACAAATTACAATGTTGCCGATTAATAATGAAATTTTGAAATTTTGAAATTACCA
AAAAAAACAAGTGCAAAACCAGAAATTTCCGGCAAATTCAGCAACTCGACAATTAGTAGGTTTGCCGATTTTAAGGAA
TTTTCAATTCGGCAAATAGCGGA

TTTGCCGGAAATTTCAATTCGGCAAATGTGGA

TTTGCCGGAAAGTTTAAATTACGGCATCTTGCGA

TTTGCCGGAAATTTAAATTCGGCATATTGAGGA

TTTGCCGAACATTTTAAATTCGGCATATTGCGAA

TTTGCCGGAAATTTCAATTCGGCAG

TTTGCCGAATCGCCGGAAATTTTCAATTCCTGCACCTTGTAGATCTGCCAGAAATTTTAAATTCGGACAATTTGCCGGA

TTTGCCGGAAATTTTCAATTCGGCAAATAGTGGA

TTTGCCGGAAATTTTCAATTCGGCAAATTCGGGA

Nr of selected repeats 6 Similarity 0.779048

Consensus:

TTTGCCGGAAATTTTcAATTCCGGCAaATTGcGGA

>Cele-UNSB01_5:1427061-1427411 Satlength=351 Nr of Repeats=8 RepeatLength=35
seed=TGCCGGAAAT

TGCCGGAAATTTTGCTTTTGGACAAATTGGCGATT

TGCCGGAAATTTTGATTTTGGTAATTTGCCGATT

TGCCGGAAATTTTGATTCACGGCAAAGTGCCGATA

TGCCGGAAATTTTGATTTTGGCAAATGCCGATT

TGCCGGAAATTTTGATTTTGGCAAATGCCGCTTGGCGTTTATCGAACATTTGCCGATTAATAATGAAAATCTGAAA

TTTCCAACAACAAAAAATGTGCAAAGCCACAAAT

TGCCGGTAATTTTTATTTCTGGCAATT

TGCCGGAACTTCAATTCGGCAATATGCCGATT

TGCCGGAAATTGTGATTTACGGCAATTTGCCGATA

Nr of selected repeats 5 Similarity 0.790476

Consensus:

TGCCGGAAATTTtGaTTtttGgcAAatTGcCGATt

>Cele-UNSB01_5:1441594-1441873 Satlength=280 Nr of Repeats=7 RepeatLength=40
seed=ATTTTTCTAG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTCCCA

ATTTCTCTAGAATGTTCTGGAACATTTCCAGAATTTTCTCG

ATTTTTCTAGAAAGTTCTGAACATTTCCAGACTTTTCCCA

ATTTTTCTAGAGAGTTCTGGAACATTTCCAGACTTTTCCCA

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCTCG

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGACTTTTCCCA

Nr of selected repeats 6 Similarity 0.880000

Consensus:

ATTTTTCTAGAAAGTTCTGGAACATTTCCAGAcTTTTCCa

>Cele-UNSB01_5:1441948-1442263 Satlength=316 Nr of Repeats=21 RepeatLength=15

seed=CGATGGGTCT

CGATGGGTCTCACCA

CGATGGGTCTCACCA

CGATGGGTCTCACCA

CGACGGGTCTCACCA

CGATGGGTCTCACCA

CGATGGGTCTCACCA

CGATGGGTCTCACCA

CGATGGGTCTCACCA
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CGATGGGTCTCACCT
CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGACGGGTCTCACCA
CGGTGGGTCTCGCTA
CGATGGGTCTCACCA
CGATGGGTCTCGCCA
CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCGCCA
CGATGGGTCTCACCA

Nr of selected repeats 21 Similarity 0.927196

Consensus:

CGATGGGTCTCACCA

>Cele-UNSB01_5:1442495-1442763 Satlength=269 Nr of Repeats=8 RepeatLength=11

seed=CTACAGTACC

CTACAGTACCT

CTACAGTACTA

CTACAGTACCCCGACCATATCCCCCTACTAACCCCAAACCTATATCTCTTCAAAAGACTAAAACACAATTTTTTCATAAA

CTACAGTAATCCTACCGTACTC

CTACAGTACTC

CTACAGTACTA

CTACAGTACCCCGACCATATCCCCTAATAACTCCAAACCTATATCTCTTCAAAAGACAAAACTCAATTTTTTCCTAAA

TTACAGTAATCCTATAGTACTC

CTACAGTACCT

CTACAGTACTA

Nr of selected repeats 6 Similarity 0.798148

Consensus:

CTACAGTACTa

>Cele-UNSB01_5:1461442-1461802 Satlength=361 Nr of Repeats=24 RepeatLength=12

seed=CCTAAGCCTA

CCTAAGCCTAAG

CCTAAGCCTAAG

CCTAAGCCTAAGACTATG

CCTAAGACTAAA

CCTAAGCCTAAGCCTAAGTCTGAG

CCTAAGCCTAAG

CCTAAGCCTAAG

CCTAAGCCTAAG

CCTAATCCTAAG

CCTAAGACTAAG

CCTAAGCCCAAG

CCTAATCCTAAG

CCTAAGACTAAGTCTAAT

CCTAAGCCTAAG

CCTAAGCTTAAG

CTTAAGCCTAAA

CCTAAGCCTAAG

CCTAAGCATAAG

CCTAAGCCTAAGACTAAA

CCTAAGCCTAAG

CCTAAGCCTAAGCCTAAGACGAAA
CCTAAGCCTAGG
CCTATGCCTAAGCCTAATCATAAGCCTCAA
CCTGAGCCTAAGACTAAACCTAAG
Nr of selected repeats 17 Similarity 0.861928
Consensus:
CCTAAGCCTAAG
>Cele-UNSB01_5:1519749-1519965 Satlength=217 Nr of Repeats=10 RepeatLength=12
seed=AGCCTAAGCC
AGCCTAAGCCTT
AGCCTAAGCCTA
AGCCTAACCCGA
AGCCTAAGACTAAGCCTCAGTTAAAATTTAAGCCTAGAAATAAGCTTAAGTCTAAGCATAAGCATAAGCATAATCCAA
AGCCTAAGCCTA
AGCCTAAGCCCCAGCCTGAGGCTGAGTTTAAATCTA
AGCCTAATCCTG
AGCCTAAGCATA
AGTCTAAGCCTAATTCTA
AGCCTTAGCCTA

Nr of selected repeats 7 Similarity 0.788360
Consensus:
AGCCTAAGCCTA

>Cele-UNSB01_5:1568984-1569144 Satlength=161 Nr of Repeats=4 RepeatLength=40
seed=GTTCTAGAAC
GTTCTAGAACATTCCAGAATTTTTCTCGAATTTTCCAGAAG
GTTCTAGAACGTTCCAGAATTTTCTCGAATTTACCAGGAA
GTTCTAGAACATTCCAGAATTTTTCTCGAATTTTCCAGAAG
GTTCTAGAACGTTCCAGAATTTTCTCGAATTTACCAGGAA
Nr of selected repeats 4 Similarity 0.875339

Consensus:
GTTCTAGAACAATTCCAGAATTTTCTCGAATTTACCAGGAAg
>Cele-UNSB01_5:1577782-1578190 Satlength=409 Nr of Repeats=5 RepeatLength=89
seed=GCACTACGTT

GCACTACGTTGCGCACACACTAAGCTACTCGTTTTACGCCAGGCTGTGGAACCCCGAACGTGTCGCCCGCTCCAAATAA
CTATCGTTCA
GCACTACGTTGCGCACACACCAAGCTACGGAACCCCGAACGTGTCGCCCGCTCCAAATAACTATCGTTCA
GCACTACGTTGCGCACACACCAAGCTACGGAACCCCGAACGTGTCGCCCGCTCCATATAAGTACCTTTTC
GCACAACGTTGTGCGCACACACTAAGCTACTCGTTTTACGCCAAGCTACGGAACCCCTAACGTGTCGCCCGCTCCAAAAG
CTACCTTTCTT
GCACTACGTTGCGCAGACACCAAGTTACTCGTTTTACGCCAAGCTACGGAACCCCTGCATGTGTCGCCCGCTTTTCATAA
CTGCCTTTTC

Nr of selected repeats 3 Similarity 0.740741
Consensus:

GCACTACGTTGCGCACACACTAAGCTACTCGTTTTACGCCAAGCTACGGAACCCCTgaAcGTGTCGgCCGCTccaaAtAa
CTaCtTtctn

>Cele-UNSB01_5:1676007-1687585 Satlength=11579 Nr of Repeats=242
RepeatLength=48 seed=AATTTCTGAA

AATTTCTGAAGATAAGCAATTTAAATTTTGGAGTTTCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTTGGAGTTGCCCgTAATTTATA
AATTTCTGAAGATGGAATAATTTAAATTTTGGAGTTGCCCgTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTTGGATTTTCCCGTAATTTATA
AATTTCTGAAAATGAGCAATTTAAATTTTGGAGTTGCCCgTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTTGGAGTTTCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTTGGAGTTTCCCGTAATTTATA

AATTTCTGAAGATGAGCAATTTAAGTTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAGATAAGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAGTTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTTGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTTGAGTTGCCCGTAATTTATA
AATTTCTGAAAATGAGCAATTTAAATTTGAGTTGCCCGTAATTTATA
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AATTTCTGAAGATGAGCAATTTAAATTTGAGTTGCCCGTAATTTATA
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AATTTCTGAAGATGAGCAATTTAAGTTTAGTGTTGCCCGTAATTTATA
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AATTTCTGAAGATGAGCAATTTAAATTTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTGAGTTGCCCGTAATTTATA
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AATTTCTGAAGATGAGCAATTTAAATTTGATTTTCCCGTAATTTATA
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AATTTCTGAAGATAAGCAATTTAAATTTGATTTTCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAGTTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAAATGAGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTGATTTTCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTGAGTTGCCCGTAATTTATA
AATTTCTGAAAATGAGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATAAGCAATTTAAATTTGATTTTCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAGTTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAGTTTAGTGTTGCCCGTAATTTATA

AATTTCTGAAGATGAGCAATTTAAAGTTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAGATAAGCAAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGGGCAATTTAAATTTGAGTTTCCCGTAATTTATA
AATTTCTGAAGATGGGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAAGTTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTGAGTTTCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTGAGTTTCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTGAGTTGCCCGTAATTTATA
AATTTCTGAAAATGAGCAATTTAAATTTAGAGTTGCCCGTAATTTATAT
ATTTCTGAAGATAAGCAATTTAAATTTGATTTTCCCGTAATTTATA
AATTTCTGAAAATGAGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATAAGCAATTTAAATTTGATTTTCCCGTAATTTATA
AATTTCTGAAGATAAGCAAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAAGTTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAAATGAGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAAATGAGCAATTTAAATTTAGAGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTAGTGTTGCCCGTAATTTATA
AATTTCTGAAGATGAGCAATTTAAATTTTATTTGCCCGTAATTTTATA

Nr of selected repeats 199 Similarity 0.901202

Consensus:

AATTTCTGAAGATgAGCAATTTAAATTTtGAGTTgCCCGTAATTTATA

>Cele-UNSB01_5:1707873-1707951 Satlength=79 Nr of Repeats=5 RepeatLength=18
seed=GCCTAAGCCT

GCCTAAGCCTAAGCATAAC

GCCTAAGCCTAA

GCCTAGGCCTACAACCTA

GCCGAAGCCTTAGCATAA

GTCTAAGCCTAA

Nr of selected repeats 3 Similarity 0.614035

Consensus:

GCCTAaGCCTaAgCaTAn

>Cele-UNSB01_5:1765405-1765535 Satlength=131 Nr of Repeats=9 RepeatLength=13
seed=GCTCAAGCTA

GCTCAAGCTAGGT

GCTCAAGCTAAGA

GCTCAAGCTAGGT

GCGCAAGCTAGGT

GCTCAGGCTAAGA

GCTCAAGCTAGGA

GCTCAAGCTAAGTGATTAAGCTAGGT

GCTCGAGCTAGGTA

CTCAAGCTAAGA

Nr of selected repeats 6 Similarity 0.815385

Consensus:

GCTCAAGCTAgGa

>Cele-UNSB01_5:1860337-1860547 Satlength=211 Nr of Repeats=7 RepeatLength=35
seed=TCCGGCAATT

TCCGGCAATTTGTCGATTTGCCGAAATTTTAAAA

TCCGGCAATTTTCCGATTTGCCGTAATTTTAAAT

TCCGGCAATTTGCCGATTTGCCGAAATTTTCAA

TCCGGCTATTTGCCTATTT

TCCGGAAATTTTCAAT

TCCGGCAATTTGCCTATTTGCCGAAATTTTAAAT

TCCGGCAATTTGCCGATTTGCCGAAAATTTTCAA

Nr of selected repeats 5 Similarity 0.833333

Consensus:

TCCGGCAATTTgcCgATTTGCCGgaAATTTnAAa

>Cele-UNSB01_5:1872631-1872733 Satlength=103 Nr of Repeats=7 RepeatLength=12

seed=AGCCTGAGCC

AGCCTGAGCCTA

AGCCTGAGCCTG

AGCCTAAGCCTAAGCCTAAGACAA

AGCCTGAGCCTA

AGCCTGAGCCTA

AGCCTGAGCCTA

AGCCTGAGCCTGAGCCTG

Nr of selected repeats 5 Similarity 0.955556

Consensus:

AGCCTGAGCCTa

>Cele-UNSB01_5:1895975-1896260 Satlength=286 Nr of Repeats=14 RepeatLength=17

seed=TAAGCCTAAG

TAAGCCTAAGCCTAAGTTTAACTATGCCTAATTTTAAAGCATAGGCCTGAGCTTAGCT

TGAGCCTAAGCTTAGCT

TAAGCCTAAGCTTAGCT

TAAGCCTAAGCTTAGCT

TAAGCCTAAGCTTAGCT

TAAGCCTAAGCTTAGCT

TAAGCCTAAGCTTAGCT

TAAGCCTAAGCTTAGCT

TAAGCCTAAGCTTAGCT

TAAGCCTAAGCTTAGCT

TAAACCTAAGCTTACCT

TAAGCCTAAGCTTAGCTTAGGCTTAAGG

TAAGCTTAAGCC

TAAGCCTAATCTTAAGTC

Nr of selected repeats 9 Similarity 0.930283

Consensus:

TAAGCCTAAGCTTAGCT

>Cele-UNSB01_5:1897354-1897674 Satlength=321 Nr of Repeats=23 RepeatLength=10

seed=GGGCGTCAGC

GGGCGTCAGCGGCCATCAGTAGGCGTAAGC

GGGCGTCAGC

GGGCGTTAGC

GGGCGTCAGC

GGGCGTCAGC

GGGCGTCAGC

GGGCGTCAGC

GGGCGTCAGT

GGGCGTCAGC

GGGCGTCAGC

GGGCGTCAGC

GGGCGTCAGC

GGGCGTCAGC

GGGCGTCAGC

GGGCGTCAGT

GGGCGTCAGCGGGCGTCCGT

GGGCGTCAGC

GGGCGTCAGCGGAAGTCAGG
GGGCGTCAGCGTCTGTAGGC
GGGCGTCTGCGGAAGTCGGG
GGGCGTCAGCGTCTGTAGGC
GGGCGTCAGCTAGCGTCAGT
GGGCGTCAGGGGGCAATAGC

Nr of selected repeats 15 Similarity 0.949206

Consensus:

GGGCGTCAGC

>Cele-UNSB01_5:1955153-1955723 Satlength=571 Nr of Repeats=7 RepeatLength=93
seed=CAGTACCCTC

CAGTACCCTCTAGGATCAGATGCTCCACAATATCGAGGATCTTCT

CAGTCCCCTCGAGGCTATGGATATGGGTCGTCATCTGCTCCACAATACCTAGGATCTTCT

CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCTGGTAACTACAATGCCTTTGCCAGCACTTCCGATGCTCCACAGT
ATCCAGGATCCTCC

CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCCGGTAACATAATGCCTTTGCCAGCACTTCCAGATGAGCCACAGT
ATCCAGGATCCTCC

CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCTGGTAACTACAATGCCTTTGCCAGCACTTCCGATGCTCCACAGT
ATCCAGGATCCTCC

CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCCGGTAACATAATGCCTTTGCCAGCACTTCCGATGCTCCACAGT
ATCCAGGATCCTCC

CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCCGGTAACATAATGCCTTTGCCAGCACTTCCAGATGAGCCACAGT
ATCTAGGATCCTCT

Nr of selected repeats 5 Similarity 0.954122

Consensus:

CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCcGGTAACTACAATGCCTTTGCCAGCACTTCCgATGctCCACAGT
ATCcAGGATCCTCc

>Cele-UNSB01_5:1958361-1958506 Satlength=146 Nr of Repeats=7 RepeatLength=11
seed=CTACAGTACT

CTACAGTACTT

CTACAGTACTA

CTACAGTACCCCGACTATATCCCGCCACTAACCCCAAAGCAATATCACATCAAAAGACGAAAAGCCAATTTTTTCCAAAA

CTACAGTAATC

CTACCGTACTC

CTACAGTACCT

CTACAGTACTA

Nr of selected repeats 6 Similarity 0.723148

Consensus:

CTACAGTACTn

>Cele-UNSB01_5:1987432-1987712 Satlength=281 Nr of Repeats=8 RepeatLength=35
seed=GGCAAATCGG

GGCAAATCGGCAATTTTCCGAAAATGAAAATTTCT

GGCAAATCGGCAATTTTCCGAAAATGAAAGTTTCC

GGCAAATCGGCAATTTTCCGAAAATGAAAATTTTCG

GGCAAATCGGCAATTTTCTGAAAATGAAAATTTTCG

GGCAAATCGGCAATTTTCCGAAAATGAAAATTTTCC

GGCAAATCGGCAATTTTCCGAGAATAAAAATTTTCC

GGCAAATCGGCAATATTCCGAAAATGAAAATTTTCC

GGCAAATCGGCAATTTTCCGAGAATTAATAATTTTCC

Nr of selected repeats 8 Similarity 0.914286

Consensus:

GGCAAATCGGCAATTTTCCGAaAATgAAAATTTCC

>Cele-UNSB01_5:2151047-2151352 Satlength=306 Nr of Repeats=21 RepeatLength=13
seed=GCCTAAGCCT

GCCTAAGCCTAAGCCTAGGGCTTAAGTTTAGT
GCCTGAGCCTATAGTTTAAAGCTTAGG
GCTTAAGCCTCGG
GCCTAAACCTAGGA
CCTAAGCCTTGG
GCCTAAGCCTATG
GCCTAAGCCTAGG
GCCTAAGACTATG
GCCTAAGCCTATG
GCCTAAGACTATG

Nr of selected repeats 17 Similarity 0.930618

Consensus:

GCCTAAGCCTATG

>Cele-UNSB01_5:2189835-2190349 Satlength=515 Nr of Repeats=18 RepeatLength=11
seed=CTACAGTACC

CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCCTAACCTAAACCGATATCCCTTCAAAAAGACGAAAAGTCAGTTTTTCCCCAAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCCTAACCTAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTTCCCCAAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCCTAACCTAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTTCCCCAAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCCTAACCTAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTTCCCCAAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACCA

Nr of selected repeats 14 Similarity 0.742063

Consensus:

CTACAGTACcn

>Cele-UNSB01_5:2213030-2213142 Satlength=113 Nr of Repeats=6 RepeatLength=16
seed=ATGCCTACAT

ATGCCTACATGCCTACATTCCAAC

ATGCCTACATGCCTAC
 ATGCCTACATGCCTAG
 ATGCCTACATGCCTGC
 ATGCCTGCATGCCTAC
 ATGCCTACATGCCTACATACCAAC
 Nr of selected repeats 4 Similarity 0.875000
 Consensus:
 ATGCCTaCATGCCTac
 >Cele-UNSB01_5:2439353-2440062 Satlength=710 Nr of Repeats=4 RepeatLength=177
 seed=GAGTCTCACG
 GAGTCTCACGTGGTGTCAAGAGTGTCCCATTTCCGGTGTGATCTACGAAGATCTACAAAAAGTGC GGGAGAAGAGACGCAG
 AGTTTTCAACTGATTTTGCATGGTTAAGAACGTGCTGACGTCAAATTTTTTTGAGAAAAAAATCCCGCATTTTTTTGTA
 GATCAAACCGTAATGGGACG
 GAGTCTCACGATGTGTCAACGTGTCTCAGTCGGCTTGATCTACGTAGATCTACAAAAAATGC GGGAGAAGAGACGCAGA
 CTTATTCTCTGATTTTGCATGAGTAAGAGCGTGTGGCGTCACATTTTTTGTCTGGCAAAAAATCCCGCATTTTTTTGTAG
 ATCAAACCGTAATGGGACG
 GAGTCTCACGATGTGTCAACGTGTCTCAGTCGGCTTGATCTACGTAGATCTACAAAAAATGC GGGAGAAGAGACGCAGA
 CTTATTCTCTGATTTTGCATGAGTAAGAGCGTGTGGCGTCACATTTTTTGTCTGGCAAAAAATCCCGCATTTTTTTGTAG
 ATCAAACCGTAATGGGACG
 GAGTCTCACGATGTGTCAACGTGTCTCAGTCGGCTTGATCTACGTAGATCTACAAAAAATGC GGGAGAAGAGACGCAGA
 GTTTTCAACTGATTTTGCATGGTTAAGAACGTGCTGGCGTCACATTTTTTGTCTGGCAAAAAATCCCGCATTTTCTTGTAG
 ATCAAACCTTAATGGGACG
 Nr of selected repeats 3 Similarity 0.943196
 Consensus:
 GAGTCTCACGATGTGTCAACGTGTCTCAGTCGGCTTGATCTACGTAGATCTACAAAAAATGC GGGAGAAGAGACGCAGA
 cTTaTTcTCTGATTTTGCATGagTAAGAgCGTGTGGCGTCACATTTTTTGTCTGGCAAAAAATCCCGcATTTtTTGTAG
 ATCAAACCGTAATGGGACG
 >Cele-UNSB01_5:2441369-2441565 Satlength=197 Nr of Repeats=4 RepeatLength=35
 seed=AAATTTTCAA
 AAATTTTCAAATTTTTCGTCATTTGCCATTTTTCCGTCAAATTCGGCAAGATTTGTGTGTTTCACTTTTCGGCAATTTTAG
 CCGATTTGCCG
 AAATTTTCAAATTCCTCCAGTTTGCCAATTTGCCGG
 AAATTTTCAAATTCGGCAATTTGCCGATTTGCCGG
 AAATTTTCAAATTCGGCAATTTCCGATTTGCCGG
 Nr of selected repeats 3 Similarity 0.780864
 Consensus:
 AAATTTTCAAATTCcggCAaTTTgCCgATTnGCCGG
 >Cele-UNSB01_5:2444425-2444473 Satlength=49 Nr of Repeats=4 RepeatLength=12
 seed=AGGCTTAGGC
 AGGCTTAGGCTG
 AGGCTTAAGCTC
 AGGCTTAGGCTG
 AGGCTTAGGCTC
 Nr of selected repeats 4 Similarity 0.870370
 Consensus:
 AGGCTTAgGCTc
 >Cele-UNSB01_5:2527844-2527991 Satlength=148 Nr of Repeats=6 RepeatLength=12
 seed=CCTAAGCCTA
 CCTAAGCCTAAG
 CCTAAGCCTGAGCCTAATCAAAAAATCAAAAAACTGGAAAAT
 CCTAAGCCTAATAGCGTCAGTAGCTGGCTGACGCTCGCCACTGACGCCAAGCTTGAT
 CCTAGGCCTAAA
 CCTAAGCCTATG
 CCTAAGCCTAAG

Nr of selected repeats 4 Similarity 0.833333

Consensus:

CCTAaGCCTAag

>Cele-UNSB01_5:2582229-2582433 Satlength=205 Nr of Repeats=7 RepeatLength=20

seed=CCCCGACGCT

CCCCGACGCTCGAGAGCAAG

CCCCGACGCTCGATGGCAAGCG

CCCCGACGCTCGAGCGCAAACGCCGAAGCTTGAGCGCAAACGCCGAACTTGAGCGCAAGCGCCGAACTTGAGCGCAA
GCG

CCCCGACGCTCGAGCTCAAA

CCCCGACGCTCGAGCTCAAA

CCCCGACGCTCGAGCTCAAA

CCCCGACGCTCGAGCTCAAA

Nr of selected repeats 5 Similarity 0.920000

Consensus:

CCCCGACGCTCGAGctCAAA

>Cele-UNSB01_5:2582360-2582560 Satlength=201 Nr of Repeats=10 RepeatLength=20

seed=GCTCGAGCTC

GCTCGAGCTCAAACCCCGAC

GCTCGAGCTCAAACCCCGAC

GCTCGAGCTCAAACCCCGAC

GCTCGAGCTCAAACCCCGAC

GCTCGAGCTCAAGCCCCGAA

GCTCGAGCTCAAGCCCCGAA

GCTCGAGCTCAAGCCCCGAA

GCTCGAGCTCAAGCCCCGAA

GCTCGAGCTCAAGCCCCGAA

GCTCGAGCTCAAGCCCCGAA

Nr of selected repeats 10 Similarity 0.928889

Consensus:

GCTCGAGCTCAAgCCCCGAa

>Cele-UNSB01_5:2584213-2584387 Satlength=175 Nr of Repeats=6 RepeatLength=21

seed=GATTAGATTT

GATTAGATTTCTCCATATTTTCATTAGAAAACAAATCTAATCCAATATGGCACGATCTCAGCCATATTT

GATTAGATTTTCGACCATATTTG

GATTAGATTTTGTCCATATTTG

GATTAGATTTGTTCCATATTTG

GATTAGATTTTCGGCCATATTTG

GATTAGATTTGTTCCACATTTG

Nr of selected repeats 5 Similarity 0.841270

Consensus:

GATTAGATTTngtCCAtATTG

>Cele-UNSB01_5:2587851-2588904 Satlength=1054 Nr of Repeats=15 RepeatLength=35

seed=TCAATTCGG

TCAATTCGGCAATTTGCCGTTTGCCGCAAGTTC

TCAATTCGGCAATTTTCCGATTTGCCGGAATTC

TCAATTCAGCAATTTGCCGTTTCCCGGAATTC

TCAATTCGGCAATTTGCCGATTTGCCGGAATTC

TCAATTCGGCAATTTGGATAGGTTTCGGGCCGGGATTTTACTTGAAAAAAAAAGAAAAAATTCGATTTTTTTTCGAAAA

AATTGAAAAATCAGATTTTTCAAAAATTTCAAATTTTTTGACATTTTTCTTATTTTTTAAGAAGGAATTTATATGTT

TTATTATATTTTTGTTTCTGACAAATTTGCCGGAATTTGCAATTTTCGGCAATTTGCCGTTTCCCGGAATTC

TCAATTCGGCAATTTGCCGATTTGCCGGAATTC

TCAATTCGGCAATTTGGATAGGTTCCGGCCGGGATTTTACTTGAAAAAAGGAAAAAATTCGATTTTTTTTCGAAAAA
TTGAAAAAATGATAAAATTCATTTTTTCATCAATTTTGTATATTTTGTATGAGAAATGCCGGTTTGCCGAAAT
GT

TCAATTCGGTAATTTGCCGATAATTGAAAATGAAAAATGGTCAGAAAATTAATTAATTTTAAATGTTTCTAAAAAT
TCTAAAATTATCAACTTTGTAAAAAACCAGATATTTTCGTTTAAAAAATCAGATTTTTCAAAAATTTTCAAATTTTTT
GTCATTTTCCTTATTTTTTTAAAGAAGGAATTTATATGTTTTATTATATTTTTGTTTCTGACAATTTGCCGATTTGCCG
GAAATTC

TCAATTCGGCAATTTGGCGATTTGCCGAAATTC
TAAATTCGGCAATTCGGCGATTTGCCGAAATTC
TCAATTCGGTCAATTTGCCGATTTGCCGAAATTC
TCATTTCCGGCAATTTGGCGATTCGCCGAAATTC
TCAATTCGGCAACTCGTCGGTTTGCCGAAATTC
TCAATTCGGCAATTTGGCGATTTGCCGAAATTC
TCAATTCGGCAATTTGCCGACTTGCCAGAAGTTC

Nr of selected repeats 10 Similarity 0.832381

Consensus:

TCAATTCGGCAATTTGcCGaTTTGCCgGAAaTTC

>Cele-UNSB01_5:2602720-2603297 Satlength=578 Nr of Repeats=16 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAATTTTCATTTTCGGCAATTTGCCAA
TTTGCCGGAAATTTTCAATTCGACAATTTGCCGG
TTTGCCGGAAATTTTATTTTTTGGCAAATTTGCCAA
TTTGCCGGAAATTTTCATGTTTCGCAAATTTGCCGA
TTTGCCGGAAATTTTCAATTTCTGCAATTTTCCGA
TTTACCGGAAATTTTCATTTTCGGCAATTTGCCAA
TTTGCCGGAAATTTTCAATTCGACAATTTGCCGA
TTTGCCGGAAATTTTCAATTCGACAATTTGCCAA
TTTGCCGGAAATTTTCAAAATTCGACAATTTGCCGA
TTTGCCGGAAATTTTAAATTTTGGCAAATTTGCCGA
TTTGCCGGAAATTTTCATTTTCGGCAATTTGCCGTTTCTCAA
TTTGCCGGAAATTTCAATTTTCGGTGATTTCCGATGAGCCGA
TTTGCCGGAAATTTTAAATTTTGGCAAATTTTCCGA
TTTGCCGGAAATGTTTCATGTTTCGCAAATTTGGCAA
TTTGCCGGAAATTTCAACTCCGGCAATCTGCCGA
TTTGCCGGAAATTTTCAACTCCGGCAATTTTCCTA

Nr of selected repeats 10 Similarity 0.790053

Consensus:

TTTGCCGGAAATTTTCAaTtCgNCAaTTTGCCaA

>Cele-UNSB01_5:2608578-2609028 Satlength=451 Nr of Repeats=10 RepeatLength=35
seed=TTTCCGGCAA

TTTCCGGCAAATCGGCGAATTTGTCGGAATTGAAAT
TTTCCGGCAAATCGGAAAAGTGTCCAAGTTTAAAA
TTCCCGGCAAACCGGCATATTGCCGGAATTTAAAA
TTTCCGGCAAATCGGAAAATTTGCCGGAATTTAAAA
TTTCCGGCAAATCGCCAAATTTGCCGGAATTTAAAAAGTTCTGGCAATTCGGCACATTGCCTGAATTTAAAA
TTTCCGGCAATTTGGCCAACTACCGGAATCGGAAT
TTTCCGGCAAACCGGCAAATTTGCCGGAATTTAAAA
TTTCCGGCAAATCGGAAAATTTGCCGGAATTTAAAA
TTTCCGGCAAATCGGCACATTTGCCGGAATTTATAA
TTTCCGGCTAATCGGAATCTTGCCGGAATTTGAAACCGTCAATTTGCCGATTTGCCGGAATTTGATTGTCGGCAAAT
TGCCGGTTTGCAGAATTTTCA

Nr of selected repeats 7 Similarity 0.807710

Consensus:

TTTCCGGCAAATCGGcAaATTGcCgGAAaTTTAAAA

>Cele-UNSB01_5:2619946-2620165 Satlength=220 Nr of Repeats=6 RepeatLength=35
seed=GCCGGAAATT
GCCGGAAATTTTGAATTCCGGCAAATTCACGATTA
GCCGGAAATTTTCAACTCCGGCAATTTGCCAGTTTGCCGATTT
GCCGGAAATTTTCAATTCCGGCAACTCCCCGATTT
GCCGGAAATTGTCAATTCCGGCGAGTTCCCCGATTT
GCCGGAAATTTTCTATTCCGCCAGTTTGCCGATGT
GCAGGAAATTTTCAATTATGGCAATTTGCCGATTT
Nr of selected repeats 4 Similarity 0.752381
Consensus:
GCcGGAAATtTCaATTccGgCaatTtcCCGATtT

>Cele-UNSB01_5:2625951-2626161 Satlength=211 Nr of Repeats=14 RepeatLength=15
seed=CTCACCACGA
CTCACCACGATGGAC
CTCACCACGAAGGGT
CTCAACACGATGGGT
CTCACCACGATGGAC
CTCACCACGATGGGT
Nr of selected repeats 14 Similarity 0.840316
Consensus:
CTCACCACGATGGGt

>Cele-UNSB01_5:2661964-2662120 Satlength=157 Nr of Repeats=13 RepeatLength=12
seed=CTAAGCCTAA
CTAAGCCTAAGC
CTAAGCCTAAGC
CTAAGCCTAAGC
CTAAGCCTAAGC
CTAAGCCTAAGA
CTAAGCCTAAGT
CTAAGCCTTAGT
CTAAGCCTAAGC
CTAATCCTAAGC
CTAAGCTTAAGC
CTAAGCCTAATC
CTAAGCCAAACC
CTAAGCCTAAAC
Nr of selected repeats 13 Similarity 0.839031
Consensus:
CTAAGCCTAAgc

>Cele-UNSB01_5:2665615-2665738 Satlength=124 Nr of Repeats=4 RepeatLength=35
seed=TTTCTCAGAA
TTTCTCAGAAAAAAACAT
TTTCTCAGAAAATTTGAATTTCCCGCCAAAATGTT
TTTCTCAAAAATTTGAATTTCCCGCCAAAATGTT
TTTCTCAGAAAATTTGACTTTCCCGCCAAAATTTT

Nr of selected repeats 3 Similarity 0.923810

Consensus:

TTTCTCAgAAAATTTGAaTTTCCCGCCAAAATgTT

>Cele-UNSB01_5:2726947-2727107 Satlength=161 Nr of Repeats=12 RepeatLength=10

seed=GCTACCGCCC

GCTACCGCCCGCTGTCCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCCGCTACTGCTA

GCTACCGCCCTCCACTGCCCGCTACCGCCC

Nr of selected repeats 9 Similarity 1.000000

Consensus:

GCTACCGCCC

>Cele-UNSB01_5:2726947-2728543 Satlength=1597 Nr of Repeats=110 RepeatLength=10

seed=GCTACCGCCC

GCTACCGCCCGCTGTCCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCC

GCTACCGCCCGCTACTGCTA

GCTACCGCCCTCCACTGCC

GCTACCGCCC

GCTACCGCCC

GCTACAGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTACCGCCCTCCACTGCC

GCTACCGCCC

GCTACCGCCC

GCTACAGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTAACGCCC

GCTACCGCCC
GCTACTGCCC
GCTACCGCCC
GCTACTGCCC
GCTACCGCCC
GCTACCGCCC
GCTACCGCCC
GCTACCGCCC
GCTACCGCCC
GCTACTGCCC
GCTACCGCCC
GCTACCGCCC

GCTACCGCCC GCTACCGACT

Nr of selected repeats 99 Similarity 0.951240

Consensus:

GCTACCGCCC

>Cele-UNSB01_5:2836474-2836692 Satlength=219 Nr of Repeats=20 RepeatLength=11
seed=GCACATTTTTT

GCACATTTTTTT
GCACATTTTTTT
GCACATTTTTTT
GCACATTTTTTC
GCACATTTTTTC
GCACATTTTTTC
GCGCATTTTTTC
GCACATTTTTT
GCACATTTTTTC
GCACATTTTTTT
GCACATTTTTTT
GCACATTTTTTT
GCACATTTTTTC
GCACATTTTTTC
GCACATTTTTT
GCACATTTTTTC
GCACATTTTTTT
GCACATTTTTTT
GCACATTTTTTT
GCACATTTTTTT
GCACATTTTTTC

Nr of selected repeats 18 Similarity 0.909685

Consensus:

GCACATTTTTc

>Cele-UNSB01_5:3006278-3006868 Satlength=591 Nr of Repeats=10 RepeatLength=59
seed=AATTTCAAAT

AATTTCAAATGTGCACTGGTTTTCAAATTTTTTAACTGAGAATTATGGAAAATATGG
AATTTCAAATGTGCACTGGTTTTCAAATTTTTTAACTGAGAATTATGGAAAATGGG
AATTTCAAATGTGCACTGGTTTTCAAATTTTTTAACTGAAAATTATGGAGAATATGG
AATTTCAAATGTGCACTGGTTTTAAAAGTTTTTAACTGAGAATTATGGAAAATGGA
AATTTCAAATGTGCACTGGTTTTCAAATTTTTTAACTGAAAATTATGGAGAATATGG
AATTTCAAATGTGCACTGGTTTTAAAAGTTTTTAACTGAGAATTATGGAAAATGGA
AATTTCAAATGTGCACTGGTTTTCAAATTTTTTAACTGAAAATTATGGAGAATATGG
AATTTCAAATGTGCACTGGTTTTAAAAGTTTTTAACTGAGAATTATGGAAAATGGA
AATTTCAAATGTGCACTGGTTTTCAAATTTTTTAACTGAAAATTATGGAGAATATGG
AATTTCAAATGTGCACTGGTTTTAAAAGTTTTTAACTGAGAATTATGGAAAATGGA

Nr of selected repeats 10 Similarity 0.895123

Consensus:

AATTTCAAATGTGCACTGGTTTTcAAAaaTTTTTAACTGAgAATTATGGAAaAATaTGGn

>Cele-UNSB01_5:3035465-3035958 Satlength=494 Nr of Repeats=4 RepeatLength=16
seed=GCATGTAGGC

GCATGTAGGCATCAGGGCTGGGAACAAAAAAAAAATTTTGGACCAAAAAACAAAAAACAAAAAATTGAAGTTTTCGAAA
AACCAAAAAACCAAAAAACAAAAAATTTGAAATTTTCGAAAAATCAAAAAACTTTTTGAAAACTTTTCAAAAA
TTTTTTATGCTTAAGTTGATTTTTAATGGGGTTATTCAAGTAATGTTTCAAATGTATCGAAATACATTTCTGACAAC
GTGTTAAATACATGTTTAAATGTATTTAATAAAGAATAGTCTCGAGTCGAAACTATTAATGGCAAAAATTTTTTTTT
TTGAATTTTTTGGTTTTTTTTGGTCCCAAAGAACCAAAAAAACGAAAAAATCGATTTTTCGTCAAATACCAAAAA
ACCAAAAAAACAACAAAAACCAAAAAATTTCCAGCCCTGGTAA

GCATGTAGGCATGTAG

GCATGTAGGCTTGTAG

GCATGTAGGCTTGTAG

Nr of selected repeats 3 Similarity 0.944444

Consensus:

GCATGTAGGCtTGTAG

>Cele-UNSB01_5:3042873-3042939 Satlength=67 Nr of Repeats=5 RepeatLength=11
seed=TTTGGCAAGA

TTTGGCAAGAATTGAGCAAGAC

TTTGGCAAGAA

TTGGGCAAGAC

TTTGGCAAGAA

TTGGGCAAGAG

Nr of selected repeats 4 Similarity 0.818182

Consensus:

TTgGGCAAGaA

>Cele-UNSB01_5:3102518-3102978 Satlength=461 Nr of Repeats=41 RepeatLength=10
seed=GGTAGCGGGC

GGTAGCGGGCGTTAGCGGGAGTCAGCGGGC

GATAGCGGGC

GGTAGCGGGC

GGTAGCGGGT

GGTAGCGGGC

GGTAGCGGGC

GGTAGCGGGT

GGTAGCGGGC

GTTAGCGGGC

GTTAGCGGGC

CTAACATTTTTCAATTTTCGT
CTAACATTTTTCAGTTTTTCGT
CTAACATTTTTCAATTTTCGC
CTAACATTTTTCAATTTTCGTCTCACGTTTTTTAAATTTTAGT
CTAACATTTTTCAATTTTCGT
CTAACATTTTTCAAGTTTGTTCAGGTGCTCGAGGTGCTCAAGGTGCTCGAGGTGCACAAGAAGCTTCAAGGTGCTCA
AATTCGGATATTTACTCTCAGAAAATATATTTGAAGCGCTGCGTGGAACCTACACCTTCGCAATTTTTTTTGCAA
TATGGGTGACCTGATTTTATAAGATTTTATAAGAGAACTTCTCGTAGCTGAAACAGCATTAATAGGTATTGTTTTTT
ATGCTCGAGGTGCTCAAGGTTTTCAATTTTCGC
CTAACATTTTTCAGTTTTTCGC
CTAACATTTTTCAATTTTCGT
CTAACATTTTTCAATTTTTCGT
CTCACATTTTTCAGTTTTTCGT
CTAACATTTTTCAATTTTCGC
CTAACATTTTTCAATTTTCGTCTCACGTTTTTTAAATTTTAGT
CTAACATTTTTCAATTTTCGT

Nr of selected repeats 12 Similarity 0.927850

Consensus:

CTAACATTTTTCAaTTTTTCGt

>Cele-UNSB01_5:3492580-3492838 Satlength=259 Nr of Repeats=7 RepeatLength=11
seed=TACTGTAGGA

TACTGTAGGAG

TACTGTAGGATTACTATATTTTTTGAAAAATTGGCTTTTCGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGTCTGGGA
TATAGTTGGGGTACTGTAGTTG

TACTGTAGAGG

TACTGTAGGAG

TACTGTAGGATTACTGTATTTTTGAAAAAATTGGCTTTTCGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGTCTGGG
ATATGGTTGGGGTACTGTAGTTG

TACTGTAGAGG

TACTGTAGGAA

Nr of selected repeats 5 Similarity 0.763889

Consensus:

TACTGTAgGAg

>Cele-UNSB01_5:3492923-3493163 Satlength=241 Nr of Repeats=6 RepeatLength=40
seed=TCCAGAACCT

TCCAGAACCTTCTGGAAAATTCGAGAAAATTCGGAATGT

TCCAGAACCTTCTGGAAAATTCGAGAAAATTCGGAATGT

TCCAGAACCTTCTGGAAAATTCGAGAAAATTCGGAATGC

TCCAGAACCTTCTGGAAAATTCGAGAAAATTCGGAATGT

TCCAGAACCTTCTGGAAAATTTGAGAAAATTCGGAATGT

TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT

Nr of selected repeats 6 Similarity 0.931111

Consensus:

TCCAGAACCTTCTGGAAAATtcGAGAAAATTCGGAATGT

>Cele-UNSB01_5:3493344-3494338 Satlength=995 Nr of Repeats=31 RepeatLength=32
seed=CGGGAATTCA

CGGGAATTCAAATTTTCTGTGAAAAATTTTGG

CGGGAATTCAACATTTTCTGTGAAAAATTTTGG

CGGGAATTCAAATTTTCTGTGAAAAATTTTAG

CGGGAATTCAAATTTTCTGTGAAAAATTTTGG

CGGGAATTCAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTTCTGTGAAAAATTTGTTGG
CGGGAATTCAAATTTTCTGTGAAAAATTTTGTAG
CGGGAATTCAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAGAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAATTTTCTGTGAAAAATTTTGG
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CGGGAATTCAAACTTTTCTGTGAAAAGTTTTGG
CGGGAATTCAAAATTTTCTATGAAAAATTTTGG
CGGGAATTCAAAATTTTCTGTGAAAAATTTTAA
CGGGAATTCAGTTTTTCTGTGAAAAATTTTGG
CGGGAATTCAAAATTTTCTGTGAAAAATTTGTTGG
CGGGAATTCAAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAAATTTTCTATGAAAAATTTTGG
CGGGAATTCAGTTTTTCTATGAAAAATTTTGG
CGGGAATTCAAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAAATTTTCTGTGAAAAATTTTGG

Nr of selected repeats 29 Similarity 0.920874

Consensus:

CGGGAATTCAAAaTTTCTGTGAAAAATTTTGG

>Cele-UNSB01_5:3593686-3593761 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=CGTGGTGAGA
CGTGGTGAGACCCAT
CGTGGCGAGACCCAC
CGTGGTGAGACCCGT
CGTGGTGAGAACCAT
CGTGGCGAGACCCAT

Nr of selected repeats 5 Similarity 0.840000

Consensus:

CGTGGtGAGAcCCat

>Cele-UNSB01_5:3602166-3602210 Satlength=45 Nr of Repeats=4 RepeatLength=11

seed=CAAAAAATGT
CAAAAAATGTG
CAAAAAATGTG
CGAAAAATGTT
CAAAAAATGTG

Nr of selected repeats 4 Similarity 0.878788

Consensus:

CaAAAAATGTg

>Cele-UNSB01_5:3604514-3604619 Satlength=106 Nr of Repeats=5 RepeatLength=21

seed=TTTCAGTTTT
TTTCAGTTTTTCGTCTATCATT
TTTCAGTTTTTCGTCTAACATT
TTTCAATTTTTCGTCTAACATT
TTTCAGTTTTTCGTATAACATT
TTTCAGTTTTTCGTATAACATT

Nr of selected repeats 5 Similarity 0.911111

Consensus:

TTTCAGTTTTCGTcTAaCATT

>Cele-UNSB01_5:3623960-3624037 Satlength=78 Nr of Repeats=4 RepeatLength=21

seed=AGTTTGTAGT

AGTTTGTAGTTTGT

AGTCTGTAGTTTGTCTGTTTGT

ATTTTGTAGTTTGTAGTCTGC

AGTTTGTAGTTTTTGCCTTGT

Nr of selected repeats 3 Similarity 0.640212

Consensus:

AgTtTGTAGTTTgTngttTgT

>Cele-UNSB01_5:3651691-3651860 Satlength=170 Nr of Repeats=4 RepeatLength=42

seed=TTTCCAGCAA

TTTCCAGCAAATTGGCAAATCGGCAAATTGTCGGAATTAATA

TTTCCAGCAAATCGGCATATCGGTAAATTGCTGGAATCGCAA

TTTCCAGAATATCGGCAAGTCAGTGATTTGCCGGAATTGAGA

TTTCCAGCAAATCGGCAAATCAGCGAATTGCCGGAATTGAGA

Nr of selected repeats 3 Similarity 0.767196

Consensus:

TTTCCAGcAaATcGGCAAATCaGcgAaTTGcCGGAATTgAgA

>Cele-UNSB01_5:3666468-3666780 Satlength=313 Nr of Repeats=8 RepeatLength=39

seed=GATTTACGGG

GATTTACGGGCATTGATCAGTTTCAAAAAATCTTGTGTC

GATTTACGGGCTTTAATCAGTTTCGAAAAGCTTGCCTGTC

GATTTACGGGCTTTAATCAGTTTCGAAAAGCTTGTGTC

GATTTACGGGCCTTAATAAGTTTCGAAAAGCTTGTGTA

GATTTACGGGCTTTAGTCAGTTTCGAATAATCTTGTGTA

GATTTACGGGATTTAATCAGTTTCGAAAATCTTGTGTC

GATTTACGGGCTTAAATAAGTTTTGAAAAGCTTGTGTCG

GTTTACGGGCTTTAATAAAATTTTCGTAAGCTTGTGTC

Nr of selected repeats 6 Similarity 0.849573

Consensus:

GATTTACGGGCTTTAATCAGTTTCGAAAAGCTTGTGTC

>Cele-UNSB01_5:3674779-3675094 Satlength=316 Nr of Repeats=9 RepeatLength=35

seed=AAAATTTCCG

AAAATTTCCGGCAAATTGACAAAATTTATGGAATTG

AAAATTTCCGGCAAACAGGCAACTTGCCGGAATTG

AAAATTTCCGGCGAACAGGCAAATTTCTGGAATTG

AAAATTTCCGGCAAATTGACAAAATTTATGGAATTG

AAAATTTCCGGCAAACAGGCAACTTGCCGGAATTG

AAAATTTCCGGCGAACAGGCAAATTTCTGGAATTG

AAAATTTCCGGCAAACAGGCAACTTGCCGGAATTG

AAAATTTCCGGCAAATTGACAAAATTTATGGAATTG

AAAATTTCCGGCAAACAGGCAACTTGCCGGAATTT

Nr of selected repeats 9 Similarity 0.834921

Consensus:

AAAATTTCCGGCaAAcaGgCAAATTTctGGAATTG

>Cele-UNSB01_5:3703054-3703534 Satlength=481 Nr of Repeats=23 RepeatLength=11

seed=AGGATTACTG

AGGATTACTGTAGGATTATTAT

AGTATTACTGTATGATTAATGTAATAATTACTGTA

AGGTTACTGT

AGGATTACTGTAGGATTATTTAGGGTTATTGTAGGTATACAGTAGGATTCCGCCGAAATTAATAATGGATTACAGTAGG

GTTATTTA

AGGATTACTGT

AGGATTGCTGTAGTTTTTGAAAAACGAGTTTTGGTAAGGGGTGAGGGTACTGTAATAGTTTTGTAGGGGCACT
AGGATTACTGT
AGGAATACTGT
ATGATTACTGT
AGAATTACTGTAGGATTATTCT
AGGATTACTGT
ACGATTACTGT
AGAATTACTGT
AGGATTACTGT
AGGATTACTGT
AGGATTGCTGT
AGGATTGCTGC
AGGATTACCGT
AGGATTACTGG
AGGATTACTGTGGGGTTATTATAGAATTATAGTAGGGTTATTCT
AGGATTACTGT
AGGGTTACTGT
AGGATTACTGTATGATTACAGT

Nr of selected repeats 15 Similarity 0.843001

Consensus:

AGGATTACTGT

>Cele-UNSB01_5:3735730-3736160 Satlength=431 Nr of Repeats=4 RepeatLength=35
seed=GCCGATTTGC

GCCGATTTGCCGAACATCAATTTGCCGGAAGTTTTTAGAGGAATTTTTATGAGACGGAACCTCTTCAAACGTGCCTT
TTTAAATTTTTCCCGTTTTCTTTAGATAATTTTCATAGAATTTGCTTACTTTTCAAAATAGATTTAGGATCATTATAG
GATACGCACAATTTTTACGATCAAAAGTTAAATTTCTGAAATTTTTCAAAAAAAGTGCAAAAACACAATTTCCAAAAATG
TTCTGCAATTGCCGTTTTTCCGACAAATCGGCAAATCAATAATTTGTGCGTTTTGCTGACTTGCCGGAAAACCTTCATTTCC
AGGCAATTA

GCCGATTTGCCGAAAATGTTTCAGTTCTGGCAAATT

GCCGATTTGCCTGAAATGTTCAATCCCTGCAATTT

GCCGATTTGCTTGAAATGTTCAAATCTGACAATTT

Nr of selected repeats 3 Similarity 0.743827

Consensus:

GCCGATTTGCctGAAATGTTCAantCTGnCAatTT

>Cele-UNSB01_5:3737155-3737311 Satlength=157 Nr of Repeats=4 RepeatLength=35
seed=TTGCCGATTT

TTGCCGATTTGCCGATTTGTCAGAAATTTTCATTTTCGGCAAATTGTCGGT

TTGCAGATTTGCCGGAAAAATTCATTTCCGGCAAT

TTACCGATTTGCCGGAAACATTCATTTCTGACAAT

TTGCCGATTTGCCAGAAATTTTCATTTCCGGCAAC

Nr of selected repeats 3 Similarity 0.784127

Consensus:

TTgCcGATTTGCCgGAAAaTTCaATTCcGgCAAt

>Cele-UNSB01_5:3739928-3740028 Satlength=101 Nr of Repeats=6 RepeatLength=10
seed=TAGCCATGCC

TAGCCATGCC

TAGCCATGCC

TAGCCATAACC

TAACCATGCCTATTCATGCCTAGTCATGAC

TAGCCATGCC

TAGCCATGCCTATTCATGCCTAGCCATGAC

Nr of selected repeats 4 Similarity 0.933333

Consensus:

TAGCCATgCC

>Cele-UNSB01_5:3789009-3789261 Satlength=253 Nr of Repeats=6 RepeatLength=42
seed=ACCGGCAATT

ACCGGCAATTGCCAGAATTGCCGATCGCTGAAAATTTCCAAA
ACCGGAAATTGCCGGAATTGTCGATTGCTGAAAATTTCCAAA
ACCGGCAATTGCCGAAATTACCGATTGCCGAAAATTTCCAAA
ACCGGCAATTGCCAAAATTGCCGATTGCTGAAAATTTCCAAA
ACCGGCAATTGCCGAAATTACCGATTGCCGAAAATTTCCAAA
ACCGGCAATTGCCAAAATTGCCGATCGCTGAAAATTTCTAAA

Nr of selected repeats 6 Similarity 0.881481

Consensus:

ACCGGCAATTGCCaaAATTgCCGATtGCTGAAAATTTCCAAA

>Cele-UNSB01_5:4001570-4002151 Satlength=582 Nr of Repeats=5 RepeatLength=42
seed=CCAGCCGACA

CCAGCCGACAGCCGAAAATTTTCACGATTTTTCGGCTGGTAGCG
CCAGCCGAAAATTTAAAAGAGTCCGGCTGGCGGCG
CCAGCCGACAGCCGAACCAGCTTTTTGTCCGGCTGGTAGCTTTAAATTTTTTCCAGTTTTTACAGAAAATTCGTCCAG
TTCTTACAGAAAATTCGCGTTTTCTATGTTTTAAATTTGATAACATTTGCAGTAACGGAGACTGCTGACCCGGCGTTTTCC
CATGAGAAAAGAGAGAGAGAGAGAGAGAGGGGGGAGACAGTGAGATATACGGCAGAGACATAGACAGGGGAGACACCATTAG
AGATCGTCTCCTATAGAGTGCTGCCGGCAGGGGGCGTTGTGGACCTGTGGGAAGAAGGGGGGAGACAACCGCACACTGT
GCGGTTGTAAATGCGGAATAATCCATTTAAACTAAGGAAAATAGTGGTCTAATGCTTAACAGTGAGCCGCCTAGATAA
AACAAAAAAAGTCCGGCTGGCTGCG

CCAGCCGACAGCCGAAAATTTTCACTATTTTTCGGCTGGTGCCA

CCAGCCGACAGCCGAAAATTTGAAGTCAATCCGGCTGTCCGGCG

Nr of selected repeats 3 Similarity 0.684755

Consensus:

CCAGCCGACAGCCGAAAAttTtAcgatttTCGGCTGgtnGCg

>Cele-UNSB01_5:4022711-4023271 Satlength=561 Nr of Repeats=14 RepeatLength=40
seed=GAACCTTCTG

GAACCTTCTGAAAAATTCGAGAAAAATTTGGAATGTTTTT
GAACCTTCTGGAAAATTCGAAAAATTTCTGAAATGTTCTA
GAACCTTCTGGAAAATTCGAGAAAATTTGGAATGTTCTA
GAACCTTCTGGAAAATTCGAGAAAATTTGGAATATTCTA
GAACCTTCTGGAAAATTCGAAAAATTTCTTGAATGTTTTT
GAACCTTCTGGAAAATTCGAGGAGATTTCTTGAATGTTTTT
GAACCTTCTGAAAAATTCGAGAAAAATTTCTGGAATGTTTTT
GACCTTCTGGAAAATTCGAGAAAAATTTCTAGAATATTCTA
GAACCTTCTGGAAAATTCGAGAAAATTTCTTGAATGTTTTT
GAACCTTCTGGAAAATTCGAGAAAATTTCTAGAATATTCTA
GAACCTTCTGGAAAATTCGAAAAATTTCTTGAATGTTTTT
GAACCTTCTGAAAAATTCGAGAAAATTTCTGGAATGTTTTT
GAACCTTCTGGAAAATTCGAGAAAATTTCTAGAATATTCTA
GAACCTTCTGGAAAATTCGAGAAAATTTCTGGAATGTTTTT

Nr of selected repeats 12 Similarity 0.857071

Consensus:

GAACCTTCTGGAAAATTCGAgAAAATTTCTgGAATgTtTt

>Cele-UNSB01_5:4024546-4025389 Satlength=844 Nr of Repeats=21 RepeatLength=40
seed=CTAGAAAGTT

CTAGAAAGTTCTGGAATATTCCAGAATTTTATTGAACTTC
CTAGAATGTTCTGGAACATTCTAGAATTTTCTTGAATTTT
CTAGAAAGTTCTGGAACATTCCAGAATTTTCTTGAATTTT
CTAGAAACTTCTGGAACATTCCAGAATTTTCTTGAATTTT
CTAGAAAGTTCTGGAACATTCCAGAATTTTCCCGGTTTTT
CTAGAAAGTTCTGAAACATTTCAGGCTTTTCTTGAATTTT
CTAGAAAGTTCTAGAACATAATAGACTTTTCCCGATTTTT

CTAGAAAGTTCTGGAACATTCCAGAATTTTCTTGAAC TTC
CTAGAAACTTCTGGAACATTCCAGATTTTCTTGAAT TTC
CTAGAAAGTTCTGGAACATTCCAGAATGGTCCCGGGTTTT
CTAGAAAGTTCTGAAAACATTCCAGAATTTTCTTGAAT TTC
CTAGAAAGTTCTGGAACATAATAGACTTTTCCCGATTTTT
CTAGAAAGTTCTGGAACATTCCAGAATTTTCTTGAAC TTC
CTAGAAACTTCTGGAACATTCCAGATTTTCTTGAAT TTC
CTAGAAAGTTCTGGAACATTCCAGATTTTCTTGAAC TTC

Nr of selected repeats 18 Similarity 0.796514

Consensus :

CTAGAAAGTTCTGgAACATTCCaGAaTTTCTtGAAtTTc

>Cele-UNSB01_5:4025406-4025890 Satlength=485 Nr of Repeats=15 RepeatLength=32
seed=TTTCACAGAA

TTTCACAGAAAATTTGAATTC CCGCCAAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAT
TTTCACAGAAAATTTGGATTCC CACCAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAT
TTTCACAGAAAATTTGGATTCC CACCAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAT
TTTCACATAAAAATTTGAATTC CCGCCAAAAGTT
TTTCACAGAAAATTTGAATTC CCGCAAAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAT
TTTCACAGAGAATTTGAATTC CACCAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAGTT
TTTCACAGAAAATTTAAATTC CCGCCAAAAT
TTTCACAGAAAATTTGAATTC CCGCCAAAAT

Nr of selected repeats 11 Similarity 0.921212

Consensus :

TTTCACAGAAAATTTGAATTC CCGC CAAAAT

>Cele-UNSB01_5:4118450-4118598 Satlength=149 Nr of Repeats=4 RepeatLength=35
seed=TTTGCCGGAA

TTTGCCGGAAAATTTAATTTT TGCCAAATG CCGT
TTTGCCGGAAAATTTTTTTTT TGGTAAATG CTGT
TTTGCCGGAAAATTTCTTTTT TCGTAAATG CCGTTTACCAA
TTTGCCAGAAAATTCATTTT CGGTAAGTTCCGA

Nr of selected repeats 3 Similarity 0.682540

Consensus :

TTTGCCgGAAAtTtTnaTTTTtGgtAAaTTgCcGt

>Cele-UNSB01_5:4162356-4162767 Satlength=412 Nr of Repeats=11 RepeatLength=35
seed=TTCCGGCAA

TTCCGGCAAATCGGCAAAC TGACAATTTGTCGAAAATGACATT
TTCTGGCAAATCGGCGAAAT TGCCGGAATTGAAAAT
TTCCGGCAAATCGGAACAC CGGCAATTTGCCGAAAACGAAAAA
TTCCGGCAAACCGGCAATTT CCGAAAACGAAAAA
TTCCGGCAAACCGGCAATTT CCGAAAACGAAAAA
TTCCGGCAAATCGGCAAAC CCGGCAATTTCCACAAATCAAAT

TTCCGGCAAACCGGCAATTTACCGAAAATGAAAAT
TTCCGGCAAACCGGCAATTTGCCAAAAATGAAAAT
TTCCGGCAAACCGGCAATTTGCCAAAAATCAAAAT
TTCCGGTAAATCGGCAATTTGCCAAAAATGAAAAT
TTCCGGCAAACCGGCGATTTGCCAAAAATCAAAAT

Nr of selected repeats 7 Similarity 0.865760

Consensus:

TTCCGGCAAACCGGCAATTTgCCaAAAAAtgAAAAt

>Cele-UNSB01_5:4165711-4166017 Satlength=307 Nr of Repeats=5 RepeatLength=35
seed=AATTTTCAAT

AATTTTCAATTCCTGCAATTTGCCGATTTGCCGGA
AATTTTAAATTCCTGCAATTTGCCAGTTTGCCAGA
AATTTTCAATTCGGCAATTTGCCGTTTTGTCGGA
AATTTTCAATTCCTGCAATTTGCCGTTTTGTCGGA

AATTTTCAATTTCCGCAAAATGCTATTTGCCGGAATAAATCGTTTTGTCGCCACCCTGAATTAAGTGACGCCATTTT
TGTGTATTCCGGCATATTAGTAGTTTTTTCTTCGTTTTTTTTTTCAATTTTAGATTAAATTTAAGTATTTATATAACT
TGAAACAC

Nr of selected repeats 4 Similarity 0.847619

Consensus:

AATTTTcAATTCCTGCAaTTTGCCGgTTTGcCgGA

>Cele-UNSB01_5:4169850-4170172 Satlength=323 Nr of Repeats=8 RepeatLength=35
seed=TTTCAATTCC

TTTCAATTCGGCAATTTGCCGATTTGCCGAAAT
TTTCAATTCGGGAAGTTTGCCGATTTGCCGAAAT
TTTCAATTCGGCAATTTGCCGATTTGCCAGAAAT
TTTCAATTCGGCAATTTGCTGATTTGCCGAAAT
TTTCAATTCGGGAAGTTTGCCGATTTGCCGAAAT

TTTCAATTCGGAAATTTGCCGATTTGTCGATTTGCCGAAATTTTCAATAACGGCAATTTGTCAATTTACCGGATA

TTTCAATTCGGCAAATTTGCTGATTTTCTGAAAT

TTTCAATTCGGCAAATTTGCCGATTTGCCGAAAT

Nr of selected repeats 7 Similarity 0.885714

Consensus:

TTTCAATTCGGcAaTTTGcGATTTGCCgGAAAT

>Cele-UNSB01_5:4216093-4219558 Satlength=3466 Nr of Repeats=18 RepeatLength=200
seed=TGTGGTCCAG

TGTGGTCCAGAAGGTATGACTGAAAATTCAGTTTTTTCTGCTTGAACCTGGCAGATTTAAAATTTTTCAAATGCTGTTT
TCAAATTTCTGAAAGAAGTTAAAATTTGCTACAAAATGGCTACGGGAATTTCTAAAAAGTTAGTTTCAAGCCAGAAAT
AATTTTCAAAGTTGGAAAATCTATTAATTTTGTATATAAAT

TGTGGTCCAGAAGGTATGACTGAAAATTCAGTTTTTTCTGCTTGAACCTGGCAGATTTCAAATTTTTCAAATGCTGTTT
TCAAATTTCTAAAAGAAGTTAAAATTTGCTACAAAATGGCTACGGGAATTTCTAAAAAGTTAGTTTCAAGCCAGAAAT
AATTTTCAATATAAAT

TGTGGTCCAGAAGGTATGACTGAAAATTCAGTTTTTTCTGCTTGAACCTGGCAGATTTCAAATTTTTCAAATGCTGTTT
TCAAATTTCTAAAAGAAGTTAAAATTTGCTACAAAATGGCTACGGGAATTTCTAAAAAGTTAGTTTCAAGCCAGAAAT
AATTTTCAATATAAAT

TGTGGTCCAGAAGGTATGACTGAAAATTCAGTTTTTTCCGCTTAAACTTGGCAGATCTAAAATTTTTTGAATGCCGTTT
TCAAATTTCTGAAAGAAGTTAAAATTTGCTACAAAATGGCTACTGGAATTTCTGAAAAAGTTAGTTTCAAGCCAGAAAT
AATTTTCAATATAAAT

TGTGGTCCAGAAGGTATGACTGAAAATTCAGTTTTTTCTGCTTGAACCTGGCAGATTTTAAAATTTTTTGAATGCCGTTT
TCAAATTTCTGAAAGAAGTTAAAATTTGCTACAAAATGGCTACTGGAATTTCTGAAAAAGTTAGTTTCAAGCCAGAAAT
AATATTCAAAGTTTGGAAAATCTATTAATTTTGCATAAATAT

TGTGGTCCAGAAGGTATGACTGAAAATTCAGTTTTTTCTGCATGAACCTGGCAGATTTCAAATTTTTCAAATGCTGTTT
TCAAATTTCTAAAAGAAGTTAAAATTTGCTACAAAATGGCTACGGGAATTTCTAAAAAGTTAGTTTCAAGCCAGAAAT
AGTTTTCAAAGTTTGGAAAATCTATTAATTTTGCATATAAAT

TGTGGTCCAGAAGGCATGACTAAAAATTCACTTTTCTGCTTAAACTTGGCAGATTTCAAATTTTTTGAATTGCCGTTT
TCAAATTTCTGAAAGAAGATAAAAAATTTGCTACAAAATGGCTACGGGAATTTTTAAAAAAGTTAGTTTCAAGCCAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTTGTATATAAAAT
TGTGGTCCAGAAGGTATGACTGAAAAATCAGTTTTCTGCTTGAACCTGGCAGATTTTAAATTTTTTGAATGCCGTTT
TTAAATTTCTGAAAGAACTTAAAAATTTGCTACAAAATGGCTACGGGATATTCTAAAAAAGTTAGTTTCAAGCCAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTTGCATATGAAC
TGTGGTCCAGAAGGTATGACTGAAAAATCAGTTTTCTGCTTGAACCTGGCAGATTTAACTTTTTTGAATGCCGTTT
TCAAATTTCTGAAAGAAGCTTAAAAATTTGCTACAAAATGGCTACTGGAATTTCTGAAAAAGTTAGTTTCAAGCCAGAAATT
AATATTCAAAGTTTGGAAAAATCTATTAATTTTTGCATATAAAC
TGTGGTCCAGAAGGTATGACTGAAAAATCAGTTTTCTGCTTGAACCTGGCAGATTTTAAATTTTTTGAATGCCGTTT
TTAAATTTCTGAAAGAAGCTTAAAAATTTGCTACAAAATGGCTACGGGATATTCTAAAAAAGTTAGTTTCAAGCCAGAAATT
AATATTCAAAGTTTGGAAAAATCTATTAATTTTTGCATAAAAAAT
TGTGGTCCAGAAGGTATGACTGAAAATTCACATTTCTGCTTGAACCTGGCAGATTTCAAATTTTTCAAATGCTGTTT
TCAAATTTCTAAAAGAAGCTTAAAAATTTGCTACAAAATGGCTACGGGAATTTCTAAAAAAGTTAGTTTCAAGCCAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTTGTATAAAAAAT
TGTGGTCCAGAAGGTATGACTAAAAATTCACTTTTCTGCTTGAACCTGGCAGATTTCAAATTTTTCAAATGCTGTTT
TCAAATTTCTAAAAGAAGCTTAAAAATTTGCTACAAAATGGCTATGGGAATTTCTAAAAAAGTTAGTTTCAAGCCAGAAATT
AATTTTCATATAAAAT
TGTGGTCCAGAAGGTATGACTGAAAATTCAGTTTTCTCGCTTAAACTTGGCAGATCTAAAATTTTTTGAATGCCGTTT
ACAAATTTCTGAAAGAAGCTTAAAAATTTGCTACAAAATGGCTACGGGAATTTCTAGAAAAGTTAGTTTCAAGCCAGAAATT
AGTTTTCAAAGTTTGGAAAAATCTATTAATTTTTGTATAAAAAAT
TGTGGTCCAGAAGGTATGACTGAAAATTCAGTTTTCTCGCTTGAACCTGGCAGATTTAACTTTTTTGAATGCCGTTT
TCAAATTTCTGAAAGAAGCTTAAAAATTTGCTACAAAATGGCTACGGGAATTTCTAAAAAAGTTAGTTTCAAGCCAGAAATT
AGTTTTCAAAGTTTGGAAAAATCTATTAATTTTTGCATATAAAAT
TGTGGTCCAGAAGGCATGACTAAAAATTCACTTTTCTGCTTAAACTTGGCAGATTTTAAATTTTTTGAATGCCGTTT
TCAAATTTCTGAAAGAAGCTTAAAAATTTGCTACAAAATGGCTACGGGAATTTCTAAAAAAGTTAGTTTCAAGCCAGAAATT
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TGTGGTCCAGAAGGCATGACTAAAAATTCACTTTTCTGCTTAAACTTGGCAGATTTTAAATTTTTTGAATGCCGTTT
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AATTTTCATATAAAAT
TGTGGTCCAGAAGGTATGACTGAAAATTCACATTTCTCCTTGAACCTGGCAGATTTCAAATTTTTCAAATGCTGTTT
TCAAATTTCTAAAAGAAGCTTAAAAATTTGCTACAAAATGGCTACGGGATATTCTAAAAAAGTTAGTTTCAAGCCAGAAATT
AATTTTCAAAGTTTGGAAAAATCTATTAATTTTTGCATATAAAC

Nr of selected repeats 13 Similarity 0.916410

Consensus:

TGTGGTCCAGAAGGtATGACTgAAAAtTCAcTtTTTCTGCTTgAACTTGGCAGATTTtAAATTTTTtgAAATGCcGTTT
TCAAATTTCTgAAAGAAGCTTAAAAATTTGCTACAAAATGGCTACGGGAatTTCTAAAAAAGTTAGTTTCAAGCCAGAAATT
AaTtTTCAAAGTTTgGAAAAATCTATTAATTTTTGcATAtAAAt

>Cele-UNSB01_5:4240718-4240800 Satlength=83 Nr of Repeats=4 RepeatLength=18
seed=AAATATTCTT

AAATATTCTTTTTTTTTTGTAATTTACAA

AAATATTCTTATTTTCAG

AAATATTCTTATTTTCAG

AAATATTCTTCGTTTTAG

Nr of selected repeats 3 Similarity 0.851852

Consensus:

AAATATTCTTatTTTcAG

>Cele-UNSB01_5:4305444-4315394 Satlength=9951 Nr of Repeats=398 RepeatLength=25
seed=AGTAAAATAT

AGTAAAATATTCTGTGAAGCCAGAG

AGTAAAATATTCTGTGAAGCCAGAG

AGTAAAATATTCTGTGAAGCCAGAG
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AGTAAAATATTCTGTGAAGCCAGAG
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AGTAAAATATACGGTGAAGCCAGAG
AGTAAAATATTCTGTGAAGCCAGAG
AGTAAAATATACGGTGAAGCCAGAG
AGTAAAATATTCTGTGAAGCCAGAG
AGTAAAATATTCTGTGAAGCCAGAG
AGTAAAATATATGGTGAAGCCAGAG

Nr of selected repeats 346 Similarity 0.935129

Consensus:

AGTAAAATATtCtGTGAAGCCAGAG

>Cele-UNSB01_5:4422681-4422875 Satlength=195 Nr of Repeats=5 RepeatLength=35

seed=ATTCCGGCAA

ATTCCGGCAAGTTGCCGGTTTGCCGGAAGTATTCA

ATTCCGGCAAGTTACCGATTTGTTCGGAAGTCTTCAATTCGGACAGTTTGCCAGAAGTTTTCG

ATTCCGGCAACATGCCGGAACCTTTTAA

ATTCCGGCAATTTGCCGATCTGCCGGACCTATTAA

ATTCCGGCAATTTGCCGATTTGCCGGAACCTTTTAA

Nr of selected repeats 3 Similarity 0.822222

Consensus:

ATTCCGGCAAtTTGCCGaTtTGCCGGAacTaTTaA

>Cele-UNSB01_5:4531686-4531763 Satlength=78 Nr of Repeats=5 RepeatLength=15

seed=CCCCTTTTCG

CCCCTTTTCGTTGCT

CCCCTTTTCGTATCT

CCCCTTTTCGCAGAT

CCCCTTTTTGCAGAT

CCCCTTTTCGTTCTGCC

Nr of selected repeats 4 Similarity 0.748148

Consensus:

CCCCTTTTcGcagaT

>Cele-UNSB01_5:4631559-4631760 Satlength=202 Nr of Repeats=8 RepeatLength=18

seed=CCTGGCTGTC

CCTGGCTGTCCATCGTTT

CCTGGCTGTCCATCGCTTCCGCGTTGT

CCTGGTTGTCTGGGCTT

CCTGGCTGTCCGTTGCCCTCCTGGGCTTCCAGCTTGTCTGGTGGTCCACGTGGT

CCTGGTTGTCCGTTTGGT

CCTGGCTGTCTGGCTCAGAAGAGCTGGAT

CCTGGCTGACCGGCTTGT

CCTGGTTGTCCATCTCTT

Nr of selected repeats 5 Similarity 0.607407

Consensus:

CCTGGtTgtCCntctnnT

>Cele-UNSB01_5:4664068-4664530 Satlength=463 Nr of Repeats=10 RepeatLength=35
seed=GCAAATCGGC
GCAAATCGGCAAATTGCCGGATTTCGAAAATGTCCG
GCAAATCGGCAAATTGCCGTATTTGAAAATGCCCG
GCAAATCGGCAAATTGTCTTATTTGAAAATGACCG
GCAAATCGGCAAATGCCCGAATCGAAAATGTCCG
GCAAATCGGCAAATCCCAGATTTCGAAAATGTCCG
GCAAATCGGCAAATTGCCGGATTCAAAAATGTCCG
GCAAATCGGCAAATTGCCGATTTCCGAATTTGCTGAAAACGGCAATTGCCGAAAATTTTCGGCAAATTGTGGTTTTT
CTTGAAAATTCCG
GCAAATCTGCAAAAATTTCCGGTTTGCCGATTTAAAAATAGATCCCTCTCAACACTTCGCCAAATGGGTATCCG
GCAAACGGCAAATGGTTCGCTTTGCCAAAAAATGAAAATTTCCG
GCAAATCGGCAAGCTGGCAAATTGCCGGAACCAAACATTTCCG
Nr of selected repeats 6 Similarity 0.837460

Consensus:

GCAAATCGGCAAATTgCCGgATTcGAAAATGtCCG

>Cele-UNSB01_5:4696924-4697115 Satlength=192 Nr of Repeats=5 RepeatLength=35
seed=CGGCAAATCG

CGGCAAATCGGCAACTTGCCGGAATTTTAAATTTTC
CTGCAAATCGGTGAATTGCCGGAATTTTATATTTCTGCATAT
CGGCAAATTTGTTCGGAATTGAATATTTCCGACAAAC
CGGCAAATCGCCAAATTGCCGGAATTGAAAATGTT
CGGCAAATCGCAAAATTGCCGGAATTGTAAATTTCCGGCAAAT
Nr of selected repeats 3 Similarity 0.479798

Consensus:

cggcaaatCGgCAAaTTGcCGGAATTgaAaATTTc

>Cele-UNSB01_5:4698132-4698369 Satlength=238 Nr of Repeats=5 RepeatLength=35
seed=CAATTCCGGC

CAATTCGGCAATTTGCCGATTTGCCGGAATTTA
CAATTCGGCAATTTGCCAGAAATTTA
CAATTCGGCAATTTGCCGATTTGCCGGAATTTAAAATTCTGGCAATTTGGCGATTTGCCGGAATTTCAAATTCTGG
CGATTTGCCGATTTGCCGGAATTTA
CAATTCGGCAATCTGCCGATTTGCCAGAAATTTA
CAATTCGGCAATTCGCCGATTTGCCGGTAATTTT
Nr of selected repeats 3 Similarity 0.873016

Consensus:

CAATTCGGCAATttGCCGATTTGCCgGaAATTTa

>Cele-UNSB01_5:4751883-4752158 Satlength=276 Nr of Repeats=22 RepeatLength=11
seed=CACGAAGTTG

CACGAAGTTGTCCCAAAGTTGT

CACAAAGTTGT

CACAAAGTTGT

CACGAAGTTGT

CACGAAGTTGT

CACGAAGTTGT

CACGAAGTTGT

CACGAAGTTGC

CACGAAGTTGT

CACGAAGTTGT

CACGAAGTTGT

CACGAAGTTGG

CACGATGTTGT

CACGAAGTTGT

CACGAAGTTGT

CACGAAGTTGT
CTCGAAGTTGT
CACGAAGTTGT
CACGAAGTTGC
CACGAAGTTGT
CACGAAGTTGTCACGTAATTGT
CACGAAGTTGTCACGTAATTGT
Nr of selected repeats 19 Similarity 0.914939
Consensus:
CACGAAGTTGT

>Cele-UNSB01_5:4763134-4763326 Satlength=193 Nr of Repeats=11 RepeatLength=16
seed=TAGGCATGTA
TAGGCATGTAGGCATG
TAGGCATGTAGGAAAG
TAGGCACGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCATG
TAGGCATGTAGGCACGCAGGCATA
TAGGCATGTACGCATGTAGGCATG
Nr of selected repeats 9 Similarity 0.944444
Consensus:

TAGGCATGTAGGCATG
>Cele-UNSB01_5:4844742-4844913 Satlength=172 Nr of Repeats=5 RepeatLength=17
seed=AAATGCCAAA
AAATGCCAAAATGCCAA
AAATGCCAAAAGTGCCAACTTACCAGAGGCCAAAATTACAAAATTTTCAAATTTAGCA
AAATGCCAAAATTTGCTG
AAATGCCAAAATTTGCCAAGTTACAAAGCTTGAAAAACGTTAAAATTTCCAAAGTTGCAG
Nr of selected repeats 3 Similarity 0.641975
Consensus:

AAATgCCAAAanTGCca
>Cele-UNSB01_5:4982997-4984483 Satlength=1487 Nr of Repeats=35 RepeatLength=11
seed=GTACTGTAGG
GTACTGTAGGA
GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTGTAGGAAAAATCAAATTTTAAACATTTTAAAGAGGTATTGGCTTGAA
GTTGGTGAAAGATAATGTCAAGGTACTGTAATG
GTACTGTAGGA
GTACTGTAGGAT
TACTGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTAGTCTACAGAAGGGGTATTGGGTGGGAGTTGCCGGGGGA
TAATGTCAAG
GTACTGTAGTG
GTACTGTAGGA
GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTAGTCTACAGAAGGGGTATTGGGTGGGA
GTTGCCGGGGGATAATGTCAAG
GTACTGTAGTA
GTACTGTAGGA
GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTGTCTACAGAAGAGGTATTGGGTGGGA
GTTGCCGGGGGATAATGTCAAG
GTACTGTAGTG

GTACTGTAGGA
GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTAGTCTACAGAAGAGGTATTGGGTTGGGA
GTTGCCGGGGGATAATGTCAAG
GTACTGTAGTA
GTACTGTAGGA
GTACTGTAGGTATACGATAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTTGTCTACAGAAGAGGTATTGGGTTGGGA
GTTGCCGGGGGATAATGTCAAG
GTACTGTAGTG
GTACTGTAGGA
GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTAGTCTACAGAAGAGGTATTGGGTTGGGA
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GTACTGTAGGA
GTACTGTAGGTATACGATAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTTGTCTACAGAAGAGGTATTGGGTTGGGA
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GTACTGTAGGA
GTACTGAAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTTAAACATTTTAAGAGGTATTGGCTTGGAA
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GTACTGTAGGA
GTACTGTAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTAGTCTACAGAAGGGGTATTGGGTTGGGA
GTTGCCGGGGGATAATGTCAAG
GTACTGTAGTG
GTACTGTAGGA
GTACTGAAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTTAAACATTTTAAGAGGTATTGGCTTGGAA
GTTGGTGAGGATAATGTCAAGGTTACTGAGTG
GTACTGTAGGA
GTACTGAAGGTATACGGTAGGGTTACTGTAGTTTGGGAAAAATTGAGTTTTTAAACATTTTAAGAGGTATTGGCTTGGAA
GTTGGTGAAAGATAATGTCAAGGTTACTGTAATG
GTACTGTAGGA

Nr of selected repeats 22 Similarity 0.888233

Consensus:

GTACTGTAGga

>Cele-UNSB01_5:4984650-4985356 Satlength=707 Nr of Repeats=46 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGAAGACCA

TCGTGGTGAGACTTTTCGTTGG

TCGTGGTGAGATCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACTCT

TCGTGGTGAGATCTT

TCGTGTTGAGACCCA

TCGTGGTGAGACCTT

TCGTGTTGAGACCCT

TCGTGGTGAGACCTT

TCGTGTTGAGACCCA

TCGTGGTGAGACCTT

TCGTGGTGAGACCTCTA

TCGTGGTGAGACCTT

TCGTGTTGAGACCCA

TCGTGGTGAGACCTT

TCGTGGTGAGACCCA

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TCGTGGTGGTGGTGAGACCTTTCGTGGAA
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TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTAAGACCTT
TCGTGGTAAGACCTT
TCGTGGTAAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGGCCCA

Nr of selected repeats 38 Similarity 0.852948

Consensus:

TCGTGGTGAGACCct

>Cele-UNSB01_5:4989154-4989259 Satlength=106 Nr of Repeats=7 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACC

GGGTCTCACC

GGGTCTCACC

GGGTCTCACC

GGGTCTCACC

GGGTCTCACC

GGGTATCACC

Nr of selected repeats 7 Similarity 0.898413

Consensus:

GGGTCTCACCAGat

>Cele-UNSB01_5:5106861-5107246 Satlength=386 Nr of Repeats=10 RepeatLength=35

seed=TGCCGAAAT

TGCCGAAATTTTCGATTTTTCGGCAAAATGCCGATT

TGCCGAAATTTGGATTTTTCGGCAAAATGCCGATT

TGCCGAAATTTGGATTTTTCGGCAAAATGCCGTTT

TGCCGAAATTTCTTTTTCGGCAACTTGTTCGATT

TGCCGAAATTTTGATTTTCGGCAATTTGTTCGATT

TGCCGAAATTTTGATTTTCGGCAATTTGTCAA

TGCCGAAATTTTGATTTTCGGAAATTTGCCGATTTGGCGGAAATTTTGATTTTTCGGCAAAATGCCGATT

TGCCGAAATTTTGATTTTCGGCAAAATACCAATT

TGCCGAAATTTTGAATTCCTGCAGTTTGACGACT

TGCCGAAATTTTGATTTTCGGCAAATGCCAGTT

Nr of selected repeats 6 Similarity 0.730794

Consensus:

TGCCGAAATTTtGATTTcCGGCAAaATGcCgATT

>Cele-UNSB01_5:5114820-5115220 Satlength=401 Nr of Repeats=8 RepeatLength=35

seed=TTGCCGATTT

TTGCCGATTTGCCGAAAATTTCAATTTTCGGTAATTTCCCGTTTTGCCGGAAGTTTCAATTCGGCTATTTGTCAATTT

ACCGAACTTTCCAATTCGGCAATTCGCCATATATTTAAATTCGGCAAG

TTGCCGATTTGCCGAAAATTTCAATTTTCGGCAATAAGCCGAAAATTTGAATTCGGAAAAT

TTGCCGATTTGCCGAACTTTCCAATTTTCGACAAG

TTGCCGATTTGCCGAAAATTTCAATTCGACAAG

TTGCCGATTTGCCGAAAATTTCCAATTCGGCAAT

TTGCCGATTTTTCGAAAATTTCAATTCCTGCAA

TTGCCGATTTTTCGAAAATTTTCAGTTACGTCGAT

TTGCCGATTTGCCGAAAATTTCAATTCGGTAAA

Nr of selected repeats 5 Similarity 0.767619

Consensus:

TTGCCGATTTgcCGGAAaTTTtCAaTtcCgnCaAn

>Cele-UNSB01_5:5204356-5204779 Satlength=424 Nr of Repeats=9 RepeatLength=35

seed=CGATTTGCCG

CGATTTGCCGGAAGTTTTCTATTCCAGCAATTTAC

CGATTTGCCGGAATTTTTATTTTGGCAAATTC

CGATTTGCCGGAATTTTTATTTCCGGCAAATTC

CGATTTGCCGATTTGCCGGAATTTTGATTTTCGG

CAATTTGCCGATTTGCCGAAAATTTTATTTCCGGCAATTTTCAGATTTGGCGGAATTTTTATTTCCGGCAAATTAC

CGATTTGCCGGTTGGTTTTTGGCAATTTTCAGAATTTGCCGAACTTTTTGTTTTCTGCAATTTTCAGAATGGCCGACAA

TTTTGATTTTCGG

CGAATTTGCCGATTTGCCGAAAATTTTCATTTCCGGCAATTTAC

CGATTTGCCGGAATTTTCGATTTTCGGCAAATTC

CGATTTGCCGGAATTTTCATATTCGGCGATTTGC

Nr of selected repeats 6 Similarity 0.576768

Consensus:

CGATTTGCCGGAATTTTtATtTtCGGCaAaTTgC

>Cele-UNSB01_5:5272176-5275211 Satlength=3036 Nr of Repeats=112 RepeatLength=26

seed=CAGAGTCACT

CAGAGTCACTAATTTTGGTGAACGGC

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTTACTAATTTTGGTGAACGGT

CAGAGTTACTAATTTTGGTGAACGGC

CAGAGTCACTATATTTGGTGAACGGT

CAGAGTCACTTTATTTGGTGAACGGC

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTTACTAATTTTGGTGAACGGC

CAGAGTTACTAATTTTGGTGAACGGC

CAGAGTCACTATATTTGGTGAACGGT

CAGAGTCACTTTATTTGGTAAACGGC

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTCACTAATTTTGGTGAACGGT

CAGAGTCACTATTTTGGTGAACGGT
CAGAGTCACTAATTTTGGTGAACGGT
CAGAGTCACTAATTTTGGTGAACGGC
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CAGAGTCACTAATTTTGGTGAACGGC
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CAGAGTCACTTTATTTTGGTAAACGGC
CAGAGTCACTATATTTTGGTGAACGGC
CAGAGTCACTAATTTTGGTGAACGGT
CAGAGTCACTTTATTTTGGTAAACGGC
CAGAGTCACTATATGTTGGTGAACGACAGAGTCTCATTGGTGAACGGTC
CGAGTCACTATATATCTAGTGAACAGCCAGGTCATAATTTTAGTGAAGAACGGCCAAGGAGTCACTAATTTTGGAGTGAA
CGGT
CGAGTCACTATATCATTGTGAGCAAC
Nr of selected repeats 99 Similarity 0.819649
Consensus :
CAGAGTCACTaatTTTGGTGAACGGc
>Cele-UNSB01_5:5413359-5414150 Satlength=792 Nr of Repeats=8 RepeatLength=96
seed=TCTGCTTAGA
TCTGCTTAGAATAGGATTAAGCCAGCCACAGTTTTCAAGAGTATTCGGGCCTGCGGCCCTCAAACCTGGTTATTAGG
CTTGAGTGAATAACATA
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Nr of selected repeats 7 Similarity 0.949735

Consensus:

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>Cele-UNSB01_5:5638035-5638095 Satlength=61 Nr of Repeats=4 RepeatLength=15

seed=CGTGGTGAGA

CGTGGTGAGACCCTT

CGTGGTGAGACCCTT

CGTGGTGAGACCCTC

CGTGGTGAGACTCTT

Nr of selected repeats 4 Similarity 0.911111

Consensus:

CGTGGTGAGACcCTt

>Cele-UNSB01_5:5649265-5649420 Satlength=156 Nr of Repeats=8 RepeatLength=19

seed=AAAAATAGAT

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AAAAATAGATTGGCAGACG

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Nr of selected repeats 5 Similarity 1.000000

Consensus:

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>Cele-UNSB01_5:5757268-5757343 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=CGAAAAGGGG

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CAAAAAGGGGATCTG

CGAAAAGGGGAGATA

CGAAAAGGGGAGATA

CGAAAAGGGGAGCAA

Nr of selected repeats 5 Similarity 0.768889

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_5:5757528-5757620 Satlength=93 Nr of Repeats=6 RepeatLength=15

seed=TCCCCTTTTC

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TCCCCTTTTCGTTCTGC

Nr of selected repeats 5 Similarity 0.733333

Consensus:

TCcCCTTTTcGtagc

>Cele-UNSB01_5:5757785-5758298 Satlength=514 Nr of Repeats=19 RepeatLength=27
seed=TGGAGGCGGC

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Nr of selected repeats 19 Similarity 0.948018

Consensus:

TGGAGGCGGCTTCTGGCCTGgTGGTGG

>Cele-UNSB01_5:6073958-6074258 Satlength=301 Nr of Repeats=20 RepeatLength=15
seed=ACCCATCGTG

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Nr of selected repeats 20 Similarity 0.901287

Consensus:

ACCCaTCGTGGtGAG

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Nr of selected repeats 4 Similarity 0.961905

Consensus:

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>Cele-UNSB01_5:6074472-6074951 Satlength=480 Nr of Repeats=12 RepeatLength=40
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Nr of selected repeats 11 Similarity 0.960000

Consensus:

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>Cele-UNSB01_5:6179564-6194498 Satlength=14935 Nr of Repeats=110

RepeatLength=117 seed=TACTTCAGAT

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TTTTGGATAGAAGTTGTTACGTATTCCAGAACATTCATCAGTAAATCTAGTTCCAAACCGGAGAACAACCTTTCAGCTTGTG
AGAAGAGGAGTTCAACTTCTACCTCCGTCCAGCAGTTCTTTGATTTCTCTTCCATGTGACATCCTTTTGCTCAACAAT
TTCAGCTGGTTT
TACTTCAGATGTTTTCTTTGAATCCACAGGAGCTAGTTTCTCAACTGTTGGTTCGACAGTAGGTGCACTAGTCTCTGGC
ACTGGAACATCCTTTTGCTCGATGATTTTCAGCTTGGTTG
TACTTCAGATGTTTTCTTTTGATTCCACAGATTTAAGTTTCTCAACTGTTGGTTCGACTGTAGGTGCACTAGTCTCTGGC
ACTGGAACATCCTTTTGCTCAACAATTTTCAGCTGGTTT
TACTTCAGATGTTTTCTTTGGATTCCACAGGAGCAAGTTTCTCAACTGTTGGTTCCTTGGGCGGGTGCAGTTGAACCT
TTTTGGATAGAAGTTGTTACGTATTCCAGAACATTCATCAGTAAATCTAGTTCCAAACCGGAGAACAACCTTTCAGCTTTTG
AGAAGAAGAGTTCAACTTCCACCTCCGTCCAGCAGTTCTTTGATTTCTCTTCCATGTGACATCCTTTTGCTCAAGAAT
TTCAGCTGGTTG
TACTTCAGGTGTTTTCTTTTGATTCCACAGGTGCAAGTTTCTCAACTGTTGGTTCGACAGTAGGTGCACTAGTCTCTGGC
ACTGGAACAACCTTTTGCTCAACAATTTTCAGCTGGTTG
TACTTCAGATGTTTTCTTTTGATTCTACAGGTGCATGTTTTCTCAACTGTTGGTTCGACTGTAGGTGCACTGGTCTCTGGC
ACTGGAACATCCTTTTGCTCGATGATTTCAACTTGGTTG
TACTTCAGATGTTTTCTTTTGATTCCACAGGTTAAGTTTCTCAACTGTTGGTTCGACTGTAGGTGCACTGGTCTCTGGC
ACTGGAACATCCTTTTGCTCGATGATTTTCAGCTTGGTTG
TACTTCAGATGTTTTCTTTTGATTCCACAGGTTAAGTTTCTCAACTGTTGGTTCGACTGTAGGTGCACTGGTCTCTGGC
ACTGGAACATCCTTTTGCTCGATGATTTCAACTTGGTTG
TACTTCAGATGTTTTCTTTTGATTCCACAGGTTAAGTTTCTCAACTGTTGGTTCGACTGTAGGTGCACTGGTCTCTGGC
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TACTTCAGATGTTTTCTTTTGATTCCACAGGAGCAAGTTTCTCAACTGTTGGTTCCTTGGGCGGGTGCAGTTGAACCT
TTTTGGATAGAAGTTGTTACGTATTCCAGAACATTCATCAGTAAATCTAGTTCCAAACCGGAGAACAACCTTTCAGCTTGTG
AGAAGAAGAGTTCAACTTCTACCTCCGTCCAGCAGTTCTTTGATTTCTCTTCCATGTGACATCCTTTTGCTCAACAAT
TTCAGCTGGTTG
TACTTCAGATGTTTTCTTTTGATTCCGCAGGTGCAAGTTTCTCAACTGTTGGTTCGACAGAAGGTGCACTAGTCTCTGGC
ACTGGAACATCCTTTTGCTCGACGATTTTCAGCTTGGTTG
TACTTCAGATGTTTTCTTTTGATTCTACAGGTGCAAGTTTCTCAACTGTTGGTTCGACAGAAGGTGCACTAGTCTCTGGC
ACTGGAACATCCTTTTGCTCAACAATTTTCAGCTGGTTT

TACTTCAGATGTTTTCTTTTGATTCCACAGGTGCAAGTTTCTCAACTGTTGGTTCTTGGGCGGGTGCGGCAGTTGAACCT
TTTTGGATAGAAGTTGTTACGTATTTCAGAACATTCATCAGTAAATCTAGTTCCAAACCGGAGAACACTTCAGCTTGTG
AGAAGAAGAGTTCAACTTCCACCTCCGTTCAGCAGTTCTTTGATTTCTCTTTCACATGTGACATCCTTTTGCTCAACAAT
TTCAGCTGGTTG

TACTTCAGATTTTTCTTTTGATTCCACAGGTGTATGTTTTTCAACTGTTGGTTCGACAGTTGGTGCAGTACTAGTCTCTGGC
ACTGGAACATCCTTTTGCTCAACAATTTTCAGCTGGTTC

Nr of selected repeats 94 Similarity 0.905974

Consensus:

TACTTCAGATGTTTCcTTTGATTCCACAGGTGCAAGTTTCTCAACTGTTGGTTCGACAGTAGGTGCAGTACTAGTCTCTGGC
ACTGGAACATCCTTTTGCTCaACaATTTTCAGCTgGTTg

>Cele-UNSB01_5:6199698-6200391 Satlength=694 Nr of Repeats=15 RepeatLength=42

seed=AGGTGCTGCT

AGGTGCTGCTTCCTTTGGAACGTCTTTAGTTGGCTCCGA

AGGTGCTGCTTCCTTTCGGAACATTTTCTTGAGTTGGCTCCGA

AGGTGCTGCTTCCTTTGGAACGTCTTCTTGAGTTGGCTCCGAAGGAGCTTCTTCCTTTCGGAACATCTTCTTGAGTTGGT
CCCGA

AGGTGCTGCTTCCTTTGGAACGTCTTCTTGGGTTGGCTCCAG

AGGTGCTGCTCCCTTTTGGAACGTCTTCTTGAGTTGGCTCCGA

AGGTGCTGCTTCCTTTGGAACCTTCTTCCCTGAATTGGCTCCAA

AGGTGCTGCTACCATTGGAACCTTCTTGTGTATTTGAGTTTGTTCAG

AGGTGCTGCTACCTTTTGGAACATCTGCTTGGCTTGGCTCCGA

AGGTGCTGCTTCCTTTGGAACATCTGCTTGGGTTGGCTCCGA

AGGTGCTGCTACCATTGGAACCTTCTTGTGTATTTGACTTTGTTCAG

AGGTGCTGCTACCTTTTGGAACATCTGCTTGGGTTGGCTCCGA

AGGTGCTGCTACCATTGGAACCTTCTTGTGTATTTGAGTTTGTTCAG

AGGTGCTGCTACCTTTTGGAACATCTGCTTGGCTCCGCTCCGA

AGGTGCTGCTTCCTTTGGAACATCTGCTTGGGTTGGCTCCGA

AGGTGCTGCTACCATTGGAACCTTCTTGTGTATTTGACTTTGTTCAG

Nr of selected repeats 9 Similarity 0.859788

Consensus:

AGGTGCTGCTtCCTTTGGAACaTCTgCTTGggTTGGCTCCgA

>Cele-UNSB01_5:6230981-6231799 Satlength=819 Nr of Repeats=13 RepeatLength=59

seed=ATGTGCACTG

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATAGGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATATGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATAGGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATATGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATATGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATATGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATATGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATAGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATATGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATATGGAATTTCAA

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATATGGAATTTCAAATGGATGGCAATACTGGATTT
GAATTTTCA

ATGTGCACTGGTTTTCAAAAATTTTTAAATAAAAAAAAAAAAAAAAAAATTTAAACTGAGAATAATGGAGAATATGGAATTT
CAG

ATGTGCACTGGTTTTCAAAAATTTTTAAACTGAGAATAATGGAGAATAGGGAATTTCAA

Nr of selected repeats 10 Similarity 0.954300

Consensus:

ATGTGCACTGGTTTTCAAAAaTTTTTAAACTGAGAATAATGGaGAATAtGGAATTTCAa

>Cele-UNSB01_5:6307822-6308103 Satlength=282 Nr of Repeats=8 RepeatLength=35

seed=AATTTCCCGC

AATTTCCCGCCAAAATTTTTTTCAGAGAAAATTTG

AATTTCCCGCCAAAATTTTTTACTGCAAATTTG
AATTTCCCGCTAAAATTTTTTCACTGAAAATTTT
AATTTCCCGCCAACATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTACTGCAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
Nr of selected repeats 7 Similarity 0.909297

Consensus:

AATTTCCCGCCAAAATTTTTTtCACTGAAAATTTG
>Cele-UNSB01_5:6309373-6309654 Satlength=282 Nr of Repeats=8 RepeatLength=35
seed=AATTTCCCGC

AATTTCCCGCCAAAATTTTTTTCAGAGAAAATTTG
AATTTCCCGCCAAAATTTTTTACTGCAAATTTG
AATTTCCCGCTAAAATTTTTTCACTGAAAATTTT
AATTTCCCGCCAACATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTACTGCAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
Nr of selected repeats 7 Similarity 0.909297

Consensus:

AATTTCCCGCCAAAATTTTTTtCACTGAAAATTTG
>Cele-UNSB01_5:6310933-6311214 Satlength=282 Nr of Repeats=8 RepeatLength=35
seed=AATTTCCCGC

AATTTCCCGCCAAAATTTTTTTCAGAGAAAATTTG
AATTTCCCGCCAAAATTTTTTACTGCAAATTTG
AATTTCCCGCTAAAATTTTTTCACTGAAAATTTT
AATTTCCCGCCAACATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTACTGCAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
AATTTCCCGCCAAAATTTTTTCACTGAAAATTTG
Nr of selected repeats 7 Similarity 0.909297

Consensus:

AATTTCCCGCCAAAATTTTTTtCACTGAAAATTTG
>Cele-UNSB01_5:6314778-6314883 Satlength=106 Nr of Repeats=7 RepeatLength=15
seed=GGGTCTCACC

GGGTCTCACC
GGGTCTCACCACGAT
GGGTATCACCACGAA
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAA
GGGTCTCACCACGAT
Nr of selected repeats 7 Similarity 0.881481

Consensus:

GGGTCTCACCACGAt
>Cele-UNSB01_5:6410601-6410727 Satlength=127 Nr of Repeats=6 RepeatLength=21
seed=TTGGTGACAA

TTGGTGACAATGTGGAAACAA
TTGGTGACAATGTGGAAACAA
TTGGTGACAATGTGGAAACAA
TTGGTGACAATGTGGAAACAA

TTGGTGACAATGTGGAAACAA

TTGGTGACAATGTGGAAACAA

Nr of selected repeats 6 Similarity 1.000000

Consensus:

TTGGTGACAATGTGGAAACAA

>Cele-UNSB01_5:6605586-6605676 Satlength=91 Nr of Repeats=6 RepeatLength=15

seed=GGTGAGACCC

GGTGAGACCCATCGT

GGTGAGACCCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCCTTCGT

GGTGAGACCCATCGT

GGTGAGACCCCTTCGC

Nr of selected repeats 6 Similarity 0.917037

Consensus:

GGTGAGACCCaTCGT

>Cele-UNSB01_5:6928533-6928671 Satlength=139 Nr of Repeats=7 RepeatLength=17

seed=CTCATTGCCT

CTCATTGCCTACCCTTG

CTCATTGACTACCCTTG

CTCTTTGCCTACCTCTTT

CTCATTGACTACCTGTG

CTCATTGCCTTCCTGTC

CTCATTGCCTACTTGTGCTTGTGACTGCCTTTT

CTCATTGCCTACTCTTT

Nr of selected repeats 5 Similarity 0.703704

Consensus:

CTCATTGcCTaCnCTTg

>Cele-UNSB01_5:6955453-6955644 Satlength=192 Nr of Repeats=10 RepeatLength=19

seed=AACAATCTAT

AACAATCTATTTTTTCGTGT

Nr of selected repeats 9 Similarity 1.000000

Consensus:

AACAATCTATTTTTTCGTGT

>Cele-UNSB01_5:6963271-6963507 Satlength=237 Nr of Repeats=4 RepeatLength=59

seed=TGGAAATTCA

TGGAAATTCAAGACTTCACTGGTTTTTCAAATTTTTTAAACCGAGAATATTGGGGAAAA

TGGAAATTCAAGACTTCACTGGTTTTTCAAATTTTTTAAACCGAGAATTATGGGGAAATA

TGGAAATTCAAGACTTCACTGGTTTTTCAAATTTTTTAAACCGAGAATTATGGGGAAATA

TGGAAATTCAAGACTTCACTGGTTTTTCAAATTTTTTAAACCGAGAATTATGGGGAAAA

Nr of selected repeats 4 Similarity 0.951036

Consensus:

TGGAAATTCAAGACTTCACTGGTTTTTCAAATTTTTTaAAACCGAGAATtaTGGGGAAaA

>Cele-UNSB01_5:6963686-6964031 Satlength=346 Nr of Repeats=23 RepeatLength=15

seed=AGACCCATCG

ACCAGTGAAGTCTTGAATTTCCATATTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATATTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCCTAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCCTAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATATTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATATTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCCTAATTCTCGGTTTTAAATTTTTTTGAAA

Nr of selected repeats 13 Similarity 0.950167

Consensus:

ACCAGTGAAGTCTTGAATTTCCATATTTCCCCAtaATTCTCGGTTTTAAATTTTTTTGAAA

>Cele-UNSB01_5:6966002-6966297 Satlength=296 Nr of Repeats=5 RepeatLength=59
seed=TGGAAATTCA

TGGAAATTCAAGACTTCACTGGTTTTCAAAAATTTTTAAACCGAGAATATTGGGGAAAA
TGGAAATTCAAGACTTCACTGGTTTTCAAGATTTTTAAACCGAGAATTATGGGGAAATA
TGGAAATTCAAGACTTCACTGGTTTTCAAAAAATTTAAACCGAGAATTATGGGGAAATA
TGGAAATTCAAGACTTCACTGGTTTTCAAAAATTTTTAAACCGAGAATTATGGGGAAATA
TGGAAATTCAAGACTTCACTGGTTTTCAAAAATTTTTAAACCGAGAATTATGGGGAAAA

Nr of selected repeats 5 Similarity 0.941243

Consensus:

TGGAAATTCAAGACTTCACTGGTTTTCAAaAttTTTTAAACCGAGAATtaTGGGGAAAtA

>Cele-UNSB01_5:6966476-6966776 Satlength=301 Nr of Repeats=20 RepeatLength=15
seed=AGACCCATCG

AGACCCATCGTGACG
AGACCCATCGTGGTG
AGACCCATCGTGGCG
AGACCCACCGTGGTC
AGACCCATCGTGGCG
AGACCCATCGTGGCG
AGACCCATCGTGGTG
AGACCCATCGTGGCG
AGACCCATCGTGGCG
AGACCCATCGTGGTG
AGACCCATCGTGGTG
AGACCCATCGTGGCG
AGACCCATCGTGGCG
AGACCCATCGTGGTG
AGACCCATCGTGGTG
AGACCCATCGTGGCG
AGACCCATCGTGGTG
AGACCCATCGTGGTG
AGACCCATCGTGGCG
AGACCCATCGTGGTG

Nr of selected repeats 20 Similarity 0.894269

Consensus:

AGACCCATCGTGGtG

>Cele-UNSB01_5:6967498-6969084 Satlength=1587 Nr of Repeats=27 RepeatLength=59
seed=ACCAGTGAAG

ACCAGTGAAGTCTTGAATTTCCATATTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAAT
ACCAGTGAAGTCTTGAATTGCCATATTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATATTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCCTAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCCTAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATATTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAAT

ACCAGTGAAGTCTTGAATTGCCATATCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATATCCCCATAATTCTCGGTTTTAAATTTTTTTGAAT
ACCAGTGAAGTCTTGAATTGCCATATCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATTTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATATCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTTCCATTTTCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAAGTTCCATATTTCCCCATAATTCTCGGTTTTAAAGTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATCCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
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ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAATTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAAGTTTTTTGAAA
ACCAGTGAAGTCTTGAATTGCCATATTTCCCATAATTCTCGGTTTTAAAGTTTTTTGAAA

Nr of selected repeats 20 Similarity 0.961939

Consensus:

ACCAGTGAAGTCTTGAATTTCCATATTTCCcCATAATTCTCGGTTTTAAATTTTTTTGAAA

>Cele-UNSB01_5:6969386-6969716 Satlength=331 Nr of Repeats=22 RepeatLength=15

seed=AGACCCATCG

AGACCCATCGTGACG

AGACCCATCGTGGTG

AGACCCATCGTGGCG

AGACCCACCGTGGTC

AGACCCATCGTGGCG

AGACCCATCGTGGCG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGCG

AGACCCATCGTGGCG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGCG

AGACCCACCGTGATG

AGACCCCGTGGCG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGTG

AGACCCATCGTGGCG

Nr of selected repeats 22 Similarity 0.899182

Consensus:

AGACCCATCGTGGcG

>Cele-UNSB01_5:6971634-6982576 Satlength=10943 Nr of Repeats=186

RepeatLength=59 seed=ATGGAAATTC

ATGGAAATTCaAGACTTCACTGGTTTTCAAATAAATAAACCAGAGAATTATGGGGAAAT

CTAGCTAGATTA AACGCTCTCAAGAGACAGCATGTTGTTGTTGCCACACAAGAAGAAGGCC
CTAGCTAGATTA AACGCTCTCAAGAGACAGCATGTTGTTGTTGCCACACAAGAAGAAGGCT

Nr of selected repeats 6 Similarity 0.943704

Consensus:

CTAGCTAGATTA AACGCTCTCAAGAGAcAGCATgTTGTTGtTGCCACACAAGAAGAAGGCT

>Cele-UNSB01_5:7379892-7380037 Satlength=146 Nr of Repeats=8 RepeatLength=18
seed=TTTCATAAGA

TTTCATAAGAAGTAAATC
TTTCATAAGAAGTAAATT
TTTCATAAGAAGTAAATT
TTTCATAAGAAGTAAATA
TTTCATAAGAAGTAAATAT
TTTCATAAGAAGTAAATA
TTTCATAAGAAGTAAATA
TTTCATAAGAAGTAAATC

Nr of selected repeats 7 Similarity 0.943563

Consensus:

TTTCATAAGAAGTAAATn

>Cele-UNSB01_5:7485041-7485201 Satlength=161 Nr of Repeats=4 RepeatLength=40
seed=GAAGGTTCTA

GAAGGTTCTAGAAATATTCAGAAATATTCAAAACCTTTCCA
GAAGGTTCTAGAACATTTCCAGCATTTTCTGAGAATTTCTA
GAAGGTTCTAGAACATTCAGAAATTTTCTCAAATTTCCA
GAAGGTTCTAGAACATTCAGAAATCTCTTGAACCTTTCCA

Nr of selected repeats 4 Similarity 0.794444

Consensus:

GAAGGTTCTAGAAcATTcCAGaATttTcTnaaAaTTTCcA

>Cele-UNSB01_5:7485330-7487566 Satlength=2237 Nr of Repeats=74 RepeatLength=11
seed=CTACAGTACC

CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTTCCAAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTTCCAAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTTCCAAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTTCCAAA
CTACAGTAATC
CTACAGTAGCC
CTACAGTACTT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTTCCAAA
CTACAGTAATC
CTACAGTAACC

CTACATTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCCCAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCCCAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
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CTACAGTACCT
CTACAGTACTA
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CTACAGTAATC
CTACAGTAGCC
CTACAGTACTT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCCCAA
CTACAGTAATC
CTACAGTAACC
CTACATTACCT
CTACAGTACTA
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CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCCCAA
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CTACAGTAACC
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CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
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CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
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CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCATTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCCCAA
CTACAGTAATC

CTACAGTAACC
CTACATTACCT
CTACAGTACTA
CTACAGTACCCCGACCATATCCCACCACTAACCTAAACCCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCCCAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA
CTACAGTACCCCGACCATATCCCACCATTAACCTAAAACCAATATCCCTTCAAAAAGACGAAAAGTCAATTTTTCCCAA
CTACAGTAATC
CTACAGTAACC
CTACAGTACCT
CTACAGTACTA

Nr of selected repeats 56 Similarity 0.675400

Consensus:

CTACAGTACct

>Cele-UNSB01_5:7745857-7745978 Satlength=122 Nr of Repeats=6 RepeatLength=17
seed=CTCATTGCCT

CTCATTGCCTACCCTTG
CTCATTGACTACCTCTTT
CTCATTGACTACCTGTG
CTCATTGCCTTCCTGTT
CTCATTGCCTACTTGTGCTCGTTGACTACTTTTT
CTCATTGCCTACTCTTT

Nr of selected repeats 4 Similarity 0.697531

Consensus:

CTCATTGcCTaCnCTgTg

>Cele-UNSB01_5:7764570-7764720 Satlength=151 Nr of Repeats=10 RepeatLength=15
seed=GGGTCTCACC

GGGTCTCACCACGAA
GGGTCTCACCACGAT
GGGTCTCACCACGAA
GGGTCTCACCACGAA
GGGTCTCACCACGAT
GGGTCTCACCACGAA
GGGTCTCACCACGAT
GGGTCTCACCACGAA
GGGTATCACCACGAA
GGGTCTCACCACGAT

Nr of selected repeats 10 Similarity 0.934815

Consensus:

GGGTCTCACCACGAa

>Cele-UNSB01_5:7956964-7957604 Satlength=641 Nr of Repeats=16 RepeatLength=40
seed=TCTGGAACAT

TCTGGAACATTCCAGAATTTCTCGATTTTTCTAGAAAGT
TCTGGAACATTCCAGAATTTCTCGATTTTTCTAAAAAGT
TCTGGAACATTCCAGAAATTTCCCGATTTTTCTAGAAAGT
TCTGGAACATTCCAGAAATTTCTCGATTTTTTTAAAAAGT
TCTGGAACATTCCAGACTTTTCCCAATTTTTCTAGAATGT
TCTGGAACATTCCAGACATTTCTAATTTTTCTAGAAAGT
TCTGGAACATTCCAGACTTTTCCCAATTTTTCTAGAAAGT
TCTGGAACATTCCAGACTTTTCCCAATTTTTCTGGAAGT
TCTGGAACATTCCAGACTTTTCCCAATTTTTCTAGAAAGT
TCTGGAACATTCCAGAATTTCTCGATTTTTCTAGAAAGT

TCTGGAACATTCCAAAAATTTCCCAATTTTTCTAGAAATA
TCTGGAACATTTTCAGAATTTTCCCAATTTTTCTAGAAAGT
TCTGGAACATTCCAGAATTTTCCCAATTTTTCTAGAAAGT
TCTGGAACATTCCAGAATTTTCTCGATTTTTTTAGAAAGT
TCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGAATGT
TCTGGAACATTCCAGACTTTTCTAATTTTTCTAGAAAGT
Nr of selected repeats 16 Similarity 0.859790

Consensus:

TCTGGAACATTCCAGAatTTTCcCaATTTTTCTAGAAAGT

>Cele-UNSB01_5:7957689-7957969 Satlength=281 Nr of Repeats=8 RepeatLength=35
seed=CAGAAAATTT

CAGAAAATTTAAATTTCCCGCAAAAATATTTTTCA
CAGAAAATTTAAATTTCCCGCAAAAATATTTTTCA
CAGAAAATTTAAATTTCCCGCAAAAATATTTTTCA
CAGAAAATTTAAATTTCCCGCAAAAATATTTTTCA
CAGAAAATTTAAATTTCCCGCAAAAATATTTTTCT
CAGAAAATTTAAATTTCCCGCAAAAATATTTTTCA
CAGAAAATTTAAATTTCCCGCAAAAATATTTTTCA
CAGAAAATTTAAATTTCCCGCAAAAATATTTTTCA

Nr of selected repeats 8 Similarity 0.964626

Consensus:

CAGAAAATTTAAATTTCCCGCcAAAATATTTTTCA

>Cele-UNSB01_5:7958037-7958202 Satlength=166 Nr of Repeats=11 RepeatLength=15
seed=CCACGATGGG

CCACGATGGGTCTCA
CCACGACGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCA
CCACGGTGGGTCTCA
CCACGATGGGTCTCG
CCACGACGGGTCTCA
CCACGATGGGTCTTA
CCACGATGGGTATCG
CCACGATGGGTCTCA
CCACGATGGGTCTCG

Nr of selected repeats 11 Similarity 0.877172

Consensus:

CCACGATGGGTCTCa

>Cele-UNSB01_5:7959905-7960085 Satlength=181 Nr of Repeats=11 RepeatLength=15
seed=ACCCATCGTG

ACCCATCGTGGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG
ACCCATCGTGGAGAT
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCGTCGTGGCGAG
ACCCATCGTGGTGAGACCCGTCGTAGCGAG
ACCCATCGTGGTGAG
ACCCATCGTGGTGAG
ACCCATCGTGGCGAG

Nr of selected repeats 10 Similarity 0.907161

Consensus:

ACCCATCGTGGtGAG

GTCTGGACTGGTGTAGTAGAACTGCTTGAGGTTCTGTGCTGGTTGTCTCTGGAGCCGTGGTAGTAGTA
GTCTGGACTGGTGTAGTAGAACTGCTTGAGGTTCTGTACTGGTTGTCTCTGGAGCCGTGGTAGTAGTA
GTCTGGACTGGTGTAGTAGAACTGCTTGAGGTTCTGTACTGGTTGTCTCTGGAGCCGTGGTAGTAGTA
GTCTGGACTGGTGTAGTAGAACTGCTTGAGGTTCTGTACTGGTTGTCTCTGGAGCAGTGGTAGTAGTA
GTCTGGACTGGTGAAGTAGAACTGCTTGAGGTTCTGTGCTGGTTGTCTCTGGAGCCGTGGTAGTAGTC
GTCTGGACTGGTGTAGTAGAGCTGCTTGAGGTTCTGTGCTGGTTGTCTCTGGAGCCGTAGTAGTAGTC

Nr of selected repeats 67 Similarity 0.948872

Consensus :

GTCTGGACTGGTGTAGTAGAACTGCTTGAGGTTCTGTaCTGGTTGTCTCTGGAGCcGTGgTAGTAGTa

>Cele-UNSB01_5:8761530-8782970 Satlength=21441 Nr of Repeats=357

RepeatLength=60 seed=ACACAATTGG

ACACAATTGGAGTGGTGCTTGAGGAGCTGAATTCAGTTGAGCTCGTTATGTTCGGTTGAAG
ACACAATTGGAGTGGTGCTTGAGGAGCTGGATTTCAGTTGAGCTCGTTATGTTCGGTTGAAG
ACACAATTGGAGTGGTGCTTGAGGAGCTGGATTTCAGTTGAGCTCGTTATGTTCGGTTGAAG
ACACAATTGGAGTGGTGCTTGAGGAGCTGAATTCAGTTGAGCTCGTTATGTTCGGTTGAAG
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GTAAGTCTCAAAGCTTCTGGCACCTATTGGGATGTTGTTGGTAAATTCTGAAAAAGCTTGGAAATTTGCAACAAAGTTT
CTGAAAGAAATTTCAAAAAAGTTGGTTTGAAGTGAATTTGCAATTTTCAAAGTTTCATAAATTTACCTATTTTGCCTA
TAAATGGTTCGTTTTTCATTTAATAATAAAAATACGAACAAAGGACTGTAGGTTTTCT

Nr of selected repeats 12 Similarity 0.965543

Consensus:

GTAAGTCTCAAAGCTTCTGGCACCTATTGGGATGTTGTTGGTAAATTCTGAAAAAgCTTGGAAATTTGCAACAAAGTTT
CTGAAAGAAATTTTCgAAAAAGTTGATTTGAAGTGATTTggGAATTTTCAAAGTTTCATAAATTTACCTATTTTGCCTA
TAAATGGTTCGTTTTTCATTTAATAATAAAAATACGCACAAAGGACTGTAGGTTTTCT

>Cele-UNSB01_5:9479420-9479630 Satlength=211 Nr of Repeats=6 RepeatLength=35
seed=AGAAAATTTA

AGAAAATTTAAATTTCCCTCCAAAATTTTTTTCTC
AGAAAATTTAAATTTACCCGCCAAAATTTTTTCAC
AGAAAATTTAAATTTCCCGCCAAAATTTTTTTCTC
AGAAAATTTAAATTTCCCTCCAAAATTTTTTTCTC
AGAAAATTTAAATTTCCCTCCAAAATTTTTTTCTC
AGAAAATTTAAATTTCCCGCCAAAATTTTTTCAC

Nr of selected repeats 6 Similarity 0.888254

Consensus:

AGAAAATTTAAATTTCCCGCCAAAATTTTTTctC

>Cele-UNSB01_5:9479685-9479850 Satlength=166 Nr of Repeats=11 RepeatLength=15
seed=CGATGGGTCT

CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATAGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCACCT
CGATGGGTCTCACCA
CGATGGGTCTCACCA
CGATGGGTCTCGCCA
CGACGGGTCTCGCCA
CGACGGGTCTCGCCA

Nr of selected repeats 11 Similarity 0.899798

Consensus:

CGATGGGTCTCaCCA

>Cele-UNSB01_5:9480075-9480332 Satlength=258 Nr of Repeats=8 RepeatLength=11
seed=GTACTCCTAC

GTACTCCTACA
GTACTCCTACA
GTACTACTACAGTACCCCGACCATATCCCACCTAATAACTCCAAACCTATATCTCTTCAAAGGCAAAAACCTAATTTTT
CCTAAACTACA
GTAATCCTACC
GTACTCCTACA
GTACTCCTACAGCACTACTACAGTACCCCGACCATATCCCACCTAATAACTCCAAACCTATATCTCTTCAAAGGCAAAA
ACTCAATTTTTCCAAAACCTACA
GTAATCCTACC
GTACTCCTACA

Nr of selected repeats 6 Similarity 0.870707

Consensus:

GTAcTCCTACa

>Cele-UNSB01_5:9642570-9642900 Satlength=331 Nr of Repeats=22 RepeatLength=15
seed=GGTGAGACCC

GGTGAGACCCTTCGT
GGTGAGACCCATCGT

GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTG
GCGGGAAATTCAAATTTTCAGGGAAAAAAAAATTTG
GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTG
GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTG
GCGGGAAATTCAAATTTTCAGTGAAAAAAAAATTTA
GCGGGAAATTCAAGTTTTCAATGAAAAAAAAATTTA
GCGGGAAATTCAAGTTTTCAATGAAAAAAAAATTTA
Nr of selected repeats 25 Similarity 0.936127

Consensus:

GCGGGAAATTCAAATTTTCAGTgAAAAAAAAATTTG

>Cele-UNSB01_5:9644299-9645659 Satlength=1361 Nr of Repeats=40 RepeatLength=40

seed=TTTCTAGAAA

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TTTCTAGAAAATTCGGGAAAACCTCTGGAATATTCCAGAAC

TTTCTAGAAA

TTCTAGAAAGTTCTGGAATGGTCCAGAAT

TTTCTAGAAAATTCGGGAAAACCTCTGGAATATTCCAGAAG

TTTCTAGAAAATTCGAGAAAATCCGGAATGGTCCAGAAT

TTTCTAGAAAATTCGGGAAAACCTCTGGAATATTCCAGAAC

TTTCTAGAAA

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TTTCTAGAAAATTCGAGAAAATCCGGAATGGTCCAGAAC

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TTTCTAGAAAATTCGAGAAAATCCGGAATGGTCCAGAAT

TTTCTAGAAAATCCGAGAAAAGTTCTGGAATGGTCCAGAAT

TTTCTAGAAAATTCGGGAAAATCTGGAATATTCCAGAAC

Nr of selected repeats 28 Similarity 0.851676

Consensus:

TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTTG
TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTCG
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TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTCG
TGTAACAATCTATTTTTTCG

Nr of selected repeats 53 Similarity 0.979833

Consensus:

TGTAACAATCTATTTTTTCG

>Cele-UNSB01_5:10311486-10312622 Satlength=1137 Nr of Repeats=33

RepeatLength=34 seed=TTGGCGGGAA

TTGGCGGGAAATTCAAATTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTCTATGAAAAAATA
TTGGCGGGAAATTCAAATTTTGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTCAGTGAAAAAATT
TTGGCGGGAAATTCAAATTTTCAGTGAAAAAATT
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TTGGCGGGAAATTCAAATTTTCAGTGAAAAACAAT
TTGGCGGGAAATTCAAATTTTCAGTGAAAAAGATT
TTGACGGGAAATTCAAATTTTCTGAGGAAAACAT

Nr of selected repeats 20 Similarity 0.915765

Consensus :

TTGGCGGGAAATTCAAATTTTCAGTGAAAAaATT

>Cele-UNSB01_5:10490005-10492889 Satlength=2885 Nr of Repeats=111

RepeatLength=26 seed=CCAGAGTCAC

CCAGAGTCACTATAATTGGTGAACGG

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CCAGAGTCACTATAATTTGGTGAACGG

CCAGAGTCACTATAATTGGTGAACGG

CCAGAGTCACTATAATTGGTGAACGG

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CCAGAGTCACTATAATTGGTGAACGG
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Nr of selected repeats 109 Similarity 0.974141

Consensus:

CCAGAGTCACTATA~~t~~TTGGTGAACGG

>Cele-UNSB01_5:10495318-10500018 Satlength=4701 Nr of Repeats=187

RepeatLength=25 seed=TTTACTCTCT

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TTTACTATCTGGCTTCACAGAATAA

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TTTACTCTCTGGCTTCACAGAATAT

AGATACACTTC
AGATACACTTC
AGATACACTTC
AGATACACTTTC
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AGATACACTTTC

Nr of selected repeats 15 Similarity 0.983838

Consensus:

AGATACACTTC

>Cele-UNSB01_5:10655040-10675549 Satlength=20510 Nr of Repeats=527

RepeatLength=39 seed=CCACCAGAAA

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CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCTAGGG
CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCTAGGG
CCACCAGAAATACCAGTTTATGGAAAAGTGGCTCTAGGG
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CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCAAGGG
CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCAAGGG
CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCTAGGG
CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCAAGGG
CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCTAGGG
CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCTAGGG
CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCTAGGG

Consensus :

CCACCAGAAATACCAGTTTATGAAAAAGTGGCTCTAGGG

>Cele-UNSB01_5:11125880-11126094 Satlength=215 Nr of Repeats=10 RepeatLength=11
seed=CACATTTTTT

CACATTTTTTG

CACATTTTTTG

CACATTTTTAA

CACATTTTTTG

CACATTTTTTG

CACATTTTTTG

CACATTTTTTG

CACATTTTTTG

CACTTTTTTTGAAGGAAATCCTCGTTACCCCTTAGGATTTTTTTATTATTTTAGAAAAAATTCCTAAGGGGGTA

ACGAGGATTTTTCTCCAAAAATAAAAAAATCCTAA

CACATTTTTTG

Nr of selected repeats 9 Similarity 0.946128

Consensus :

CACATTTTTTG

>Cele-UNSB01_5:11176286-11176509 Satlength=224 Nr of Repeats=5 RepeatLength=45

seed=TCTGATCCTT

TCTGATCCTT CAGCTCCGAAGGATCACATGGGTACCTTCTGATGT

TCTGATCCTT CAGATAAGAAGAATCGTAAGGGTACCTCCTGATGG

TCTGATACTT CAGCTCCAAAGGATCATGAGGCTCGTTCTGATGT

TCTGATCCTT CAGATAAGAAGAATCGTAAGGGTACCTCCTGATGG

TCTGATACTT CAGCTCCAAAGGATCATGAGGCTCTCCTGATGT

Nr of selected repeats 3 Similarity 0.822222

Consensus :

TCTGATCCTT CAGaTaaGAAGaATCgtAaGGGTACCTcCTGATGg

>Cele-UNSB01_5:11176622-11177248 Satlength=627 Nr of Repeats=14 RepeatLength=45

seed=CTGAAGGATC

CTGAAGGATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTAT

CTGAAGGATCAGAACATCAGAAGGTACCCATGTGATCCTTCGGAG

CTGAAGGATCAGAACATCAGGAAAAGCCTCGTGATCCTTTGGAG

CTGAAGGATCAGACCATCAGGAGGTACCCTTACGATCCTTCTTAT

CTGAAGGATCAGAACATCAGAAGGTACCCATGTGATCCTTCGGAG

CTGAAGGATCAGAACATCAGGAAAAGCCTCGTGATCCTTTGGAG

CCAAGCACATCTACAGAGACACCTACAACCTGAATCAACTGCAGCA
Nr of selected repeats 85 Similarity 0.985127

Consensus:

CCAAGCACATCTACAGAGACACCTACAACCTGAATCAACTGCAGCA
>Cele-UNSB01_5:12149471-12149551 Satlength=81 Nr of Repeats=5 RepeatLength=16
seed=AAAAATTATT
AAAAATTATTGAATAC
AAAAATTATTGAATAC
AAAAATTATTGAATAC
AAAAATTATTGAATAC
AAAAATTATTGAATAC

Nr of selected repeats 5 Similarity 1.000000

Consensus:

AAAAATTATTGAATAC
>Cele-UNSB01_5:12442637-12442985 Satlength=349 Nr of Repeats=5 RepeatLength=18
seed=GCACTCCCTA
GCACTCCCTATTAGTATTGCCCTCGGAGACCTTCCGAAAATTAGTATG
GCACTCCCTATTAGTCTT
GCACTCCCTAATAGCCTTGCCTTTACTCTTTTTTTATTGCAGGCCCGTCTTGTTAACTTCAGGATTTCAACGAAAAAATT
TGCCTATTTTGCAACAATTTTTCACAACATTTCTACGAGATTGAAGTTTTTGAAGTTATATGTTACAATTTAAAATCAA
TTTTCTGAATTTTTACATAAGATTCGAGCTTTTTTCAGAAAAAACTAGTAAGCTCAAAGTCAGAAAAATGTTCTGAAA
TTAGTATT

GCACTCCCTAATAGTCTT

GCACTCCCTAATAGTCTT

Nr of selected repeats 3 Similarity 0.950617

Consensus:

GCACTCCCTAaTAGTCTT

>Cele-UNSB01_5:12601066-12601185 Satlength=120 Nr of Repeats=8 RepeatLength=14
seed=CTATACGCTA

Nr of selected repeats 26 Similarity 0.979703

Consensus:

GTTACACGAAAAATAGATT

>Cele-UNSB01_5:13461673-13462167 Satlength=495 Nr of Repeats=26 RepeatLength=19
seed=GTTACACGAA

GTTACACGAAAAATAGATT

Nr of selected repeats 26 Similarity 0.979703

Consensus:

GTTACACGAAAAATAGATT

>Cele-UNSB01_5:13535913-13536380 Satlength=468 Nr of Repeats=12 RepeatLength=40
seed=TCTGGAATGT

TCTGGAATGTTCCAGAACTTTCTAAAAAAATCGGGAAAAT

TCTGGAATGTTCCAGAACTTTCTAGAAAAATCGGGAAAAT

TCTGGAATGTTCCAGAACTTTCTAGAAAAATCGGAGAAAAT

TCTGGAATGTTCCAGAACTTTCTAAAAAAATCGGGAAAAT

TCTGGAATGTTCCAGAACTTTCTAGAAAAATCGGAAAAT

TCTGGAATGTTCCAGAACTTTCTAGAAAAATCGGGAAAAT

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TCTGGAATGTTCCAGAACTTTCTAGAAAAATCGGGAAAAT

TCTGGAATGTTCCAGAACTTTCTAGAAAAATCGGAGAAAAT

TCTGGAATGTTCCAGAACTTTCTAAAAAAATCGGAGAAAAT

TCTGGAATGTTCCAGAACTTTCTAGAAAAATCGGGAAAAT

Nr of selected repeats 11 Similarity 0.922424

Consensus:

TCTGGAATGTTCCAGAACTTTCTAgAAAAATCGgGAAAT

>Cele-UNSB01_5:13735981-13739186 Satlength=3206 Nr of Repeats=193

RepeatLength=16 seed=GAAAAATTTT

GAAAAATTTTGCTGTT

GAAAAATTTTGCTGCT
GAAAAATTTTCGTGGCG
GAAAAATTTTCCTGGT
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Nr of selected repeats 167 Similarity 0.786698
Consensus:
GAAAAATTTtGctGct
>Cele-UNSB01_5:13735981-13740432 Satlength=4452 Nr of Repeats=256
RepeatLength=16 seed=GAAAAATTTT
GAAAAATTTTGCTGTT
GAAAAATTTTGCTGCT
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Nr of selected repeats 212 Similarity 0.783548

Consensus:

GAAAAATTTtGctGct

>Cele-UNSB01_5:13735981-13741243 Satlength=5263 Nr of Repeats=280

RepeatLength=16 seed=GAAAAATTTT

GAAAAATTTTGCTGTT
GAAAAATTTTGCTGCT
GAAAAATTTTCGTGGCG
GAAAAATTTTCCTGGT
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Nr of selected repeats 227 Similarity 0.784063

Consensus:

GAAAAATTTtGctGcn

>Cele-UNSB01_5:13735981-13743674 Satlength=7694 Nr of Repeats=334

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Nr of selected repeats 260 Similarity 0.786925

Consensus:

GAAAAATTTTgctGcg

>Cele-UNSB01_5:13979410-13979500 Satlength=91 Nr of Repeats=6 RepeatLength=15

seed=TCGTGGTGAG

TCGTGGTGAGACCCT

TCGTGGTGAGACCCT

TCGTGGTGATACCAA

TCGTGGTGAGACCTT

TCGTGGTGAGACCCT

TCGTGGTGAGACCAA

Nr of selected repeats 6 Similarity 0.857778

Consensus:

TCGTGGTGAGACCt

>Cele-UNSB01_5:13979523-13981831 Satlength=2309 Nr of Repeats=66

RepeatLength=35 seed=GCGGGAAATT

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Nr of selected repeats 50 Similarity 0.968964
Consensus:
GCGGGAAATTCAAATTTTCAGTGAAAAAAATTTTg
>Cele-UNSB01_5:13979521-13982440 Satlength=2920 Nr of Repeats=68
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CGCGCTCCATTGGACTGAAA

Nr of selected repeats 50 Similarity 0.947124

Consensus:

TGGCGGGAAATTCAAATTTTCAGTGAAAAAATTT

>Cele-UNSB01_5:14055771-14055849 Satlength=79 Nr of Repeats=6 RepeatLength=12
seed=TCTTTCTCCTT

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TCTTTCTCCTTT

TCTTTCTCCTTG

TCCTTCTCCTTC

TCTTTCTCCTTG

TCTTTTCTCCTTCTCCCTT

Nr of selected repeats 5 Similarity 0.866667

Consensus:

TcTtTCTCCTTn

>Cele-UNSB01_5:14155473-14156076 Satlength=604 Nr of Repeats=4 RepeatLength=151
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Nr of selected repeats 3 Similarity 0.988227

Consensus:

CATTTTCAGATATTCCATCACCACCAACcACCTTCATCCACTTCTTCGCCTGGAACGACGGGATTTTCTACAAAAATCGGA

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>Cele-UNSB01_5:14159253-14159397 Satlength=145 Nr of Repeats=6 RepeatLength=11

seed=CTACAGTACC

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Nr of selected repeats 4 Similarity 0.818182

Consensus:

CTACAGTACcc

>Cele-UNSB01_5:14206302-14207970 Satlength=1669 Nr of Repeats=22

RepeatLength=57 seed=GAACTCAACA

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GAACTCAACAAGCTGATCAAGAATCGCAACGTCCAGCTAGAGCCGCTGACAACCTCACACAAAGGATCCCTTGACGCTGA

TGCTGATATGAAACGACCCAGAGCTGCCGGCCAAAAA

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GAACTCAACAAGCTGATCAAGAGCGACACCGTGGATCCCGAGCTGCCGGAGAGAAGG

GAACTCAACAAGCTGATCAAGAGCAACACCGTGGATCCCGAGCTGCCGGACAGAAGG

GAACTCAACAAGCTGATCAAGAGCAACACCGTGGATCCCGAGCTGCCGGACAGAAGG

GAACTCAACAAGCTGATCAAGAATCAAAGCGTCCAGCAAGAGCTGCCGACAATCCACAAAGGATCCCTTGATGCTGA

TGCCGATATCAAACGACCCAGCAAGAGGTGCCGCAGACATTTCTCAACATGGATCAGTTCATACCGAGGTGAAACGTCCA

GCTAGAGATGCCGGCCAAAAAGGAACCCAGCAATTCGGAGGAGACCATCACCGCAATCCAGAGCTGCCGGCCAAAAAG

Nr of selected repeats 15 Similarity 0.952771

Consensus:

GAACTCAACAAGcTGATCAAGAGCaACACCGTGGATCCCGAGCTGCCGGAcAGAAGG

>Cele-UNSB01_5:14209723-14211643 Satlength=1921 Nr of Repeats=32

RepeatLength=60 seed=CTGCTGATTC

CTGCTGATTCGAGAAGAAGGCCCAACCAAGAGAGAAGCTGATCCACCAAAGACTGAAT

CTGCTGATTCGAGAAGAAGGCCCAACCAAGAGAGAATCTGATAAGCCAAAGACTGAAT

CTGCTGATTCGAGAAAAATGCCCCAGCCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

CTGCTGATTCGAGAAGAAGGCCCCAGCCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

CTGCTGATTCGAGAAGAAGGCCCCAGCCAAGAGAGAATCTGATAAGCCAAAGACTGAAT

CTGCTGATTCGAGAAGAAGGCCCCAGTCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

CTGCTGATTCGAGAAGAAGGCCCCAGCCAAGAGAGAATCTGATAAGCCAAAGACTGAAT

CTGCTGATTCGAGAAGAAGGCCCCAGTCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

CTGCTGATTCGAGAAGAAGGCCCCAGTCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

CTGCTGATTCGAGAAGAAGGCCCCAGTCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

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CTGCTGATTCCGAGAAAAATGCCCCAGCCAAGAGAGAAGCTGATAAGCCAAAAGACTGAAT
CTGCTGATTCCGAGAAGAAGGCTTCAGCCAAGAGAGAAGCTGATCCACCAAAGACTGAAT

Nr of selected repeats 32 Similarity 0.925493

Consensus:

CTGCTGATTCCGAGAAGAAGGCCCCAGC CAAGAGAGAAGCTGATAAGCCAAAAGACTGAAT

>Cele-UNSB01_5:14226001-14226091 Satlength=91 Nr of Repeats=6 RepeatLength=15

seed=CGTGGTGAGA

CGTGGTGAGACCCAT

CGTGTTGAGACCCTA

CGTGGTGAGACCCTT

CGTGGTGAGACCCTT

CGTGGTGAGACCCAT

CGTGGTGAGACCCTT

Nr of selected repeats 6 Similarity 0.893333

Consensus:

CGTGGTGAGACCCTT

>Cele-UNSB01_5:14226151-14226968 Satlength=818 Nr of Repeats=21 RepeatLength=35

seed=GGAAATTCAA

GGAAATTC AAATTTTAAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTAGCA

GGAAATTC AAATTTTCAGTTAAAAAAATTTTGGCG

GGAAATTC AATCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTAAAAAAATTTTGGCG

GGAAATTC AATCAGTGAAAAAAATTTTGGCA

GGAAATTC AAATTTTCAGTAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTAGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTGAAAAAAATTTTGGCG

GGAAATTC AAATTTTCAGTAAAACTTTTTGTTAGCTTAAGTACCACCTGGAACTGGCGAGACCCATCGTGGTGGGACCT

TTAAAAATATGGGCGGGAGCTTCAAATTTATGAGAAAAGAAATTTTGGCG

GGAATTCAAATTTCCAAGAAAAATTTGGCG
GGAAATTCAAATTTTCTGAGAAAAAGATTTTGACG
GGAAATTCAAATTTTCTGAGGAAAACATTTGGCG

Nr of selected repeats 14 Similarity 0.922554

Consensus:

GGAAATTCAAATTTTCAgTgAAAAAAaTTTTGGCG

>Cele-UNSB01_5:14260478-14260568 Satlength=91 Nr of Repeats=6 RepeatLength=15

seed=GGGTCTCACC

GGGTCTCACCACGAA

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGAA

GGGTCTCACCACGTA

GGGTCTCACCACGAT

Nr of selected repeats 6 Similarity 0.917037

Consensus:

GGGTCTCACCACGAa

>Cele-UNSB01_5:14309212-14310008 Satlength=797 Nr of Repeats=14 RepeatLength=64

seed=GTAGTCAAAA

GTAGTCAAAAAGTCAAAAAGTGCgAATGTAGCTATTTTTTcAGTCAGTAGCGAAAAAGACATTCA

GTAGTCAAAAAGACAAAAGTGCgAATGTAGCTATTTTTTtAGTCAGTAGCGAAAAAGACATTCA

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GTAGTCAAAAAGACAAAAGTGCgAATGTAGCTATTTTTTtCGGCCAGTAGCGAAAAAGACACTC

GTAGTCAAAAAGCAAT

GTAGTCAAAAATCCA

Nr of selected repeats 9 Similarity 0.983796

Consensus:

GTAGTCAAAAAGaCAAAAAGTGCgAATGTAGCTATTTTTTcAGTCAGTAGCGAAAAAGACATTCA

>Cele-UNSB01_5:14425209-14425464 Satlength=256 Nr of Repeats=5 RepeatLength=24

seed=GCCGCTCCAG

GCCGCTCCAGCTCCGGCACCAGAT

GCCGCTCCAACAGCCCCAGCAGCAGGCGCAGGTGGATATTCGCCGCGCAGATGCTCCAActGGTGGTGGATCTTATC

CATCCAAGAAGAGAAGAGTTGCTCGTGATTATGCTGAAGAAGGT

GCCGCTCCAGCTGCGCCAGCAGAACC GCCCAGTTCTGCACCAGAACCAGCACCAGAA

GCCGCTCCAGCACCAGCACCAGAA

GCCGCTCCAGTTCCGGCACAAGAT

Nr of selected repeats 3 Similarity 0.814815

Consensus:

GCCGCTCCAGctCCgGCACcAGAt

>Cele-UNSB01_5:14452450-14453298 Satlength=849 Nr of Repeats=19 RepeatLength=45

seed=TCTGATCCTT

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TCTGATCCTTcAGATAAGAAGGATCGTAAGGGTACCTCCTGATGG

TCTGATACTTcAGCTCCAAAGGATCACGAGGCTCTTCTGATGT

TCTGATCCTTcAGCTCCGAAGGATCACATGGGCACCTTCTGATGT

TCTGATCCTTCAAATAAGAAGGATCGTAAGGGTACCTCCTGATGG

TGTGAAGCCAGAGAGTAAATTATTC
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TGTGAAGCCAGAGAGTAAATTAATC
TGTGAAGCCAGAGAGTAAATTATTA
TGTGAAGCCAGAGAGTAAATTAATC
TGTGAAGCCAGAGAGTAAATTAATC

Nr of selected repeats 41 Similarity 0.923265

Consensus:

TGTGAAGCCAGAGAGTAAATTATTC

>Cele-UNSB01_5:14878525-14883699 Satlength=5175 Nr of Repeats=182

RepeatLength=27 seed=GGAAGCCACA

GGAAGCCACAGAGGGTAAAAATATGGTG
GGAAGCCACAGAGAGTAGAATATGGTG
GGAAGCCACAGAGAGTAGAATATGGTG
GGAAGCCACAGAGGGTAAAAATATAGTT
GGAAGCCACAGAGAGTAGAATATGGTG
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Nr of selected repeats 139 Similarity 0.948635

Consensus:

GGAAGCCACAGAGAGTAAAAATATGGTg

>Cele-UNSB01_5:15130293-15130341 Satlength=49 Nr of Repeats=4 RepeatLength=12
seed=TCTAAGTCTA

TCTAAGTCTAAG

TCTAAGTCTAAA

TCTAAGTCTAAG

TCTAAGTCTAAG

Nr of selected repeats 4 Similarity 0.944444

Consensus:

TCTAAGTCTAAg

>Cele-UNSB01_5:15289065-15289259 Satlength=195 Nr of Repeats=6 RepeatLength=35
seed=GGAATTGAAA

GGAATTGAAAATTTCCGGCAAATTGGCAAATTGGC

GGAATTGAAAATTTCCGGCAAATTGGC

GGAATTGAAAATTTCCGACAAATCGGCAAATTGGC

GGAATTGAAAATGTCCGGCAAATCGGCAAATTGGC

GGAATTGAAAATTTCTGCAAATCGGCAAATTGCC

GGAATTGAAAATTTCCGGAAAATTGAA

Nr of selected repeats 4 Similarity 0.904762

Consensus:

GGAATTGAAAATtTCCggCAAATcGGCAAATTGgC

>Cele-UNSB01_5:15290454-15290610 Satlength=157 Nr of Repeats=6 RepeatLength=26
seed=TTCACCTAAA

TTCACCTAAAATATGACTCTAACCA

TTCACCTAAAATAATGACTCTAACAA

TTCACCTAAAATAATGACTCTAACCA

TTCACCTAAAATATGACTCTGACCA

TTCACCTAAAATAATGACTCTTACCA

TTCACCTAAAATAATCACTCTAATCA

Nr of selected repeats 6 Similarity 0.846154

Consensus:

TTCACCTAAAAtaATGACTCTaACCA

>Cele-UNSB01_5:15415879-15416665 Satlength=787 Nr of Repeats=8 RepeatLength=15
seed=TCTCACCACG

TCTCACCACGAATATTCAGAAATTTTTTTTCGAATTTTTTCAGAAGGTTCTGGAACTTTCCAGAAGGTTCTGGAACTTTCC

AGAAGGTTCTGGAACTTTCCAGAAAGTTCTGGAACATTCCAGAAATTTCTCGAATTTTCCAGAAAGTTCTAGAACATTA

TAGAATTTTCTGGAATTTTCCAGATGTTTCCAAAACCAATATTGAAATTTCCCGCCAAAATCTTTTTCTCAGAAAATTTG

AATTTCCCTCCAAAATTTTTTTCTCAGAAAATTTGAAATTTCCCGCCAAAATTTGTTTTCACTGAAAATTTGAATTTCCC

GCCAAAATTTTTTTCACTGAAAATTTGAATTTCCCGCCAAAATTTTTTTCACTGAAAATTTGAATTTCCCGCCAAAATTT

TTTTTTCACTGAAAATTTGAATTTCCCGCCAAAATTTTTTTCACTGAAAATTTGGATTTCCCGCCAAAATTTTTTTTTTTCAC

TGAAAATTTGAATTTCCCGCCAAAATTTGTTTTCACTGAAAATTTGAATTTCCCGCCAAAATTTTTTTCACTGAAAATTTG

AATTTCCCGCCAAAATTTTTTTCACTGAAAATTTGAAGTTCCCGCCAAAATTTGTTTTCACTTAAAATTTGAATTTCCC

GCCAAAATTTGTTTTCACTTAAAATTTGAATTTCCCGCCAAATTTTGGG

TCTCACCACGAAGGG

TCTCACCACGATGGG

TCTCACCACGAAGGG

TCTCACCACGATGGG

TCTCACCACGAAGGG
TCTCACCACGAAGGA
TCTCACCACGATGGG

Nr of selected repeats 7 Similarity 0.923810

Consensus:

TCTCACCACGAaGGG

>Cele-UNSB01_5:15441112-15445831 Satlength=4720 Nr of Repeats=118

RepeatLength=40 seed=ATTTTCTAG

ATTTTCTAGAAAGTTCTGGAACATTCAGAATTTTCTCG
ATTTTCTAGAAAATTCTGGAACACTCCAGAATTTTCCCG
ATTTTCTAGAAAATTCTGGACCCTCCAGAATTTTCTCG
ATTTTCTAGAAAGTTCTGGAACATTCAGAATTTTCCCG
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 CCACGATGGGTCTCG
 CCACGATGGGTCTCA
 CCACGATGGGTCTTT
 CCACGATGGGTCTCA

Nr of selected repeats 70 Similarity 0.859308

Consensus:

CCACGATGGGTCTCa

>Cele-UNSB01_5:15447313-15447447 Satlength=135 Nr of Repeats=5 RepeatLength=11

seed=GTA¹CTCCTAC

GTACTCCTACA

GTACTCCTACA

GTACTACTACAGTACCCCGACCATATTCCTACTACTAACC CGAAACCTATATCTCTTC AAAAGACAAAACACAAATTTT

CATAAACTACA

GTAATCCTACC

GTACTCCTACA

Nr of selected repeats 4 Similarity 0.878788

Consensus:

GTAcTCCTACa

>Cele-UNSB01_5:15668468-15668848 Satlength=381 Nr of Repeats=5 RepeatLength=73
seed=TTAGGCTTAA

TTAGGCTTAAGCCGCCATACCGCCGGTGTGTGCATAATGATTTCCAATATTTTCTTCCAGTTGGGCATCCTAGTATGT
TTTTCGGGCCT

TTAGGCTTAAGTGTGTGCATAAGGATTTCCAATATTTTCTTCCAGTTGGGCATCCTAGTATGTTTTTCGGGCCT

TTAGGCTTAAGTGTGTGCATAAGGATTTCCAATATTTTATTCCAGTTGGGCATCCTAGTTTTTTTTTCGGGCC

TTAGGCTTAAGTGTGTGCATAAGGATTTCCCTATATTTTATTCCAGTTGGGCATCCTAGTTTTTTTTTCGGGCCT

TTAGGCTTAAGTGTGTGCATAAGGATTTCCAATATTTTATTCCAGTTGGGCATCCTAGTTTTTTTTTCGGGCC

Nr of selected repeats 3 Similarity 0.939117

Consensus:

TTAGGCTTAAGTGTGTGCATAAGGATTTCCaATATTTTaTTCCAGTTGGGCATCCTAGTtTtTTTTTCGGGCct

>Cele-UNSB01_5:15725489-15725564 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=AGACCCATCG

AGACCCATCGTGGTG

AGACCCATCGTAGTG

AGACCCATCGTGGTG

AGACCCGTCGTGGTG

AGACCCATCGTGGTG

Nr of selected repeats 5 Similarity 0.928889

Consensus:

AGACCCaTCGTgGTG

>Cele-UNSB01_5:15725600-15726976 Satlength=1377 Nr of Repeats=36

RepeatLength=35 seed=TTCAAATTTT

TTCAAATTTTCAGTGAAAAAATTTTGGCGGGAAA

TTCAAATTTTCTGTGAGAAAAAATTTTGGGGGGAAA

TTCAAATTTTCAGTGAAAAAATTTTGGCGGGAAA

TTCAAATTTTCTGTGAGAAAAAATTTTGGGGGGAAA

TTCAAATTTTCAGTAAAAAACATTTTGGCGGGAAT
TTCAAATTTTCAGTGAAAAACGTTTTGCCGGGAAA
TTCAAATTTTCTGAGAAACTTTTTGTTAGCTTAAGTACCACCTGGAAGTAGCGAGACCCATCGTGGTGAGACCCTTAAA
AATATGGGCGGGAAC
TTCAAATTTTATGAGAAAAAGAAATTTTGGCGGGAA
TTCAAATTTTCTGAGATAAAATTTTGGCGGGAA
TTCAAATTTTCTGGGAAAAAAATTTTGGCGGGAAA
TTCAGATTTTCTGAGAAAAAAGATTTTGGCGGGAAA

Nr of selected repeats 30 Similarity 0.828501

Consensus:

TTCAAATTTTCaGTGAaAAAaATTTTGGcGGGAAa

>Cele-UNSB01_5:15757927-15757998 Satlength=72 Nr of Repeats=5 RepeatLength=12
seed=CTTAGGCTTA

CTTAGGCTTAGG
CTTAGGCTTAAACTAGT
CTTAGACTTAGG
CTTAGGCTTAGG
CTTAAGCTTAAACGTAGG

Nr of selected repeats 3 Similarity 0.925926

Consensus:

CTTAGgCTTAGG

>Cele-UNSB01_5:15913508-15913600 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=CGAAAAGGGG

CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGATA
CGAAAAGGGGAGATA
CGAAAAGGGGAGCAA

Nr of selected repeats 5 Similarity 0.768889

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_5:15966117-15966182 Satlength=66 Nr of Repeats=4 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGG
GTACTGTAGAGACTGTAAAAACTGTAGTA
GTACTGTAGGG
GTACTGTAGGC

Nr of selected repeats 3 Similarity 0.919192

Consensus:

GTACTGTAGGg

>Cele-UNSB01_5:16082522-16083430 Satlength=909 Nr of Repeats=7 RepeatLength=37
seed=GCGGGAATTC

GCGGGAATTCAAATTTTAATTATTTGAAATCATTTTG
GCGGGAATTCAAATTTTAATTATTTGAAATCATTTTG
GCGGGAATTCAAATTTTAATTATTTGAAATCATTTTG
GCGGGAATTCAAATTTTAATTTTTCTAAAACATTTTG
GCGGGAATTCAAATTTTAATTTTTTTAGGAATAATATTACTTGAGTTTTCGAAAAAATCTGTTTTTTAGAATTGATTC
TGTGACAACACACACTTATAAATAATTACGAGCATTATAATTTTGAGTCCTCTATTCACTGAACTACACGTTTTTAAAA
AGAGAGGATAGATATGTCCAAAATTGAATTTTTCTGCAAATATTACTTGAGTTTTCGAAAGAAATCTGTTTTTTAGAA
TTGATTCTGTGACAACACACTTATAAATAATTACGAGCATTATAATTTTGAGTCCTATCCACTGAACTACACGTTT
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GCGGGAATTCAAATTTAAATTTTCCGAAACATTTTGACGGGAAATTCGAGAAAATTCGGAATGTTCCAGAACCTTCT
TGAAAATTTGGGAAAGTTCTGGAATCTTCTTGAATCATCGAAAAATTGGGGAAAAATTCGGATTGTTCTAGAACCTTC

TCGAAAATTCGAGAAAATTTTGGATTGTTCCAAAATCTTTTGAAAATTCGAGAAAATCTGAATGTTTCGTGGCGAGAC
CTATCGTGGTTAGACCCATCATGGTGAGACCCTTAAAACCTTCGGTGGGAAAATTGCTGGAATAAATATTTTGCCGCGA
AGTTCGAATTTTAATTTTTTTGAAATAATTTTG

GCGAGAATTCAAAATTTAATTTATTGAAATCACTTTG
Nr of selected repeats 5 Similarity 0.877477

Consensus:

GCGgGAATTCAAAAtTTTAATtAtTtgAAAAtCAtTTTG

>Cele-UNSB01_5:16332671-16332882 Satlength=212 Nr of Repeats=6 RepeatLength=42
seed=TTTCGGCAAC

TTTCGGCAACTGGCAATTGCCGACGTTGCCGAACCTTAAAAA
TTTCGGCAACCCGGCAATTGCCGATGTTGCCGAACCCGAAAAA
TTTCGGCAACCCGGCAATTGTCGAAGTTGCCGAACCCAAAAA
TTTCGGCAACCCGGCAATTGCCGATGTTGCCGAACCCGAAAAA
TTTCGGCACCCGGCAACTTTTTGTTGCCGAAAA
TTTCGGCAACT

Nr of selected repeats 4 Similarity 0.899471

Consensus:

TTTCGGCAACcGGCAATTGcCGAtGTTGCCGAACCCgAAAAA

>Cele-UNSB01_5:16414638-16414819 Satlength=182 Nr of Repeats=5 RepeatLength=36
seed=GGGAATTCAA

GGGAATTCAAATTTTAATTTTTGAAAACATTTTGGC
GGGAATTCAAATTTCAATTTTTGAAAACATTTTGGC
GGGAATTCAAATTTTAATTTTTGAAAAAATTTTGGC
GGGAATTCAAATTTTAATTTTTGAAAACATTTTGGC
GGGAATTCAAATTGGAATTTTTTTGAAAACATTTTGGC

Nr of selected repeats 4 Similarity 0.962963

Consensus:

GGGAATTCAAATTTtAATTTTTGAAAAcATTTTGGC

>Cele-UNSB01_5:16414904-16415369 Satlength=466 Nr of Repeats=31 RepeatLength=15
seed=TGGTGAGACC

TGGTGAGACCCGTCG
TGGTGAGACCTTTTCG
TGGTGAGACCCATCG
TGGTGAGGCCTTTTCG
TGGTGAGACCCGTCG
TGGTGAGACCTTTTCG
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TGGTGAGACCCATCG
TGGTGAGACCTTTTCG
TGGCGAGACCCATTG
TGGTGAGACCTTTTCG
TGGTGAGACCCATCG
TGGTGAGACCTTTTCG
TGGTGAGACCCATCG
TGGTGAGACCCATCG

TGGTGAGACCTTTTCG
TGGTGAGACCCGTCG
TGGTGAGACCTTTTCG
TGGTGAGACCAATCG
TGGTGAGACCCATCG
TGGTGAGACCCTTCG
TGGTGAGACCTTTTCG

Nr of selected repeats 31 Similarity 0.865806

Consensus:

TGGTGAGACCnTCG

>Cele-UNSB01_5:16471613-16475389 Satlength=3777 Nr of Repeats=23

RepeatLength=164 seed=CGTACAAGCT

CGTACAAGCTATTATACTTTGATTGGCATATTTTGGTGTTTTTGACTATGCTGAACATTTTTATGAAATAAAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTATCAATTTTTAAAAAAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAAATAAAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTATCAATTTTTAAAAAAA
TACTTC

CGTACAAGCTATTATACTTTGATTAGCATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAAATAAAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTATCAATTTTTAAAAAAA
TACTTC

CGTACAAGCTATTATACTTTGATTGACATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAAATAAAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTATCAATTTTTTAAAGAA
TACTTA

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAATTA AAAAAGGAAT
GACTCCATATGATTTTCTAGA ACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTTAACAATTTTTAAAAAAT
ACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTTGGTGTTTTTGACAATGCTGAACATTTTTATGAATTA AAAAAGAAT
GACTCCATATGATTTTCTAGA ACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTTATCAATTTTTAAAAAAA
AAACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAAATAAAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTATCAATTTTTAAAAAAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAAATAAAAAAGAAT
GACTCCATATGATTTTCTAGA ACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTAACAATTTTTTAAAGAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAATTA AAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTAACAATTTTTTAAAGAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTTGGTGTTTTTGACTATGCTGAACATTTTTATGAATTA AAAAAGAAT
GACTCCATTTGATTTTCTAGA ACTTTTGAATTTTTGAAAAAATCAGCTTTTATATTTTTTTATCAATTTTTTAAAGAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAATTA AAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTCATCAATTTTTAAAAAAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTTGACTATGCTGAATATTTTTATGAAATAAAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTATCAATTTTTAAAAAAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTTGGTGTTTTTGACTATGCTGAACATTTTTATGAAATAAAAAAGAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTTATCAATTTTTTAAAGAA
TACTTA

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTTGACTATGCTGAACATTTTTATGAATTA AAAAAGGAAT
GACTCCATATGATTTTCTAGA ACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTTAACAATTTTTAAAAAAT
ACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTTGGTGTTTTGACTATGCTGAACATTTTTATGAATTAATAAGAAAT
GACTCCATATGATTTTCTAGAACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTTATCAATTTAAAAA
AAAACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTGACTATGCTGAACATTTTTATGAAATAATAAGAAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTATCAATTTTAAAAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTGACTATGCTGAACATTTTTATGAAATAATAAGAAAT
GACTCCATATGATTTTCTAGAACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTAACAATTTTTTAAAGAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTGACTATGCTGAACATTTTTATGAATTAATAAGAAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGATTTTATATATTTTTAACAATTTTTTAAAGAA
TACTTC

CGTACAAGCTATTATACTTTGATTAGCATATTTCTGGTGTTTTGACTATGCTGAACATTTTTATGAAATAATAAGAAAT
GACTCCATATGATTTTCTAGGGCTTTTGAATTTTTGAAAAAATCTGATTTTATATATTTTTATCAATTTTTAAAAA
TACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTTGGTGTTTTAGACTATGCTGAACATTTTTATGAAATAATAAGAAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTTATCAATTTTTTAAAGAA
TACTTA

CGTACAAGCTATTATACTTTGATTGGCATATTTCTGGTGTTTTGACTATGCTGAACATTTTTATGAATTAATAAGAAAT
GACTCCATATGATTTTCTAGAACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTTAACAATTTTTAAAAAAT
ACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTTGGTGTTTTGACTATGCTGAACATTTTTATGAATTAATAAGAAAT
GACTCCATATGATTTTCTAGAACTTTTGAATTTTTGAAAAAATCAGCTTTTATATATTTTTATCAATTTAAAAA
AAACTTC

CGTACAAGCTATTATACTTTGATTGGCATATTTTGGTGTTTTAGACTATGCTGAACATTTTTATGAAATAATAAGAAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGCTTTTACATATTTTTATCAATTTTTTAAAGAA
TACTTC

Nr of selected repeats 17 Similarity 0.961741

Consensus :

CGTACAAGCTATTATACTTTGATTGGCATATTTcGGTGTTTTGACTATGCTGAACATTTTTATGAAaTAAAAAGAAAT
GACTCCATATGATTTTCTAGGACTTTTGAATTTTTGAAAAAATCAGaTTTTATATATTTTTAtCAATTTTTtAAAGAA
TACTTC

>Cele-UNSB01_5:16591935-16597985 Satlength=6051 Nr of Repeats=50

RepeatLength=121 seed=GTTGCAAACC

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGACAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGCTCGTAG

ACTATAATTTCTCTGAAAAGATAGTTGCCCTAATAGCAGAAG

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGACAAGCCACCCAAGTACTCGTTGCCCTACCTATCATATAATCGTAG

ACTATAATTTCTCTAAAAAGATAGTTGCCCTAATAGCAAAAG

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGACAAGCCACCCAAGTACTCGTTGCCCTACCTATCATATAATCGTAG

ACTATAATTTCTCTAAAAAGATAGTTGCCCTAATAGCAGAAG

GTTGCAAACCGCGAGAGCAAACCTTGCCAAATGACAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGCTCGTAG

ACTATAATTTCTCTGAAAAGATAGTTGCCCTAATAGCAGAAG

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGACAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGCTCGTAG

ACTATAATTTCTCTGAAAAGATAGTTGCTCTATGAGCAAAG

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGAAAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGCTCGTAG

ACTATAATTTCTCTGAAAAGATAGTTGCTCTATGAGCAAAG

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGAAAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAAATCGTAG

ACTATAATTTCTCTGAAAAGATAGTTGCCCTAATAGCAGAAA

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGAAAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGCTCGTAG

ACTATAATTTCTCTGAAAAGATAGTTGCCCTAATAGCAGAAA

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGAAAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGCTCGTAG

ACTATAATTTCTCTGAAAAGATAGTTGCCCTAATAGCAGAAA

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ACTATAATTTCTCTGAAAAGATAGTTGCTCTATGAGCAAAG

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ACTATAATTTCTCTGAAAAGATAGTTGCTCTATGAGCAAAG
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GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGACAAGCCACCCAAGTACTCGTTGCACCTACCTATCATATAATCGTAG
ACTATAATTTCTCTAAAAAGATAGTTGCCCTAATAGCAAAG
GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGACAAGCCACCCAAGTACTCGTTGCACCTACCTATCATATAATCGTAG
ACTATAATTTCTCTAAAAAGATAGTTGCCCTAATAGCAAAG

Nr of selected repeats 50 Similarity 0.958478

Consensus:

GTTGCAAACCGCAAGAGCAAACCTTGCCAAATGAAaAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGCTCGTAG
ACTATAATTTCTCTGAAAAGATAGTTGCcCTAatAGCAgAAG

>Cele-UNSB01_5:16677048-16677311 Satlength=264 Nr of Repeats=16 RepeatLength=12
seed=CATTGACTTG

CATTGACTTGGG

CATTGACTTGAG

CATTGACTTGAG

CATTGACTTGAG

CAGTGACTTGAG

CATTGAATTGAACCATTGGGCTGAACCATTGGATTGATCCATTGGGCTGATC

CATTGACTTGGG

CATTGACTTGAG

CATTGACTTGAG

CATTGACTTGAG

CAGTGACTTGAG

CATTGAATTGAACCATTGGGCTGAACCATTGGATTGAG

CATTGACTTGAG

CATTGACTTGGA

CATTGACTTGAG

CATTGACTGACTTGAAC

Nr of selected repeats 13 Similarity 0.842209

Consensus:

CATTGACTTGaG

>Cele-UNSB01_5:16682435-16683237 Satlength=803 Nr of Repeats=14 RepeatLength=22
seed=GGGTACTGTA

GGGTACTGTAGTACTGTAT

GGGTACTGTAGGAATACTGTGG
GGGTACTGTAGTAGTACTGTAT
GGGTACTGTAGGAATACTGTGG
GGGTACTGTAGTAGTACTGTAT
GGGTACTGTAGAAGTACGGTGGGATTACTGTAGTTTGGGAAAAATTGACTTTTCATCTTTTGAAGGGATATTGGTTTGG
GGTTAGTAGGGGGTATTGTCTG
GGGTACTGTAGTAGTACTGCAT
GGGTACTGTAGGAATACTGAGG
GGGTACTGTAGTAGTACTGTAT
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GGGTACTGTAGTACTGTAG
GGGTACTGTAGGATGTAG
GAGTACTGTAGGATATAAGTTTTTTGCGGTAAGTCAAATTTTCTGATAAAAAATTTTGGCGGGAATTTAGAATTTTCTGA
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ACGTCAGTCGGAGCACGCGTTTTGCGGCTGGTTCAAGATACATTGGAAAGATATTTCTTCTCGTGGCGAGACCTATTAA
AATGTCTGTGCACCTTTAAGAAATCTTGG

Nr of selected repeats 9 Similarity 0.840067

Consensus:

GGGTACTGTAGtAgTACTGtat

>Cele-UNSB01_5:16693408-16693990 Satlength=583 Nr of Repeats=10 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGATTTCTTTTTAATCTTTTTTTGGCATTAAAAAACTTGAAAAAATATTTAAATTTCTAAAGAAAATTGC
CTTTTTTTCAATTTTTTCGATATCTAAAACTAAAAATCGAAAACTTCGGTTTTTCGAAAAATATCCCAATTTTTGGT
CATTTTTCTAGAAAAATGTAATACTATTATATATAAAAAAATACATGAGGGATGTTACAATTTGTAGTTTGTAGTCT
GTGACGTACACTTGCAAGGTGTTTCCGGCTGTTGAAGGGATTGTGGGTTGGGGTTAGTGGTGGGATATGGTCCGGATA
CTGTAGTA

GTACTGTAGGG

GTACTGTAGGGT

TACTGTAGGATTACTGTAGTTTTGGAAAAATTGACTTTTTGTCTTTTGAAGTGATATTGGTTTTGAGGTTAGTGGTGGGA
TATGATCGGG

GTACTGTAGTA

GTACTGTAGTA

GTACTGTAGGA

GTACTGTAGGATTACTGTATTTTTGAAAAAAATGGCTTTTCGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGTCTGG
GATATGGTTGGG

GTACTGTAGAG

GTACTGTAGGA

Nr of selected repeats 6 Similarity 0.846465

Consensus:

GTACTGTAGga

>Cele-UNSB01_5:16694107-16694865 Satlength=759 Nr of Repeats=17 RepeatLength=40
seed=CTGGAATGTT

CTGGAATGTTCCAAAACCTTCTGGAAAAATTTGAGAAAATG

CTGGAATGTTCCAGAACCTTCTGGAAAAATTTGAGAAAATTCGGAATGCTCCAGAACCTTCTAGAAAATCCGAGAAAAT
T

CTGGAATGTTCCAAAACCTTCTGGAAAAATTTGAGAAAATG

CTGGAATGTTCCAGAACCTTCTGGAAAAATTTGAGAAAAT

CTGGAATGTTCCAAAACCTTCTGGAAAAATTTGAGAAAATG

CTGGAATGTTCCAGAACCTTCTGGAAAAATTTGAGAAAAT

CTGGAATGTTCCAGAACCTTCTGGAAAAATTTGAGAAAAT

CTGGAATGTTCCAGAACCTTCTGGAAAAATTTGAGAAAAT

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT
CTGGAATGTTCCAGAACCTTCTGGAAAATCCGAGAAAATG
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATCCGGAATGCTCCAGAACCTTCTAGAAAATCCGAGAAAAT
T

CTGGAATGTTCCAAAACCTTCTGGAAAATTTGAGAAAATG
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT
CTGGAATGTTCCAAAACCTTCTGGAAAATTTGAGAAAATG
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATG
CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT
Nr of selected repeats 13 Similarity 0.950427

Consensus:

CTGGAATGTTCCAgAACCTTCTGGAAAATTTGAGAAAATg

>Cele-UNSB01_5:16694107-16695183 Satlength=1077 Nr of Repeats=18

RepeatLength=40 seed=CTGGAATGTT

CTGGAATGTTCCAAAACCTTCTGGAAAATTTGAGAAAATG

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATCCGGAATGCTCCAGAACCTTCTAGAAAATCCGAGAAAAT

T

CTGGAATGTTCCAAAACCTTCTGGAAAATTTGAGAAAATG

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT

CTGGAATGTTCCAAAACCTTCTGGAAAATTTGAGAAAATG

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT

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CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT

CTGGAATGTTCCAAAACCTTCTGGAAAATTTGAGAAAATG

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATG

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAAT

CTGGAATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATCCGGAATGCTCCAGAACCTTCTAGAAAATCCGAGAAAAT

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TGGCGGAAATTCAAATTTTCTGTGAAAATTTTGTAGCGGAAATTCAAATTTTCTGTGAAAATTTTGGCGGAAATTCAA

TTTTCTGTGAAAATTTGTGGCGGAAATTCAAATTTTCTGTGAAAATTTTGGCGGAAATTCAAATTTTCTGAAAAAAA

TT

Nr of selected repeats 13 Similarity 0.950427

Consensus:

CTGGAATGTTCCAgAACCTTCTGGAAAATTTGAGAAAATg

>Cele-UNSB01_5:16699381-16699441 Satlength=61 Nr of Repeats=4 RepeatLength=15

seed=CGAAAAGGGG

CGAAAAGGGGATCTG

CAAAAAGGGGATCTG

CGAAAAGGGGAGATA

CGAAAAGGGGAGCAA

Nr of selected repeats 4 Similarity 0.748148

Consensus:

CgAAAAGGGGAgcta

>Cele-UNSB01_5:16699651-16699786 Satlength=136 Nr of Repeats=7 RepeatLength=15

seed=GCAGATCCCC

GCAGATCCCCTTTTTC

GCAGATCCCCTTTTT
GCAGATCCCCGTTTCGTTGCTCCCCTTTTCGTATCTCCCCTTCTC
GCAGATCCCCTTTTT
GCAGATCCCCTTTTT
GCAGATCCCCTTTTT
GCAGATCCCCTTTTT

Nr of selected repeats 6 Similarity 0.946667

Consensus:

GCAGATCCCCTTTTTc

>Cele-UNSB01_5:16730521-16730649 Satlength=129 Nr of Repeats=4 RepeatLength=32
seed=GCTGATTGGT

GCTGATTGGTGAGATACTGAGCATTCTGAAA
GCTGATTGGTAAGATAAAACTGGTGGTGAAC
GCTGATTGGTGAGCGACTGGGCGTGGCTGAAT
GCTCATTGGTAAGCAAGTGGGTGTGACTAAAC

Nr of selected repeats 4 Similarity 0.508488

Consensus:

GCTgATTGGTaAGaaAcTGgGcgTggcTgAAa

>Cele-UNSB01_5:16772051-16772198 Satlength=148 Nr of Repeats=7 RepeatLength=21
seed=ATTTTTCAAT

ATTTTTCAATCTTCGTCTAAA
ATTTTTCAATTTTCGTCTAAC
ATTTTTCAATTTTCGTCTAAA
ATTTTTCAATTTTCGCCTAAC
ATTTTCCAATTTTCGTCTAAT
ATTTTTCAACTTTCCTCTAAC
ATTTTTCAATTTTCGTCTAAC

Nr of selected repeats 7 Similarity 0.848828

Consensus:

ATTTTTCAATTTTCGTCTAAc

>Cele-UNSB01_5:16819160-16819347 Satlength=188 Nr of Repeats=11 RepeatLength=17
seed=TAACCTGACT

TAACCTGACTGCAACAG
TAACCTGACTGCTATAT
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG
TAACCTGACTGCTACAG

Nr of selected repeats 11 Similarity 0.957219

Consensus:

TAACCTGACTGCTACAG

>Cele-UNSB01_5:16845717-16846129 Satlength=413 Nr of Repeats=25 RepeatLength=16
seed=ACATACCTAC

ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT

ACAAACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACAAACCT
ACATACCTACATACCT
ACATACTTACATACCAACGAACCT
ACATACCTACATACCA
ACATACCTACATACCT
ACATATCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACATACT
ACATACCTACATACCT
ACATACCTACATACCT
ACATACCTACATACCT

ACAAACCTACATACCTACATACCT
Nr of selected repeats 22 Similarity 0.969697

Consensus:

ACATACCTACATACCT

>Cele-UNSB01_5:17041242-17041488 Satlength=247 Nr of Repeats=7 RepeatLength=11
seed=CTACAGTACC

CTACAGTACCCCGACCATATCCCCTACTAACCCCAAATCTATATCTCTTCAAAGACAAAAACACAATTTTTCTTAA
TTACAGTAGTCCTACCGTACTC

CTACAGTACCT

CTACAGTACTA

CTACAGTACCCCGACCATATCCTATCACTAACCTCAAACCAATATCCCTTCAAAGGCGAAAAGTCAATTTTTCCCAA

CTACAGTAATC

CTACAGTACTC

CTACAGTACCT

CTACAGTACTA

Nr of selected repeats 5 Similarity 0.786111

Consensus:

CTACAGTACTn

>Cele-UNSB01_5:17104481-17104658 Satlength=178 Nr of Repeats=5 RepeatLength=21
seed=CTAATTAGCG

CTAATTAGCGCTAAAGCGATGCTAATGTTAAAAATAGATGTTATAAGTTGCCCCACCTAGCTATGCTTTTTT

CTAAGTAGCGTCGCTTCCTTT

CTAATTAGCGTCGCTTTCGTTCTAGTTAGCAGCGCCCCTCCG

CTAATTAGCAGCGCAACGATT

CTAATTAGCGTCGCTTTCGTT

Nr of selected repeats 3 Similarity 0.640212

Consensus:

CTAAtTAGCgtCGcttccnTT

>Cele-UNSB01_5:17108364-17108469 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=TGCTAATTAG

TGCTAATTAGCGCTGGTGCTG

TGCTAATTAGCGGGCTGCGT

TGCTAATTAGTGGAGGGGCGAC

GCTAATTAGAACGAAAGCGAC

GCTAATTAGAATCGTTGCGC

Nr of selected repeats 3 Similarity 0.545455

Consensus :

tGCTAATTAGcgCggntGCgtn

>Cele-UNSB01_5:17207041-17207511 Satlength=471 Nr of Repeats=12 RepeatLength=40
seed=AAAATTCTGG

AAAATTCTGGAATGTTCTAGAGCCTTTTGGAAAATTTGAA
AATATTCTGGGATGTTCTAGAACCCTTCTGGAAAAATTGAG
AAAATTCTGGAATGTTCTAGAGCCTTTTGGAAAATTCGAG
AAAATTCTGGAATGTTCTAGAGCCTTTTGGAAAATTTGAA
AAAATTCTGGGATGTTCTAGAACCCTTCTGGAAAAATTGAG
AAAATTCTGGAATGTTCTAGAGCCTTTTGGAAAATTTGAG
AAAATTCTGGAATGTTCTAGAGCCTTTTGGAAAATTTGAG
AAAATTCTGGAATGTTCTAGAGCCTTTTGGAAAATTTGAG
AAAATTCTGGAATGTTCTAGAGCCTTTTGGAAAATTTGAA
AAAATTCTGGGATGTTCTAGAACCCTTCTGGAAAAATTGAG
AAAATTCTGGAATGTTCTAGAGCCTTTTGGAAAATTTGAG

Nr of selected repeats 11 Similarity 0.899394
Consensus :

AAAATTCTGGaATGTTCTAGAgCCTTtTGGAAAAtTTGAg

>Cele-UNSB01_5:17249920-17250872 Satlength=953 Nr of Repeats=8 RepeatLength=119
seed=AACTGTGGGC

AACTGTGGGCTGGCTTTAATCCTAACCCAAGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCAATCAAGCCTA
ACAACCAGGTTTGAGGGCCGAGGCCCGAAAACCTCTTGGA
AACTGTGGGCTGGCTTTAATCCTAACCCAAGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCAATCAAGCCTA
ACAACCAGGTTTGAGGGCCGAGGCCCGAAAACCTCTTGGA
AACTGTGGGCTGGCCTTAATCCTAACCCAAGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCAATCAAGCCTA
ACAACCAGGTTTGAGGGCCGAGGCCCGAAAACCTCTTGGA
AACTGTGGGCTGGCCTTAATCCTAACCCACGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCAATCAAGCCTA
ACAACCAGGTTTGAGGGCCGAGGCCCGAAAACCTCTTGGA
AACTGTGGGCTGGCCTTAATCCTAACCCACGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCACTTAAGCCTA
AAAATTAGGTTTGAGGGCCGAGGCCCGAAAACCTCTGGT
AACTGTGGGCTGGCCTTAATCCTAACCCACGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCACTTAAGCCTA
ACAACCAGGTTTGAGGGCCGAGGCCCGAAAACCTCTTGGA
AACTGTGGGCTGGCCTTAATCCTAACCCACGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCACTTAAGCCTA
ACAACCAGGTTTGAGGGCCGAGGCCCGAAAACCTCTTGGA
AACTGTGGGCTGGCCTTAATCCTAACCCACGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCACTTAAGCCTA
AAAATTAGGTTTGAGGGCCGAGGCCCGAAAACCTCTTGGA

Nr of selected repeats 8 Similarity 0.947979

Consensus :

AACTGTGGGCTGGCcTTAATCCTAACCCAcGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCAaTcAAGCCTA
AcAAccAGGTTTGAGGGCCGAGGCCCGAAAACCTCTTGGA

>Cele-UNSB01_5:17487338-17487635 Satlength=298 Nr of Repeats=8 RepeatLength=37
seed=AAAACATTTT

AAAACATTTTGGCGGAATTCAAAATTTAATTTTTTG
AAAACATTTTGGCGGAATTCAAAATTTAATTTTTTG
AAAACATTTTGGCGGAATTCAATATTTAATTTTTTG
AAAACATTTTGGCGGAATTCAAAATTTAATTTTTTG
AAAACATTTTGGCGGAAATTCAAATTTTAATTTTTTC
AAAACATTTTGGCGGAAATTCAAATTTTAATTTTTTG
AAAACATTTTGGCGGAAATTCAAATTTTAATTATTCA
AAAATTTTGGCGGAAATTCAAATTTTAATTTTTTC

Nr of selected repeats 5 Similarity 0.894737

Consensus :

AAAACATTTTGGCGGgAATTCAAaTTTAATTTTTtg

>Cele-UNSB01_5:17569173-17569281 Satlength=109 Nr of Repeats=9 RepeatLength=12
seed=CGCAACGCGA

CGCAACGCGATA
CGCAACGCGATA
CGCAACGCGATA
CGCAACGCGATA
CGCAACGCGATA
CGCAACGCGATA
CGCAACGCGATA
CGCAATGCGACG
CGCAACGCGACA

Nr of selected repeats 9 Similarity 0.907407

Consensus:

CGCAACGCGAtA

>Cele-UNSB01_5:17588702-17608641 Satlength=19940 Nr of Repeats=337
RepeatLength=59 seed=TTATGGTGAA

TTATGGTGAATATGGAAATTC AAGACTTCACTGGTTTTCAAATTTTTTAAAACCGAAAA
TTATGGTGAATATGGAAATTC AATGTGCACTGGTTTTCAAATTTTTTAAAACCGAGAA
TTATGGTGAATATGGAAATTC AAGACTTCACTGGTTTTCAAATTTTTTAAAACCGAAAA
TTATGGTGAATATGGAAATTC AATGTGCACTGGTTTTCAAATTTTTTAAAACCGAGAA
TTATGGTGAATATGGAAATTC AAGACTTCACTGGTTTTCAAATTTTTTAAAACCGAGAA
TTATGGTGAATATGGAAATTC AATGTGCACTGGTTTTCAAATTTTTTAAAACCGAGAA
TTATGGTGAATATGGAAATTC AAGACTTCACTGGTTTTCAAATTTTTTAAAACCGAGAA
TTATGGTGAATATGGAAATTC AATGTGCACTGGTTTTCAAATTTTTTAAAACCGAGAA
TTATGGTGAATATGGAAATTC AAGACTTCACTGGTTTTCAAATTTTTTAAAACCGAGAA
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TTATGGTGAATATGGAAATTC AAGACTTCACTGGTTTTCAAATTTTTTAAAACCGAGAA
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TTATGGTGAATATGGAAATTC AAGACTTCACTGGTTTTCAAATTTTTTAAAACCGAGAA
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TTATGGTGAATATGGAAATTC AATGTGCACTGGTTTTCAAATTTTTTAAAACCGAGAA
TTATGGTGAATATGGAAATTC AAGACTTCACTGGTTTTCAAATTTTTTAAAACCGAGAA
TTATGGTGAATATGGAAATTC AATGTGCACTGGTTTTCAAATTTTTTAAAACCGAGAA

TTATGGTGAATATGGAAATTCAAATGTGCACTGGTTTTCAAATTTTTTAAAAACAGAGAA
TTATGGTGAATATGGAAATTCAAATGTGCACTGGTTTTCAAATTTTTTAAAAACAGAGAA
TTATGGTGAATATGGAAATTCAAATGTGCACTGGTTTTCAAATTTTTTAAAAACAGAGAA
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TTATGGTGAATATGGAAATTCAAATGTGCACTGGTTTTCAAATTTTTTAAACCCAGAA
TTATGGTGAATATGGAAATTCAAATGTGCACTGGTTCTCAAATTTTTTCAAATGTACACTGGTTTTCAAATTTTTTAA
ACCCAGAA

TTATGGTGAATATGGAAATTCAAATGTGCACTGGTTTTCAAATTTTTTAAACCCAGAA
TTATGGTGAATATGGAAATTCAAATGTGCACTGGTTTTCAAATTTTTTAAACCCAGAA
Nr of selected repeats 283 Similarity 0.948621
Consensus :

TTATGGTGAATATGGAAATTCAAaTGTGCACTGGTTTTCAAATTTTTtAAACcGAGAA
>Cele-UNSB01_5:17626210-17626494 Satlength=285 Nr of Repeats=15 RepeatLength=19
seed=TTTTCGTGTA

TTTTCGTGTAACAATCTAT
TTTTCGTGTAACCATCTAT
TTTTCGTGTAACAATCTAT
TTTTCGTGTAACAATCAAT
TTTTCGTGTAACAATCTAT
TTTTCGTGTAACAATCTAT
TTTTCGTGTAACCATCTAT
TTTTCGTGTAACAATCAAT
TTTTCGTGTAACCATCTAT
TTTTCGTGTAACAATCTA
TTTTCGTGTAACCATCTAT
TTTTCGTGTAACAATCAAT
TTTTCGTGTAACAATCTAT
TTTTCGTGTAACCATCTAT
TTTTCGTGTAACAATCAAT

Nr of selected repeats 14 Similarity 0.934452
Consensus :

TTTTCGTGTAACaATCtAT

>Cele-UNSB01_5:17709602-17709736 Satlength=135 Nr of Repeats=5 RepeatLength=11
seed=CCTACAGTAC

CCTACAGTACT

CCTACAGTACC

CCTACAGTACTA

CTACAGTACCCCGCCATATCCCGCCACTATCCCCAAAGCAATACCATTTCAAAAGACGGAAAGTCAATTTTTCCGAAA

CTACAGTAAT

CCTACAGTACT

Nr of selected repeats 3 Similarity 0.919192

Consensus:

CCTACAGTACT

>Cele-UNSB01_5:17737089-17738916 Satlength=1828 Nr of Repeats=7

RepeatLength=255 seed=AACAAGTCGG

AACAAGTCGGGAACGTTTCGGAAAAGCTCTGAGGAAAACCTCCGACAGTATTATGCTTAAGTACGCAATTGAGCTATCTTTA

TTAGATTCGAAAAGAGGACGCTTCAAAAATTGAAGCAATAACGAAGAAGCTTAAGTTGGAACTGGCGAAGCTTAAATTGA

GAATTACGCAGTCTTTATCAGATTCAAAAGACGACTCTTTGTCCAATGAAGCAAATCTGCAGAACGATCTACCTTCGAC

TTCTGATAGCAAACTCC

AACAAGTCGGGAACGTTTCGGAAAAGCTCTGAGTCAAACATTAGCAACATCTTGCGTGAATTGGAAAATGAGCAGTCTTTA

TTAGATTCGAAAAACGACTCTTCAAACCCCTGAATACATGATGAAGATGCTTAAGTTGGATCTGGCGAAGCTTAAATTGG

TATTTTTTCAAGCTGTATTAGATGCGAAAAGGCAATTCGCGACCGATGAAACACGTCCGGGAGACGTTCCATCCTTGAA

TTCCGAAGGCAGAACACC

AACAAGTCGGGAACGTTTCGGAAAAGCTCTGAGTCAAACATCGAAAACATCCTTTTGAAGTTGGCAATGAAGGAGTCTTTA

TTAGAATCAAAGACGATTCCTCAACCAATGGAGCAAGTCTGCAGAAAGATCTACCTTCGACTTCTGATGACAGAACTC

C

AACAAGTCGGAAAACCTTTCGGAAAACCTTGAAGAAAACCTCCGACAATATCATGCTTAAGTACGCAATTGAGCTATCTTTA

CTAGATTCAAAAAAGGACTCTACAAAAATTGAAGCAATACCGGAGAAGCTTAAGTTGAACTGGCAAAGCTTAAATTGG

GACTTATGAAGTCTTTATCAAATTCAAAAGACGATCCTTCAACCAATGGAGCAAGTCTGCAGAATGATCTACCTTCGAC

TTCTGATGACAGAACTCC

AACAAGTCGGGAACGTTTCGGAAAAGCTCTGAGTCAAACATTAGCAACATCATGCGTAAAATTGGAAATCGAGCAGTCTTTA

TTAGATTCGAAAAACGACTCTTCAAACCCCTGAATCAATGATGAAAATGCTTAAGTTGGATCTGGCGAAGCTTAAATTGG

TATTTTTTCAAGGTGTATTAGATGCGAAAAGGCAATTCGCGACCGATGAAACACGTCCAGGAGACGTTCTATCCTTGAA

TTCCGAAGGCAGAAATCC

AACAAGTCGGGAACGTTTCGGAAAATCTCTGAGTCAAACATCGAAAACAAGATGATAAAGTTGGCAATGAAGGAGTCTTTA

TTGGGTTTCGGAAAGACGGTCTTCAACCGATGGAGCAATGGCAAAGATGCTTAAGATGGCACTTGTGCAGTCTTTATTGG

GTTCCGATGATTATTCTTCAATCCGATGAAGCAAGCAAGCAAGACGATCCACCTTCAAACCTCTGATAACAAGACTCCGAC

AAGTGGGAAACGTTTGGAAAGCTATGAGTCACGCATCGAAAACATCCTTTTGAAGTTGGCAATGAAGGAGTCTTTATTA

GAATCAAAGACGATTCTTCAACCAATGGAGCAAGTCTGCAGAAAGATCTACCTTCGACTTCTGATGACAGAACTCC

AACAAGTCGGAAAACCTTTCGGAAAACCTTGAAGAAAACCTCCGACAATATCATGCTTAAGTACGCAATTGAGCTATCTTTA

TTAGATTCGAAAAAAGGACTCTTCAAAAATTGAAGCAATAACGAAGAAGCTTACGTTGGAACTGGCGAAGCTTAAATTGG

GAATCAGCAGTCTTTATCAGATTCAAAAGAAGATCCTTCAACCAATGAAGCAAGCCCGGAAGACGATCTACCTTCGAC

TTCTGATAACAGAACTCC

Nr of selected repeats 5 Similarity 0.720930

Consensus:

AACAAGTCGGgAACgTTCGGAAAAGCTcTGAggaAAACTccGaCAatATcaTGcTtaAgTacGcAAttGAGCtaTCTTTA

tTAGATTCgAAAaAgGACtCTtCAAAAatTGAAGcaATaacGaAgAaGCTTAAgTTgGAaCTGGCgAAGCTTAAATTGg

gAnTtatgcAgtcTtTATcAgATtCaAAAGacgAttCttcgaCCaATGaAgCAagtCcGgAgnAcGaTctACCTTcGAc

TTctGatggCAGAActCC

>Cele-UNSB01_5:17801402-17801541 Satlength=140 Nr of Repeats=10 RepeatLength=12

seed=ACGCGACACG

ACGCGACACGCA

ACGCGACACGCAACGCGGCACCCA

ACGCGGCACGCA

ACGCGACACGCA

ACGCGACACGCGACACGCA

ACGCGACACGCA

ACGCGACACGCA

ACGCGACACGCA

ACGCGACACGCA

ACGCGACACGCA

Nr of selected repeats 8 Similarity 0.972222

Consensus:

ACGCGACACGCA

>Cele-UNSB01_5:17834079-17834336 Satlength=258 Nr of Repeats=8 RepeatLength=11

seed=CCTACAGTAC

CCTACAGTACT

CCTACAGTACC

CCTACAGTACTATTACAGTCCCCGACTATATCCCACTACTAACCGCAAACCTATATCTCTTCAAAGACAAAACTCA

ACTTTTCCTAAATTACAGTAAT

CCTACAGTACT

CCTACAGTACC

CCTACAGTACCCCCACCATATCCCACTACTAACCGCAAACCTATATCACTTCAAAGACAAAACTCAATTTTTCCTAA

ATTACAGTAAT

CCTACAGTTCT

CCTACAGTACC

Nr of selected repeats 6 Similarity 0.886869

Consensus:

CCTACAGTACC

>Cele-UNSB01_5:17844176-17844688 Satlength=513 Nr of Repeats=32 RepeatLength=16

seed=CCAGGGTTCC

CCAGGGTTCCAGGGTT

CCAGGGTTCCAGGGTT
CCAGGGTTCCAGGGTT
CCAGGGTTCCAGGGTT
CCAGGGTTCCAGGGTT

Nr of selected repeats 32 Similarity 1.000000

Consensus:

CCAGGGTTCCAGGGTT

>Cele-UNSB01_5:17844176-17845043 Satlength=868 Nr of Repeats=35 RepeatLength=16

seed=CCAGGGTTCC

CCAGGGTTCCAGGGTT

CCAGGGTTCCAGGGCAGGGGTGCGCGGCAATCGAATTTTCGGCAATTTCCGGCAATTGCCGAAAATTCGATTGCTGGAAA

TCAGAATTGAAATGTAAAGTTGATACTTTTTGTACATTTATGAGCCTAAACAGGCATTTCAATGAACAATTTTCTCTTT

TCAAGCTCGAAATGTAAAATGTCCGGCAATCGCCAACTTCGGCAATTTCCGGCAATTGCCGAAAATTTTCATTTTCGGAA

ATTGCTGATTGCCGAAAATTCAAAACCGGCAATTGCCGAAAATTTCCGATTGCCGCGCAGCCCTGCT

CCAGGGTTCCAGGGTTCCGAGGTT

CCAGGGTTCCCGTGTT

Nr of selected repeats 33 Similarity 0.989899

Consensus:

CCAGGGTTCCAGGGTT

>Cele-UNSB01_5:17868232-17868328 Satlength=97 Nr of Repeats=6 RepeatLength=16

seed=GAATAATATT

GAATAATATTGGAGAA

GAATAATATTGGAGAT

GAATAATATTGGAGAA
GAATAATATTGGAGAA
GAATAATATTGGAGAA
GAATAATATTGGAGAA

Nr of selected repeats 6 Similarity 0.972222

Consensus:

GAATAATATTGGAGAA

>Cele-UNSB01_5:17962175-17963525 Satlength=1351 Nr of Repeats=6

RepeatLength=143 seed=CAGTGGGATT

CAGTGGGATTCTGAATTTATCCAATCAAACGTCGGGGTTCGAGTCCGCACAGGGTATTTATTTTTTGAAGCTGTG
ATTTACAAGTTTATAGCTGAAAAAGTGATTTTTATCGAATTTTTAGGAAAATGTCCGAATGGCA
CAGTGGGATTTTCCATGTCTATCAATCAGAGGTCCGGGGTTCGAGTCCACACAGGGTATTTATTTTTTGAAGCTTTA
GAAATTGAGGTTTCGAGTTGGGAAATTCATTTTTAGCGAATTTTCAGGAAAATGTCTAATGACG
CAGTGGGATTTTTAGTGTCTTTCAATCAGATGTCAGTGGTTCGAGTCCGCACAGGGTATTTATTTTTTGAAGCTGTG
ATTAACAAGTTTATAGCTGCAAAAGTCATTTTAATCGAACTTTTCGGGAAAAGTGTCCGATTGGCG
CAGTGGGATTTTCAACGTCTTCCAATCAAACGGCTGGGGTTCGAGTCCGCACAAGGGTATTTATTTTTTGAAGCTGTG
ATTAACAAATTTCAAGCTGCAAAAGTCATTTTAATCGAACTTTTCGGGAAAAGTGTCCGATTGGCG
CAGTGGGATTTTTAATGTCTTCCAATCAGAGGTCCGTGGTTCAAACCCGCACAGTGACAAATATTTTTGTTATGATGTT
TATGAGCCTCAATTGTAACATAATAACTTTATCCGAAAACAATATGAGTTTATGACTGATTATCAAATTTAACTTT
CTCCAATTTTCTTCATTTTTCTTTATTTTTTTTTCTCAATTTTTTCAATATTTATGACTGAATTCACAATTCCTCA
AAACCTTTTCTGGCATCGAAAATGAACATTTGCATGACAATCCGTGCACTGAACGCCCTGCTTCGTGAGCCCATAGAG
CATACTTCCACAGTGATCAGAAAATGTCGGGCGAGTGAAGAAATGCTTGTAAAAGTGATGAGTATTTGATGGAGGTTCT
TCCGAAGCAGATCGGCTACGACGAGTTTTAGATTTGTAGTTTCAGCAGGAACCGGAGCTCGGGAAGATGGTCCGAAGG
TGCAGCGGGCGGTGATGAGGGCATGGCACCCTTATGAACGACTGTCTCACAGCCTGGAATAATGAAATATGAACTAATA
TTCCTAGAAAATCAGGTTCCGTGCTTAAAATCTAGCTTTTGCCTAATTTTTGAGAAAATGCACCAATGGCT
CAGTGGGATTTTCCAGAATATCGCGCACAAGTCCGGGGTTCAGCCCGCCATGTGGTCAAATATTTTTGTACGCAGTG
TTTAGACATATAAAGACCAGCTTGTAATGAACAAACGATTTTACAGGTTTTAAGGAAAAGTGCCCGAATGGCG

Nr of selected repeats 4 Similarity 0.759132

Consensus:

CAGTGGGATTtTcaatgTcTtcCAATCAaAcGtCcGgGGTTCGAGTCCgCACAgGGGTATTTATTTTTTGAAGCTgTG
ATTaAcaagtTTatAGcTGcaAAAgtTcATTTTaAtCGAAcTTTcaGGAAAaTGTCCgAaTGgCg

>Cele-UNSB01_5:17995705-17996016 Satlength=312 Nr of Repeats=5 RepeatLength=20

seed=ATTTGACCTA

ATTTGACCTACTTTTTTAAA

ATTTGACCTACTTTTTAAAAATTTGGGTACTAGTCTGAAATCACCCCGCCACTTTTTTTTTATCATTTTAATATTATCCA
TTTTAATAAAACGTGATGTCCATTTCCATCTTTAGGCTTAGAAATGGTTATTTCTAAGCCTAAAAATACAAAACCTC
CACACGTTTTTATTTGAAAAATTTATTTAAATTTAAAGAAAAAAGTGGCGGGGTGATTTAGACTAGTACCCAA

ATTTGACCTACTTTTTTAAA

ATTTGACCTACTTTTTACAA

ATTTGACCTACTTTTTAAAT

Nr of selected repeats 4 Similarity 0.900000

Consensus:

ATTTGACCTACTTTTTTaaAa

>Cele-UNSB01_5:18032604-18033134 Satlength=531 Nr of Repeats=13 RepeatLength=34

seed=TCAAATTTTC

TCAAATTTTCCGAGAAAATTTTGGCGGGTAT

TCAGATTTTCTGAAAAAAACTTTATCGGGAAAT

TCAAATTTTCTGAAAAAAACATTTTGGCGGGAATTTCTAATTTTTTTTTAATCTGGCGAGAAATTTCTAATTTCTAAAAAA
AAATTTTTGACGGGTAT

TCAAATGTTCTGAAAAAAATTTGGCGGGAATTTCAAATTTTTGAAAAAATGTTTGGCGGAAAT

TCAAATTTTCTCAAAAAACGTTTGGCGGAACT

TCAAATTTTCTTTTTAAAAAACTTTGGCGGAAAC

TCAAATTTTCTTTTTAAAAAACTTTGGCGGAAAC

TCAAATTTTCTTTTTAAAAAACTTTGGCGGAAAC

TCAAATTTTCTTTTTAAAAAACTTTGGCGGAAAT
TCAAATTTTCTTTTTAAAAAACTTTGGCGGAAAT
TCAAATTTTCTTTTTAAAAAACTTTGGCGGAAAT
TCAAATTTTCTTTTTAAAAAACTTTGGCGGAAAT
TCAAATTTTCTCAAAAAACGTTTGGCGGGTAT

Nr of selected repeats 8 Similarity 0.860204

Consensus:

TCAAATTTTCTTTTTaAAAAAACTTTGGCGGAAAt

>Cele-UNSB01_5:18100660-18102309 Satlength=1650 Nr of Repeats=32

RepeatLength=44 seed=TTGCCGAAA

TTGCCGAAAATTTTCAATTCTGGCAAATGTTCGGTTTTGCCTAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATTTTCAATTCTGGCAAATGTTCGGTTTTGCCTAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATTTTCAATTCTGGCAAAGTGTTCGGTTTTCCGAAA

TTGCCGAAAATAGTAATTTTGGCAAATGTTCGGTTTTGCCTAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATTTTCAATTCTGGCAAAGTGTTCGGTTTTCCGAAA

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATTTTCAATTCTGGCAAAGTGTTCGGTTTTCCGAAA

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATTTTCAATTCTGGCAAAGTGTTCGGTTTTCCGAAA

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAC

TTGCCGAAAATTTTCAATTCTGGCAAATGTTCGGT

TTGCCGAAAATTTTCAATTCTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATTTTCAATTCTGGCAAATGTTCGATTTTCCGAAA

TTGCCGAAAATTTTCAATTCTGGCAAATGGCCGTTTTGCCTAAT

TTGCCGAAAATATTCAATTTTCGGCTAATGTTCGGTTTTGCCACAT

TTGCCGAAAATTTTCAATTCTGGCAAATGTTCGGT

TTGCCGAAAATTTTCAATTCTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATAGTAATTTTGGCAAATGGCCGTTTTGCTGAAT

TTGCCGAAAATTTTCAATTCTGGCAAATGTTCGATTTTCCGAAA

TTGCCGAAAATTTTCAATTCTGGCAAATGGCCGTTTTGCCTAAT

TTGCCGAAAATATTCAATTTTCGGCTAATGTTCGGTTTTGCCACAT

TTGCCGAAAATGTTCAATTCTGGCAACTGGCCGTTTCGTGCAATTTGCCGAAAGTTTTCAATTCGCAACTTTTGTGTTTTGCTTT

GCTGAATTAGCCGAAAATGTTCAATTCTGGCAACTGGCCGTTTCGTGCAATTTGCTGAAAATTTTATATTCCGGCAAAT

TACCGGT

TTGCCGAAATTGCAACAAACTTCAATTTTGGTAAATGGCCGTTAACCGAAAACGGCGAGTATTTTTAATTCCTGCAAAT

TGCCGTTTTGCCGAAAT

TTGCCGAAAATTTATCAATTCCGACGAATGGCCGTTGTGCGGAACGTGCAGGAAAATTTTCAATTCGGCAAATACCGAT

TTGCCGATTTTTCGGAATTTTCAATTCGGTCAAATGGTTCGGTTTTGCTGAAT

Nr of selected repeats 27 Similarity 0.807908

Consensus:

TTGCCGAAAATatTcAaTTtTGGCAAATGnCGGTTTTgCtgAAt

>Cele-UNSB01_5:18206252-18206609 Satlength=358 Nr of Repeats=5 RepeatLength=35

seed=AATTCGGCA

AATTCGGCAATATGCCGTTTTGCCGAAAATTTTC

ACTTCCGGCAAGTTGCCGATTTGCCGAAAATCTTC

AATTCGGCAATTTGCCGATTTCTTGAAACTTTCCATTCGGAAAATATGCCGATTTCCGGAAAATTTTC

AATTGCGGCAATATGCCGTTTTGCCGTAATTTTC
AATTCCGGCAACTTTTTAGATGGATTTTTTTATAAAAGGCGAAACACTTGAAACTGTGCCTTTTTGAAAATTTTTTCCC
GTTTCCAATTTTGCCGATGAAAACTGAAATTTCTGAAATTTCCAAAAAAAAAAAAATGTGCAGAACCACAAATTTTCCGGCAA
TTGCCGTTTTTCCGGCAATTTCAA

Nr of selected repeats 3 Similarity 0.822222

Consensus:

AaTTcCGGCAAtaTGCCGtTTTGCCGgAAATtTTC

>Cele-UNSB01_5:18261348-18261785 Satlength=438 Nr of Repeats=10 RepeatLength=35
seed=TTTCCGGCAA

TTTCCGGCAAATACGGCAAATAGCCGTTTTTTCGAATTTTGGGCAAACCGGCAATTTGCCGAATTTTCAAAAAGGCACAG
TTTCAAGTGTTAACCGTCTTATTAAAAATCTTTCTGAAAA

TTTCCGGCAAATCGGCGATTTGCCTGAATTGAAAG

TTTCCGGCAGAACGGAAATTTTCCGAAAATGACAA

TTTCCGGCAAATCGTAATTTTGCCGGAATTTAAAA

TTTCCGGCAAATTAGCACTTTGCCGGAATTGAAAG

TTTCCGGCAGAACGGAAATTTTCCGAAAATGACAA

TTTCCGGCAAATCGTCATTTTGCCGGAATTTAAAA

TTTCCGGCAAATCGGCGATTTGCCTGAATTGAAAG

TTTCCGGCAGAACGGAAATTTTCCGAAAATAACAA

TTTCCGGCAAATCGTCATTTTGCCGGAATTTGAAA

Nr of selected repeats 6 Similarity 0.790432

Consensus:

TTTCCGGCAAATCGgCatTTTGCCgGAAtTTgAAAg

>Cele-UNSB01_5:18345564-18345809 Satlength=246 Nr of Repeats=7 RepeatLength=35
seed=AAATTTTTCGG

AAATTTTTCGGCAAATTTGATAATTGCCGGTTTTGG

AAATTTTTCGGCAAATTCGATAATTGCCGGTTTTGT

AAATTTTTCGGCAAATTTGATAATTGCCGGTTTTGT

AAATTTTTCGGCAAATTCGATAATTGCCGGTTTTGG

AAATTTTTCGGCAAATTTGATAATTGCCGGTTTTGT

AAATTTTTCGGCAAATTCGATAATTGCCGGTTTTGG

AAATTTTTCGGCAAATTTGAAAATTGCCGGTTTTGG

Nr of selected repeats 7 Similarity 0.945578

Consensus:

AAATTTTTCGGCAAATTTtGATAATTGCCGGTTTTTgG

>Cele-UNSB01_5:18406789-18410349 Satlength=3561 Nr of Repeats=114
RepeatLength=31 seed=GTCAATTTTT

GTCAATTTTTTGCGGGAAATTCAAATTTTCA

GTCAATTTTTTGCGGGAAATTCAAATTTTCA

GTCAATTTTTTAGCGGGAAATTTAAATTTTCA

GTCAATTTTTTATCTGGAACTTCAAATTTTCA

GTCAATTTTTTATCTGGAAGTTCAAATTTTCA

GTCAATTTTTTGCGGGAAATTCAAATTTTCA

GTCAATTTTTTGCGGGAAATTCAAATTTTCA

GTCAATTTTTTATCTGGAAGTTCAAATTTTCA

GTCAATTTTTTGCGGGAAATTCAAATTTTCA

GTCAATTTTTTGCGGGAAATTCAAATTTTCA

GTCAATTTTTTAGCGGGAAATTTAAATTTTCA

GTCAATTTTTTATCTGGAAGTTCAAATTTTCA

GTCAATTTTTTAGCGGGAAATTTGAATTTTCA

GTCAATTTTTTATCTGGAACTTCAAATTTTCA

GTCAATTTTTTATCTGGAAGTTCAAATTTTCA

GTCAATTTTTTGCGGGAAATTCAAATTTTCA

GTCAATTTTTTGCGGGAAATTCAAATTTTCA

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TTGGCGCAATTCTAGTGAC
TTGACGCAATTATCGTGCC
TTGGCGCAATTCTAGTGTA
TTGACGCAATTCTGGTGAC

Nr of selected repeats 77 Similarity 0.809381

Consensus:

TTGaCGCAATTCTAGTgnC

>Cele-UNSB01_5:18442188-18442272 Satlength=85 Nr of Repeats=4 RepeatLength=21

seed=GCACTGACCA

GCACTGACCAAATGCAATGTT

GCACTGACCAAATGCAATGTT

GCACTGACCAAATGCAATGTT

GCACTGACCAAATGCAATGTT

Nr of selected repeats 4 Similarity 1.000000

Consensus:

GCACTGACCAAATGCAATGTT

>Cele-UNSB01_5:18556604-18557205 Satlength=602 Nr of Repeats=6 RepeatLength=45

seed=GGGGGACCCT

GGGGGACCCTTTGGACTTTTTTTTCTGAAAAAATTGAAAAAATTTTTTTTCAAAAATTTTCAAATATTTATCAGATAT

TGGAGAAATCACTTACTTGGTTGTTTCTATACATTTTCTTGCCAAAATAGGTGTTTTCTATAAGTCAAACCGACATTCC

TTGGGGCTCTGAACAATAAAACCTCCCGTCTTAAATGGATGTATCCAATTCTAGAGGCGAGGTATCAAAAAGCCTTCA

ACTACAACCATGTTAAGCTTGAAGCAATAAACGTTTTTCATAGTTGTAGGCATCTTTTCATCTTTGTCCAGAAGTGAAGAT

ATTGTTGAGCACAGATCTAGCAACTTGTGATCCTTTGGAGCTGAAGATTCAAGTCATAAG

GGGGGACCCTTATGATCCTTTGGAGCTGAAGATTCAAGTCATAAG

GGGGGACCCTTATGATCCTTTGGAGCTGAAGATTCAAGTCATAAG

GGGGGACCCTTATGATCCTTTGGAGCTGAAGATTCAAGTCATAAG

GGGGGACCCTTATGATCCTTTGGAGCTGAAGATTCAAGTCATAAG

GGGGGACCCTTATGATATTTTGGAGCTGAAGATTCAAGTCATAAG

Nr of selected repeats 5 Similarity 0.940741

Consensus:

GGGGGACCCTTATGATccTTTGGAGCTGAAGATTCAgtTCaTAAG

>Cele-UNSB01_5:18596071-18596370 Satlength=300 Nr of Repeats=14 RepeatLength=14

seed=ACAAACTACA

ACAAACTACAAACT

ACAAACTACAAACT

ACAAACCACAAACT

ACAAACTACAAACTACAAGCA
ACAAACTACAAACT
ACAAACTACAAACAACAACCTTATAAACTGCAATTCATGTACCTACAGAATGTACCAATTTTTTCGAAAAATGTTCTGA
TCGGTTTTGAAAAGTACATATTATT
AAAACCTACAAACT
ACAAACTACAAACT
ACAAACTATAAACT
ACAAACTACAAACT
ACATACTACATACTGCATACT
ACAAACTACAAGCT
ACAAACTACAAACT
ACAAACTACAAACT

Nr of selected repeats 10 Similarity 0.942857

Consensus:

ACAAACTACAAACT

>Cele-UNSB01_5:18630095-18630532 Satlength=438 Nr of Repeats=22 RepeatLength=19
seed=CAAGGCACTA

CAAGGCACTAGAAATGCGT
CAAGGCACGAGAATTGCGC
CAAGGCACTAAAATCGCGC
CAAGGCACTAAAAATGTGT
CAAGGCACGATAATTACGT
CAATGCACTAAAATCGCGC
CAAGGCACTAGAAATGTGT
CAAGGCACGATAATTACGT
CAATGCACTAAAATCGCGT
CAAGGCATTAGAATTGCGT
CAAGGCGCTAGAAATGCCC
CAAGGCACTAGAAATGCGTCAATGCGCTAGAATTGCGA
CAAGGCACTAAAATCGCGC
CAAGGCACTAGAAATGTGT
CAAGGCACGATAATTACGT
CAATGCACTAAAATGCGT
CAAGGCATTAGAATTGCGT
CAAGGCACTAGAACTACGC
CAAGGCACTAAAATGCGT
CAAGGCACTAGAATTGCGT
CAAGGCACTAGAACTACGC
CAAGGCACTAAAATGCGC

Nr of selected repeats 21 Similarity 0.750042

Consensus:

CAAGGCACTAnAAtTgCGt

>Cele-UNSB01_5:18631640-18632148 Satlength=509 Nr of Repeats=18 RepeatLength=19
seed=TGACGCAATT

TGACGCAATTCACGTGCCT
TGACGCATTTCTAGTTCAT
TGACGCATTTTCAGTGCCT
TGGCGCAATTTTAT
TGACGCAATTCACGTGCCT
TGACGCAATTCTAGTGGCT
TGACACAATTCTAGCGCCT
TGACGCAATTCTAGTGCCTTTGACGCAGTCCCTAGCGCCTTGGCGCGATTATAGTGCCTTGGCGTAATTCTAGTGCAC
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TGACGCAATTCTAGTGGCT

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ACACGAAAAAATAGATTGAT

GTCTGGGGTCTGGG
GTCTGGGGTCTGGG
GTCTGGGGTCTGGG
GTCTGGGGTCTGGG

Nr of selected repeats 9 Similarity 0.978836

Consensus:

GTCTGGGGTCTGGG

>Cele-UNSB01_5:18669912-18670449 Satlength=538 Nr of Repeats=16 RepeatLength=31
seed=TTGGCCCAGA

TTGGCCCAGAGCTCTCTTGACCTAAGCCCC
TTGACCCAGAGCTTTCTTGACCCAAGCCCC
TTGGCCCAGAGCTCTCTTGACCCAAGCCCC
TTGGCCCAGACCAAGTACCCGTGGCTCAGAGCATTCTTGACTCAAGTCCCC
TTGGCCCAGAGCTCTCTTGACCTAAGCCCC
TTGGCCCAGAGCTCTCTTGACCTAAGCCCC
TTGACCCAGAGCATTCTTGACTCAAGCCCC
TTGGCCCAGAGCTCTCTTGACCTAAGCCCC
TTGGCCCAGAGCTCTCTTGACCTAAGCCCC
TTGACCCAGAGCTTTCTTGACCCAAGCCCC
TTGGCCCAGAGCTCTCTTGACCCAAGCCCCAGACCCATCCACC
TTGGCCCAGAGCTCTCTTGACCCACACCCCT
TTGGCCCAGAGCTTTTTTTGACCCAAGCCCC
TTGGCCCAGAGCTCTCTTGACCCAAGCCGCC
TTGGCCCAGAGCTCTCTTGACCCAAGCCCC
TTGGCCCACAGCTCTCTTGACCCAAGCCAGACCAAGAGCCT

Nr of selected repeats 11 Similarity 0.885826

Consensus:

TTGgCCCAGAGCTcTCTTGACCcAAGCCCC

>Cele-UNSB01_5:18701783-18702035 Satlength=253 Nr of Repeats=9 RepeatLength=28
seed=CCAAGAGAAT

CCAAGAGAATTTCAACCGCCTAGAAATT
CCAAGAGAATTTCAACCACCTGGAAATT
CCAAGAGAATTTCAACCACCTGGAAATT
CCAAGAGAATTTCAACCACCTGGAAATC
CCAAGAGAATTTCAACCACCTGCAAATT
CCAAGAGAATTTCAACCGCCTAGAAATT
CCAAGAGAATTTCAACCACCTGGAAATC
CCAAGAGAATTTCAACCACCTGCAAATT
CCAAGAGAATTTCAACCGCCTAGAAATT

Nr of selected repeats 9 Similarity 0.915344

Consensus:

CCAAGAGAATTTCAACCcCCTggAAATt

>Cele-UNSB01_5:18728400-18728559 Satlength=160 Nr of Repeats=4 RepeatLength=32
seed=GAATTCAAAT

GAATTCAAATTTTCTGAAAAAATTTTGGCGT
GAATTCAAATTTTCTGAAAAAATTTTGGCGT
GAATTCAAATTTTCTGAGAAAAAATTTGGCGG
GAATTCAAATTTTCTGAGAAACAATTTGGCGTGAATTCGCATTTTTGAGAAAAATTTGGTGG

Nr of selected repeats 3 Similarity 0.888889

Consensus:

GAATTCAAATTTTCTGAaAAAatTTTGGCGt

>Cele-UNSB01_5:18730021-18731423 Satlength=1403 Nr of Repeats=114
RepeatLength=12 seed=GTATATGTAT

GTATATGTATAATTTAAATGTATAGTGTATATTTATAATATGTAAATA

GTATACGTATAT
GTATACGTATAT
GTATATGTATAT
GTATATGTATAT
GTATATGTATAT

Nr of selected repeats 110 Similarity 0.972866

Consensus:

GTATATGTATAT

>Cele-UNSB01_5:18793643-18794338 Satlength=696 Nr of Repeats=5 RepeatLength=31
seed=AAAATTTTGA

AAAATTTTGAATTTTCAGCCCCTAACTTTTGAATTTTCGAAAAATCAAGTTTAAATTCGAATTCCTCCGTGCCAAATTAC
CCCTTACCCCGATTTTCAGAATTTTAGTGCAAAATTCGTCAAATATGGTGTCTGGTACGCAAACACCACGCTACAGT
AACCCAAAACACCGGATTTGACGGAAGTTTGCCTAAAATTCAAAAATCAAGGGTCAGGGTAATTTGCCAAGGCGAA
TTCAAATTTGCACTGATTTTTC

AAAATTTTACCAATTGGGCCAGTTTTCGTGCGCCTAAAAAGACCGAATTTTGGGGTCTAAATCCGAAAATTTCCCAA
TTTTTTTACAATTTTCAGAACCCTACTCCAAGGCTCAATCATCACATTTACTGGAATCGGGTGCCGAGCAATTCCGCA
CCTACGTCATTGAAATTTCAAGCCGAAAAACGGTCCAAACGGGCGGTCCGGCCGTGTTGAACATTATTCAGACAGAGTA
CGAGCACAAATTTGCGCGGATTTCCGACGTTTTCACTTTTTGATGCAAAAAACCGAATCCCGAGCTGCAGGAGGCCGTT
AGCCAGCTTATTGTGGTAAAAATCGC

AAAATTTTGAATTTTCAGAAAATTCGAAAAATTCGC

AAAATTTTGAATTTTCAGAAAATTCGAAAAATTCGC

AAAATTTTGAATTTTCAGAAAATTCGAAAAATTCGC

Nr of selected repeats 3 Similarity 0.971326

Consensus:

AAAATTTTGAATTTTCAGAAAATTCGAAAAATTCGC

>Cele-UNSB01_5:18824768-18825020 Satlength=253 Nr of Repeats=16 RepeatLength=12
seed=AGGCTTAGGC

AGGCTTAGGCTTAGACCTAGACTCGGACTC

AGGCCTAGGCTT

AGGCTTAGGCTT

AGGCGTAGGCTT

AGGCTTAGGCTT

AGGCTTAGGCTT

AGGCTTAGGCTA

AGGCTTAGGCTT

AGGCTTAGGCTT

AGGCTTAGGCTT

AGGCTTAGGCTT

AGGCTTAGGCTTAGGCGTACGCTT

AGTCTTAGGCTTAAGCAT

ATGCTTAGGCTTAGGCCCA

AGCTTAGGCTTAGTCTT

AGGATTAGGCTTAGGCTCAGGTTT

Nr of selected repeats 10 Similarity 0.935802

Consensus:

AGGCTTAGGCTT

>Cele-UNSB01_5:18831834-18832119 Satlength=286 Nr of Repeats=11 RepeatLength=19
seed=TTGACGCAAT

TTGACGCAATTCTCGTGCT

TTGACGCAATTCTAGTGCTTCGCCGTATTTCAAGTGTGTTTGGTGCAATTCTAGTACC

TTGACACAATTTTAGTACC

TTGGCGCAATTCTATTGCT

TTGACACAATTTTAGTACC

TTGGCGCAATTCTATTGCT

TTGACACAATTTTTGCGCC
TTGACGCATTTCTAGTGCC
TTGACGCAATTCTCGTGCG
TTGACGCAATCCTGGTGCCTCGGCGAAATTCTAGTGCCCTGACGCATTTCCAGTTTC
TTGGCGCAATTCTCGTGTC

Nr of selected repeats 9 Similarity 0.666667

Consensus:

TTGaCgCAATTcTagTgCn

>Cele-UNSB01_5:18833669-18833973 Satlength=305 Nr of Repeats=15 RepeatLength=19

seed=TAGTGCCTTG

TAGTGCCTTGCCACAATTT
TAGTGCCTTGATGCAATTT
TAGTGCCTTGGCGCAATTC
TAGTTCCTTGGCGCATTTTC
TAGTGCCTTGGCGCAATTC
TAGTGCCTTGACGCATTTTC
TAGTCCCTTGACGACATTCTAGTGCCTAACGCAATTC
TAGTTCCTTGACGCATTTTC
TAGTGCCTTGGCGCAATTC
TAGTGCTTTGACACAATTC
TAGTGCCTTGGCGCAATTC
TAGTTCCTTGACACATTTTC
TAGTGCCTTGGCGCAATTCA
AGTGCCTTGGCGCATTTTC
TATTGCCTTGGCGCAATTC

Nr of selected repeats 12 Similarity 0.808612

Consensus:

TAGTgCCTTGgCgCAaTTC

>Cele-UNSB01_5:18836263-18836629 Satlength=367 Nr of Repeats=11 RepeatLength=33

seed=TGTCGGCTGC

TGTCGGCTGCTAAAAGTGTAGCCACCCGGCAGG
TGTCGGCTGCTAAAAGTATAGCCTCCCGGTAGG
TGTCGGCTGCTAAAAGTATAGCCTCCCGGCAGG
TGTCGGCTGCTAAAAGTATAGCGACCCGGCAGA
TGTCGGCTGCTAAAAGTATAGCCACCCGGCAGG
TGTCGGCTGCTAAAAGTATAGCCTCCCGGCAGG
TGTCGGCTGCTAAAAGTATAGCCACCAGGTAAG
TGTCGGCTGCTAAAAGTATAGCCTCCCGGCAGG
TGTCGGCTGCTAAAAGTATAGCCTCCCGGAAGG
TGTCGGCTGCTAAAAGTATAGCCACCCGGTAAG

Nr of selected repeats 10 Similarity 0.876094

Consensus:

TGTCGGCTGCTAAAAGTATAGCctCCCGGcAgG

>Cele-UNSB01_5:18839756-18840116 Satlength=361 Nr of Repeats=22 RepeatLength=12

seed=AGCCTAAGCC

AGCCTAAGCCTA
AGCCTAAGCCTA
AGCCTAAGCCTA
AGCCTAAGCCTAAGACTATCCCTA
AGCCTAAGCCTA
AGCCAAAGCCTACGCCTAAATCTAAGCATT
AGCTTAAGCCTA
AGCCTAAGCCTAAATCTA

AGCCTGAGCCTA
AGCCTAAACCAC
AGCCTAAGCCTG
AGCCTAAGACTATCCCTA
AGCCTAAGCCTA
AGCCAAAGCCTACGCCTAAATCTAAGCCTTAGCTGA
AGCCTAAGACTA
AGCCTAAGCCTA
AGCCTAAGCCTA
AGCCTAAACCAA
AGCCTAAGCCTG
AGCCTAAGACTATCCCTA
AGCCTAAGCCTA
AGCCAAAGCCTACGCCTAAATCTAAGCCTTAGATTA

Nr of selected repeats 15 Similarity 0.860317

Consensus:

AGCCTAAGCCTa

>Cele-UNSB01_5:18842565-18843912 Satlength=1348 Nr of Repeats=50

RepeatLength=20 seed=GTAAATCTAC

GTAAATCTACATTGACATCC
GTAAATTTACATTGGCCTCC
GTAAATCTACATCGACTACC
GTAAATCTACCTGACTACTGTAAAATTACACAGAGCTCC
GTAAATCTACAGTTGCCTCC
GTAAATCTACATAGACCTCC
GTAAATCTACATAGACCTCC
GTAAATCTACATCGACCTCC
GTAAATCTACAATAACCTTC
GTGAATCTACATTGACCACC
GTAAATCTACATAGTGCTCC
GTAAATCTACAATAACCTCC
GTAAATCTACATTGACTACT
GTAAATTTACAAAGACCTCC
GTAAATCTACATAGACGTCC
GTAAATCTACATTGGCCTTCATGAATCTACATTGACATCCGTAAATTTATATTGACTACC
GTAAATCTACAATAACCTCCGGGAATCTACATTAACTTTCGTAAAATTGCATGGACTACCGTAATTTACATCGACCTCA
GAAATCTACATTTACCACC
GTAACCTCTACCTACACCTTC
GTAAATCTACAGTTGCCTTC
GTAAATCTACACTGGCCCCC
GTAAATCTACATCGACCTCA
GTAAATCTACATCAACCTTC
GTAAATTTACATTTACCACC
GTAAATCTACACATAACCGTC
GTAAATCTACTTTGACCTTT
GTAAATTTACATTTACCACC
GTAAATCTACACAGAACTCTGTAAATTTGCATTGACCTCC
GTAAATCTACACAGACCTTC
GTAAATCTACATCGACCTCA
GTAAATCTACATTGACTACC
GTGAATCTACGCAGACCTTTGGAGTTCTAGGTATATCTTC
GTAAATCTGCATAGGCCTCGGTAAATCCCATCGATCTTT
GTGAATCTACATAGACCACCGAAAATCCATACACCCCTCT
GTAAATCGACAGAGATCTCC

GTAAATCTACACGTTCCCTTT
GTAAATCTACATAGATCTCC
GTAAATTTACATTTACCACC
GTAAATCTACATGGATATTCT
TAAATCTACATAGACCTCC
GTAAATCAACATTGATTTTTGTAACTCTAAATTACTGTGAATTCATATTAACCTCC
GTAAATCTAAATGTTCCCTCT
GTAAATCGACGTAGTTCTCC
GTAAATCTACATACCCTCCACAAATTTTCATACCACACC
GTAAATCCACACAAGCTACC
GTAAATCTACATAAGCTTCCACAAATC
GTAAATCTACGTTGGCACCTGTAAGGTAAGTAGACTTTTGTCTCCATTAAAGATTTTTTAAACTTCAGAAAGTTTCAG
AGATCTCT
GTAAATCTACATACCCCTGC
GTAAATCGACATACTCCTCC
GTAAATCTACACGGACTTTTGTAAAACCTTGTGGACTACC
Nr of selected repeats 35 Similarity 0.635294

Consensus:

GTAAATCTACAtngaCCtC

>Cele-UNSB01_5:18846370-18846628 Satlength=259 Nr of Repeats=18 RepeatLength=12
seed=TAAGCCTAAG

TAAGCCTAAGCC
TAAGCCTAAACCTAAGCG
TAAACCTAAGCG
TCAGCCTAAGCG
TAAGCCTAAGCCTAAGTT
TAAGCCTAAGCC
TAAGCCTAAGCC
TAAGCCTAAGAC
TAAGCCTAAGCC
TAAGCCTAAGCC
TAAACCTAAGCG
TAAGCCTAAGCG
TAAGCCTAAGCG
TAAGCCTAAGCG
TAAGCCTAAGCCTAAGTT
TAAGCCTAAGCCTAATCCTAATTC
TAAGCCTAAGCC
TAAACCTAAGTCTAAGCCGAAACC

Nr of selected repeats 13 Similarity 0.874644

Consensus:

TAAGCCTAAGCc

>Cele-UNSB01_5:18856264-18856396 Satlength=133 Nr of Repeats=9 RepeatLength=12
seed=AGCCTAAGCC

AGCCTAAGCCTACGTCTAAGCCTACCCCTA
AGCCTAAGCCTA
AGCCTAAGCCCG
AGCCTAAGCCTA
AGTCTAAGCCTG
AGCCTAAGCCTA
AGCCTAAGCCTG
AGCCTGAGCCTG
AGCCCAAGCCTAAGCCTA

Nr of selected repeats 7 Similarity 0.841270

Consensus :

AGCCTAAGCCTg

>Cele-UNSB01_5:18874657-18874753 Satlength=97 Nr of Repeats=6 RepeatLength=12

seed=CTAAGCCTAA

CTAAGCCTAAGC

CTAATCCTAAGC

CTAACCTAAGTTTAAAGAATTAGCCGACGT

CTAAGCCTAAGC

CTAAGCCTAAATCTAGGT

CTAAGCCTTAGC

Nr of selected repeats 4 Similarity 0.888889

Consensus :

CTAAGCCTaAGC

>Cele-UNSB01_5:18877478-18878086 Satlength=609 Nr of Repeats=29 RepeatLength=19

seed=GTGCCTTGAC

GTGCCTTGACGCATTTCTA

GTGCTTTGACGCAATTCTA

GTGCCTTGACGCATTTCTA

GTGCCTTGGCGCAATTCTT

GTGCCTTGACTCAATTATA

GTGTCTTGACGCATTTCTA

GTGCCTTGGCGCAATTCTT

GTGCCTTGACGCAATTATAGTGTATTGACGCAATTCTA

GTGCCTTGACGCATTTCTA

GTGCCTTGACGCATTTCTA

GTGCCTTGACGCAATTCTA

GTGCCTTGACGCAATTCTT

GTGCCTTTACGCATTTCTA

GTGTCTTGACGCAATTCTT

GTGCCTTGACGCATTTCTA

GTGCCTTGACGCAATTCTT

GTGCCTTGGCGCAATTCTAGTACTGGACGCAATTCTA

GTGCCTTGACGCAATTCTA

GTGCCTTGACGCATTTCTA

GTGCCTTGACGCATTTCTA

GTGCCTTGACGCATTTCTT

GTGCCTTGGCGCAATTCTA

GTGCCTTGACGCAGTTCTA

GTGCCTTGACGCATTTCTA

GTGCCTTGACGCAATTCTT

GTGCCTTGGCGCAATTCTA

GTGCCTTGACGCAGTTCTA

GTGCCTTGACGCAATTCTTGTGCTTTGGCCAATTCTA

GTGCCTTGACGCAGTTCTA

Nr of selected repeats 26 Similarity 0.876923

Consensus :

GTGCCTTGACGCAnTTCTa

>Cele-UNSB01_5:18890478-18890638 Satlength=161 Nr of Repeats=8 RepeatLength=20

seed=GATTTTTCTG

GATTTTTCTGAAAATTTATT

GATTTTTTTGAAAATTTATT

GATTTTTTTGAAAATTTATT

GATTTTTTTGAAAATTTATT

GATTTTTCTGAAAATTTATT

GATTTTTCTGGAAATTTATC
GATTTTTCTGAAAATTTATC
GATTTTTCTGAAAATTTATC

Nr of selected repeats 8 Similarity 0.871429

Consensus:

GATTTTTcTGaAAaTTTATt

>Cele-UNSB01_5:18891023-18891077 Satlength=55 Nr of Repeats=4 RepeatLength=12
seed=TAAGCCTAAG

TAAGCCTAAGCG

TAAGCCTAGGCC

TAAGCCTAAGCC

TAAGCCTAAGCCTAAGCC

Nr of selected repeats 3 Similarity 0.851852

Consensus:

TAAGCCTAaGCc

>Cele-UNSB01_5:18895119-18895676 Satlength=558 Nr of Repeats=15 RepeatLength=39
seed=GTAATTTATA

GTAATTTATAAATTTTTTAAAGATGAATAATAGATTGCC

GTAATTTATAAATTTTTTAAATATGAGTTATGTATTGCC

GTAATTTATAAATTTTTTAAAGATGAGTAATATATTGCC

GTAATTTATAAATTTTTTGAAGATGAGTAATATATTGCC

GTAATTTATAAATTTTTTGAAGATGAATAATATATTGCC

Nr of selected repeats 13 Similarity 0.917598

Consensus:

GTAATTTATAAATTTTTTaAAgATGAgTaATATATTGCC

>Cele-UNSB01_5:18898055-18898199 Satlength=145 Nr of Repeats=9 RepeatLength=12
seed=GCTTAGGCTT

GCTTAGGCTTAATCATAG

GCTTCGGCTTAG

GCTTAGGCTTAA

GCTTAGACTTTGGCTCAGGGTTAGACTCTG

GATTAGGCTTAGGCTTAATCGTAG

GCTTAGGCTTAG

Nr of selected repeats 6 Similarity 0.925926

Consensus:

GCTTAGGCTTAG

>Cele-UNSB01_5:18899719-18900018 Satlength=300 Nr of Repeats=5 RepeatLength=11
seed=TTTCAGGCCT

TTTCAGGCCTA

TTTCAGGCCTAAAAAATAATTTTCAGAAGCAAAGTGAATGAGTGTGCGAGAATTCTGGAAGTTCTGAAAATTTAAACT
CACTTTGATTAGATTTAAAAATTATTGCATTTGTGGCCCGATTTCAGACTAT

TTTAGGCCTAC
TTTAGGCCTGAAAAACAACATTTTTCCAAAAAAGCTGAAAAATGTCATTTTTTTTACAATAGCGTTTTTTTTAGAATTTTT
ATCCAATATTTTGACACCCATATTGACTTGGGTGTGAGCTTTGGGTTCGATTCAAGCTA
TTTCAGGCCTA

Nr of selected repeats 3 Similarity 0.796296

Consensus:

TTTcAGGCCTA

>Cele-UNSB01_5:18902702-18903276 Satlength=575 Nr of Repeats=24 RepeatLength=21
seed=AAAAATCGAT

AAAAATCGATGAAATTTGGAG
AAAAATCGATAAAAATATGGAG
AAAAATCTATAAAAATATGGAG
AAAAATCGATAAAAATTTGGAG
AAAAATCGATAAAAATTTGGAG
AAAAATCGATAAAAATATGGAG
AAAAATCGATAGAATTTGGAG
AAAAATCGATAAAAATTTGGAA
AAAAATCGTTAAAACTTAAAT
AAAAATCTATAAAAATTTAGATGAAAATCAATAAAAATTTAGTG
AAAAATCTATGAAAATTTGGACA
AAAAATCGATAAAAATATGGAT
AAAAATCGATGAAATTTGGCCAGAAATCGTTAAAACTTGGAT
AAAAATCTATAAAAATTTGGCC
AAAAATCGTTAAAACTTGAAT
AAAAATCTATAAAAATTTAGAT
AAAAATTGATAAAAATTTGGCC
AAAAATCGTTAAAACTTGGAT
AAAAATCTATAAAAATTTAGAT
AAAAATCAATAAAAATTTAGTG
AAAAATCTATGAAAATTTGGACA
AAAAATCAATAAACTTTGGAT
AAAAATCGATGAAATTTGGACAAAAAATCAACAAAATTTGAACA
AAAAATCAATAAAAATTTAGAGA

Nr of selected repeats 18 Similarity 0.739602

Consensus:

AAAAATCgATAAAAATtTgGAn

>Cele-UNSB01_5:18924789-18925018 Satlength=230 Nr of Repeats=6 RepeatLength=35
seed=GGAAATTCAA

GGAAATTCAACTTTCTGAGAAATAACTTTGGTG
GGAAATTCAAATTTTTCTGAAAAAAAAAATTTTTGGTGAAAATTTTTTTTTGGCG
GAAATTCAAATTTTTCTGAGAAAAATTTTTTTTTGGC
GGAAATTCAAATTTTTGGAGAAAAATAATTTGGCG
GAAATTCAAATTTTTCTGAGAAAAATTTTTTTTTGGC
GGAAATTCAAATTTTTGGAGAAAAATTTTTTTTTGGCG

Nr of selected repeats 4 Similarity 0.776235

Consensus:

GaAAATTCAAATTTTTcgGAGAAAAtaTttTTTTGGCg

>Cele-UNSB01_5:18933758-18934184 Satlength=427 Nr of Repeats=12 RepeatLength=20
seed=AGAAAAATCA

AGAAAAATCAAAAAATTC
AGAAAAATCAATAAATTTTT
AGAAAAATCAATAAATTTTC
AGAAAAATCAAAAAATTC
AGAAAAATCAATAAATTTTT

AGAAAAATCAATAAAATTTTC
AGAAACATCAAAAAATTTTC
AGAAAAATCAATAAAATTTTT
AGAAAAATCAATAAAATTTTC
AGAAAAATCGATTAATTTTC
AGAAAAATCGATAAAATTTCC
AGAAAAATCAATGAAAGTCAATTTAATTTCTAAAAATTTGAAAATTTTCAGTTCTGTATCGAAGCCAAAAACGGAACCGC
TACCACAAAAGCCCCGGCAAAATGCCTACCCGGGTGCACTTGCCGGCCAGCTTACAAGCGAGATTCTGACAGTGGCCAG
TGTGTCCATTCCAGGCAATGTTTTGGGAGTAAGTCGGAGCTCAGAATTTCC
Nr of selected repeats 8 Similarity 0.902381

Consensus:

AGAAAAATCaATAAAATTTTc
>Cele-UNSB01_5:18934684-18935273 Satlength=590 Nr of Repeats=23 RepeatLength=19
seed=TGACGCAATT
TGACGCAATTCTAGTGCCT
TGACGCAATTCTAGTGCATTGAAGCTATTCTATTTCCCT
TGACGCATTTTTAGTGCCT
TGACGCAATTTTAGTGCCTTTGCGCAGTTCGAGTGTCT
TGACGCAATTCTAGTGCGC
TGACGCAATTCTAGTGCCT
TGACGCAATTCTAGTGCGC
TGACGCAATTCTAGTGCCT
TGACGCAATTTTAGTGCCTTGACAAAATTCTAGGGCCT
TGACGCAATTCTAGTGGCT
TGACGCAATTCTAGTGCTTCGACGCGATTTTAATACCT
TGACGCAATTCTAGTGTCTTGCCGCGATTCCAGTGCCT
TGACGCAATTCTAGTGCCT
TGACGCAATTCTAGTGCCT
TGACGCAATTCTAGTGCAT
TGACGCAATTCTAGTACATTGGCACAATTCTAATGCCT
TGACGCAATTTTAGTGTCT
TGACGAAATTCTAGGGCCT
TGACGCAATTCTAGTGGCT
TGACGCAATTCTAGTGCTTCGACGCGATTTTAATACCT
TGACGCAATTCTAGTGTCTTGCCGCGATTCCAGTGCCT
TGACGCAATTCTACTGCCT
TGACGCAATTCTAGTGCAT
Nr of selected repeats 15 Similarity 0.830476

Consensus:

TGACGCAATTCTAGTGCCcT
>Cele-UNSB01_5:18935616-18936186 Satlength=571 Nr of Repeats=26 RepeatLength=19
seed=ACTAGAATTG
ACTAGAATTGCGCCAAGGC
ACTAGAAGTGCGCCAATAC
ACGAGAATTGCGCCAAAAC
ACTAGAATTGCGCTAAGGT
ACTAGACTTGCGTCAAGGC
ACTATAATTGCGTCAAAAAC
ACTAGAATTGCGTCAAGGC
ACTAGAATCGCGTCAAGGC
ACTAGAATTGCGCCAATGC
ACGAGAATTGCGCCAAGGC
ACTAAAATTGCGTCAAGAC
ACTAGAATTGCGTCAAGGC

ACTAGAATTGCGGCAAGGT
ACTCGAATTGCGTCAAGGT
ACTAGAATTGCGTCAAGGC
ACTGGAATTGCGCCAAGGC
ACTAGAATTGCGTCAAGGC
ACTAGAAATGCGTTCGAGGCTCTAGTACTGCGCCAAGAC
ACTAGAATTGCGTCAAGGT
ACTAGAATTGCGTCAAGGC
ACTGGAATTGCGTCAAGGT
ACTAGAATTGCGTCAAGGC
ACTAGAATTGCGTCAAGGC
ACTAGAATTGCGTCAAGGC
ACTAGAATTGCATCAAGGC
ACTAGAATTGCGTCAAGGA
ACTAGAATTGCGTCAAGGCACGAGAAATGCGCCAAGGCACGAGAAATGCGCCAAGGC
Nr of selected repeats 23 Similarity 0.820539

Consensus:

ACTAGAATTGCGtCAAGGc

>Cele-UNSB01_5:18937116-18937194 Satlength=79 Nr of Repeats=6 RepeatLength=12
seed=GGCTCAGGCT

GGCTCAGGCTCA
GGCTCCGGCTCA
GGCTCAGGCTCA
GGCTCAGGCTCA
GGCTCAGGCTCA
GGCTCAGGCTCA
GGCTCAGGCTCAGGCTCA

Nr of selected repeats 5 Similarity 0.955556

Consensus:

GGCTCaGGCTCA

>Cele-UNSB01_5:18944459-18944687 Satlength=229 Nr of Repeats=8 RepeatLength=19
seed=TTCTAGTGCC

TTCTAGTGCCTTGACGCAAATCTAGTGCATTGACGCAA
TTCTAGTGCCTTGACGCAATTCAGTATCTTGACGCAA
TTCTAGTGCCTTGGCGCTT
TTCTAGTGCCTTGGCGCAA
TTCTAGTGTCTTGACGCAATCTGGTGCTTTGAAGCAATTTTAGTGTCTTGACGCAT
TTCTGGTGCCATGACGCAA
TTCTAGTGCCTTGGCGCAT
TTCTAGTGCATTGGCGCAA

Nr of selected repeats 5 Similarity 0.817544

Consensus:

TTCTaGTGCctTGgCGCaa

>Cele-UNSB01_5:18982935-18983047 Satlength=113 Nr of Repeats=7 RepeatLength=12
seed=AGCCTGAGCC

AGCCTGAGCCTG
AGCCTGAGCCTG
AGCCTGAGCCTG
AGCCTGAGCCTG
AGCCTGAGCCTG
AGCCTGAGCCTGAGCCTAATCCTTTCTAGCCCTAAGTCTA
AGCCTGAGCCTG

Nr of selected repeats 6 Similarity 1.000000

Consensus:

AGCCTGAGCCTG

AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGAAAAA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACG
AAAAATAGATTGTTACACGA
AAAAATAGATTGTTACACGA

Nr of selected repeats 52 Similarity 1.000000

Consensus:

AAAAATAGATTGTTACACGA

>Cele-UNSB01_5:19020255-19020473 Satlength=219 Nr of Repeats=6 RepeatLength=31
seed=TGTAAAAATG

TGTAAAAATGCATGAAATTTTCGTATTTTCTATGAAAAAATGTCTGAAAGTTTGATTTTCCGG
TGAAAAAATGTCTGAAACTTCCAATTTACAA
TGTAATAATGTATGAAATTATGAATTTCCCAA
TGGAAAAATGTATGGAAAAATTGAATTTCCAG
TGTAATAATGCCTGGAATTATAAATTTCCGG
TGTAATAATATCTGAAATTACGAATTTTCTA

Nr of selected repeats 5 Similarity 0.651613

Consensus:

TGtAAAAATgtcTGaAAttatgAATttcCaa

>Cele-UNSB01_5:19059372-19059511 Satlength=140 Nr of Repeats=4 RepeatLength=35
seed=TCAGAAAATT

TCAGAAAATTTAAATTTCCCGCCAAAATATTTTTTC
TCAGAAAATTTAAATTTCCCTCCAAAATTTTTTTTC
TCAGAAAATTTAAATTTCCCGCCAAAATATTTTTTT
TCAGAAAATTTAAATTTCCCGCCAAAATATTTTTTT

Nr of selected repeats 3 Similarity 0.923810

Consensus:

TCAGAAAATTTAAATTTCCCGCCAAAATaTTTTTc

>Cele-UNSB01_5:19079815-19080004 Satlength=190 Nr of Repeats=5 RepeatLength=24
seed=GCCTAAGCCT

GCCTAAGCCTAA
GCCTAAGCCTAATCAACACTACCTTTTCATGAAAAAATAATTTTCAGAATTTTTTTTTTAAATTTTCAGACAAACTAC
CAAAAAAATACTAGAAAAATGTTTTAA
GCCTAAGCCTAAGCCTGAGTCTAG
GCCTAAGCCTAAGCCTGAGTCTAG
GCCTAAGCCTGAGTCTAGGCTAG

Nr of selected repeats 3 Similarity 0.666667

Consensus:

GCCTAAgCcTaAgcCtgaGtCTAG

>Cele-UNSB01_5:19138115-19138319 Satlength=205 Nr of Repeats=6 RepeatLength=31
seed=TCGTTTTTTC

TCGTTTTTTTCGCAAATTTTCAATTTTGGAGGGATTTGTCTAATTTTTCGG
TCGTTTTTTTCATGAAAAAACTCAATTTTCCG
TCGTTTTTTTCATGAAAAAACAAAATTTTTCGT
TCGTTTTTTCCGTGAGAAAACTCAATTTTTCGG
TGGTTTTTTTCACGAAAAAACTCAATTTTTCGT
TCGTTTTTTTCATGAAAAAACTCAATTTTTCGG

Nr of selected repeats 5 Similarity 0.819355

Consensus:

TcGTTTTTtCatGAaAAAActcAaTTTTcGg

>Cele-UNSB01_5:19147729-19148084 Satlength=356 Nr of Repeats=7 RepeatLength=40
seed=GAATTTTTTG

GAATTTTTTGGGGGAAAAATTCGAAAAATTGAAGAATTTTGGAGAAAAATCATATTTTTCCGTTAAAAAGTGCCTAGCAG
CAGCGCCCAAATCCGGTTTTGTTTCAAATTTTTCAGC
GAATTTTTTGAATTTTATTGAATTTTCCAAATTTTTCAGC
GATTTTTTTGAATTCTACTTAATTTTCCAAATTTTTCAGC
GAATTTTTTGAATTCTACTTAATTTTCCAAATTTTTCAGC
GAATTTTTTGAATTCTACTGAAATTTTCCAAATTTTTCAGC
GAATTTTTTGAATTCTACTGAAATTTTCCAAATTTTTAGC
GAATTTTTTGAATTCTACTGAAATGTCCAAATTTTTCAGC

Nr of selected repeats 6 Similarity 0.926667

Consensus:

GAATTTTTTGAATTCTACTgAATTTTCCAAATTTTTCAGC

>Cele-UNSB01_5:19162213-19162392 Satlength=180 Nr of Repeats=5 RepeatLength=40
seed=TTTTGCCGAA

TTTTGCCGAAAATTGCAAAGTTTCTGACAT
TTTTACCGAAAATTGCAAATTTTGTGGAATGTATCACATT
TTTTGCCAAAATCTGTCAATTTTGGGAATTTCTATAAT
TTTTGCCGAAGCTGCAAATTTCTGACAT
TTTTGCCGAAAATTTGTCAATTTTGTGGAATTTCTGTCA

Nr of selected repeats 3 Similarity 0.629630

Consensus:

TTTTgCCaAAAAtnTgtcAATTTTgtGGAATtTcTntcAt

>Cele-UNSB01_5:19164473-19167625 Satlength=3153 Nr of Repeats=148
RepeatLength=17 seed=ATTAGCAGCG

ATTAGCAGCGCCCAAAAATAGGTGTAGTTTGTAGTCAAATATCGATTTTTTGCATGATTTTTTGTATGAAAAATATATAAA
ATCGGCGATTTTCTAGCTCTTCAGGAACTTTTTCTCATCAAAATGTGCTTTATGCTTCGAAATGGGATTTTTTAAA
GCAAAAACGAGAAAATTTGGGTTTTTAGATGTAATGGCTGGCTAATATACCGTATTTCTTCTATTAATATGGCTGCAA
TACTATTTTTTCGATGGCCTTCCCGTTTGCAATACTAATAGGGAGTGCAAGACTATTAGGGAGTGCAATACTAATTTTCA
GAACATTTTCTGACTTTGAGCTTACTAGTTTTTTTTTCTGAAAAGCTCGAATCTTATGTAAAAATTCAGAAAATTTGTT
CTTAATTGTAAACATATAAGTTCAAAAACCTCAATCTCGTAGAAATGTTGTAAAAAACTGTTGCAAAATAGGCAAAAAAT
GCTGTTGAAATCTGAAATCAGCGATACGGGATTGCAATAAAAAAGAGTAAACGCAAGACTATTAGGGAGTGCAAGACT
AATAGGGAGGCCATATTAATAGAAGATATACGGTATTGTAGTTTGTAGTG
TTAGCAGCGACCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGACCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCTAAAA
ATTAGCAGCGACCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA

ATTAGCAGCGCCTAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA
ATGAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCTAAAA
ATTAGCAGCGCCCAAAA
ATGAGCAGCGCCCAAAA
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ATTAGCAGCGACCGAAAA
ATTAGCAGCGCCTAAAA
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ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGACCAAAAA
ATTAGCAGCGCCTAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGACCAAAAA
ATTAGCAGCGCCTAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGACCAAAAA
ATTAGCAGCGCCTAAAA
ATTAGCAGCGCCCAAAA
ATTAGCAGCGCCCAAAA

Nr of selected repeats 97 Similarity 0.880902

Consensus:

ATTAGCAGCGCCcAAAA

>Cele-UNSB01_5:19170107-19171106 Satlength=1000 Nr of Repeats=12

RepeatLength=18 seed=AATTAGCAGC

AATTAGCAGCGACCAAAA
AATTAGCAGCGACCAAAA
AATTAGCAGCGCCCAAAA
AATTAGCAGCGACCAAAA
AATTAGCAGCGCCCAAAA
AATTAGCAGCGACCAAAA
AATTAGCAGCGCCCAAAA
AATTAGCAGCGACCAAAA
AATTAGCAGCGCCCAAAA
AATTAGCAGCGACCAAAA
AATTAGCAGCGCCCAAAA
AATTAGCAGCGACCAAAA

AATTAGCAGCGCCCGAAGACTTTTGCAGTTTGTAGTCTAAACCGCATTTTCAGCACATTTTCCGGGCAAAAAATGTGATT
TTCAAAACTTTTTTATACGAAACTAGGAGTTTCAACACTTTTTTTTTCGCTGTGAAACTAATTTTTAGACAACTTTTTAT
ATGGAAAATCCGATTCTCAGCACTTTTCCATCGAAAAATCGATGTAACTACTCAAAAAATCGATTTTTTAGCCGATTT
TCCACACACAACTTACAAGTGGATTCCAACCTGAAAAAGGTTGAAATTCCTCAGCAAATAGTCGTGAAGTGTGAGAAAT
TGGAGATTAAGCTTATCCAATGCGAGCACACCGTCTCCTGTATAATTCTCGTATGGAATGATATTTCTCGTCCCAAATCA
CTTTTTCCGTCCGGAAAAGAGGCTTTTTCGTTGAGTTGTGTGAGTTGATTTGGGCGTCTTCACAGTGCAAAGTGATTGT
TTCCAGCAGATGTTGGTGTGGATAGAGATGGAGAAGAGATGTCTGGTGATTTGGGTCTTCTGCAAAAAATTGGGGGTTT
TTTGAGGGAAAAATCGTTAATTTTCATGATTTTTTCAGTATAAAAAACCGAAAAATTCATTACATACAGGTGTAGTTTGTA
GTCCAGGCCAAAAATTGGATTTCGCAGCGCCCAAAATATTGTAGTTTGTAGTCTTAGCATCGCCCAAAATTG

AATTAGCAGCGCCCAAAATATTGTAGTTTGTAGTTTTAGCAGCGCCCAAAACTTGTAGTTCGTAGTCTAAGCAGCGCCCA
AAATTTGTAGTTTGTAGTGTTAGCAGCGCCCAAAATTG

Nr of selected repeats 10 Similarity 0.960494

Consensus:

AATTAGCAGCGaCCAAAA

>Cele-UNSB01_5:19172684-19173158 Satlength=475 Nr of Repeats=14 RepeatLength=32
seed=TTGTAGTTTG

TTGTAGTTTGTAGTCTAAGCAGCGCCCAAAAC
TTGTAGTTTGTAGTCTAAGCAGCGCCCAAAAC
TTGTAGTTTGTAGTCTAAGCAGCGACAAAAAAAAAATT
TTGTAGTTTGTAGTCTAAGCACCGCCCTAAAT
TTGTAGTTTGTAGTCTAAGCAGCGCCCAAAAC
TTGTAGTTTGTAGTCTAAGCAGCGCCCAAAATA
TTGTAGTTTGTAGTCTAAGCACCGCCCTAAAT
TTGTAGTTTGTAGTCTAAGCAGCGCCCAAAAT
TTGTAGTTTGTAGTCTAAGCAGCGCCCAAAAT
TTGTAGTTTGTAGTCTAAGCAGCGCCCAAAATTC
TTGTAGTTTGTAGTCTAAGCAGCGCCCTAAAT
TTGTAGTTTGTAGTCTAAGCAGCGCCCTAAAT
TTGTAGTTTGTAGTCTAAGCACCCAAAAT
TTGTAGTTTGTAGTCTAAGCAGCGCCCAAAATTGAATTAGCCGCGCCTAAAATA

Nr of selected repeats 9 Similarity 0.939815

Consensus:

TTGTAGTTTGTAGTCTAAGCAgCGCCCaAAAt

>Cele-UNSB01_5:19225003-19225171 Satlength=169 Nr of Repeats=8 RepeatLength=21
seed=ATTATTGATT

ATTATTGATTTTTCAAGAAAA
ATTATCGATTTTTGAAGGGAA
ATTATTGATTTTTCAAAAATG
ATTATTGATTTTTGAAGGGAA
ATTATTGATTTTTCAAGAAAA
ATTATCGATTTTTGAAGGGAA
ATTATTGATTTTTCAAGAAAA
ATTATCGATTTTTGAAGGGAA

Nr of selected repeats 8 Similarity 0.778409

Consensus:

ATTATTGATTTTTcAAGaaAA

>Cele-UNSB01_5:19249579-19249688 Satlength=110 Nr of Repeats=6 RepeatLength=18
seed=AGCAGCGCCC

AGCAGCGCCCAAAAAAAAA
AGCAGCGCCCAAAAAAAT
AGCAGCGCCCAAAAAAAAA
AGCAGCGACCAAAAAATT
AGCAGCGCCCAAAAAAAAA
AGCAGCGCCCAAAAAAAT

Nr of selected repeats 5 Similarity 0.896296

Consensus:

AGCAGCGcCCAAAAAAat

>Cele-UNSB01_5:19251983-19252110 Satlength=128 Nr of Repeats=5 RepeatLength=18
seed=GCAGCGCCCA

GCAGCGCCCAGAAAATTAGTAGCGCCTAAAAAATTA
GCAGCGCCCAAAAAGATTA
GCAGCGCCCAAAAAAATTAACAGCGCCTAAAAAATTA
GCAGCGCCCAAAAAATTA

GCAGCGCCCAAAAATTA

Nr of selected repeats 3 Similarity 0.950617

Consensus:

GCAGCGCCCAAAAaATTA

>Cele-UNSB01_5:19255197-19255501 Satlength=305 Nr of Repeats=17 RepeatLength=18

seed=TGCTAATTTT

TGCTAATTTTTTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTCTGGGCGC

TACTAATTTTTTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTCTGGGCGC

TGCTAATTTTCTGGGCGC

TGCTAATTTTCTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTCTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTTTGGGCGC

TGCTAATTTTTTGGGCGC

Nr of selected repeats 15 Similarity 0.936508

Consensus:

TGCTAATTTTTtGGGCGC

>Cele-UNSB01_5:19270843-19271693 Satlength=851 Nr of Repeats=31 RepeatLength=20

seed=ATTTATTGAT

ATTTATTGATTTTTCTGAAA

ATTTATCGATTTTTCTGTAA

ATTTATTGATTTTTATTGAAAATACAGTGATTTTTCTAAAAATTATCAATTTTTCTGAAA

ATTTATTGATTTTTCCGGAA

ATTTATTGATTTTTCCGGAA

ATTTATCGATTTTTCTAAAA

ATTTATCGATTTTTCTGGAA

ATTTATTGATTTTTATTGAAAATTCAGTGATTTTTCTAAAA

ATTTATCGATTTTTCTGTAA

ATTTATTGATTTTTATTGAAAATTCAGTGATTTTTCTAAAA

ATTTATCGATTTTTCTGAAA

ATTTATCGATTTTTCTAAAA

ATTTATTGATTTTTCTAGAAAATTATCGATTTTTCTAGGA

ATTTATCGATTTTTCTGGAA

ATTTATCGATTTTTCTGAAAACGTATCGATTTTTCTAAAA

ATTTATCGATTTTTCTGGAA

ATTTATCGATTTTTCTGAAAATTCAGTGCTTTTTGTAAAA

ATTTATCGATTTTTACTGGAA

ATTTATTGATTTTTATTGAAAATTCAGTGATTTTTGTAAGA

ATTTATTTATTGATTTTTCTGGAA

ATTTATTGATTTTTCTAAAA

ATTTATCGATTTTTCTGGAA

ATTTATTGATTTTTATTGAAAATTCAGTGCTTTTTGTAAAA

ATTTATTGATTTTTCTGGAA

ATTTATTGATTTTTCTAAAA

ATTTATCGATTTTTCTGGAA

ATTTATTGATTTTTCTGGAA
ATTTATTGATTTTTATTGAAAAATTCAGTGATTTTTGTAAAA
ATTTATCGATTTTTCTGGAA
ATTTATTGATTTTTATTGAAAAATTCAGTGCTTTTTGTAAAA
ATTTATTGATTTTTCTGGAA

Nr of selected repeats 20 Similarity 0.886667

Consensus:

ATTTATcGATTTTTCTggAA

>Cele-UNSB01_5:19272660-19272781 Satlength=122 Nr of Repeats=6 RepeatLength=20

seed=ATAAATTTTC

ATAAATTTTCCATAGAAATCG

ATAAATTTTCAGAAAAATCG

ATAAATTTTCAGAAAAATCA

ATAAATTTTCAGAAAAATCG

ATAAATTTTCAGAAAAATCA

ATAAATTTTCAGAAAAATCA

Nr of selected repeats 5 Similarity 0.960000

Consensus:

ATAAATTTTcAGAAAAATCa

>Cele-UNSB01_5:19273514-19273585 Satlength=72 Nr of Repeats=4 RepeatLength=18

seed=TAGCAGCGCC

TAGCAGCGCCCAAGAAAT

TAGCAGCGCCCAAGAAAT

TAGCAGCGCCCAAAAAAA

TAGCAGCGCCCAAAAAAT

Nr of selected repeats 3 Similarity 0.901235

Consensus:

TAGCAGCGCCCAAgAAAt

>Cele-UNSB01_5:19275863-19276354 Satlength=492 Nr of Repeats=14 RepeatLength=32

seed=TGTAGTTTGT

TGTAGTTTGTAGCTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGCTTTAGCAGCGCCCAAAATCT

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATGAATTAGCAGCGCCCAAACT

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATCT

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATG

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATCT

TGTAGTTTGTAGTTTAGCAGCGCCCAAAATGAATTAGCAGCGCCTAAAATG

Nr of selected repeats 9 Similarity 0.905443

Consensus:

TGTAGTTTGTAGTTTAGCAGCGcCCAAaATTg

>Cele-UNSB01_5:19279992-19280235 Satlength=244 Nr of Repeats=8 RepeatLength=20

seed=TATCGATTTT

TATCGATTTTTCTGCAAATT

TATCGATTTTTCTGCAAATT

TATCGATTTTCTGAAAATTTGTCGAATTTTCTGCAATTTTATTGACTTTTCTGGAATT

TATCGATTTTTCTCTCAATTAATTGATTTTTCTGCAAATT

TATCGATTTTTCTGCAAATT

TATCGAGTTTTCTGGAAGTT
TATCGATTTTTCTGAAAATT
TATCGATTTTTTTAAAAATTAATTGATTTTTTTTTTGCAAATT
Nr of selected repeats 5 Similarity 0.900000
Consensus:
TATCGAtTTTTCTGcAAaTT
>Cele-UNSB01_5:19309007-19310074 Satlength=1068 Nr of Repeats=10
RepeatLength=19 seed=TGGCGCATT
TGGCGCATTCTCGTGCCTTACTAAATCCTCCATAAATGTTTCCTTTCTTTTTGGTCTCCTGAATACAATTTGTCACA
TCTTTTCCAGGACATGAGATAAAGTTGACGATTCCTAGTACACTGGCGCCAAGGAACACACCGAACAGAAGTTTTCTGG
AAAAAAAAAACTAGTCAATATTAATTAATAAAAAAAAAAAAAACCAAAACTGCACGAGAATTGCGCCAAGACACCGGAAATGC
GTCCACAATAGAATATTCAAAGTCAGTGCCTCAGAGCTTTCAAATTAGTGTACATCATTGC
TGGCGCGTTTTCTGGTGTGT
TGGCGCAATTTTTCTGCCT
TGGCGCATTCTCGATTTCTTACCTACATTTCCAAATCGCTGAATCTTTCGCTCCACTGGTTCAAATTTCTGTGGAATTC
TTCAAATTTTGATAATTTCCCGAGAATCCAATGTCATGTGAGTCACCGTTCGCCAAAATCCAGACGACAGTAATAGGC
TGAAAATATGTACAGAAAATCTTTTGTGGGTGGAGTCTAAAATTACCAAATGCATCCGACACACCACGCAATGTTAATA
TTAGATTCGATGGTCTTACGTGTTGAGTGGGAAGTCAGGTAACCGCCATGTCCTTGGTAATACACTGAAAGAGAATGTA
TCGAGAATTGCGCCAAGGCACCGGAAATGCGTCAACAACCTATTTTTTAAACTCAGCTTGCCGAGAGCTTTCAAATAAG
TATAATATCGAGCT
TGGCGCAATTTTGGTGAGT
TGGCGCATTCTGGTGCCT
TGGCGCAATTCTCGATACGCATATTTCTCGGTTGTTTTGCTCCAAATTCCTACAGATTTAATTTTTGAATTCAGTTTG
CCGAGAACTTCGAAATAAGTATAATATCGACCT
TGGCGCAATTTTGGTAAGT
TGGCGCATTCTGGTGCCTTGGCACAATTCTCGATACGCATATTTCTCAGTTGTTTTTGCTCCAATCTTTATACAGATT
CATTAAATTAATTCGGTATGCAGACAGCTATAAAATTAGTTAAATATCGACGC
TGGCGCATTGTGGTGTGAGT

Nr of selected repeats 6 Similarity 0.714620

Consensus:

TGGCGCAaTTTtGGTGagT
>Cele-UNSB01_5:19313130-19313974 Satlength=845 Nr of Repeats=33 RepeatLength=20
seed=AAAATCGATA
AAAATCGATAAAATTTCCAGAC
AAATCGATACATTTCCAGA
ATAATCGATAAAATTTCCAGA
AAAATCGATAAACTTTCCAGA
AAAATCGATAAAATTTCCAGA
AAAATCGATAAAATTTCCAGA
AAAATCAATAAAATTTCCAGA
AAAATTGATAAAATTTCCAGA
AAAATCAATAAAATTTCCAGA
AAAATCGATAAAATTTCCAGA
AAAATCAATAAAATTTCCAGA
AAAATTGATAAAATTTTAGA
AAAATCAATAAAATTTCCAGA

AAAATCAATAAAATTTCCAGC
AAAATCAATAAAATTTCCAGC
AAAATCAATAAAATTTTCAGAAAAATCACTAAATTTTCAGAACCTGGATTCTCCGATATTCGACGAAAATGAGAAAATGT
TCTACGGAAAAGTGTGCGATTTTCATGTCCCCGGTGGAAATTTGCTCCAACCAAAAATATCTGAGCACC GCCCG
AAAATCGATAATGGAACAGTTGAATGCCACGTATCAAAGTACACAAGTTGCTGAGTTTCAAGAAGATCAGGTAACGA
AAAATCGATAAAATTTCTGA
AAAATCGATAAAATTTCTGA
AAAATCGATAAAATTTCCAGAAA
AAAATCGATAAAATTTCTGA
AAAATCGATAAAATTTCTGA
AAAATCGATAAAATTTCTGA
AAAATCGATAAAATTTCTGA
AAAATCGATAAAATTTCCAGAA
AAAATCGATAAAATTTCTGA

Nr of selected repeats 22 Similarity 0.814643

Consensus:

AAAATCgATAAAATTTcCAGA

>Cele-UNSB01_5:19325271-19325379 Satlength=109 Nr of Repeats=9 RepeatLength=12
seed=ATACATATAC

ATACATATACAT
ATACATATACAT
ATACATATACAT
ATACATATACAT
ATACATATACAT
ATACATATACAT
ATACATATACAT
ATACATATACAT
ATACATATACAT
ATACATATACAA

Nr of selected repeats 9 Similarity 0.975309

Consensus:

ATACATATACAT

>Cele-UNSB01_5:19329973-19330169 Satlength=197 Nr of Repeats=8 RepeatLength=12
seed=ATATGTATAT

ATATGTATATGT
ATATGTATATGT
ATATGTATATGTATGGGCCTTAACCTTATTCATGTCTATTCACTATTTATTTATTTTGGATCACGATTTCAATCGTAATA
AATACAATACAATACAATACA
ATATCTATATCTATGTTC
ATATCTATATCT
ATATTTATATTT
ATATTTATATCA
ATATGTGTATTTATATGC

Nr of selected repeats 5 Similarity 0.777778

Consensus:

ATATnTATATnt

>Cele-UNSB01_5:19334298-19334625 Satlength=328 Nr of Repeats=23 RepeatLength=14
seed=TATATGTTAT

TATATGTTATGTGG
TATATGTTATATGT
TATATGTTATATGT
TATATGTTATATGT
TATATGTTATATGT
TATATGTTATATGT
TATATGTTATATGT
TATATGTTATATGT

TATATGTTATATGT
TATATGTTATATG
TATATGTTATATGT
TATATGTTATATG
TATATGTTATATGT
TATATGTTATATGTTATATGT

Nr of selected repeats 20 Similarity 0.980952

Consensus:

TATATGTTATATGT

>Cele-UNSB01_5:19338537-19338764 Satlength=228 Nr of Repeats=7 RepeatLength=33

seed=GGAATTCAAA

GGAATTCAAATTTATTTCAGAAAAATTTTGGC
GGAATTCAAATTTTCATCAAAAAAATTTTGGC
GGAATTCAAATTTCTTCAAAAAAATTTTGGCG
GGAATTCAAATTTATTTCAAAAAATTTTGGCG
GGAATTCAAATTTATTTCAAAAAATTTTGGCG
GGAATTCAAATTTATTTCAAAAAATTTTGGCG
GGAATTCAAATTTATTTCAAAAAATTTTGGCG
GGAATTCAAATTTATTTCAAAAAATTTTGGCG

Nr of selected repeats 5 Similarity 0.967677

Consensus:

GGAATTCAAATTTaTTCAAAAAAaTTTTGGCG

>Cele-UNSB01_5:19352170-19352944 Satlength=775 Nr of Repeats=29 RepeatLength=26

seed=TGAAATTTCA

TGAAATTTCAAAAAATCGATTTTC
TGAAATTTCACAAAATATCGATTTTC
TGAAATTTTCAGAAAATCGATTTTC
TGAAATTTTCACAAAAATCGATTTTC
TGAAATTTCTCAGAATATCGATTTTC
TGAAATTTTCAGAAAATCGATTTTC
TGAAATTTTCACAAAATATCGATTTTC
TGAAATTTTCACAGAATATCGATTTTC
TGAAATTTTCACAAAATATCGAATTTTC
TGAAATTTTCACAAAATATCGATTTTC
TGAAATTTTCGCAGAATATCGATTTTC
TGAAATTTTCACAAAAATCGATTTTTTAATAGATTTTGGAAATTTTGGAAATTATTGATTTT
TGAAATTTTCAAAAATCGATTTTC
TGAAATTTTCACAAAATATCGATTTTC
TGAAATTTTCAGAAAATCGATTTTC
TGAAATTTTCACAAAAATCGATTTTC
TGAAATTTCTCAGAATATCGATTTTC
TGAAATTTTCAGAAAATCGATTTTC
TGAAATTTTCACAAAATATCGATTTTC
TGAAATTTTCACAGAATATCGATTTTC
TGAAATTTTCACAAAATATCGAATTTTC
TGAAATTTTCACAAAATATCGATTTTC

TGAAATTTTCGCAGAATATCGATTTTC
TGAAATTTTCAGAAAATCGATTTTT
TGAAATTTTCACAAAAAATCGATTTTC
TGAAATTTTCTCAGAATATCGATTTTC
TGAAATTTTCAGAAAATCGATTTTC
TGAAATTTTCACAAAAATCGATTTTT
TGAAATTTTCACAGAATATCGAATTTTC

Nr of selected repeats 20 Similarity 0.904453

Consensus:

TGAAATTTTCaCaAaAATATCGATTTTC

>Cele-UNSB01_5:19385136-19386466 Satlength=1331 Nr of Repeats=44

RepeatLength=20 seed=AAAAATCAAT

AAAAATCAATAAAATTTCCCG

AAAAATCAATCAATTTCCGA

AAAAATCGATAAAATTTCCCG

AAAAATCAATAAAATTTCCAT

AAAAATCAATAAAATTTCCCG

AAAATTCAATAAAATTTTTAGAAAAATTGATAAAATTTCCCG

AAAAATCAATAAAATTTCTAT

AAAAATCAATAAAATTTCCAG

AAAAATCAAAAAATTTTCAG

AAAAATCAATAAAATTTGGCTCCGCCCTTTTTACAGTACCCCATGAAGTTTTCGGTGGATGATGAATCGGTGTCTCGA

AGGATGCCGGCGGATGTGACTGATAATTTGACGTGCATTTTGTAGTTTGTGCTTTTGAACGA

AAAAATCGATAATTTTCA

AAAAATCGATAAAATTTCCA

AAAAATCGATATTTTTCTAG

AAAAATCAATAAAATTACCAGAAAATCGATAATTTTGTCCA

AAAAATCGATAATTTCCA

AAAAATCGATATTTTTCTAG

AAAAATCGATAAAATTACCAGAAAATCGATAATTTTGTCCA

AAAAATCGATAAAATTACCCTGGCGATTTGGCAGGCGCCTCGGCCTCGGCCTCTGCCTTCGCCTGTGCCTTCGTAAATCT

TCTCTGAATTTGAACGGGCGTCTCATACATTGAATCACTGAATACACGCATCATTGACGGTGTCTCCAGACTCCGCGAA

CTCGCCACTTTTCAGAGAATTTGAACGGGGCGGAGTCTGAGGGGGCGGAGCCTGCTCGGCCAGTTGCTTTTTTTAGTTTCG

AAATTTTCGTGTTCTTTTCGATTTGAGCAGGTGGTACGCCTCTTCGAGTTGTCTGAAATATAA

AAAAATCGATAATTTTTCAG

AAAAATCAATAATTTTTCAG

AAAAATCAATAATTTTTCAG

AAAAATCAATAATTTTTCAG

AAAAATCAATAATTTTTCAG

AAAAATCAATTAATTTCCA

AAAAATCGATAAAATTTCCGA

AAAAATCAATAAAATTTTCAG

AAAAATCAATAAAATTTCCA

AAAAATCAATAAAATTTTCAG

AAAAATCAATAAAATTTCCA

AAAAATCAATAAAATTTTCAG

AAAAATCAATAAAATTTCCA

AAAAATCAATAAAATTTTCAG

AAAAATCAATAAAATTTCCA

AAAAATCAATAAAATTTTCAG

AAAAATCAATAAAATTTCCA

AAAAATCAATAAAATTTTCAG

AAAAATCAATAAAATTTCCA

AAAAATCAATAAAATTTTCAG

AAAAATCAATAAAATTTTCAG

AAAAATCAATAAAATTTCCAA
AAAAATCAATAAAATTTTCAG
AAAAATCAATAAAATTTCCA
AAAAATCAATAAAATTTTCAG
AAAAATCAATAAAATTTCCAA
AAAAATCAATAAAATTTTCAG

Nr of selected repeats 31 Similarity 0.770186

Consensus:

AAAAATCAATAAAATTTTCAG

>Cele-UNSB01_5:19386514-19386960 Satlength=447 Nr of Repeats=10 RepeatLength=20
seed=ATTGATTTTT

ATTGATTTTTCCGTACTTTTTATAGTGTTCTTTTTTGGTTTTTCTTCACTATAAGCATCACGTAGTCGATCGAATGCC
GCTACTTTTTCGTTCCAAAAATGTCGATAAACTCGCCGTTGGCGGTGTTGGAATGTTAAAACACGTGTCAAATCACGTG
TATACTGATTGATTTCTCCGAAATGGGGTGAAC

ATTGATTTTTATCTGAAAAAATTAATAAATTAATAAATTAATAATTTGAAGAAAAATCGATAAATTTTTATAATTATCGAG
TTTTCTGAAAATTT

ATTGATTTTTCTGAAAATTT

ATCGATTTTTCTAAAAATTT

ATTGATTTTTCTGAAAATTT

ATTGATTTTTTTGAAAATTTG

ATTGATTTTTCTGAAAATTT

ATCGATTTTTCTAAAAATTT

ATTGATTTTTCTGAAAATTT

ATTGATTTTTCTGAAAATTT

Nr of selected repeats 8 Similarity 0.861905

Consensus:

ATTGATTTTTCTGAAAATTT

>Cele-UNSB01_5:19387732-19388133 Satlength=402 Nr of Repeats=17 RepeatLength=20
seed=CAGAAAAATC

CAGAAAAATCGATAAATTTT

CAGAAAAATCGATAAATTTT

CAAAAAATCGATAAATTTT

CAGAAAAATCGATAAATTTT

CAGAAAAATCAATAAATTTT

CAGAAAAATCGATAAATTTT

CAAAAAATCGATAAATTTT

CAGAAAAATCGACAAATTTT

CAGAAAAATCAATAAATTTT

CAGAAAAATCAATAAATTTT

CAGAAAAATCAATAAATTTT

CAGAAAAATCGATAAATTTT

CAAAAAATCAATAAATTTT

CAGAAAAATCAATAAATTTTCAAAAAAATCGATAAATTTT

CAAAAAATCAATAAATTTTCAAAAAAAGCATAGAAATTT

CAGAAAAATCGATAAATTTTCAAAAAAATCGATAAATTTT

Nr of selected repeats 12 Similarity 0.905051

Consensus:

CAGAAAAATCaATAAATTTT

>Cele-UNSB01_5:19392335-19392460 Satlength=126 Nr of Repeats=6 RepeatLength=18
seed=ATTAGCAGCG

ATTAGCAGCGCAAAAAATTAGAACCGACCAAAAA

ATTAGCAGCGACCAAAAA

ATTAGCAGCGACCAAAAA

ATTAGCAGCGACCAAAAA
ATTAGCAGCGACCAAAAA
ATTAGCAGCGACCAAAAA
Nr of selected repeats 4 Similarity 1.000000
Consensus:
ATTAGCAGCGACCAAAAA
>Cele-UNSB01_5:19398669-19400674 Satlength=2006 Nr of Repeats=80
RepeatLength=20 seed=TATCGATTTT
TATCGATTTTTTTGAAAATT
TATTGATTTTTCTGAAAATT
TATTGATTTTTCAGGAAATT
TATTGATTTTTCAGGAAATT
TATTGATTTTTGGGAATTTACTGATTTTTCTGAAAATT
TATTGATTTTTCAGGAAATT
TATTGATTTTTCTAGAAATT
TATCGATTTTTCTAGAAATT
TATCGATTTTTCTGGAATTT
TATCGATTTTTCTGAAAATT
TATTGATTTTTCAGGAAATT
TATTGATTTTTCAGGAAATT
TATTGATTTTTGGGAATT
TATTGATTTTTCTGAAAATT
TATTGATTTTTCAGGAAATT
TATTGATTTTTTGTAATTTTTGATTTTTCGGAAAGT
TATTGATTTTTCTGAAAATT
TATTGATTTTTGGGAATT
TATTGATTTTTCTGAAAATTTTTGATTTTTGGGAATT
TATTGATTTTTCTGAAAATTTTTGATTTTTGGGAATT
TATTGATTTTTCTGAAAATT
TATTGATTTTTCTGAAAAGGTAGTTTTTTTACGGGTTTTGGGTGATTTTTCTTAATATTCGCAATATTTGAGCATT
TTTTCATTTTTAAAAGGAAAATAGCGAAGTTAAGCTAATTTTCAGAGTTTTGGGCAAAAAACTGGGACAGTTTTAGGTT
TTGATAGTTTTTATGAAAAAATCGAATTTTTGGCAAAAAAAATTGAGAAAAACGCTGGGTTTTCGCTGAAATTGTA
AATTTGAACAAAAATTTAGAAAATTTGCTCATTTTTTCGATAAAAACTTCAAATTTGAGCTTTTCACATATTTTGAAT
GGAATTTCAAACCTTTGTCTTTTTTACGAATAT
TATTGATTTTTCTGAAAATG
TATCGATTTTTCTAGAAATT
TATCGATTTTTCTAGAAATT
TATCGATTTTTCTGGAATTT
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TATCGAATTTTTCTAGAAATT
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TATCGATTTTTCTGAAAATT
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TATTGATTTTTCTGGAATTT
TATCGATTTTTCTGGAATTT

TATCGATTTTTCTGAAATT
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TATCGATTTTTCTGGAATTT
TATCGATTTTTCTAGAAATT
TATCGATTTTTCTGGAATTT
TATCGATTTTTCTAGAAATT
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TATCGATTTTTCTGGAATTT
TATTGATTTTTCTGGAATTT
TATCGATTTTTCTGGAATTT
TATCGATTTTTCTGAAATT
TATCGATTTTTCTGGAATTT
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TATCGATTTTTCTAGAAATT
TATCGATTTTTCTAGAAATT
TATCGATTTTTCTGGAATTT
TATCGATTTTTCTAGAAATT
TATCGATTTTTCTGAAAATT
TATCGATTTTTCTGGAATTT
TATTGATTTTTCTAGAAATT
TATTGATTTTTCTAGAAATT

Nr of selected repeats 72 Similarity 0.876291

Consensus:

TATcGATTTTTCTgGAAaTT

>Cele-UNSB01_5:19404337-19404490 Satlength=154 Nr of Repeats=5 RepeatLength=33
seed=TTAGCAGCGC

TTAGCAGCGCCCAAAAACCTTGTAGTTTGTAGTC
TTAGCAGCGCCCAAAATCTTGTAGTTTGTAGTC
TTAGCAGCGCCCAAAATTGAA
TTAGCAGCGCCCAAAATCTTGTAGTTTGTAGTC
TTAGCAGCGCCCAAAATCTTGTAGTTTGTAGTC

Nr of selected repeats 4 Similarity 0.979798

Consensus:

TTAGCAGCGCCCAAAAtCTTGTAGTTTGTAGTC

>Cele-UNSB01_5:19407563-19408121 Satlength=559 Nr of Repeats=25 RepeatLength=20
seed=AATTTATTGA

AATTTATTGATTTTTCCGGA

AATTTATTGATTTTTCCGGA
AATTTATTGATTTTTCCGGA
AATTTATTGACTTTTTTGGG
AATTTATTGATTTTTTGGG
AATTTATTGATTTTTTGGG
AATTTATTGATTTTTCTGAA
AATTTGTTGATTTTTCTGAATATTCATTGATTTTTCTGAA
AATTTATTGATTTTTCTGAA
AATTTATTGATTTTTCTGAATGTTCACTGATTTTTCTGGA
AATTTATTGATTTTTCTGG
AATTTATTGATTTTTCTGAA
AATTTATTGATTTTTTGG
AATTTATTGATTTTTCTGGG
AATTTATAGATTTTTCTGAA
AATTTATTGATTTTTTGGG
AATTTATTGATTTTTCTGGG
AATTTATTGATTTTTCTGG
AATTTATTGATTTTTCTGAA
AATTTATTGATTTTTTGG
AATTTATTGATTTTTCTGGG
AATTTATAGATTTTTCTGAA
AATTTATTGATTTTTCTGAA
AATTTATTAATTTTTTGGG

Nr of selected repeats 16 Similarity 0.823333

Consensus:

AATTTATTGATTTTTtTGga

>Cele-UNSB01_5:19408877-19410842 Satlength=1966 Nr of Repeats=65

RepeatLength=33 seed=AGCAGCGCCC

AGCAGCGCCCAATTTATGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATCTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATCTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATTTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATTTGAATT
AGCAGCGCCCAAAATCTTGTAGTTTGTAGTGT
AGCAGCGTCCAAAATTTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATTTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATTTGAATT
AGCAGCGCCCAAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATCTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATTTGAATT
AGCAGCGCCCAAAATTTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATTTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATTTGAATT
AGCAGCGCCCAAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATCTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATTTGAATT
AGCAGCGCCCAAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAAATCTTGTAGTTTGTAGTCTT

AGCAGCGCCCAAATGAATT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATGAATT
AGCAGCGCCCAAATTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATGAATT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCTAAAATTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTA
AGCAGCGCCCAAATCCTGTAGTTTGTAGTGTT
AGCAGCGTCCAAAATTTGTAGTTTGTAGCTTT
AGCAGCGCCCAAATTTAATT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTA
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTA
AGCAGCGCCCAAATCCTGTAGTTTGTAGTGTT
AGCAGCGTCCAAAATTTGTAGTTTGTAGCTTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTGTT
AGCAGCGTCCAAAATTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATGAATT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCTAAAATTTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTA
AGCAGCGCCCAAATCCTGTAGTTTGTAGTGTT
AGCAGCGTCCAAAATTTGTAGTTTGTAGCTTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT
AGCAGCGCCCAAATTTAATT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTA
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTA
AGCAGCGCCCAAATCCTGTAGTTTGTAGTGTT
AGCAGCGTCCAAAATTTGTAGTTTGTAGCTTT
AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT

Nr of selected repeats 49 Similarity 0.900143

Consensus:

AGCAGCGCCCAAATCCTGTAGTTTGTAGTCTT

>Cele-UNSB01_5:19416239-19417040 Satlength=802 Nr of Repeats=34 RepeatLength=20
seed=GATTTTCTG

GATTTTCTGAAAATATATC
GATTTTCTGAAAATATATC
GATTTTCTGAAAATTTAT
GATTTTCTGAAAATTTAT
GATTTTCTGAAAATTTAT
GATTTTCTGAAAATTTAAT
GATTTTCTGAAAATTTATCGACTTTCCTGAAAATATATC
GATTTTCTGAAAATTTAT
GATTTTCTGAAAATTTATTTGATTTTGTAGAAAATTTACT

GATTTTTCTGGAAATTTATC
GATTTTTCTGGAAAATTTATC
GATTTTTCTGAAAATTTATT
GATTTTTTTGAAAATTTATT
GATTTTTCTGAAAATTTATT
GATTTTCCTGAAAATTTATTGATTTTTTAGAAAATTTACT
GATTTTTCTGGAAATTTATC
GATTTTTCTGGAAAATTTATC
GATTTTTCTGAAAATTTATT
GATTTTTTTGAAAATTTATT
GATTTTTCTGGAAAATTTATT
GATTTTTCTGAAAATTTATT
GATTTTTCTGAAAATTTATT
GATTTTTCTGAAAATTTATT
GATTTTTCTGAAAATTTATT
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GATTTTTCTGAAAATTTATT
GATTTTTCTGAAAATTTATT
GATTTTTCTGAAAATTTATT
GATTTTTCTGAAAATTTATT
GATTTTCCTGAAAATTTATT
GATTTTTCTAAAATTTATTAACTTTCTGAAAATTTATT
GATTTTTCTGAAAATTTATTGATTTTTTAGAAAATTTATT
GATTTTTCTGGAAAATTTATT
GACTTTCTGGAAAATTTATCGATTATTCGAAAATTTATC
GACTTTCTGAAAATTTATT

Nr of selected repeats 28 Similarity 0.875661

Consensus:

GATTTTTCTGAAAATTTATt

>Cele-UNSB01_5:19434732-19435093 Satlength=362 Nr of Repeats=16 RepeatLength=19
seed=TGGCGCATTT

TGGCGCATTTCTCGTGCGT
TGGCGCATTTCTTGAGCCT
TGGCGCAATTCTCGTGCGT
TGGCACATTTCTGGTGCCTTGACGCAGTTCTAGTGACT
TGGCGCATTTCTCGTGCTT
TGGCGCATTTTTCTCGTGCTT
TGGCGCAATTCTCGTTTCT
TGGCGCATTTCTGATGCCT
TGGCGCATTTTTCTCGTGCTT
TGACGCATTTCTTGTTGCCA
TGGCGCATTTCTCGTGCA
TGGCGCATTTCTGGTGCCT
TGGCGCATTTCTTGTTGCCCTGTCGTCAGTATAGTGCCTTGGCACAAATTCTCGTGCA
TGGCGCATTTCTCGTGCTT
TGGCGCATTTCTCGTGAGT
TGTGCGATTTCCCGTGTAT

Nr of selected repeats 14 Similarity 0.787160

Consensus:

TGGCGCATTTCTcGTGccT

>Cele-UNSB01_5:19480245-19483641 Satlength=3397 Nr of Repeats=189
RepeatLength=18 seed=GCTGCTAATT

GCTGCTAATTTTCTGGAC
GCTGCTAATTTTTTGGTCA
CTGCTAATTATTTGGTC

GCTGCTAATTTTTTGGGC
GCTGCTAATTATTTGGTC
GCTGCTAATTTTTTGGTC
GCTGCTAATTATTTGGTC
GCTGCTAATTTTTTGGTCA
CTGCTAATTATTTGGTC
GCTGCTAATTTTTTGGGC
GCTGCTAATTATTTGGTC
GCTGCTATTTATTTGGGC
GCTGCTAATTATTTGGGC
GCTGCTAATTTTTTGGGC
GCTGCTAATTATTTGGTC
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GCTGCTAATTTTTCTGGGC
GCTGCTAATTTTTTGGTC
GCTGCTAAATTTTTGGGC
GCTGCTAATTTTTTGGTC
GCTGCTAATTATTTGGTC
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GCTGCTAATTTTTTTGGTC
GCTGCTAATTTTTTTGGTC
GCTGCTAATTTTTTTGGGC
GCTGCTAATTTTTTTGGTC
GCTGCTAATTTTTCTGGGC

Nr of selected repeats 161 Similarity 0.900696

Consensus:

GCTGCTAATTTtTtTGGtC

>Cele-UNSB01_5:19517858-19518362 Satlength=505 Nr of Repeats=37 RepeatLength=12
seed=AGGCTCAGGC

AGGCTCAGGCTC
AGGCTCAGGCC
AGGCTCAGGCTC
AGGCTTAGGCTT
AGGCTTAGGCTGAGGATT
AGGCTTAGGCTC
AGGCTTAGGCAC
AGGCTCAGGCTC
AGGCTCAGGCTC
AGGCTCAGGCTT
AGGCTCAGGCTT

AGGCTTAGGCTTAGGCTGAGGATT
AGGCTTAGGCTC
AGGCTTAGGCAC
AGGCTCAGGCTC
AGGCTCAGGCTC
AGGCTCAGGCTT
AGGCTCAGGCTT
AGGCTTAGGCTTAGGCTTAGGTTTCATTCTT
AGGCTTAGGCTT
AGGCTTAGGCCTTAGGCTTTGGCTT
AGGCTAAGGCTTAAACTAAGATTT
AGGCACAGGCTC

Nr of selected repeats 32 Similarity 0.903226

Consensus:

AGGCTCAGGCTC

>Cele-UNSB01_5:19521326-19521536 Satlength=211 Nr of Repeats=15 RepeatLength=12
seed=GCCTAAGCCT

GCCTAAGCCTAA
GCCTGAGCCTGA
GCCTGAGCCTGT
GCCTAAGCCTAAGCCTGA
GACTAAGCCTAA
GCCTAAGCCTAA
GCCTAAGCCTAA
GCCTTAGCCTAA
GCCTAAGCCTGA
GCCCAAGCCTTA
GTCTAAGCCTAAT
CCTAAGCCTACTCATAAACCTAAATCTAA
GCCTAAGCCTAA
GCCTAAGCCTGA
GCCTGAGCCTGAGCCTGA

Nr of selected repeats 11 Similarity 0.818182

Consensus:

GCCTaAGCCTaA

>Cele-UNSB01_5:19549755-19549902 Satlength=148 Nr of Repeats=7 RepeatLength=21
seed=CACACGAGCT

CACACGAGCTTGAGAGCCCGG
CACACGATCTTCAGATTCCAC
CACACGAGCTTGAGAGCCCGG
CACACGAGCTACAGTCTCTAC
CACACGAGCTTGAGAGCCCGG
CACACGATCTTCAGATTCCAC
CACACGAGCTTGAGAGCCCGG

Nr of selected repeats 7 Similarity 0.727891

Consensus:

CACACGAgCTTgAGAgcCCgg

>Cele-UNSB01_5:19567297-19567464 Satlength=168 Nr of Repeats=5 RepeatLength=29
seed=CTCGTCAGTG

CTCGTCAGTGGATGGACGAGGAATGAGCG
CTCGTCAGTGGGTGGACGAGGAATGAGCG
CTCGTCAGTGGGTGGACGAGGAATGAGCG
CTCGTCAGTGGGTGGACGAGGAATGAGCA
CTCGTCAGTGGATGGACGAGGAGTGAGCACTCGTCAGACGAGGAGTGGACG

Nr of selected repeats 4 Similarity 0.954023

Consensus:

CTCGTCAGTGGgTGGACGAGGAATGAGCg

>Cele-UNSB01_5:19604230-19604355 Satlength=126 Nr of Repeats=4 RepeatLength=22
seed=GTGCGCAGAA

GTGCGCAGAATGTGTGCTGAAT

GTGCGCAGAATCTGCTCAGGGG

GTGCGCAGATTGTGCGCACGAGGCTAGGCCACCAAGAAAAAGCCACAACAACAGCAAT

GTGCGCAGAATCGGCGCAGGGG

Nr of selected repeats 3 Similarity 0.676768

Consensus:

GTGCGCAGAATctGcgCaGggg

>Cele-UNSB01_5:19643678-19643940 Satlength=263 Nr of Repeats=11 RepeatLength=21
seed=TCTAATTAGA

TCTAATTAGAAAAATAGGTGATCTAACGTGTCCCAATTAGAAATGCTTTTTT

TCAAATTAGATTACCTTTTTTT

TCTAATTAGACTACCTTTTTTT

TCTAATTAGATCACCATTTTTT

TCTAATTAGATCACCTTTTTTT

TCTAATTAGATCACCTTTTTTT

TCTAATTAGATCACCTTTTTTT

TCTAATTAGATCACCTTTTTTT

TCTAATTAGATCACCTTTTTTT

TCTAATTAGATCACCTTTTTTT

TCTAATTAGATCACCTTTTTTT

Nr of selected repeats 10 Similarity 0.939330

Consensus:

TCTAATTAGATcACCTTTTTTT

>Cele-UNSB01_5:19645516-19645794 Satlength=279 Nr of Repeats=13 RepeatLength=21
seed=TTCTAATTAG

TTCTAATTAGATCACGCTCCT

TTCTAATTAGATGCGCATTCC

TTCTAATTAGATCACCCCTCTT

TTCTAATTAGATATGATTTTGCGT

TTCTAATTAGACGCGCCTTCT

TTCTAATTAGATCACGCTCCT

TTCTAATTAGATTAGCATTCC

TTCTAATTAGATCACCATCTT

TTCTAATTAGACATGGTTTTGTGT

TTCTAATTAGACGCGCCTTCT

TTCTAATTAGAAATGCCTATT

TTCTAATTAGAAATGCCCTT

TTCTAATTAGAAGTGCTTCTT

Nr of selected repeats 10 Similarity 0.650000

Consensus:

TTCTAATTAGATnCGCcnTctt

>Cele-UNSB01_5:19666114-19666380 Satlength=267 Nr of Repeats=11 RepeatLength=19
seed=GATCCTTGGC

GATCCTTGGCGCTTTTCGC

GATCCTTAGCGCTTTTCTCGATTATTGGCGCTTTTCTCGATCCATTGTGCTTCTCTC

GATCCTTGGCACATTTCCCGATCCATTGCGCTTTTCTC

GATCCTTAGCGCTTTTTTTT

GATCCTTGGCGCCTTTTTTT

GATCCTTGGCGCTTTTCTC

GATCCTTGGCGCTTTTCTC
GATCCTTGGCGCTTTTCTC
GATCCTTGGCGCTTTTCTC
GATCCTTGGCGCTTTTCTC
GATCCTTGGCGCTTTTCTC

Nr of selected repeats 9 Similarity 0.898636

Consensus:

GATCCTTGGCGCTTTTcTc

>Cele-UNSB01_5:19667001-19667210 Satlength=210 Nr of Repeats=9 RepeatLength=19
seed=TTGCGCCAAG

TTGCGCCAAGACTCGAA
TTGCGTCAAGACTAAAA
TTGCGCCAAGGCACTGAAG
TTGCGCCAAGGCACTAGAAA
TGCGCCAAGGCACTAGAAAATGCGCTAAGGCACTAAAACGGCGGCAATGCACTAGAA
TTGCGTCAAGGCACTGGAA
TTGCGTCAAGGACGAGAA
TTGCGCCAAGGCACTAGAA
TTGCGCCAAGACACAATAA

Nr of selected repeats 7 Similarity 0.744444

Consensus:

TTGCGcCAAGgCACTagAA

>Cele-UNSB01_5:19670399-19670678 Satlength=280 Nr of Repeats=9 RepeatLength=31
seed=CGGGAAATTC

CGGGAAATTCAAATTTTCAGTTAATTTTGT
CGGGAAATTTGAATTTTCAGTCAATTTTGGT
GGGAAATTCAAATTTCCAATCAATTTTGG
CGGGAAATTTGAATTTTCGAATAATTTTGG
CGGGAAATTTCAAATTTTCAGTTAATTTTAGG
CGGGAAATTCAAATTTTAAATTAATTTTGA
CGGGAAATTCAAAATTTTCAGTCAATTTTAGG
CGGGAAATTCAAATTTTGTAAATTTTGA
CGGGAAATTCGAATTTTCAGTCGACTTTCCG

Nr of selected repeats 7 Similarity 0.774706

Consensus:

CGGGAAATTCaAATTTTcAgTtAATTTTtGg

>Cele-UNSB01_5:19673680-19673832 Satlength=153 Nr of Repeats=5 RepeatLength=19
seed=AGAATTGCGC

AGAATTGCGCCAAGGCACG
AGAATTGCGCCAAGGCACG
AGAATTGCGTCAAGGCACGAAAAGTGCGTCAAGGCACAAGAAATACGTCAAGACT
AGAATTGCGCCAGGACT
AGAATTGCGTCAAGGCACCAATTTTGCGTTAATGCACT

Nr of selected repeats 3 Similarity 0.859649

Consensus:

AGAATTGCGCCAaGgCACg

>Cele-UNSB01_5:19673879-19674316 Satlength=438 Nr of Repeats=16 RepeatLength=19
seed=GCCTTGACGC

GCCTTGACGCAATTCTAGT
GCCTTGACGCAATTCTAGC
GCCTTGACGCAATTCTAGT
GCCTTGACGCAATTCTAGT
GCCTTGACGCAATTCTACC
GCCTTGACGCAATTCTAGTGCCTTGGCACAATTCTAGTGCATTAACGAAATTCTCGT

GCCTTGGCGCCTTTCTCGTTCCTGACGTATTTCTAGA
GCCTTGACGCAATTCTAGTGACTTAGCGTAATTCTCGTTCCTTGACACAATTCTCGT
GCCTTGGCGCCTTTCTCGTCTGACGTATTTCTAGA
GCCTTGGCGCATTTCCTATTCCTTGGCGCAACTCTAGT
GCCTTGACGCAATTCTAGT
GCCTTGACGCAATTTAAT
GCCTTGACGCAATGCTAGT
GCCTTGACGCAGTTCTAGT
GCCTTGACGCAACTCTAGT
GCCTTGACGCAATTCTCGT

Nr of selected repeats 11 Similarity 0.888995

Consensus:

GCCTTGACGCAATTCTAGT

>Cele-UNSB01_5:19696042-19696279 Satlength=238 Nr of Repeats=14 RepeatLength=17
seed=GAATTAGAAA

GAATTAGAAAACCTTTGA
GAATTAGAAAACCTTTGA
GAATTAGAAAACCTTTGA
GAATTAGAAAACCTTTGA
GAATTAGAAAACCTTAA
GAATTAAGAAAAAGTAA
GAATTAGAAAATTTCTG
GAATTAGAAAATTTGAA
GAATTAGAAAATTCGAA
GAATTAGAAAATGAAA
GAATTAAGAAAATTTTG
GAATTAGAAAATTTTA
GAATTAGAAAATTTTCG
GAATTAGAAAATTTAA

Nr of selected repeats 13 Similarity 0.554584

Consensus:

GAATTAGAAAATttga

>Cele-UNSB01_5:19714208-19714335 Satlength=128 Nr of Repeats=5 RepeatLength=25
seed=AAAAATCTGT

AAAAATCTGTTCTTCGAGGTCCCTA
AAAAATCTGTTCTCAGAGGTCCCTG
AAAAATCTGTTTATGAGGTCCCTG
AAAAATCTGTTCTGTGAGGTCCCTT
AAAAATCTGTTCTCCGAGCTATCTGG

Nr of selected repeats 3 Similarity 0.822222

Consensus:

AAAAATCTGTTcTnnGAGGTCCCTg

>Cele-UNSB01_5:19721189-19721423 Satlength=235 Nr of Repeats=7 RepeatLength=22
seed=ACGTATACAG

ACGTATACAGGCATATACACAT
ACGTATACAGTCATATACACAT
ACGTATACAGGCATATACATAT
ACGTATACAGTCATATACACAT
ACGTATACAGGCATATACACTT
ACGTATACAGGCATATACACATACGTACATACGCATGGACACGTGTGAATGTACACAAGTACGCAAGAACATACGCATA
GAC

ACGTATAAAGGTACCCAAGCACACATGTACATACCCATAGCT

Nr of selected repeats 5 Similarity 0.915152

Consensus:

ACGTATACAGgCATATACaT

>Cele-UNSB01_5:19721079-19721595 Satlength=517 Nr of Repeats=5 RepeatLength=21
seed=TATTTTCAAA

TATTTTCAAAAAAAAAATTCGAAATACTATTATTTTTCCTATGAAAATTCCTTTTTTCTCCTTTTTTAATACAGAAGTGG
GGTTTCAACTGTTTTTAACTGTTTTTACACACGTATACAGGCATATACACATACGTATACAGTCATATACACATACGT
ATACAGGCATATACATATACGTATACAGTCATATACACATACGTATACAGGCATATACACTTACGTATACAGGCATATA
CACATACGTACATACGCATGGACACGTGTGAATGTACACAAGTACGCAAGAACATACGCATAGACACGTATAAAGGTAC
CCAAGCACACATGTACATACCCATAGCTACGTATACAGATACATATGTACACATGTACATACACTTAACCTCGCATAAA
ATTTGTATACACACACAAAAACAGAAAAAATTTAAAG

TATTTTCAAAAAAAAAATTTAAAA

TATTTTCAAAAAAAAAATTTAAAA

TATTTTCAAAAAAAAAATTTGAAA

TATTTTCAAAAAAAAAATTTAAAA

Nr of selected repeats 3 Similarity 0.957672

Consensus:

TATTTTCAAAAAAAAAATTTaAAA

>Cele-UNSB01_5:19764010-19764338 Satlength=329 Nr of Repeats=4 RepeatLength=82
seed=CCCCGAACGT

CCCCGAACGTGTGGTTCGCTTTCAAACAACCACCTCCTTGCACTACGTTGCGCACACACTCATTTCACGCCAAGCTGCG
GAG

CCCCGAACGTGTGGCCGCTTCAAATAACCACCTCCTTGCACTACGTTGCGCACACACTCATTTCACGCCAAGCTGCG
GAA

CCCCGAACGTGTGGCCGCTTCAAATAACCACCTCCTTGCACTACGTTGCGCATACTCATTTCACGCCAAGCTGCG
GAA

CCCCGAACGTGTGGCCGCTTCAAATAACCACCTCCTTGCACTACGTTGCGCATACTCATTTCACGCCAAGCTGTG
GAA

Nr of selected repeats 4 Similarity 0.948510

Consensus:

CCCCGAACGTGTGGGcCGCTTcCAAAtAACCACCTCCTTGCACTACGTTGCGCacACACTCATTTCACGCCAAGCTGcG
GAa

>Cele-UNSB01_5:19784949-19785086 Satlength=138 Nr of Repeats=6 RepeatLength=23
seed=TTTTTCAGAAA

TTTTTCAGAAAAAACGTATGGAT

TTTTTCAGAAATAGACATTTTCAGA

TTTTTCAGAAAAAAGTCTGGGGAG

TTTTTCAGAAATAGGTATTTTCAGA

TTTTTCAGAAATAGGTATTTTCAGA

TTTTTCAGAAAAAAGTCTGGGAG

Nr of selected repeats 5 Similarity 0.631944

Consensus:

TTTTTCAGAAAtAggtaTttcaGA

>Cele-UNSB01_5:19785568-19787058 Satlength=1491 Nr of Repeats=85
RepeatLength=17 seed=TTGCAAGAAA

TTGCAAGAAAATCTGCA

TTGCAAGAAAATCTGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAAACGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAAACGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAAACGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAAACGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAAACGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAATCTGCA
TTGCAAGAAAAACGCAAGAAAAACCGCAAAAAGTGGGTATAAAAGGTATTAGGTCC

Nr of selected repeats 83 Similarity 0.953951

Consensus:

TTGCAAGAAAATCTGCA

>Cele-UNSB01_5:19792773-19792843 Satlength=71 Nr of Repeats=5 RepeatLength=10
seed=TGGCGAAAGC

TGGCGAAAGC

TGGCGAAAGC

TGGCAAAGCTGACAAAAGC

TGGCGAAAGC

TGGCGAAAGCTGGCGAAAGC

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TGGCGAAAGC

>Cele-UNSB01_5:19792863-19792928 Satlength=66 Nr of Repeats=5 RepeatLength=13
seed=TTGGGGTGGCCT

TTGGGGTGGCCT

TTGGGGTGGCCT

TTGGGGTGGCCT

TTGGGGTGGCCT

TTGGGGTGGCCT

Nr of selected repeats 5 Similarity 1.000000

Consensus:

TTGGGGTGGCCT

>Cele-UNSB01_5:19795988-19796719 Satlength=732 Nr of Repeats=4 RepeatLength=183
seed=TTTCTCTGCG

TTTCTCTGCGTCTCGCCTTGGCTCACAGTATTTTTTACACCAAACCTTCGAGGCTATGTATCTTCGCAACGGGTCGAGAT
ATTGAAAAAGTTCCAACCTAACAAAATATTTCAAATTTTGCTCTGCATCTAATGAATTTAAAATTTAAAATCTGGGCAAG
AAGCAGACAGCGAGGCACCTCAAT

TTTCTCTGCGTCTCGCCTTGGCTCACAGTATTTTTTACACCAAACCTTCGAGGCTATGTATCTTTGCAACGGGTTGAGAT
ATTGAAAAATTTCCAACCTAACAAAATGCTCTAAAATTTATTCTGTATCTTGTGAAATAAACCTTTAAAACCTTAGGCAAA
TCGCAACAGCGAAATACACCCAAG

TTTCTCTGCGTCTCGCCTCGCCTCACACTCTCTTACCCTCAACATTTTAAATGTGTGTATCTCAGTAACGGTTTGCGC
TTTCTAAAAATTTCCAACCTGATGGGATATATAAAATTTTGAATTTCTTCTGACCGTTAAAAAACCTAAGCACATAGGCAA
GACGACAGCAGGAGAAACCTAAT

TTTCCCTGCGTCTCACCTCGCCTCACACTATTTTGCACACCAAACCTTTGCGACTATGTAACCTCTGTAACGGGTTGCGCT
TTCTGAAAAATTCCAACCTGACGGGATACATGAAATTTTGAATTCTTCTCACCGTTCAAAAACCTATACACCTAGACAAG
ACGCAGACAACAAGACACCCCCAAT

Nr of selected repeats 3 Similarity 0.615789

Consensus:

TTTCTCTGCGTCTCGCCTcGcCTCACAcTaTtTTnCACaCCAAAcTTtgagncTaTGTAtCTctGtAACGGgTTGcGcT
tTcTgAAAAATTCCAACCTgAcgggATataTaAAATTTngaATTCTttcTcaccGTtaAAAAACTAaacaCcTAGgCAAg
aCGCAGACAgCgAgAnAccCCcAAt

>Cele-UNSB01_5:19815492-19815850 Satlength=359 Nr of Repeats=22 RepeatLength=12
seed=CTTAGGCTTA

CTTAGGCTTAGG

CTTGGGCTTAGG

CATAGGCTTAAG

CTTAGGTTTAAGATTAGC

CTTAGGTTTAAG

CTTAGCCTTACA

CTTAGGCTTAGG

CTTAGGCTTAGG

CTTAGGCTTAGGCTAAGGCATAGA

CTTAGGCTTAGG

CTTAGGATTACATTAGGCTGAGA

CTTAGGCTTAGGCTTAAGTCTACGCTTATGTTTAGGCTCCGG

CTTAGGCTTATG

CTTAGGCTTAAG

CTTAGGTTTAAGATTAGC

CTTAGGTTTAAG

CTTAGCCTTACA

CTTAGGCTTAGG

CTTAGGCTTAGG

CTTAGGCTTAGGCTAAGGCATAGA

CTTAGGCTTAGG

CTTAGGATTACATTAGGCTGAGACTTAGG

Nr of selected repeats 15 Similarity 0.813757

Consensus:

CTTAGGCTTAAG

>Cele-UNSB01_5:19826165-19826303 Satlength=139 Nr of Repeats=11 RepeatLength=12
seed=CTTAGGCTTA

CTTAGGCTTAGG

CTTAGGCTTAGG

CTTGGGCTTAGG

CTTAGGCTTAGG

CTTAGCCTTAGG

CTTAGGCTTAGG

CTTAGGCTTAGG

CTTAGCCTTAGG

CTTAGGCTTAGG

CTTAGGCTTAGG

CTTAGGCTTAGGCTTAGG

Nr of selected repeats 10 Similarity 0.938272

Consensus:

CTTAGgCTTAGG

>Cele-UNSB01_5:19832755-19833004 Satlength=250 Nr of Repeats=6 RepeatLength=31
seed=AATTTCCCGC

AATTTCCCGCTAAAATTTAACAGAAAATTTA

AATTTCCCGCTAAAAATTAAGTAAAAATTTG
AATTTCCCGCCGAAAAATTGATCTAAAAATTTG
AATTTCCCGCCGAAAGTTGACTTAAAAATTTGAATTAACCGCTAAAAAATTTGACTGGAAATGTGAATTTTCAGGCAAAAAT
TCAACTGGAAATTTT
AATTTCCCGCCGACAATTGACTGAAATTTTG
AATTTCCCGCCAAAAATCGACTGAAATTTTG
Nr of selected repeats 5 Similarity 0.756250

Consensus:

AATTTCCCGCcaAaAaTtgACtgAAAaTTTg

>Cele-UNSB01_5:19848468-19849404 Satlength=937 Nr of Repeats=7 RepeatLength=14

seed=TTTGTAGTTT

TTTGTAGTTTGTGT

TTTGTACTTTGTAG

TTTATAGTTTTTTAGCCTCTAAAAATCAAAAGTTAAATAAACACATTTATTTTTTTAAAAATTAACAATGAAAAAATGAGT
CAAACAGTCTCCAAAATTCCTCAGCAATCTCCTTGAACACTTTATCACACTTTGCCACTGCGGGACCCGTCAAATGTA
TGTGATTATCCACGTATGATAGTTTGTAGTCTGTGCGAATGTCAGGTACACGTGCGCGTTCGAGAAACAGCTCACCGAG
GTTGAAAACCTGGAATTAGTTGGGGAAAAATGTTGAAAATTCGCAGAAATTTGCACCCAAACCTTGCATTTTGTGCACT
TTATCCTACTGAAACGTTTACGAGCCGTTCTCCAATCCTCATCCACGTGATTTTTTTTCAAGTGAAGGCTCTCCAGCTC
CGCTGGCTTCTGGGTTACTGTATCGAGGTACTTGTTCATAAAATTCAAAGGGTATAGCGGGTGAGGTGCCAGGATGTAG
ATTTTCTTGGCGAATCTGGAATTTTTTTTTAAAAGATATTGAAAATTTAGGACGTACAAAATTAACAACCTGCCCACTT
AAAATAAACTAGGCTTCTAGGTACGGTATGTCAGGTCTAGGTAGGTTAGGTCTAGGTAGGTCATATTGAAATAAGACTA
GGCTTCTAGTACTCTACGTTACAGGAAAAAAAACCTCAATTTTTTAAATTTTTTTTTGTCTTATGTTTTTATCAGATTTT
CAAACTTTTCTAATTTTTCAGAGTTCGATG

TTTGTAGTTTGTAG

TTTGTAGTTTGTAG

TTTGTAGTTTTCGTTTCATTGTTTTTTATTTTCTCCTCGCTGAAAAAACTTTAATAAGCAACAAAAAATAAATCGAGAACC
CGAAAATTAATAATTAATAATAGAAAGTTGTAGGTTGTTGTTTGCAG

TGTGTAGTTTGTAG

Nr of selected repeats 5 Similarity 0.804444

Consensus:

TtTGTAgtTTGTaG

>Cele-UNSB01_5:19849444-19849810 Satlength=367 Nr of Repeats=11 RepeatLength=14

seed=ACAAACTACA

ACAAACTACAACCTTTGTTGTTGAATTTTGAATTTCTCGGGTTCTTGATTAATTGTTTTTTTTTTGTTGCTTTTTTTAGT
GGTTTTCCACCGAGGAAACAAAAAATTGAAA

ACAAACTACATACT

ACAAACTACAACTGCGGACT

ACAAACTACAAACT

ACAAACTACATACT

ACAAACTACACACT

ACAAACTACAACTACAACATTTATTGTTGAATTTTGAATTTTTCGGGTTCTCGTTTTGTTGTTTTTTTTTTGTTGCTTTTT
TTTAGTGGTTTTTCCACCGAGGAAACAAAAAATTGAAA

ACAAACTACATACT

ACAAACTACAAACT

ACAAACTACAAACT

ACAAACTACAAACTACATACT

Nr of selected repeats 7 Similarity 0.931973

Consensus:

ACAAACTACAnACT

>Cele-UNSB01_5:19852888-19853192 Satlength=305 Nr of Repeats=8 RepeatLength=27

seed=GCAGCCGACA

GCAGCCGACACTTTACAGGGGTTTTTACTGCGCTAAAGTCTCTTGAAACCTGACTGATCAC

GCAGCCGACACCTCACAGGTCCCTGTA

GCAGCCGACACATCACTGGTCCCTCCAA

GCAGCCGACACCCGGCTGGCCAGTGGA
GCAGCCGACCTCTCACAGGTTTCTCAAACAGTCGACGCCGAAGTCTCTAATGCTGCCGACCCTTCCCAGGCCCTC
AA

GCAGCCGACACCTAACTAGTCCCTAAG
GCAGCCGACACCTCCCTGGCCCCCTCAA
GCAGCCGACGCCGAAGTCTCCAAA

Nr of selected repeats 6 Similarity 0.584291

Consensus:

GCAGCCGACACCTcaCTgGtCCctnaA

>Cele-UNSB01_5:19913255-19913615 Satlength=361 Nr of Repeats=8 RepeatLength=31
seed=TTCAAATTTT

TTCAAATTTT TAGTTAAAAATAAATTATTACAATATTGGAAAAAATTAATAAATTTTATTATTACGCACTCGTCAA
AAATTTGAACCACTGATTTTGACGAATGTGTAATAATTTTTTTTTTTGGAAATTCAGAAAAA

TTCAAATTTT CAGTCAATTTTGGCGGGAGT

TTCAAATTTT CACTTAATTTT CAGCGGAAAA

TTCAAATTTT CAGTCAATTTTGGCGGGAAAT

TTCAAATTTT CACTTAATTTT CAGCGGAAAA

TTCAAATTTT CAGTCAATTTTGGCGGGAAAT

TTCAAATTTT TAGTCAATTTTGGCGGGAAAT

TTCAAATTTT TAGTCAATTTTGGCGGGAAAT

Nr of selected repeats 7 Similarity 0.819764

Consensus:

TTCaAATTTTcAgTcAATTTTtgGCGGgAAt

>Cele-UNSB01_5:19928437-19928836 Satlength=400 Nr of Repeats=12 RepeatLength=31
seed=GGCGGGAAAT

GGCGGGAAATTCAAAAATTCAAATTTTCAATTAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTTGAAAAATTCAAAGTTTCAATTAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTTAAAATTTCAATCAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTTGAAAAATTCAAAGTTTCAATTAATTTTT

GGCGGGAAATTCAAATTTTCAATTAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

Nr of selected repeats 8 Similarity 0.930876

Consensus:

GGCGGGAAATTCAAATTTTcAgTcAATTTTT

>Cele-UNSB01_5:19938977-19939376 Satlength=400 Nr of Repeats=12 RepeatLength=31
seed=GGCGGGAAAT

GGCGGGAAATTCAAAAATTCAAATTTTCAATTAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTTGAAAAATTCAAAGTTTCAATTAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTTAAAATTTCAATCAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

GGCGGGAAATTTGAAAAATTCAAAGTTTCAATTAATTTTT

GGCGGGAAATTCAAATTTTCAATTAATTTTT

GGCGGGAAATTCAAATTTT CAGTCAATTTTT

Nr of selected repeats 8 Similarity 0.930876

Consensus:

GGCGGGAAATTCAAATTTTCAGTcAATTTTT

>Cele-UNSB01_5:19953202-19953370 Satlength=169 Nr of Repeats=6 RepeatLength=21
seed=ACCCCGATTT

ACCCCGATTTTTACCCAAAAACCGTCAAATTTTACCCAAAAACTCCTATTTTCATCCAAAAA

ACTCCGATTTTCATCCAAAAA

ACCCCGATTTTCACCCAAAAA

ACCCCGATTTTCACCCAAAAAC

ACCCCGATTTTCACCCAAAAA

ACCCCGATTTTCACCCAAAAA

Nr of selected repeats 5 Similarity 0.911111

Consensus:

ACCCCGATTTTCACCCAAAAa

>Cele-UNSB01_5:19987417-19987506 Satlength=90 Nr of Repeats=4 RepeatLength=22
seed=ATTGGATTTT

ATTGGATTTTTCAGCCAAAAAAA

ATTGGATTTTTCACCCAAAAA

ATTGGATTTTTCACCCAAAAA

ATTGGATTTTTCACCCAAAAA

Nr of selected repeats 3 Similarity 0.959596

Consensus:

ATTGGATTTTTCACCCAAAAa

>Cele-UNSB01_5:19998052-19998541 Satlength=490 Nr of Repeats=10 RepeatLength=31
seed=AAAATTTGAA

AAAATTTGAATTTCCCGCCGAAAATTGACTG

AAAATTTGAATTTCCCGCCAAAAATTGACTG

AAAATTTGAATTTCCCGCCGAAAATTGACTG

AAAATTTGAATTTCCCGCCAAAAATTGACTG

AAAATTTGAATTTCCCGCCAAAAATTGACTG

AAAATTTGAATTTCCCGCCAAAAATTGACTG

AAAATTTGAATTTCCCGCCGAAAATTGACTG

AAAATTTGAATTTCTCGCCAAAAATTGACAG

AAAATTTGAATTTCCCCCAAAAAATTGACAG

AAAATTTGAATTTCCCCCAAAAAATTGACACAAAAATAAGGGTAAAGTGGGCGGAGCCTATTCTACAGTACCCATCCG

AAAAAAAAACAATTTTTTTCTTATTATACATTTCGTAATAATTTTTGAACCACTTTTGACGAATGTGTAATATTAAAT

TGTTTTTTTAAAGTTTTTTTCCGATATTGTAATAATTTTTTTTTTAATCAA

Nr of selected repeats 9 Similarity 0.942652

Consensus:

AAAATTTGAATTTCCCGCCaAAAATTGACTg

>Cele-UNSB01_5:20061429-20063397 Satlength=1969 Nr of Repeats=117
RepeatLength=16 seed=CTTAGATCTC

CTTAGATCTCAGTTCT

CTTAGATCTCAATTCA

CTTAGATCTCAATTCC

CTTAGATCTCAATTCA

CTTAGATCTCAATTTT

CTTAGATCTCAATTCCCTCAGATTTCAATTTT

CTTAGATCGCAATTCC

CTTAGATCTCAATTCC

CTTAGATCTCAATTTT

CTTAGATCTCGATTCC

CTTAGATCCCAATTCC

CTTAGATCTCAATTCA

CTTAGATCTCAGTTCCCTCAGTTTTCAATTCC
CTTAGATCCCAATTCC
CTTAGATCTCAATTCA
CTTAGATCTCAATTCC
CTTAAATCTCAATTCC
CTTAGATCTCAATTCC
CTTAGATCTCAGCTCT
CTTAGATCTCAGTTCC
CTTAGATCCCAATTCC
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CTTAGATCTCAGTTCC
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CTTAGATCTCGATTCC
CTTAGATCTCAATTCC
CTTAGATCTCGATTCC
CTTAGATCTCAATTCC
CTTAGATCTCGATTCC

Nr of selected repeats 111 Similarity 0.886787

Consensus:

CTTAGATCTCaaTTCC

>Cele-UNSB01_5:20065513-20066023 Satlength=511 Nr of Repeats=14 RepeatLength=34
seed=TTTCCCGCCA

TTTCCCGCCAAAATTTTTGTTGAAATTTTGAT
TTTCCCGCCAAAATAATTTCTCCGAAAATTTGTA
TTTCCCGCTAAAATGATTTCTCCGAAAATTTAAA
TTTCCCGCCAAAATATTCACCTCAAAAAATTTGAA
TTTCCCGCCAAAATATTCACCTCAAAAAATTTGAA
TTTCCCGCCAAAATAATTTCTCCGAAAATTTAAA
TTTCCCGCCAAAATATTCACCTCAAAAAATTTGAA
TTTCCCGCCAAAATAATTTCTCCGAAAATTTAAA
TTTCCCGCCAAAATATTCACCTCAAAAAATTTGAA
TTTCCCGCCAAAATATTCACCTCGAAAAATTTGAA
TTTCCCGCCAAAATATTCACCTCGAAAAATTTGAA
TTTCCCGCCAAAATATTCACCTCGAAAAATTTGAA
TTTCCCGCCAAAATAATTTCTCCGAAAATTTGAATATTCGCCAAAATATTTTCTCAGAAAAATTTGAA

Nr of selected repeats 12 Similarity 0.859774

Consensus:

TTTCCCGCCAAAATAtTcaCTCnaAAAAATTTgAA

>Cele-UNSB01_5:20072393-20073779 Satlength=1387 Nr of Repeats=40
RepeatLength=35 seed=CCGGCAAATC

CCGGCAAATCGACAAACTGCCGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGAATTTAAAATTC
CCGGCAAATCGACAAATTGCCGATTTAAAATTC
CCGGCAAATTGGTAGATTACCGGATTTGTAAATTT
CCGGCAAATCGAAAAATTACCGAATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGATTTAAAATTC
CCGGCAAATCGACAAATTGCCGATTTAAAATTC
CCGGCAAATTGGTAGATTACCGGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGAATTTAAAATTC
CCGGCAAATCGACAAATTGCCGATTTAAAATTC
CCGGCAAATTGGTAGATTACCGGATTTGTAAATTT
CCGGCAAATCGAAAAATTACCGAATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGAATTTAAAATTC
CCGGCAAATTGGTAGATTACCGGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGAATTTAAAATTC
CCGGCAAATTGGTAGATTACCGGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGAATTTAAAATTC
CCGGCAAATTGGTAGATTACCGGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGATTTGTAAATTT
CCGGCAAATCGACAAATTGCCGAATTTAAAATTC

CCGGCAAATTGGTAGATTACCGGATTTGTAAATTT
CCGGCAAATCGACAAAATTGCCGGATTTGTAAATTT
CCGGCAAATCGACAAAATTGCCGGATTTGTAAATTT
CCGGCAAATCGACAAAATTGCCGAAATTAATAATTC
CCGGCAAATTGGTAGATTACCGGATTTGTAAATTT
CCGGCAAATCGACAAAATTGCCGGATTTGTAAATTT
CCGGCAAATCGACAAAATTGCCGGATTTGTAAATTT

Nr of selected repeats 26 Similarity 0.887707

Consensus:

CCGGCAAATcGanAaATTaCCGGATTTGTAAATTT

>Cele-UNSB01_5:20105608-20107135 Satlength=1528 Nr of Repeats=40

RepeatLength=35 seed=GAAATTTTCA

GAAATTTTCATTTTTGGAAAAATTACCAATTTGCCT

GAAATTTTCATTTCCGGCAAATTAAGTATCTGCCG

GAAAATTTTCATTTTTAGCGATTTGCCGATTTGCCAA

AAATTTTCAATTTTCAGCAATTTGCCGATTTGCCG

GAAATTTTCATTTTTGGAAAAATTACCAATTTTCCT

GAAATTTTCATTTCCGGCAAATTAAGTATCTGCCG

GAAAATTTTCATTTTTAGCGATTTGCCGATTTGCCG

GAAATTTTCATTTCCGGCAAATTCAGATTTGCTG

GAAATTTTCAATTTTCAGCAATTTGCCGATTTGCCG

GAAAATTTTCATTTTTGGAAAAATTACCAATTTGCCT

GAAATTTTCATTTCCGGCAAATTAAGTATCTGCCG

GAAAATTTTCATTTTTAGCGATTTGCCGATTTGCCG

GAAATTTTCAATTTTTGGCAAATTTGCCGATTTGCCAA

AAATTTTTCATTTTCAGCAATTTGCCGATTTGCCG

GAAATTTTCATTTTTGGAAAAATTACCAATTTGCCT

GAAATTTTCATTTCCGGCAAATTAAGTATCTGCCG

GAAAATTTTCATTTTTAGCGATTTGCCGATTTGCCAA

AAATTTTCAATTTTCAGCAATTTTCCAATTTGCCGATTTGCCG

GAAATTTTCATTTTTGGAAAAATTACCAATTTTCCT

GAAATTTTCATTTCCGGCAAATTAAGTATCTGCCG

GAAAATTTTCATTTTTAGCGATTTGCCGATTTGCCG

GAAATTTTCATTTCCGGCAAATTCAGATTTGCTG

GAAATTTTCAATTTTCAGCAATTTGCCGATTTGCCG

GAAATTTTCATTTTTGGAAAAATTACCAATTTGCCT

GAAATTTTCATTTCCGGCAAATTAAGTATCTGCCG

GAAAATTTTCATTTTTAGCGATTTGCCGATTTGCCG

GAAATTTTCAATTTTTGGCAAATTTGCCGATTTGCCAA

AAATTTTTCATTTTCAGCAATTTGCCGATTTGCCG

GAAATTTTCATTTTTGGAAAAATTACCAATTTGCCT

GAAATTTTCATTTCCGGCAAATTAAGTATCTGCCG

GAAAATTTTCATTTTTAGCGATTTGCCGATTTGCCG

GAAATTTTCATTTCCGGCAAATTCAGATTTGCTG

GAAATTTTCAATTTTCAGCAATTTGCCGATTTGCCG

GAAATTTTCATTTTTGGAAAAATTACCAATTTGCCT

GAAATTTTCATTTCCGACAAAATTCAGATTTGCTG

GAAATTTTCAATTTTCGTCAATTTGCCG

GAAATTTTACAATTTTTGGCAAATTTGCCGTTTGCAGGGGGTGGGCGGCAATTTGCCGTTTCGGCAAATTTTTTACGGTTTTT
CGGCAAATTTGCCA

GAAATTTTGAATTTTCGTCAATTTGCCGATTTGCCG

GAAATTTTAATTTTCGGAAAAATTACCGATTTGCCG

GAATTTTTTCATTTTCAGCAATTTGCCGATTTGCCGATTTACCAAAAATTTCCAATCCCAGCAGTTTTCGGGAAATTTTTT

GTTTTTCAGCGATTTGTGCGATTTGCCG

Nr of selected repeats 29 Similarity 0.756979

Consensus:

GAAAtTTTCATTTtcgGcAAaTTaCngATtTGCCg

>Cele-UNSB01_5:20109112-20109540 Satlength=429 Nr of Repeats=12 RepeatLength=35
seed=AATTTCCGGC

AATTTCCGGCAAATCGGCAAATAACTGGAATTTAA
AATTTCCGGCAATACGGCAAATTACCAGAATTTAA
AATTTCCGGCAAATTGGCAAATAAGCGGAATTTAA
AATTTCCGGCAACTCCGCAAATCAACACATTGCCGGAATTAAG
AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA
AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA
AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA
AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA
AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA
AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA
AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA
AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA

Nr of selected repeats 11 Similarity 0.926580

Consensus:

AATTTCCGGCAAATCGGCAAATAACCGGAATTTAA

>Cele-UNSB01_5:20111577-20111694 Satlength=118 Nr of Repeats=5 RepeatLength=12
seed=AAGCCTAAGC

AAGCCTAAGCCTAACTAAGCTCAAGACTATGCCTAGGATAAGTCTAACCTTAAGCTTAAATCT
AAGCCTAATCTT
AAGCCTAAGCCT
AAGCCTAAGCCT
AAGCCTAAGCCCAAGCCT

Nr of selected repeats 3 Similarity 0.851852

Consensus:

AAGCCTAAGCcT

>Cele-UNSB01_5:20131328-20132164 Satlength=837 Nr of Repeats=37 RepeatLength=19
seed=TAGTGCCTTG

TAGTGCCTTGACGCATTTT
TAGTGCATTGGCGCAATTC
TAGTGCCTTGACGCATTTT
TAGTGCCTTGTCGCATTTT
TAGTGCCTTGACGCAGTTC
TAGTGCCTTGACGCAGTTC
TAGTGCCTTGACGCAGTTC
TAGTGCCTTGACGACATTCTGGTGCCTTAGCACAATTA
TAGTGCATTGGCGCAATTC
TAGTGCATTGACGCAATTC
TAGTGCCTTGACGCATTTT
TAGTGCCTTGACGCATTTT
TAGTGCCTTGTCGCATTTT
TAGTGCCTTGTCGCATTTT
TAGTGCCTTGTCGCATTTT
TAGTGCCTTGACGCAGTTC
TAGTGCCTTGACGCAGTTC
TAGTGCCTTGACGCAGTTC
TAGTGCCTTGACGACATTCTGGTGCCTTAGCACAATTA
TAGTGCATTGGCGCAATTC
TAGTGCATTGACGCAATTC
TAGTGCCTTGCGCAATTC

TAGTGCCTTAATGCAATTC
TAGTGTCTTGGCGCAATTCT
TGTGCCTTGACGCATTTTC
TAGTGCCTTGACGCAATTC
TAGTGCCTTGAGGCAATTA
TAGTGCCTTGGTGCAATTT
TAGTGCATTGGCGCGATTTC
TAGTGCCTTGGCGCAAATC
TAGTGTCTTGGCGCAATTCTGTGCATTGGCGCAATTCTGGTGCCTCGGCGCAATTCTGGTGCCTCGGCGCAATTC
TGGTGCCTTGACGCAATTC
TAGTGCCTTGGCGTAATTC
TAGTGCATTGGCGCAATTCAGTGTCTTGACGCAATTC
TAGTGCCTTGACGCAATTC
TAGTGCATTGACGCAATTC
TAGTGCCTTGACGCATTTTC

Nr of selected repeats 30 Similarity 0.844807

Consensus:

TAGTGCcTTGaCGCAaTTC

>Cele-UNSB01_5:20173699-20174897 Satlength=1199 Nr of Repeats=28

RepeatLength=31 seed=TTCCCGCCTA

TTCCCGCCTAAAACACTACTCGAAAAATTCAAATTTCCCTCTTAAAATCACACGAAAAATTCAAAT
TTCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TTCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TTCCCACCTAAAACACTACTCAAAAAATTCAAATTTCCCTCTTAAAATCACAAAGAAAAATTCAAAT
TTCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TTCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TTCCCACCTAAAACACTACTCAAAAAATTCAAAT
TTCCCGCCTAAAAGTACTCAAAAAATTCAAATTTCCCTCTTAAAATCACAAAGAAAAATTCAAATTTCCCTCTTAAAATCAC
AAGAAAAATTCAAAT
TTCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TTCCCGCCTAAAATTAATCAAAAAATTCAAAT
TTCCCGCCTAAAATTAATCAAAAAATTTTAAATTACCGCCTTAAACAACCTTAAAAATGTAATT
TTCCCGCCTAAAACACTACTTAAAAATTCAAAAATTTAAATTTTCCGTTTAAAAACCACTCAAAAAATTTAAAT
TTCCCGCCTAAAAGCTACCCAAAAATTCAAAA
TTCCCGCCTAAAATTAATCAAAAAATTCCTAAT
TTCCCGCCTAAAATTAATCAAAAAATTCCTAAT
TTCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TTCCCGCCTAAAACACTACTCAAAAAATTCAAATTTCCCTCTTAAAATCACAAAGAAAAATTCAAAT
TTCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TTCCCGCCTAAAACACTACTCGAAAAATTCAAAT
TTCCCACCTAAAACACTACTCAAAAAATTCAAAT
TTCCCGCCTAAAAGTACTCAAAAAATTCAAAT
TTCCCGCCTAAAATTAATCAAAAAATTTTAAA
TTACCGCCTAAAATTAATCAAAAAATTTTAAA
TTACCGCCTAAAATTAATCAAAACATTTTAAATTACCGCCTTAAACAACCTTAAAAATGTAATT
TTCCCGCCTAAAACACTACTTAAAAATTCAAAAATTTAAATTTTCCGTTTAAAAACCACTCAAAAAATTTAAAT
TTCCCGCCTAAAAGCTACCCAAAAATTCAAAA
TTCCCGCCTATAATTAATGAAAAATTCCTAATTTTCAGCCTAAAATTAATCAAAAAATTCCTAAT

Nr of selected repeats 17 Similarity 0.854243

Consensus:

TTCCCGCCTAAAACACTACTCgAAAAATTCAAaT

>Cele-UNSB01_5:20176707-20177444 Satlength=738 Nr of Repeats=21 RepeatLength=33

seed=TTTGAATTTTC

TTTGAATTTCCCGCCAAAATTTTTTTGAGAAAG
TTTGAATTTCCCGCTAAAATTTTTCCAAAATTTCTTTAGAAA
TTAGAATTTCCACCAAAAATTTTTCAAAAAATGTGAATATCCCGCCAAAAGTTTTTATTAAATAA
TTTGAATTTCCCGCTAGAAAAATTTTCTCATAAAA
TTTGAATTTCCCTGCAAAAATTTTCTCGGAAA
TTTGAATTTCCACCAAAATTTTTCTCAAAAAT
TTTGAATTTCCCGACAAAATTTTCTCGAAAAA
TTTGAATTTCCCGCCGAAAAATTTTCTCATAAAA
TTTGAATTTCCACCAAAATTTTTCTCAAAAAT
TTTGAATTTCAAACCAAAATTTTTCTCAAAAAT
TTTGAATTTCAAACCAAAATTTTTCTCAAAAAT
TTTGAATTTCCCGCCAAAATTTTCTCAAAAAT
TTTGAATTTCCCGCCAAAATTTTCTCAAAAAT
TTTGAATTTCCACCAAAAGATATTTCTAAAAAAA
TTTGAATTTCAAACCAAAATTTTTCTCGAAAAA
TTTGAATTTCCCGCCGAAAAATTTTCTCATAAAA
TTTGAATTTCCACCAAAAATTTTCTCAAAAAT
TTTGAATTTCCACCAAAATTTTTCATATAAAT
TTTGAATTTCAAACCAAAATTTTTCTCAAAAAT
TTTGAATTTCCCGCCAAAATGCTTTCAAAAAT
TTTGAATTTCCGGCCAAAATTTTCTCAAAAAT

Nr of selected repeats 17 Similarity 0.722086

Consensus:

TTTGAATTTCCcaCCAAAATTTTCTCAaAAAA

>Cele-UNSB01_5:20212391-20212631 Satlength=241 Nr of Repeats=10 RepeatLength=20
seed=TTATTGATTT

TTATTGATTTTTCTGGAAAT
TTATTGATTTTTCTGGAAATTTATCAATTTTTCTGGAATT
TTATTGATGTTTCTGGAAATTTTTTAATTTTTCTGAAATT
TTATTGATTTTTCTGGGAAT
TTATCGATTTTTCTGGAAAA
TTATCGATTTTTCTGGAAAT
TTATTGATTTTTCTGGAAAT
TTATTGATTTTTCTGGAAAT
TTATTGATTTTTCTGGAAAT
TTATTGATTTTTCTGGAAAT

Nr of selected repeats 8 Similarity 0.866667

Consensus:

TTATtGATTTTTctGGAAAT

>Cele-UNSB01_5:20217981-20218181 Satlength=201 Nr of Repeats=9 RepeatLength=20
seed=CAGAAAAATC

CAGAAAAATCGATAAAATTC
CAGAAAAATCAATAAATTTT
CAGAAAAATCAATAAATTTT
CAGAAAAATCAATAAATTTT
CAGAAAAATCAATAAATTTCCGAAAAATCGATAAATTTT
CAAAAAATCGATAAATTTT
CAGAAAAATCAATGAATTTT
CAGAAAAATCAATAAATTTT
CAGAAAAATCAATGAATTTT

Nr of selected repeats 8 Similarity 0.873810

Consensus:

CAGAAAAATCaATaAATTTc

>Cele-UNSB01_5:20220047-20220618 Satlength=572 Nr of Repeats=12 RepeatLength=20
seed=TTATTGATTT

TTATTGATTTTTCTGGAAGT
TTATTGATTTTTATGGAAATT
TTATCGATTTTTATGGAAAT
TTATTGATTTTTATGGAAAT
TTATTGATTTTTCTGGAAGT
TTATTGATTTTTATGGAAATT
TTATCGATTTTTATGGAAAT
TTATTGATTTTTCTGGAAGT
TTATTGTTTTTGGAAATTTATCAATTTTTCTGAAATT
TTATTGATTTTTCTGAAATT
TTATTGATTTTTATGGAAAT
TTATTAATTTTTTCGTCAATTTTCCGCGATTTTTCAGTGAATTTTCATCATTTTTTCGCCAGAAATCTCCAATTTTTGACCT
TTTTACAGGTCCAGCTTGTGTAGTTTGTAGTGCAGCTGGAGCTGCTGCTGAAATCGGCTTAATACTCTTCAAATATC
CTGTTTTCGAGTACGACAATCCGCACATTTTCATCCATTGAGTACTCATTAGTTTCGACGGCAGACGGGCGTTTTGATGGC
TGAAAATTGAGGAAATTTAGCTCTGAAAAATGGGATTTTAAGGCGAAGAAATTTTTGAAGTTTTGGCCGTTTTTAGAG
CGAACATTTAGGAAA

Nr of selected repeats 8 Similarity 0.876190

Consensus:

TTATtGATTTTTaTGGAAaT

>Cele-UNSB01_5:20243571-20245480 Satlength=1910 Nr of Repeats=58

RepeatLength=32 seed=ACTACAAACT

ACTACAAACTACAATTTTTCGAATTTTTCAATTTTTTGCCAAATTTCTGAAGATTTTTGAGATTTTCATAATTTAAAAA
AAAAAATTTATCTTAAA

ACTACAAACTACAAGTTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTTGGGCGCTGCTTAG

ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
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ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTGGGCGCTGCTAA
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACAAGTTTTGGGCGCTGCTTAG
ACTACAAACTACACGTTTTGGGCGCTGCTAG

Nr of selected repeats 46 Similarity 0.942073

Consensus:

ACTACAAACTACAAGTTTTGGGCGCTGCTTAG

>Cele-UNSB01_5:20247169-20247404 Satlength=236 Nr of Repeats=11 RepeatLength=20
seed=TTTGAATTTT

TTTGAATTTTTAAGTGAAAA
TTTGAATTTTTGAGTGAAAA
TTTGAATTTTTAAGTGAAAA
TTTGAATTTTTGAGTGAAAA
TTTGAATTTTTGAGTGAAAA
TTTGAATTTTTGAATGAAAA
TTTGAATTTTTCAGTGAAAA
TTTGAATTTTTCAGTGAATATCTAATTATTGTGTGAAAA
TTTGATTTTTTTGAAAGAATT
TTTGAATTTTTCGGTAAAAAT
TTTGAATTTTTTTT

Nr of selected repeats 7 Similarity 0.936508

Consensus:

TTTGAATTTTTgAGTGAAAA

>Cele-UNSB01_5:20269010-20269323 Satlength=314 Nr of Repeats=8 RepeatLength=12
seed=TATGTATATG

TATGTATATGTA
TATGTATATGTA
TATGTATATGTA
TATGTATATGTA

TATGTATATGTGGTACTTGTGTATTACATGGCCTCATTTTAATAGTAATTTTTTCAGTTATGCGAAAGAAAAACGTGAAC
CACACTTTTGCATTTTTAGGCTTAGGAAATAGCAATTTCTAAGCCTAAAAAGAGAAAAATGTATATCACGTTTAATTTAA
ATGGAGAAATTAATGAACATTTAAATTTAATTCAAAAATGTGGGCATGTAATACACAAGTACCGTA

TATGTATATGTA

TATGTATATGTA

TATGTATATGTATATGTA

Nr of selected repeats 6 Similarity 1.000000

Consensus:

TATGTATATGTA

>Cele-UNSB01_5:20275164-20275248 Satlength=85 Nr of Repeats=4 RepeatLength=21

seed=CTCAATTCAA

CTCAATTCAATCAAGGGAATC

CTCAATTCAATCAAGGAAATT

CTCAATTCAATCAATGGAATC

CTCAATTCAATCAAGGAAATT

Nr of selected repeats 4 Similarity 0.883598

Consensus:

CTCAATTCAATCAAgGaAATc

>Cele-UNSB01_5:20277753-20277891 Satlength=139 Nr of Repeats=11 RepeatLength=12

seed=ATATACATAT

ATATACATATAC

ATATACATATACATATAC

Nr of selected repeats 10 Similarity 1.000000

Consensus:

ATATACATATAC

>Cele-UNSB01_5:20304611-20305126 Satlength=516 Nr of Repeats=14 RepeatLength=32

seed=AAATTTGAAT

AAATTTGAATGTTCCGCCACAATTTTTCAAAC

AAATTTGAATTTCCCGCCAAAATTTTTACCGA

AAATTTGAATTTCCCGCCAAAATTTTTCTCAGA

AAATTTGAATTTCCCGCCAAAATTTTTCTCGGA

AAATTTGAATTTCCCGCCAAAATTTTTCAAAGA

AAATTTGAATTTCCCGCCAAAATTTTTCACAGA

AAATTTGAATTTCCCGCCAAAATGATTCTCTTACAATTTGACCTCCCGCCAATTTGTTTCACAAA

AAATTTGATTTCCCGCCACAAATTTTCACACAA

AAATTTAAATTTCCCGCCACAATTTTTCTCAGA

AAATTTGAATTTCCCGCCAAAATTTTTCTCGGA

AAATTTGAATTTCCCGCCAAAATTTTTCAAAGA

AAATTTGAATTTCCCGCCAAACATTTTCTAGAAAATTTTATTTTCCGCTAAATTTGTTTCACAAA

AAATTTGATTTCCCGCCACAAATTTTCACACAA

AAATTTAAATTTCCCGCCACAATTTTTCTCAGA

Nr of selected repeats 9 Similarity 0.806958

Consensus:

AAATTTgAATTTcCGCCAAaAATTTTTTctcaGA

>Cele-UNSB01_5:20312857-20314295 Satlength=1439 Nr of Repeats=50

RepeatLength=12 seed=GCTTGGGCTT

GCTTGGGCTTAAGCTTAGGTTCAAGGCTTAACCCCTAGGCTTAGGCGTAAGCTTCTTTTTAAAAATTTGCTAG

GCTTAGGCTTATGGCTTAATCCTTAGTGTAGTGGCTAAGGCTTAGACTTGGG

GCTTAGGGCTTAGGTTTAGGCTTAGACTTGGTTTTAGGCTTTGAGCGTAGACTTAGGCTCAACCCTAGGTTTAGGCGTA

AGCTTCTTTTTAAAAATGAGCATATTTTCCGACTAATTTCGATTTTCAAGAAAATCCCTAAAATATTCCCTAATTTAGAGCT

TAGGCCTAGTTTTAGCTTTAGGTTTAA

GCTTGGGCTTAG

GCTTAGGCTTAGGATTATGCTTAGGCTCAGGCTTAGGCGTAGGTTTAGGCTTAACCCCTGGGTTAGGCTTAACCCCTAGG

CTAAGGCGTAAGCTTCTTTTTAAAAATTTGCAATTTTCCGACTAATTTCGATTTTCAAGAAAATCCCTAAAATATTCCCTAA

TTTAGAGTTTAAAGCCTAGTTTTAGGTTGAAGTTTTAA

GCTTAGGCTTAGGCTTAGGATTATGCTTAGGCTCAGGCTTAGGCGTAG

GCTTAGGCTTAGGCTTAGGCCCTAGTTTTAGGCTTAGGTTTTAA

GCTTGGGCTTTAGGCATTTTTAGGCTAAATTTTCCGACTAATTTCGATTTTCAAAAAATCTCTCAAATATTCCCTAAAT

TTTCAGAAAACCTCGTCACTTTCCCGTTGAACTTTTATTAGGTCTATTTCAGAAAAGCTTGACAAAATCCATAAAAATTAGC

AACGTTCAAACCTTAAATTACCTTCAAATCACGATGTACGATGCCCTTTTTGTGGATCGCTTCCAACGCGTGAGCTGAA

AATTTGAGAGTTTATAGAAAAGGAAAAATATCTATATTTTTGAGTTTTGAAAAAAAAGGGCTTGATTTCGG

GCTTAGGCTTTG

GCTTGGGCTTGG

GCTTGGGCTTAG

GCTTAGGCTTAGGCTTAA

GCTTAGGCTTAA

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTGGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGGGCGTGT

GCTTGGGCTTGGGCTTCA

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTGGGCTTGG

GCTTTGGCTTGG

GCTTGGGCTTGG

GCTTAGGCTTTG

GCTTGGGCTTGG

GCTTGGGCTTGGGA

CTTGGGCTTGG
GCTTAGGCTTAA
GCTTAGGCTTGG
GCTCGGGCTTGG
GCTTGGGCTTGGGCTTGG

Nr of selected repeats 36 Similarity 0.903704

Consensus:

GCTTGGGCTTGG

>Cele-UNSB01_5:20413138-20414402 Satlength=1265 Nr of Repeats=44

RepeatLength=32 seed=TTTTGGGCGC

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTATAAACTACAAT

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTTAGACTACAACTACACG

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTACAAATCACAAT

TTTTGGGCGCTGCTAATTCAATTTTCAA

TTTTGGGCGCTGCTTAGACTACAAATCACAAT

TTTTGGGCGCTGCTAATTCAATTTTCAA

TTTTGGGCGCTGCTAAAACTACAACTACAAT

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTTAGACTACAAAATACAAT

TTTTGGGCGCTGCTAATTCAATTTTCAA

TTTTGGGCGCTGCTAAAACTACAACTACAAT

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTAAAACTACAACTACAAG

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTTAGACTACAAAATACAAT

TTTTGGGCGCTGCTAATTCAATTTTCAA

TTTTGGGCGCTGCTAAAACTACAACTACAAT

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTACAAATCACAAT

TTTTGGGCGCTGCTAATTCAATTTTCAA

TTTTGGGCGCTGCTAAAACTACAACTACAAT

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTAAAACTACAACTACAAG

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTTAGACTACAACTACAAT

TTTTGGGCGCTGCTTAGACTACAAAATACAAT

TTTTGGGCGCTGCTAATTCAAT

TTTTGGGCGCTGCTTAGACTACAACTACACG

TTTTGGGCGCTGCTAATTCAA

TTTTGGGCGCTGTTTAGACTACAAATCACAAT

TTTTGGGCGCTGCTAATTCAATTTTCAA

Nr of selected repeats 27 Similarity 0.907170

Consensus:

TTTTGGGCGCTGCTtAgACTACAAAcTACAAT

>Cele-UNSB01_5:20465532-20465791 Satlength=260 Nr of Repeats=7 RepeatLength=37
seed=AATTTGAATT

AATTTGAATTCCCGCCAAAACATTTTTGTAAAATTAA
AATTTGAATTCCCGCCAAAATATTTTTGAAAAATTAA
AATTTGAATTCCCGCCAATATATTTTTGAAAAATTAA
AATTTGAATTCCCGCCAAAATATTTTTGTAAAATTAA
AATTTGAATTCCCGCCAAAATATTTTTGTAAAATTAA
AATTTGAATTCCCGCCAAAATATTATTGAAAAATTAA
AATTTGAATTCCCGCCAATATATTTTTGAAAAATTAA

Nr of selected repeats 7 Similarity 0.941656

Consensus:

AATTTGAATTCCCGCCAAAaATATTTTTGaaaaATTAA

>Cele-UNSB01_5:20522553-20523111 Satlength=559 Nr of Repeats=29 RepeatLength=18
seed=CATTGTCACT

CATTGTCACTGGCTTCTC
CATTGTACGTTCTTCTC
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTC
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTT
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTC
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTT
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTC
CATTGTCACTTTCATCTC
CATTGTCACTGGCTTCTCCATTGCCACGTTCTTCTC
CATTGTCACTTTCTTCTC
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTT
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTC
CATTGTCACTTTCATCTC
CATTGTCACTGGCTTCTCCATTGCCACGTTCTTCTC
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTT
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTC
CATTGTCACTGGCTTCTT
CATTGTCACTTTCTTCTC
CATTGTCACTTTCTTCTC
CATTGTCACTGGCTTCTC

Nr of selected repeats 27 Similarity 0.884774

Consensus:

CATTGTCACTtctTTCTC

>Cele-UNSB01_5:20548445-20548748 Satlength=304 Nr of Repeats=5 RepeatLength=41
seed=GCATTTTTTCG

GCATTTTTTCGCGATTTTTGATTAATTTTCAGTTAAAATTC
GCATTTTTTCGCGATTTTTCACTATTTTTTCGTGAAAATTC

GCATTTTTTCGTGAATTTTCGGCTAATTGTCACCTCTAAATGTGAAGTTTTCTCGATTTTAACTAATTTTCAGTGAAAAT
TTGCAATATTTTCATGATTTTCTCCATTTAGACGATTTTTAATCAATTTTCAGCGAAAAAAT

GCATTTTTTCGTGATTTTTTATCAATTTTCTGCAAAAAATC

GCATTTTTTCGCCGATTTTAAATCAATTTTCAGTGAATTTTT

Nr of selected repeats 3 Similarity 0.772358

Consensus:

GCATTTTTTCGCCGATTTTnAttAaTTTTcaGTgAAaaTTc

>Cele-UNSB01_5:20558603-20558932 Satlength=330 Nr of Repeats=11 RepeatLength=30

seed=CTCAAATTTG

CTCAAATTTGCACTGAAAATTTCCAATTATC

CTCAAATTTGCACTAAAAATTTCCAATTTTT

CTCAAATTTGCACTAAAAATTTCCAATTTTT

CTCAAATTTGCACTAAAAATTTCCAATTTTT

CTCAAATTTGCACTAAAAATTACAATTTTT

CTCAAATTTGCACTAAAAATTTCAAATTTT

CTCAAATTTGCACTGAAAATTTCCAATTTTT

CTCAAATTTGCACTGAAAATTTCAATTTTT

CTCAAATTTGCACTAAAAATTTCCAATTTT

CTCAAATTTGCACTGAAAATTTCCAATTTTT

CTCAAATTTGCACTGAAAATTTCCAATTTTT

Nr of selected repeats 10 Similarity 0.911111

Consensus:

CTCAAATTTGCACTaAAAAATTTcCAATTTTT

>Cele-UNSB01_5:20572226-20572853 Satlength=628 Nr of Repeats=16 RepeatLength=11

seed=CTACAGTACT

CTACAGTACTT

CTACAGTACTA

CTACAGTACCTTGACATTATCCCTCCAGCAACTCCCAACCCAATACCTCTTCTGTGGACAAAACTAAATTTTTCTCTAA

ACTACAGTAACGCTACCGTATAC

CTACCGTACTT

CTACAGTACCA

CTACAGTACCTTGACATTATCCCCCAGTAACTCCCAACCCAATACCTCTTCTGTAGACAAAACTCAATTTTTCTCTAA

CTACAGTAACGCTACCGTATAC

CTACAGTACTT

CTACAGTACTA

CTACAGTACCTTGACATTATCCCCCAGCAACTCCCAACCCAATACCTCTTCTGTGGACAAAACTAAATTTTTCTCTAA

CCTACAGTAACGCTACCGTATAC

CTACAGTACTT

CTACAGTACCA

CTACAGTACCTTGACATTATCCCCCAGCAACTCCCAACCCAATACCTCTTCTGTAGACAAAACTCACATTTTCTCAAAC

TACAGTAACCCTACCGTATGA

CTACAGTACTC

CTACAGTACTA

CTACAGTACCTTGACATTATCCCCCAGCAACTCCCAACCCAATACCTCTTCTGTAGACAAAACTCACATTTTCTCAA

CTACAGTAACCCTACCGTATAC

CTACAGTACTC

Nr of selected repeats 11 Similarity 0.854545

Consensus:

CTACAGTACTn

>Cele-UNSB01_5:20575835-20576061 Satlength=227 Nr of Repeats=7 RepeatLength=32

seed=TTAGCAGCGC

TTAGCAGCGCCCAAAATCTTGTAGTTTGTAGT

TTAGCAGCGCCCAAAACTTGTAGTTTGTAGT

TTAGCAGCGCCCAAAACTTGTAGTTTGTAGT

TTAGCAGCGCCCAAAAaCTTGTAGTTTGTAGTT
TTAGCAGCGCCCAAAAaCTTGTAGTTTGTAGT
TTAGCAGCGCCCAAAAaCTTGTAGTTTGTAGTT
TTAGCAGCGCCCAAAAaCTTGTAGTTTGTAGT

Nr of selected repeats 5 Similarity 0.931313

Consensus:

TTAGCAGCGCCCAAAAaCTTGTAGTTTGTAGT

>Cele-UNSB01_5:20579964-20580501 Satlength=538 Nr of Repeats=15 RepeatLength=31
seed=CTACAAACTA

CTACAAACTACTAGTTTTGGGCGCTGCTAAACTACAAAATTACAAGATTTGGGCGCTGCTAAA

CTACAAACTACAAGCTTTTGGGCGCTGCTAATTCGCTTTTGGGAGCTGCTAAA

CTACAAACTACTAGTTTTGGGCGCTGCTAAG

CTACAAACTACGATTTTGGGCGCTGCTAGA

CTACAAACTACAAGATTTGGGCGCTGCTAATTTAATTTTGGGCGCTGCTAAG

CTACAAACTACGATTGTGGGCGCTGCTAGA

CTACAAACTACGAGTTTTGGGCGCTTCTAAG

CTACAAACTACAAGATTTGGGCGCTGCTAAA

CTACAAACTACGAGTTTTGCGCGCTGCTAAG

CTACAAACTACGAGCTTTGGGCGCTGCTAAG

CTACAAACTACAAGATTTGGGCGCTGCTAAG

CTACAAACTACGATTGTGGGCGCTGCTAGA

CTACAAACTACGAGTTTTGGGCGCTGCTAAG

CTACAAACTACAAGATTTGGGCGCTGCTAAA

CTACAAACTACGAGTTTTGGGCGCCGCTAAG

Nr of selected repeats 9 Similarity 0.899642

Consensus:

CTACAAACTACgAGtTTTGGGCGCTGCTAAG

>Cele-UNSB01_5:20584979-20587201 Satlength=2223 Nr of Repeats=68

RepeatLength=31 seed=GGCGCTGCTA

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAAATCGATTTTG

GGCGCTGCTAAACTACAAACTACAAGAATTG

GGCGCTGCTAATACAATTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTATTCGATTTTG

GGCGCTGCTAATTCGATTTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAATTCGATTTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAATTCGATTTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAAGCTACAAACTACAAGATTTG

GGCGCTGCTAAACTACAAACTACTAGATTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAAACTACAAACTACTAGATTTG

GGCGCTGCTAATTCGATTTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAATACAATTTG

GGCGCTGCTAAACTACAAACTACTAGATTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAAACTACAAACTACAAGATTTG

GGCGCTGCTAATACAATTTG

GGCGCTGCTAAACTACAAACTACTAGATTTG

ATTGCCGGTTTTTAAAAATGTTTGGCAATCGGCAATTTCCGGCA
ATTGCCGGTTTTTAAAAATGTTTGGCAATCGGCAATTTCCGGCG
ATTGCCGGTTTTTAAAAATATTTGGCAATCGACAGTTTCCGGTA
ATTGCCGGTTTTTAAAAATTTCCGGCAAACGGCAATTTCCGGCC
ATTGCCGGTTTTTAAAAATTTCCGGCAATCGGCAATTTCCGGCA
ATTGCCGGTTTTTGAACATTTTTGGCGATCGGCAATTTTCGATAATTGCTGATTTTTTAAATTTCCAGCAATCGGCAATTT
CGGCG
ATTGCCGGTTTTTAAAAATGTTTGGCAATCGACAGTTTCCGGTA
ATTGCCGGTTTTTAAAAATTTCCGGCAAACGGCAATTTCCGGCA
ATTGCCGGTTTTTAAAAATTTCCGGCAATCGGCAATTTCCGGCA
ATTGCCGGTTTTTGAACATTTTTGGCGATCGGCAATTTTCGACAATTGCCGGAAACTTTGGAAACCGGCAAAAATTTTCATC
TTGTTTTTTTTAGTAGTCGGTTTTTTCTAAAAGAAAACGATCAATCCTTATAAGATTAAACCATTGACTATAAGATGAAA
AAGAGAAAATTGTTTTCGTAAAAATTCATCTTTAAGCTCCTAAAACCTACAAAATGTATCAAATTCGTATTTCCGGCAGTTC
TGATTTCCAGCA

Nr of selected repeats 9 Similarity 0.803351

Consensus:

ATTGCCGGTTTTtAAaAtTtTcGGCAAtCGgCAaTTTCCGGca

>Cele-UNSB01_5:20719213-20719394 Satlength=182 Nr of Repeats=9 RepeatLength=20
seed=AAAATTCAAA

AAAATTCAAATTTTGACAG
AAAATTCAAATTTTACTG
AAAATTCAAAATTTCTACTG
AAAATTCAAATTTCTGACTA
AAAATTCAAATTTTCATGACTA
AAAATTCAAATTTTCATGACTA
AAAATTCAAATTTTACTG
AAAATTCAAAATTTCTACTG
AAAATTCAAATTTCTGAGGG

Nr of selected repeats 6 Similarity 0.778836

Consensus:

AAAATTCAAATTTcTgACTG

>Cele-UNSB01_5:20720350-20720568 Satlength=219 Nr of Repeats=4 RepeatLength=31
seed=GAAAAAGTGC

GAAAAAGTGCCTGAAAATCACATTTTTGAACT
GAAAAAGTGCCTGAAATTTCCAGATAAGAACTGCCTAAAAATTAGATTTTCAGGTAGAAAAATGAACAAAA
GCTACTTTTCTCGGCGAAAAAGTATTGTAACTCCAACGTTTCATATA
GAAAAAGTGCCTGAAAAGCACATTTTCAGAAG
GAAAAAGTTCGAAAATCGCATTTTTGAACT

Nr of selected repeats 3 Similarity 0.784722

Consensus:

GAAAAAGTgCTGAAAAtCaCATTTTTtGAAct

>Cele-UNSB01_5:20786599-20786882 Satlength=284 Nr of Repeats=9 RepeatLength=32
seed=CCGCCAAAAT

CCGCCAAAATTTTTTAAAGAAAATATGAATTC
CCGCCAAAATTTAAAAAAATTTGAATTC
CCGCCAAAATGTTTCTTTGAAAATTTGAATTC
CCGCCAAAATTTTTCTTTGAAAATTTGAATTC
CCGCCAAAATTTTTCTTTGAAAATTTGAATTC
CCGCCAAAATTTTTTAAAGAAAATTTGAATTC
CCGCCAAAATTTTTTAAAGAAAATTTGAATTC
CCGCCAAAATTTTTCTTTGAAAATTTGAATTT
CCGCCAAAATTTTCAAAGAAAATTTGAATTC

Nr of selected repeats 7 Similarity 0.853175

Consensus:

CCGCCAAAATTTTTctttGAAAATTTGAATTC

>Cele-UNSB01_5:20839531-20839647 Satlength=117 Nr of Repeats=5 RepeatLength=16

seed=GTACTAGGGT

GTACTAGGGTACTAGG

GTACTTGGGTACTAGGGTACTATGTAGA

GTACTAGGGTACTAGGGTAATGGGATACTAGGGGACTATT

GTACTGGGGTACTGGG

GTACTGGGGTACTGGG

Nr of selected repeats 3 Similarity 0.888889

Consensus:

GTACTgGGGTACTgGG

>Cele-UNSB01_5:20903761-20903966 Satlength=206 Nr of Repeats=5 RepeatLength=11

seed=CCTACAGTAC

CCTACAGTACT

CCTACAGTACCCCCCCCCACTAACCCCAAAAAGATATATTTTCAGAAGACAATTAATCAATTTTTGCTAAACTACAGT
AAT

CCTACAGTACT

CCTACAGTACT

CCTACAGTACCCTGACCATATCCTCCAACCTAACCCCTCAACCACTATCCCTTCAAAAAGACAAAACTCAATTTTTCCAAA
ACTACAGTAAA

Nr of selected repeats 3 Similarity 1.000000

Consensus:

CCTACAGTACT

>Cele-UNSB01_5:20920761-20921207 Satlength=447 Nr of Repeats=40 RepeatLength=11

seed=GTTGCGGTTG

GTTGCGGTTGC

GTTGCGATTGC

GTTGCGGTTGC

GTTGCGATTGC

GTTGCGGTTGC

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GTTGCGATTGC

GTTGCGGTTGC

GTTGCGGTTGC

GTTGCGGTTGC

GTTGCGGTTGC

GTTGCGGTTGC

GTTGCGGTTGC

GTTGCGGTTGC

GTTGCGATTGC

GTTGCGATTGC

GTTGCGGTTGC

GTTGCGGTTGC

ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATAATCGATGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
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ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATAATCGATGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC
ACAGAGAGTAAAATATAGTGGGAAGCC

Nr of selected repeats 396 Similarity 0.948514

Consensus:

ACAGAGAGTAAAATATAGTGGGAAGCC

>Cele-UNSB01_6:161019-161648 Satlength=630 Nr of Repeats=17 RepeatLength=35
seed=GGGAAATTCA

GGGAAATTCAAATTTTTTAGTGAAAAATATTTTTGGC
GGGAAATTCAAATTTTTTATGAAAAATATTTTTGGC
GGGAAATTCAAATTTTTTATGAAAAATATTTTTGGC
GGGAAATTCAAATTTTTATGAGAAAATATTTTTGGC
GGGAAATTCAAATTTTCTGAGAAAAATATTTTTGGC
GGGAAATTCAAATTTTTTATGAAAAATATTTTTGGC
GGGAAATTCAAATTTTTTATGAAAAATATTTTTGGC
GGGAAATTCAAATTTTTTAGTGAAAAATCTTTTTGGC
GGGAAATTCAAATTTTTTAGTGAAAAATATTTTTGGC
GGGAAATTCAAATTTTCTGAGAAAAATATTTTCGGC
GGGAAATTCAAATTTTCTGAGAAAAATATTTTCGGC
GGGAAATTCAAATTTTCTGAGAAAAATATTTTCGGG
GGGAAATTCAAATTTTTTAGTGAAAAATTTTTCGGC
GGGAAATTCATATTTTTTAGTGAAAAAGTTTTCGGC
GGGAAATTCAAATTTTTTAGTGAAAAATTTTTGGCGGGTAATTTAAATTTTCGGAGAAAAATTTTTGGA
GGGAAATTCAAATTTTCTGAGAAAAATATTTTCGGG
GGGAAATTCAAATTTTTTGTGAAAAATATTTTTGGC

Nr of selected repeats 14 Similarity 0.796654

Consensus:

GGGAAATTCAAATTTTtTgtGaAAAAATATTTtGGC

>Cele-UNSB01_6:161741-162501 Satlength=761 Nr of Repeats=19 RepeatLength=40
seed=GAAAATTCTG

GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCACAACCTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTACAGAACTTTCTAGAAAAATCGA
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGA
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGA
GAAAATTCTGGAATGTTCCAGAACTTTCTAAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG

GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGA
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGA
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGA
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG
GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGG

Nr of selected repeats 19 Similarity 0.974269

Consensus:

GAAAATTCTGGAATGTTCCAGAACTTTCTAGAAAAATCGg

>Cele-UNSB01_6:179889-180069 Satlength=181 Nr of Repeats=5 RepeatLength=32

seed=TTAGCAGCGC

TTAGCAGCGCCCAAACTTGTAGTTTGTAGTG

TTAGCAGCGCCCAAACTTGTAGTTTGTAGTG

TTAGCAGCGCCCAAACTCGTGTAGTTTGTAGTCTAAACAGCGCCCAAACTTGAA

TTAGCAGCGCCCAAACTTGTAGATTGTAGTG

TTAGCAGCGCCTAAATCTTGTAGTTTGTAGT

Nr of selected repeats 3 Similarity 0.944444

Consensus:

TTAGCAGCGCCCAAAaCTTGTAGtTTGTAGTG

>Cele-UNSB01_6:180452-180557 Satlength=106 Nr of Repeats=7 RepeatLength=15

seed=GTCTCACCAC

GTCTCACCACGAAGG

GTCTCACCACGATGG

GTCTCACCACGATGC

GTCTCACCACGATGC

GTCTCACCACGATGG

GTCTCACCACGATGG

GTCTCACCACGATGG

Nr of selected repeats 7 Similarity 0.932275

Consensus:

GTCTCACCACGATGg

>Cele-UNSB01_6:187518-187756 Satlength=239 Nr of Repeats=6 RepeatLength=40

seed=TTCCAGAATT

TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA

TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA

TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA

TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA

TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA

TTCCAGAATTTTCTGAAATTTTCCAGAAGATTCTAGAT

Nr of selected repeats 5 Similarity 0.986667

Consensus:

TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA

>Cele-UNSB01_6:188088-188493 Satlength=406 Nr of Repeats=27 RepeatLength=15

seed=ACGATGGGTC

ACGATGGGTCTCACC

ACGACGGGTCTCACT

ACGATGGGTCTCACC

ACGATGGGTCTCACC

ACGATGGGTCTCACT

ACGATGGGTCTCACC

ACGATGGGTCTCACT

ACGATGGGTCTCATC

>Cele-UNSB01_6:210105-210613 Satlength=509 Nr of Repeats=10 RepeatLength=20
seed=AAAAATCAAT
AAAAATCAATAAATTTCTTAAATGTTTCGCTCTAAAAACGGCCAAAACCTTCAAAAAATTTTCGCATTAAAATCCCATTTTTTC
AGCTAAAATTTCTCAATTTTCAGCCATTAATCCGCCCGTCTGCCGTGAACTAATGAGTACTCAATGGATGAAATGTGC
GGATTGTCTTTCTGCGAAACAGGATATTTTGAAGAGTATTTCAGCCGATTTTCAGCAGCTCCAGCTGCACTACAACTACA
CAAGCTGGACCCGTGTAAGGTCAATTTTGGATTTGGAGATTTCTGGCGAAAAATGATGAAAATTCAGTAAAATCGC
GGAAAATTGACG
AAAAATCAATAAATTTCCAA
AAAAATCAATAAATTTCCAT
AAAAATCAATAAATTTCCAT
AAAAATCAATAAATTTCTAG
AAAAATCAATAAATTTTCAT
AAAAATCAATAAATTTCCAT
AAAAATCAATAAATTTCCAG
AAAAATCAATAAATTTCTAG
AAAAATCAATAAATTTCTAG
Nr of selected repeats 9 Similarity 0.907407
Consensus:
AAAAATCAATAAATTTTCcAn
>Cele-UNSB01_6:229151-229455 Satlength=305 Nr of Repeats=8 RepeatLength=36
seed=ATAAAAAATTT
ATAAAAAATTTCCGTCAAATGGGCAATTTGTCAGAAA
ATAAAAAATTTCCGGCAAACCGCAATTTGTCAGAAA
ATAAAAAATTTCCGGTAAATCGGCAATTTGCCAGGAA
ATAAAAAATTTCCGGCAAATCGGCAATTTGCCAGGAA
ATAAAAAATTTCCGGCAAATCGGCAATTTGCCAGGAA
ATAAAAAATTTCCGGCAAACCGGCAATTTGTCAGAAA
ATAAAAAATTTCCGGCAAATCGCCAATTCGCTAGAGA
ATAAAAAATTTCCGGCAAACCGGCAATTCAGCAAATCGGCAATTTGTCAGAAA
Nr of selected repeats 7 Similarity 0.865961
Consensus:
ATAAAAAATTTCCGGCAAAtCGGCAATTTGcCAGaAA
>Cele-UNSB01_6:276570-276632 Satlength=63 Nr of Repeats=4 RepeatLength=15
seed=CGAAAAGGGG
CGAAAAGGGGAGCAGAA
CGAAAAGGGGATCTG
CAAAAAGGGGATCTG
CGAAAAGGGGAGCAA
Nr of selected repeats 3 Similarity 0.762963
Consensus:
CgAAAAGGGGAtCtg
>Cele-UNSB01_6:276806-276883 Satlength=78 Nr of Repeats=5 RepeatLength=15
seed=TCCCCTTTTC
TCCCCTTTTCGTTGC
TCCCCTTTTCGTAGA
TCCCCTTTTCGTATC
TCCCCTTTTGCAGA
TCCCCTTTTCGTTCTGC
Nr of selected repeats 4 Similarity 0.762963
Consensus:
TCCCCTTTTcGtaga
>Cele-UNSB01_6:309569-317496 Satlength=7928 Nr of Repeats=66 RepeatLength=119
seed=GGCCACCGTT

GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTGAGTACCCACAC
GGCTTGGTTTAATTTTTAAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCAAGGTTTAATTTTTGAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCTTGGTTTAATTTTTAAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCAAGGTTTAATTTTTGAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCAAGGTTTAATTTTTGAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCAAGGTTTAATTTTTGAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATACTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCACTTATTTGTCCACACGCTTTTT
TTTTTGTCCGATTTCCCCACCGTGCATTTTCGCAATTTTAGGAACGTATCTCCACGTCACCAGGCCATTAGTAACACGGT
TTAATTTTTTTGAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCAAGGTTTAATTTTTGAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCAAGGTTTAATTTTTGAAAATTTGGTCGCGGATTTTCTC
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCAAGGTTTAATTTTTGAAAATTTGGTCGCGGATTTTCTC

Nr of selected repeats 63 Similarity 0.981664

Consensus :

GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTACCCACAC
GGCAAGGTTTAATTTTTGAAAATTTGGTCGCGGATTTTCTC
>Cele-UNSB01_6:350789-351447 Satlength=659 Nr of Repeats=7 RepeatLength=94
seed=GCAGTAATTC
GCAGTAATTCTCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTTCGATGCCCTTTGTAGACAAATCAATGAGAAAAT
TGTC AATTTCTGAAG
GCAGTAATTCTCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTTCGATGCCCTATGTAGACCATCCAATGGGAAAAT
TGTC AATTTCTGAAG
GCAGTAATTCTCAAAATCTCCTGTTCTCTAAATATTGGGTGCTTTTTCGATGCCCTTTGTAGACAAATCAATGAGAAAAT
TGTC AATTTCTGAAG
GCAGTAATTCTCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTTCGATGCCCTTTGTAGACAAATCAATGAGAAAAT
TGTC AATTTCTGAAG
GCAGTAATTCTCAAAATCTTCTGTTCTTTAAATATTGGGTGCTTTTTCGATGCCCTATGTAGACCATCCAATGGGAAAAT
TGTC AATTTCTGAAA
GCAGTAATTCTCAAAATCTCCTGTTCTCTAAATATTGGGTGCTTTTTCGATGCCCTTTGTAGACAAATCAATGAGAAAAT
TGTC AATTTCTGAAG

Nr of selected repeats 7 Similarity 0.944613

Consensus :

GCAGTAATTCTCAAAATCTtCTGTTCTCTAAATATTGGGTGCTTTTTCGATGCCCTtTGTAAGACaAatCAATGaGAAAAT
TGTC AATTTCTGAAG
>Cele-UNSB01_6:356210-356329 Satlength=120 Nr of Repeats=8 RepeatLength=14
seed=ATAGCGTATA
ATAGCGTATAGCGT
ATAGCGTATAGCGT
ATAGTGTATAGCGC

ATAGCGTATAGCGT
ATAGCGTATAGCGT
ATAGCTTATAGCTT
ATAGCGTATAGCGT
ATAGCGTATAGAGTATAGCGT

Nr of selected repeats 7 Similarity 0.891156

Consensus:

ATAGCGTATAGCGT

>Cele-UNSB01_6:444285-444373 Satlength=89 Nr of Repeats=7 RepeatLength=11
seed=CATAACTGAG

CATAACTGAGA
CATAACTGAGA
CATAACTGAGACATGACTGGGA
CATAACTGAGA
CATAACTGAGA
CATAACTGAGA
CATAACTGAGA

Nr of selected repeats 6 Similarity 1.000000

Consensus:

CATAACTGAGA

>Cele-UNSB01_6:483296-484174 Satlength=879 Nr of Repeats=19 RepeatLength=40
seed=AAAATTCTGG

AAAATTCTGGAAAGCTCTAGAACCTTCTGAAAAATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAAGTTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAAGTTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAAGTTCGAGAAAAAACTGGAATGTTCTAGAACCTTCTGGAAATTCGA
G

AAAATTCTGGAATGTTCTAGAACCTTCTGGAAATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAAGTTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAATTCGAAAAA
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AAAATTCTGGAATGTTCTAGAAAGCTTCTGAAAAATTCGAG
AAAATTCTGGAATTTTCTAGAACCTTCTGGAAATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAAGTTCGAG
AAAATTCTGGAATGTTCTAGAACCTTTTGGAAATTCGAAAAA
AAAATTCTGGAATTTTCTAGAACCTTCTGGAAATTCGAG
AAAATTCTGGAATGTTCTAGAACCTTCTGGAAATTCGAGAAAAATTCGTG
AAAATTCTGGAATGTTGTGGTGAGACCTATCGTGCTGAGACCCATTGTGGTGAGACCCCTTA
AAAATTTTGGCGGGAAATTCAAAAATTTATGAGAACATTTTTTTGAGGGAAATTCAGTTTTTCTGAGAACTATTTTTGT
ATTAGTACCTTCTGGAAGTTTCAAGAACTGG
AAAATTTGGA

Nr of selected repeats 12 Similarity 0.943434

Consensus:

AAAATTCTGGAATgTTCTAGAACCTTCTGGAAAaTTCGAG

>Cele-UNSB01_6:556288-556934 Satlength=647 Nr of Repeats=15 RepeatLength=15
seed=CCACGATGGG

CCACGATGGGTCTTGCCAGTTCAGGTGGTACTTAAGCTAACAAAAAGTTTCTCAGAAAATTTGAATTTCCCGCCAAAA
ATTTTTTCTCAGAAAATTTGAATTTCCCGCCAAAAATGTTTTCACAGAAAATTTGAATTTCCCGCCAAAAATTTTTTCTCAG
AAAATTTGAGTTTTCCCGCCAAAAATTTTTTTCACAGAAAATTTGAATTTCCCGCCAAAAATTTTTTCACTGAAAATTTGAA
TTTGCCCGCCAAAAATTTTTTCACTGAAAATTTAAATTTCCCTCCAAAAATTTTTTCTCAGAAAATTTAAATTTCCCGCCA
AAATATTTTTTTCACAGAAAATTTAAATTTCCCGCCAAAAATTTTTTTCACAGAAAATTTAAATTTCCCGCCAAAAATTTTT
TCTCAGAAAATTTAAATTTCCCGCCAAAAATTTGGGTCTTA

CCACGGTGGGTCTCA
CCACGACGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTTT
CCACGATGGGTCTCA
CCACGGTGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCA
CCACGATGGGTCTTT
CCACGATGGGTCTCA
CCACGGTGGGTCTCG
CCACGATGGGTCTCG

Nr of selected repeats 14 Similarity 0.873016

Consensus:

CCACGaTGGGTCTCn

>Cele-UNSB01_6:556993-557132 Satlength=140 Nr of Repeats=5 RepeatLength=30
seed=AATTTTCCAG

AATTTTCCAGAAGGTTCTAGAACAATCCAGAATTTTTCG
AATTTTCCAGAAGGTTCTGGAACATTCCAG
AATTTTCTAG

AATTTTCCAGAAGGTTCTAAAGCTTTTCAG
AATTTTCCAGAAGGTTCTGGAACGTTCTAG

Nr of selected repeats 3 Similarity 0.807407

Consensus:

AATTTTCCAGAAGGTTCTggaAaCnTTccAG

>Cele-UNSB01_6:743518-743644 Satlength=127 Nr of Repeats=5 RepeatLength=21
seed=GGTCAGTGCA

GGTCAGTGCATTACCAATTTT
GGTCAGTGCATTACCAATGTT
GGTCAGTGCATTACCAATTTT
GGTCAGTGCATTTCCAATTTT
GGTCAGTGCAAATTGAAAATCGGCCAGTGAATTACCAATTTT

Nr of selected repeats 4 Similarity 0.904762

Consensus:

GGTCAGTGCATTaCCAATtTt

>Cele-UNSB01_6:763886-764130 Satlength=245 Nr of Repeats=5 RepeatLength=22
seed=TGGTCAGTGC

TGGTCAGTGCAACTAAAAATGTTGAGAGCAGTGCTAATTTTAAAAATGATTAGTCAATGAAAACGTAATAATGTTACAC
TGAAAAAACTATTTCCACCTTTCTTGTTAGAATTTTAAATTTATCGGCAAAAGACTTGGTTCCTACATGCTTGCGGTT
TGGTCAGAGCTGGCGCCAATC
TGGTCAGTGCTGGCGACCAATT
TGGTCAGTGCTCGCGCCAATT
TGGTCAGTGCTGATAACCAATT

Nr of selected repeats 4 Similarity 0.777778

Consensus:

TGGTCAGtGCTggcgcaCCAATt

>Cele-UNSB01_6:903956-904040 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=ACTGACCAAA

ACTGACCAAAAATAGATATTC
ACTGACCAAAAATAGACATGC
ACTGACCAAAAATAGATATGC
ACTGACCAAAAATAGATATGC

Nr of selected repeats 4 Similarity 0.936508

Consensus:

ACTGACCAAAAATAGAtATgC

>Cele-UNSB01_6:960884-960987 Satlength=104 Nr of Repeats=5 RepeatLength=20

seed=ATGCACTGAC

ATGCACTGACCAAAAATATG

ATGCACTGACCGAAAATATG

ATGCACTGACCAAAGCTATG

ATGCACTGACCAAAAATTAT

ATGCACTGACCAAAAATTAG

Nr of selected repeats 3 Similarity 0.866667

Consensus:

ATGCACTGACCaAAaaTATG

>Cele-UNSB01_6:983566-988244 Satlength=4679 Nr of Repeats=290 RepeatLength=15

seed=CACGATGGGT

CACGATGGGTCTTGCCAGTTCAGGTGGTACTTAAGCTAGCAAAAAGTTTCTCAGAAAAGTTGAATTTCCCGCCAAAAT

GTTTTTCACTGAAAATTTGAATTTCCCGCCAAAATGTTTTTCACTGAAAATTCGAATTTCCCGCCAAAATGTTTTTAC

TGAAAATTTGAATTTCCCGCCGAAATGTTTTTCACTGAAAATTCGAATTTCCCGCCAAAATGTTTTTCACTGAAAATTT

GAATTTCCCGCCAAAATTTTTTCACTGAAAATTTGAATTTCCCGCTAAAATTTTTTCACTGAAAATTTGAATTTCCCG

CCAAAATTTTAC

CACGATGGGTCTCGT

CACGATGGGTCTCAC

CACGATGGGTCTCAC

CACGATGGGTCTCGT

CACGATGGGTCTCAC

CACAATGGGTCTCGT

CACGATGGGTCTCAC

CACGATGGGTCTCAC

CACGATGGGTCTCGT

CACGATGGGTCTCAC

CACGATGGGTCTCAC

CACGATGGGTCTCAC

CACGATGAGTCTCAC

CACGATGGGTCTCAC

CACGATGGGTCTCAC

CACAATGGGTCTCGT

CACAATGGGTCTCAC

CACGATGGGTCTCAC

CACGATGGATCTCAC

CACAATGGGTCTCGT

CACGATGGGTCTCGT

CACGATGGTTCTCAC

CACGATGGGTCTCAC

CACGATGGGTCTCGT

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CACGATGGGTCTCGT

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CACGATGGGTCTCCA
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CACGATGGGTCTCAC
CACGATGGGTCTCAC
CACGATGGGTCTCAC
CACGATGGGTCTCAC
CACGATGGGTCTCGT
CACGATGGGTCTCAC
CACGATGGGTCTCAC

Nr of selected repeats 284 Similarity 0.839014

Consensus:

CACGATGGGTCTCac

>Cele-UNSB01_6:988331-988610 Satlength=280 Nr of Repeats=13 RepeatLength=11

seed=CTACAGTACT

CTACAGTACTC

CTACAGTACCT

CTACAGTACTA

CTACAGTACCCCGACCACATCCCATCACTAACCTCAAACCAATATCCCTTTAAAAGGCGAAAAGTCAATTTTTCCCAA

CTACAGTAATC

CTACAGTACTC

CTACAGTACCT

CTACAGTACTA

CTACAGTACCCCGACCTCATCCACCCTAACCTCAAACCAATATCCCTTCAAAGGCGAAAAGTCAATTTTTCCCAA

CTACAGTAATC

CTACAGTACTC
CTACAGTACCA
CTACAGTACTA

Nr of selected repeats 11 Similarity 0.823691

Consensus:

CTACAGTACTn

>Cele-UNSB01_6:998781-998865 Satlength=85 Nr of Repeats=4 RepeatLength=21

seed=CAGTGCATTC

CAGTGCATTCAGAACTTTGAT
CAGTGCATTCGAACTTTTCGT
CAGTTCATTCAGAAAGTTTGGT
CAGTGCATTCAGAAAGTTTGGT

Nr of selected repeats 4 Similarity 0.830688

Consensus:

CAGTgCATTCaGAAcTTTggT

>Cele-UNSB01_6:998801-998992 Satlength=192 Nr of Repeats=6 RepeatLength=21

seed=TCAGTGCATT

TCAGTGCATTCCGAACTTTTCG
TCAGTTCATTCAGAAAGTTTGG
TCAGTGCATTCAGAAAGTTTGG
TCAGTGCATTCAGAAAGTTTGGCCCTGGGAATTTTCAAATTCGATTAGTCCATTTCAAATTCGG
TCAGTGCATTTTCAAATTCGATATGTGCGTTTTCAAATTAGG
TCAGTGCATTGTCAAATTCGG

Nr of selected repeats 4 Similarity 0.735450

Consensus:

TCAGTgCATTcagAAgTTtgG

>Cele-UNSB01_6:1033071-1033155 Satlength=85 Nr of Repeats=4 RepeatLength=21

seed=TGGTCAGTGC

TGGTCAGTGCAAGAAACAATT
TGGTCAGTGCAAGAAACAATT
TGGTCAGTGCAAGAAACAATT
TGGTCAGTGCAAGAAACAATT

Nr of selected repeats 4 Similarity 0.968254

Consensus:

TGGTCAGTGCAAGAAACAaTT

>Cele-UNSB01_6:1052300-1052972 Satlength=673 Nr of Repeats=4 RepeatLength=21

seed=TGACAAAACA

TGACAAAACATCTGGAAGACGTCGACCAAGTGTAATAATATCGAAAAAGAAAACGCCTGCTCCGAATGCAAATCTTCCT
TTAAAGTAGTTCCCTTTTTCCCTTATTTTCCTCACCGTTCAAATCAATTTTCAGATCAAATCTAGAAGAGTTTGTGT
CAAAAACCTTATGCTCTTGGAGAGTACAATAATTTGGCAAGTCCAGCTTACGCCTACACATCCGAAATTCACGACGAGAG
AGAAGTAGACGTGGGGAACGATGTGCGATATGAGGTAGAGTTTTCCATTTAATTTTGGGAAAGGCTAGGTTGAAACTAT
TGGGAAACTTGAGAAGGAAAACAATTTTCCAGAAATAAGACTGCCTATGAAATTTGAAGGAAAGCTCATCATATTAACA
GTAATATATTTTCATTGAAAACTGAACAGCTCCTAACGTATTTTGTGCTGATTCCAGAAGCCGTACGAAAAAGAAGTGC
CAGCAAACCAAGAGCCCCAAGAGTCGAGGACGGAGCAGTATCATCATTCCGATCAATCACTGAAATTTGTTTCATGCCGCG
GAGACAGCAACCACATCGCAAGGTGAGGAATGCAGTAACCAGATGAGTTTTTGCAC
TGACAAAACATAACTTTGCAC
TGACAAAACATAACTTTGCAC
TGACAAAACATAACTTTGCAC

Nr of selected repeats 3 Similarity 1.000000

Consensus:

TGACAAAACATAACTTTGCAC

>Cele-UNSB01_6:1060978-1061104 Satlength=127 Nr of Repeats=6 RepeatLength=21

seed=GTCAGTGCAT

GTCAGTGCATTGATAGTTTCT

GTCAGTGCATTGATAGTTTCT
GTCAGTGCATTGATAGTTTCG
GTCAGTGCATTGATAGTTTCG
GTCAGTGCATTGATAGTTTCG
GTCAGTGCATTGATAGTTTTG

Nr of selected repeats 6 Similarity 0.944974

Consensus:

GTCAGTGCATTGATAGTTTCg

>Cele-UNSB01_6:1066955-1067057 Satlength=103 Nr of Repeats=5 RepeatLength=20
seed=TTGGTCAGTG

TTGGTCAGTGCAATTTCAACT
TTGGTCAGTGCATTTTAGTC
TTGGTCAGTGCAATTTCAACT
TTGGTCAGTGCATTTTAGTC
TTGGTCAGTGCATTTTAGTT

Nr of selected repeats 3 Similarity 0.955556

Consensus:

TTGGTCAGTGCATTTTAGTc

>Cele-UNSB01_6:1102792-1102897 Satlength=106 Nr of Repeats=4 RepeatLength=21
seed=GTCAGTGCAA

GTCAGTGCAATTGAAGTTGTG
GTCAGTGTAATTAGAATAATG
GTCAGTGCAATAAGAGTGTTG
GTCAGTGCAAATAGAACTTTAGACAGTAGAATTGAAGTTTTG

Nr of selected repeats 3 Similarity 0.661376

Consensus:

GTCAGTGcAATtagAgTnnTG

>Cele-UNSB01_6:1106813-1106897 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=GTCAGTGCAA

GTCAGTGCAAAAACTAATTTT
GTCAGTGCAAATTCAAATATT
GTCAGTGCAAATTCAAATATT
GTCAGTGCAACTTCAAATATT

Nr of selected repeats 4 Similarity 0.841270

Consensus:

GTCAGTGCAAattCaAAaTt

>Cele-UNSB01_6:1138488-1138593 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=TTGGTCAGTG

TTGGTCAGTGGAATTTTGGAT
TTGGTCAGTGCGATTTTTTAA
TTGGTCAGTGCAAATTTAAAA
TTGATCAGTGCAAATTTAGAA
TTGGTCAGTGCGATTTTTTAA

Nr of selected repeats 5 Similarity 0.746032

Consensus:

TTGgTCAGTGcaAtTTTnnAa

>Cele-UNSB01_6:1180467-1185764 Satlength=5298 Nr of Repeats=52 RepeatLength=102
seed=TGTACACTTC

TGTACACTTCTCCAAAATGACTGTAAGAATGGACTCCTTATATGATTTTTAAACCCGACTCTGGACATACAAACTTCTC
TCAAAAAGAAAATAGACTTCACA
TGTACACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTTAAACCCGACTCTGGACATACAAACTTCTC
TCAAAAAGAAAATAGACTTCACA
TGTACACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTTAAACCCGACTCTGGACATACAAACTTCTC
TCAAAAAGAAAATAGACTTCACA

TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACAG
TGTACTTCTCCAAAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCAAAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCAAAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCAAAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATAACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCAAAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA
TGTACTTCTCCATAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA

Nr of selected repeats 37 Similarity 0.984062

Consensus:

TGTACTTCTCCCAaAtTGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAACTTCTC
TCAAAAGAAAATAGACTTCACA

>Cele-UNSB01_6:1259650-1260300 Satlength=651 Nr of Repeats=6 RepeatLength=21
seed=GTCAGTGCAA

GTCAGTGCAAAGTATTTTTG
GTCAGTGCAAATGCATTGTTG
GTCAGTGCAAAGGTATTTTTG
GTCAGTGAAATGCATTTTCG

GTCAGTGCAAGTCTGTCATTTTGTTCATGTACCAAAGCACCTTTGTTTTAAATCAAACATTTCCAGCACAAATTTTACCG
ATCTTTGAATTTAATCAACCATCAACTCACCAATAGTCTGTAGATCATAACCTTGCTTCAAGAAAACCGCAAATAATT
GTCATATTGATACTATCCAGCCAGTTGGCCAAAACCTCCGCGTGCGGCACACCACTCTGCACCATGCTGGTCACATCG
ACCTCGTGAATGGAGCGATACAAGGAATCATCCAATCCATGAATTGATGATGAGGAGCCGCTTCCACTCTCCACAGAAC
GCACACTGTGTGCTGATTTCGCATCCAGATTCATTGCTTTGCACACCCGACGGGAATGATGAGGCGGACGTTGACGTCTGA
GCACTGGAAATTTGGTTTTGGGATTTGGAGAAGGTGTGGGTAGGAATTCAACTTCTCAGTGATTTGAAAATTCGCCAAT
TTGGAAATTTGCCTAATATGTAGATTGTCACTGAATTTAACCCAAAGATCTAAATTTTCAGTAGGAGCTCTTTA
GTCAGTGCAATTACCTTTT

Nr of selected repeats 4 Similarity 0.809524

Consensus:

GTCAGTGcAAAtGcATtTtG

>Cele-UNSB01_6:1324054-1324372 Satlength=319 Nr of Repeats=7 RepeatLength=22

seed=GTCAGTGCAA

GTCAGTGCAAATTGTGCACATG

GTCAGTGCAAATTGTGCACATG

GTCAGTGCAAATTGTGCACATG

GACAGTGCAAATTCTGAAATGCAAAGTTCCCAATAGTCGGAACACTTATTTTATAATTATTATATTTAACTCCGAATT

GTACAAATTCTATTAGAAGTCAACAGAAAATCATGGTCTTACCAAGTTTTTCATGCTAATTTTTGATTTCTTTTTCT

TTTCAAAGTTTACCAAAAAATATAGAAAA

TCAGTGCAAATTCATTTG

GTCAGTGCAAATTCAGGTA

GTCAGTGCAAATTCCTCCAATTT

Nr of selected repeats 5 Similarity 0.692754

Consensus:

GTCAGTGCAAattgTgCacaTg

>Cele-UNSB01_6:1338339-1338633 Satlength=295 Nr of Repeats=14 RepeatLength=21

seed=TTTGCCTGA

TTTGCCTGACCAACACGAAT

TTTGCCTGACCAACACGAGT

TTTGCCTGACCAACACGAAT

TTTGCCTGACCAACCTTAT

TTTGCCTGACCAACACGAAT

TTTGCCTGACCAACACAAAT

TTTGCCTGACCAACACAAAT

TTTGCCTGACCAACACAAAT

TTTGCCTGACCAACACAAAT

TTTGCCTGACCAATACGAAA

TTTGCATTGACCAATACAAAA

TTTGCCTGACCAATACGAAA

TTTGCCTGACCAATACAAAA

TTTGCCTGACCAATACGAAA

Nr of selected repeats 14 Similarity 0.853480

Consensus:

TTTGCCTGACCAAACgAAAt

>Cele-UNSB01_6:1342228-1342338 Satlength=111 Nr of Repeats=5 RepeatLength=22

seed=TCGCACTGAC

TCGCACTGACCAAACCTTAGAAA

TCGCACTGACCAAACCTTAGAAA

TCGCACTGACCAAACCTTAGAAA

TCGCACTGACGAAACCTTATAAA

TCGCACTGACCAAACCTTATAAG

Nr of selected repeats 5 Similarity 0.915152

Consensus:

TCGCACTGACcAAACCTTAgAAa

>Cele-UNSB01_6:1365926-1366333 Satlength=408 Nr of Repeats=5 RepeatLength=21
seed=TTGCACTGAC
TTGCACTGACCAAAATTAAGC
TTGCACTGACCAAAATTCAGTTGACACCAGGGGTGGGCGGCAAAACAAAATTTTCCGCCGAATTGATTATTCGTTAGTTC
TCAATTAATAAAAAATACTTTAAAAACAATATTCCTACTGTAATAAGTGTTATTTTGGAGAATAAGTGTAATTTTTTTTCCA
ACTTAAATATTTAGAGATTCTGAATTTTTATTCTGGCAAAAAAGTGTTGGCCGGTAATTCCAAATTCAAAATTTTCGG
CAGATCAAAACTCAGGGAGTTGCCGAAATAAACATTTTTTTGAATAAAATTAGCAATCGGCCCTTTCGACAATTGCCGCC
CACCCATGGT
TTGCACTGACAAAATTTTCGTT
TTGCACTGACAAAACCT
TTGCACTGACAAAATTTTCGTG

Nr of selected repeats 3 Similarity 0.747475

Consensus:

TTGCACTGACAAAATTTcGtn

>Cele-UNSB01_6:1371051-1371242 Satlength=192 Nr of Repeats=7 RepeatLength=21
seed=TTGCACTGAC

TTGCACTGACCAAAATTTATTGAACTATTAATTATTTGATTCTGATTAACAATGACCAAAAGAT
TTGAACTGACAAAGTGCAAAAT
TTGCACCGACCAAAAAACAGT
TTGCACTGACCACCTCTTCAT
TTGCACTGACCACCTCTTCAT
TTGCACTGACCAACTTTTCAT
TTGCACTGACCATCTCTTCAT

Nr of selected repeats 6 Similarity 0.630303

Consensus:

TTGCACTGACCAAcTcttCAT

>Cele-UNSB01_6:1379546-1379614 Satlength=69 Nr of Repeats=4 RepeatLength=17
seed=TGGTCAGTGTC

TGGTCAGTGCAAAAAGT
TGGTCAGTGCAAAAAGT
TGGTCAGTGCAAAAAGT
TGGCCAGTGCAAAAAGA

Nr of selected repeats 4 Similarity 0.882353

Consensus:

TGGtCAGTGCAaAAAGt

>Cele-UNSB01_6:1420400-1420757 Satlength=358 Nr of Repeats=9 RepeatLength=40
seed=ATTTTTCTAG

ATTTTTCTAGAAAGTTCTGGAACACTCCAGAATTTTCTCG
ATTTTTCTAGAAAGTTTGAACATTCAGAATTTTCTCG
ATTTTTCTAGAAAGTTCTGGAACATTCAGAGTTTCTCG
ATTTTTCTAGAAAGTTCTGGAACGTTCCAGAATTTTCTCG
ATTTTTCTAGAAAGTTCTGGAACATTCAGACTTTTCCCA
ATTTTTCTAGAAAGTTCTGGAACATTCAGAATTTTCTCG
ATTTTTCTAGAAAGTTCTGGAACATTCAGAATTTTCTCG
ATTTTTCTAGAAAGTTCTGGAGCGTTCCAGAATTTTCTCG
ATTTTTCTAGAAAGTTCTGGAACATTCAGAATTTTCCCG

Nr of selected repeats 6 Similarity 0.937778

Consensus:

ATTTTTCTAGAAAGTTCTGGAACaTTCAGAATTTTCTCG

>Cele-UNSB01_6:1420856-1421521 Satlength=666 Nr of Repeats=19 RepeatLength=35
seed=CCCGCCAAA

CCCGCCAAAATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAATTTTTTTTTTCAGAAAATTTAAATTT
CCCGCCAAAACATTTTTTCACAGAAAATTTAAATTT

CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAATTTTTTTTTTCAGAAAATTTAAATTA
CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAACATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAACATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAACATTTTTTCACAGAAAATTTCAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTCAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTCAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT
CCCGCCAAAATATTTTTTCACAGAAAATTTAAATTT

Nr of selected repeats 19 Similarity 0.932275

Consensus:

CCCGCCAAAAtATTTTTTCACAGAAAATTTAAATTT

>Cele-UNSB01_6:1421556-1421900 Satlength=345 Nr of Repeats=23 RepeatLength=15

seed=CGATGGGTCT

CGATGGGTCTCACCT

CGATGGGTCTCACCA

CGATGGGTCTTACCA

CGATGGGTCTCACCA

CGACGGGTCTCACCA

CGATGGGACTCACCA

CGATGGGTCTCACCT

CGATGGGTCTCACCA

CGATGGGTCTCATCA

CGGTGGGTCTCACCA

CGGTGGGTCTCACCA

CGATGGGTCTCACCA

CGGTGGGTCTCGCCA

CGATGGGTCTCACCA

CGATGGGCCTCGCCA

CGATGGGTCTCGCCA

CGATGCGTCTCGTCA

CGATGGGTCTCGCCA

CGATGCGTCTCGTCA

CGATGGGTCTCACCA

CGATGGGTTTTTTCA

CGATGGGTCTCACCA

CGATGGGTCTTGCCA

Nr of selected repeats 22 Similarity 0.845695

Consensus:

CGATGGGTCTCaCCA

>Cele-UNSB01_6:1421957-1422097 Satlength=141 Nr of Repeats=5 RepeatLength=30

seed=AATTTTCCAG

AATTTTCCAGAAGTTCTAGAACAATCCAGAATTTTTTCG

AATTTTCCAGAAAGTTCTGGAACATTCCAG

AATTTTCTAG

AATTTTCCAGAAGTTCTAAAGCTTTTCAG

AATTTTCCAGAAGTTCTGGAACATTCTAG

Nr of selected repeats 3 Similarity 0.792593

Consensus:

AATTTTCCAGAAgGTTCTggAaCaTTccAG

>Cele-UNSB01_6:1422210-1422590 Satlength=381 Nr of Repeats=13 RepeatLength=11
seed=GTACTCCTAC

GTACTCCTACA

GTACTCCTACA

GTACTACTACAGTACCACGACCATATTCCTACTAACCAGCAAACCTATATCTCTTCAAAGACAAAAACACAATTTTT

CGTAAACTACA

GTAATCCTACC

GTACTCCTACA

GTACTCCTACA

GTACTACTACAGTACCCCGACCATATCCCACTAATAACTCCAAACCTATATCTCTTCAAAGACAAAAACTCAATTTTT

CCTAAACTACA

GTAATCCTACC

GTACTCCTACA

GTACTCCTACA

GTACTACTACAGTGCCCCGACCATATCCCACTACTAACCCCAAACCTATATCTCTTCAAAGACAAAAACACAATTTTT

CCCAAACCTACA

GTAATCCTACC

GTACTCCTACA

Nr of selected repeats 10 Similarity 0.886869

Consensus:

GTAcTCCTACa

>Cele-UNSB01_6:1553970-1554390 Satlength=421 Nr of Repeats=18 RepeatLength=20
seed=AGGCAGACCT

AGGCAGACCTAGCTTACCCA

AGGCAGACCTAGCCTACCCT

AGGCAGACCTAGCTTACCCA

AGGCAGACCTAGCCTACCCT

AGGCTGACCTAGTTTACCCA

AGGCAGACCTAGCCTACCCT

AGGCAGACCTAGCTTACCCA

AGGCAGACCTAGCCTACCCT

AGGCAGACCTAGCCTACCCT

AGGCTGACCTAGTTCACCCAAAACAGACTCAGCCTACCCC

AGGCAGACCCAGCCTACCCT

AGGCAGACCTAGCCTACCCT

AGGCAGACCTAGCCTACCCA

AGGCAGACCTAGCCTACCCT

AGGCAGACTTAGCCTACTCT

AGGCAGACCTAGCCTACCCTAGGCAAACCCAGCCTACCCTGGGCAGCCCAAGTCTACCCA

AGGCAGACCCAGCCCACCCT

AGGCAGACCTAGCCTACCCT

Nr of selected repeats 16 Similarity 0.885556

Consensus:

AGGCAGACCTAGCCTACCCT

>Cele-UNSB01_6:1555230-1555302 Satlength=73 Nr of Repeats=5 RepeatLength=12
seed=CTAAGCCTAA

CTAAGCCTAAGC

CTAAGCCAAAGA

CTAAGCCTAAGC

CTAAGCCAAAGA

CTAAGCCTAACTTTAAGCATAAAC

Nr of selected repeats 4 Similarity 0.851852

Consensus:

CTAAGCCaAAGa

>Cele-UNSB01_6:1569817-1569931 Satlength=115 Nr of Repeats=5 RepeatLength=23
seed=AAAAAATTTG

AAAAAATTTGTTTCGCACTGAAC

AAAAAATTTGTTTCGCACTGACC

AAAAAATTTGTTTCGCACTGAC

AAAAAATTTGTTTCGCACTGACC

AAAAAATTTGTTTCGCACTGACC

Nr of selected repeats 4 Similarity 0.971014

Consensus:

AAAAAATTTGTTTCGCACTGAcC

>Cele-UNSB01_6:1590254-1590338 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=TCTGAGCACT

TCTGAGCACTGACCAAAAATTA

TCTGAGCACTGACCAAAAATTA

TCTGAGCACTGACCAAAAATTA

TCTGAGCACTGACCAAAAATTT

Nr of selected repeats 4 Similarity 0.925926

Consensus:

TCTGAGCACTGACaAAAATTa

>Cele-UNSB01_6:1594210-1594900 Satlength=691 Nr of Repeats=19 RepeatLength=30
seed=ACTACCCAAC

ACTACCCAACCGGCTCCGGCAACTAGTCCG

ACTACTCAACCGGCTCCGGCAACTAGTCCG

ACTACTCAACCAGCTCCCGCAACCAGCCCG

ACTACCCAGCCGGCTCCCGCAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ACTACCCAAACCGACTCCGGCAACCAGTCCA

ACTACCCAAACCGACTCCGGCAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ACTACCCAAACCGACTCCGGCAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ACTACCCAAACCGACTCCGGGAACCAGTCCA

ACTACCCAAACCGGCTCCGGCAACCAGTCCA

ATCCTCAACACCAATAGCTTCATCTAGCTCATCTGGTTCTACTGTCACCGTTGTCTCAGGATCTTCCAGCACATACGG
ATCGTCAACACCATCCGCGTCATCTAGTTCGCTGGAACCTGCGTCGACAATCTCAGGATCAACTGGTTCAACAGCTACA
ATTGTACCAGGATCTTCAAGCTCGGTTGG

Nr of selected repeats 3 Similarity 0.732510

Consensus:

ATCcTCAACACCATCnGcGTCATCTAGtTCctCcGGAACtatGTcGACaAttTCaGGATCAACTGGTTCnACAGtTACa
gTtGtaCCaGgATCnTctAGcaCatTTGg

>Cele-UNSB01_6:1598138-1600934 Satlength=2797 Nr of Repeats=10 RepeatLength=249
seed=CTGGAAGCAC

CTGGAAGCACAGTTACCACCTGGATCTACAGAAGGAAGCAGTACATCAGGTAGTTCATCTGCTACTTCTTTAAGTAGCAG
TTCCCCCGTCCCATCAACTTCCAATCCCCTAACCCCTTCCACGTCCGGTAGTAGTACTCCAACCCCCAACCCATCCCAA
TCCACTAGTCCAGTTGTTTCAACAACAACCTGGAGAAATGACATCTCATGGTTCAACTCAGACACCAAGTACTATTGGAT
CAACAGTGACTCAACCGTCTACTGTcAGTGGATCGAACAGTT

CTGGAAGCACAGTTACCATTGGATCTTTCGGAAGCAAGCACCTCAGGTAGTTCGTTTAAAACATCCCCGAGTAGCATTTC
CCCAGTTCCTACCTCTTCCCCTATCCCCTCGACAACATTTCGCAAGTAGCACATCAGGTAAGTGAATTCATAAAAAATTGA
AAATATCCAGAAAGTGCAGAAAAAATTAGTTTTGACTAACTGCTAGGGTAAATATTGATACTCTAAATAATTCAAAAA
AAACAAGTGAATCAAAAGCTTCTCAGGTTCCACGATCTCGGATGTCTCTTcAGTCTCTACGACTTCACTAGCGCCTTT
GTCTAGTTCCCTCCCATCAACAGTCCCATCTAGTACCCAATCCTTcAGTAGCACGTCCGAAGGATCTTCGAAAGCCTCT
TCCTCCCCAGTTCCCTCCAAACAAGTAGTACCCCCACAAATCCAACCGGCTCGACTGAGTCCCAACACTTCTATCTT
CGACCATATCGGGCTCCACTCAGCACACAACAATGTCAAAGCTAGCTCGGGCTCCACAAGCCCTTCGACAAATTCTCA
GA

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTCACATCTTCAGCATCCAGTACTCAGCCTCAGAT
GAGCACTTCAACAAGGAAGTTCAGCAGGATCCACAGTTGCTTCTTCAACAGCTAGCCCTGCTGCGAGTTCCACAGCTCCA
TCTTCAACTGGAACATGAGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAATCATCGACAACAGCATCTG
CAAGTTCTCAGA

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTCACATCTTCAGCATCCAGTACTCAGCCTCAGAT
GAGCACTTCAACAAGGAAGTTCAGCAGGATCCACAGTTGCTTCAACAGCTAGCCCTGCTGCGAGTTCCACAGCTCCA
TCCTCGACAGGAACAATGGGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAATCATCGACAGCAGCATCTG
CAAGTTCTCAGA

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTCACATCTTCAGCATCCAGTACTCAGCCTCAGAT
GAGCACTTCAACAAGGAAGTTCAGCAGGATCCACAGTTGCTTCTTCAACAGCTAGCCCTGCTGCGAGTTCCACAGCTCCA
TCTTCAACTGGAACATGAGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAATCATCGACAACAGCATCTG
CAAGTTCTCAGA

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTCACATCTTCAGCATCCAGTACTCAGCCTCAGAT
GAGCACTTCAACAAGGAAGTTCAGCAGGATCCACAGTTGCTTCAACAGCTAGCCCTGCTGCGAGTTCCACAGCTCCA
TCCTCGACAGGAACAATGGGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAATCATCGACAACAGCATCTG
CAAGTTCTCAGA

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTCACATCTTCAGCATCCAGTACTCAGCCTCAGAT
GAGCACTTCAACAAGGAAGTTCAGCAGGATCCACAGTTGCTTCAACAGCTAGCCCTGCTGCGAGTTCCACAGCTCCA
TCCTCGACAGGAACAATGGGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAATCATCGACAGCAGCATCTG
CAAGTTCTCAGA

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTCACATCTTCAGCATCCAGTGGTCAGCCTCAGAT
GAGCACTTCAACAAGGAAGTTCAGCAGGATCCACAGTTGTTTCTTCAACAGCTAGCCCTGCTGCGAGTTCCACAGCTCCA
TCTTCAACTGGAACATGAGCTCCACTTCTAGTGGAACAGTTGGATCAACGATGTCTCAGTCTTCAACAGCAGCTTCCA
CAACTTCTCACA

CGGGAAGCACAGTAACCCCTCGGATCTTCAAGTACCTCCAGTAATCAAATGAGCACTTCAACAAGGAAGTTCGGTAGGATC
CACAGTAGCTTCATCAACCGCTGGCCTTGTTCCTCAACTTCCACAGTTCCATCCTCGACAGGAACAATGGGCTCCACTTCT
AGTGGAACAGTTGGATCTACAATTTCTGAATCATCGACAACAGCATCTGCAAGTTCTCAGA

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTCACATCTTCAGCATCCAGTACTCAGCCTCAGAT
GAGCACTTCAACAAGGAAGTTCAGCAGGATCCACAGTTGCTTCAACAGCTAGCCCTGCTGCGAGTTCCACAGTTCCA
TCCTCGACAGGAACAATGGGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAATCATCGACAACAGCATCTG
CAAGTTCTCAGA

Nr of selected repeats 7 Similarity 0.929623

Consensus:

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTCACATCTTCAGCATCCAGTACTCAGCCTCAGAT
GAGCACTTACAAGGAAGTTCAGCAGGATCCACAGTTGCTTCaTCAACcGCTgGCCtTgTtCaAcTTCCACAGtTCCA
TCcTCgACaGGAACaATGgGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAATCATCGACAaCAGCATCTG
CAAGTTCTCAGA

>Cele-UNSB01_6:1657466-1657754 Satlength=289 Nr of Repeats=10 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGATTACTGTAGTTTAGGAAAATTGAGTTTTTTGTCTTTTAAAGGGATATTGGTTAAGGGTTAGTGCCGG
AACATGACCGG

GTACTGTAGTA

GTACTGTAGAG

GTACTGTAGGAGTACTATAGAG

GTACTGTAGGA

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Nr of selected repeats 6 Similarity 0.790741

Consensus:

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>Cele-UNSB01_6:1682621-1693139 Satlength=10519 Nr of Repeats=404

RepeatLength=26 seed=AACGGTCAGA

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Nr of selected repeats 393 Similarity 0.943434

Consensus:

AACGGTCAGAGTCACTaTTTTTGGTG

>Cele-UNSB01_6:1697161-1700255 Satlength=3095 Nr of Repeats=119 RepeatLength=26
seed=GACTCTAACC

GACTCTAACCATTTCACCTAAAAATAT
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Nr of selected repeats 119 Similarity 0.954495

Consensus:

GACTCTAACCATTTCACCTAAAAATAT

>Cele-UNSB01_6:1700308-1706287 Satlength=5980 Nr of Repeats=323 RepeatLength=11
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Nr of selected repeats 14 Similarity 0.970132

Consensus:

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>Cele-UNSB01_6:1780465-1781641 Satlength=1177 Nr of Repeats=4 RepeatLength=165
seed=CTTTTCCAAA

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AGGAATCAAAAAAATTGTTTCGAAAGAAATTTGAAAACGATTTAGAAATAGTGGTGACAGTTTGAATACTTTATCAGT
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TCAATAAATATACATTTTGTGTATACAGGGTGGCGCCCAATTACCCGTACAAAAGTTTGACATAACGATGACGCGCGCT
TACGCATGATATGCGCTTCAATACTATTTTATTTAATCATTAATAATTTGTTTATTTGTTGTTGAAAATTTTTCAGCTCAA
TCGGGCAATTTTCAACAGAAATGGCACCCTTCAGCGCACATCGTGTGTTGAATTATCAACTTATTTTCGGAAGGGAGTGAGC
CGAGTTACCATTGCTAAAAAGCTTGCCGTTGCTCGCCAGACAGTTTAAAGATAAAAATTTGAAGGTCCGGGGAGCTTGGCA
ATTTACAGGACCGTAAACTCGTGCCTACCTTCAGGCATTTCAGTTTTTAC

CTTTTCCAAAATGGCAATTTTGTATGAAAAAATCCGAATTTTCACAAATTTCAAAAAAATTTTTAACTTTTATAATTT
TAGCTTTGAATATTCCAAATGGAACGTGCATAACCTATCAATTTGATATATAAACTCGTGCCTACCTTCAGGCATTTCAG
TTTTTAC

CTTTTCCAAAATGGCAATTTTGTATGAAAAAATCCGAATTTTCACAAATTTCAAAAAAATTTTTAACTTTTATAATTT
TAGCTTTGAATATTCCAAATGGAACGTGCATAACCTATCAATTTGATATATAAACTCGTGCCTACCTTCAGGCATTTCAG
TTTTTAC

CTTTTCCAAAATGGCAATTTTGTATGAAAAAATCCGAATTTTCACAAATTTCAAAAAAATTTTTAACTTTTATAATTT
TAGCTTTGAATATTCCAAATGGAACGTGCATAACCTATCAATTTGATATATAAACTCGTGCCTACCTTCAGGCATTTCAG
TTTTTAC

Nr of selected repeats 3 Similarity 1.000000

Consensus:

CTTTTCCAAAATGGCAATTTTGTATGAAAAAATCCGAATTTTCACAAATTTCAAAAAAATTTTTAACTTTTATAATTT
TAGCTTTGAATATTCCAAATGGAACGTGCATAACCTATCAATTTGATATATAAACTCGTGCCTACCTTCAGGCATTTCAG
TTTTTAC

>Cele-UNSB01_6:1814276-1830201 Satlength=15926 Nr of Repeats=595

RepeatLength=27 seed=TTACTCTCTG

TTACTCTCTGTGGCATCCACTATATT

TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTATATT

TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTGGCTTCCCACCATATT

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TTACTCTCTGTGGCTTCCCACCATATT

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TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTATATT

TTACTCTCTGTGGCTTCCCACCATATT

TTACTCTCTGTGGCTTCCCACATATTTCTCTGTGGCTCCCACCATATT

TTACTCTCTGTGGCTTCCCACATATT

AAGCCTATGCCTAAGTCTAAACCTAAGTCTGAGCCTTTCCCA
AACCCCTATGCCATTCCCA
AAGCCTAAGCCTATGCCTAAGCAT
AAGCCTAAGCCTTTCCCA
AAGCCTATGCTTTTCCCA
AAGCCTATGCCTATCCCA
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AAGCCTATGCTTTTCCCA
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AAGCCTATGCTTTTCCCA
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AACCCCTATGCCATTCCCA
AAGCCTATGCCGAAGCCG
AAGCCTAAGCCT
AAGCCTATGCCTAAGCAT
AAGCCTAAGCCTTTCCCA
AAGCCTATGCTTTTCCCA
AAGCCTATGCCTATCCCA
AAGCCTATGCCTTTCCCA
AAGCCTATGCCT
AAGCCCATGCCTAAGCAT
AAGCCTAAGCCTTTCCCA
AAGCCTATGCTTTTCCCA
AAGCCTATGCCTATCCCA
AAGCCTATGCCATTCCCA
AAGCCTATGCCGAAGCCG
AAGCCTAAGCCT

Nr of selected repeats 44 Similarity 0.776212

Consensus:

AAGCCTATGCcttttCCa

>Cele-UNSB01_6:1926117-1926284 Satlength=168 Nr of Repeats=11 RepeatLength=14

seed=TAGGCCCTCA

TAGGCCCTCAAGCG

TAGGCCCTCAAGCG

TAGGCCCTCAGGCT

GAATTTTCTCGATTTTCTAGAAAGTTCTGGAACATTCCA
GAATTTTCTCGATTTTCTAGAAAGTTCTGGAACGTTCCA
GAATTTTCTCGATTTTCTAGAAAGTTCTGGAACGTTCCA
GAATTTTCTCGATTTTCTAGAAAGTTCTGGAACATTCCA
GAATTTTCTCGATTTTCTAGAAAGTTCTGGAACATTCCA

Nr of selected repeats 34 Similarity 0.961200

Consensus:

GAATTTTCTCGATTTTCTAGAAAGTTCTGGAACaTTCCA

>Cele-UNSB01_6:2088902-2090459 Satlength=1558 Nr of Repeats=79 RepeatLength=15

seed=CCACGATGGG

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCACGACGGGTCTCA

CCACGGTGGGTCTCG

CCACGATGGGCCTCA

CCACGACGGGCCTCGG

CACGATGGGTCTCG

CCACGATGGGTCTCG

CCACGATGGGCCTCA

CCACGATGGGTCTTT

CCACGATGGGTCTCG

CCACGATGGGTCTCGCCACGAATTTAAAATTTTCGATTTTCTAGAAAGTTCTGGAACATTCAGAATTTTCTCGATTT

TTCTAGAAAGTTCTCCGAAAATTTAAATTACCCGCCAAAATATTTTTTACAGAAAATTTAAATTTCCCGCCAAAATATT

TTTTACAGAAAATTTAAATTTCCCGCCAAAATTTGGGTCTCA

CCACGATGGGTCTCA

CCACGATGGGTCTCA

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CCTCGATGGGTCTCA

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CCACGACGGGTCTCA

CCACGGTGGGTCTCA

CCACGATGGGTCTCA

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CCACGATGGGTCTCG

CCACGATGGGTCTTG

CCACGATGGGTCTCG

CCACGATGGGTTTCA

CCACGATGGGTCTTT

CCACGATGGGTCTCA

CCACGATGGGTACG

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CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGACGGGTCTCA
CCACGGTGGGTCTCG
CCACGATGGGTCTCA
CCACGACGGGCCTCGG
CACGATGGGTCTCG

Nr of selected repeats 73 Similarity 0.860748

Consensus:

CCACGATGGGTCTCa

>Cele-UNSB01_6:2088902-2090835 Satlength=1934 Nr of Repeats=85 RepeatLength=15

seed=CCACGATGGG
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGATGGGTCTCA
CCACGACGGGTCTCA
CCACGGTGGGTCTCG
CCACGATGGGCCTCA
CCACGACGGGCCTCGG
CACGATGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGCTTCA

TTAGAGTAAATATTTGGCAGAACA
TTAGAGTAAATATTTGGCAGAACA
TTAGAGTAAATTATTTGGCAGAACA
TTAGAGTAAATATTTGGCAGAACA
TTAGAGTAAATATTTGGCAGAACA
TTAGAGTAAATAAATAAATATTTGG
CAGAACA
TTAGAGTAAATATTTGGCAGAACA
TTAGAGTAAATATTTGGCAGAACA
TTAGAGTAAATATTTGGCAGAACA
TTAGAGTAAATATTTAGCAGAACA
TTAGAGTAAATATTTGGCAGAACA

Nr of selected repeats 71 Similarity 0.941451

Consensus:

TTAGAGTAAATtATTTGGCAGAACA

>Cele-UNSB01_6:2093711-2093945 Satlength=235 Nr of Repeats=9 RepeatLength=26
seed=ATAGTGACTC

ATAGTGACTCTGGCCGTTCAACCAAT
ATAGTGACTCTGGCCGTTCTCCAAA
ATAGTGACTCTGGCTGTTCAACCAAT
ATAGTGACTCTGGCTGTTCAACCAAT
ATAGTGACTCTGGCTGTTTACCAAT
ATAGTGACTCTGGCCGTTCAACCAAT
ATAGTGACTCTGGCCGTTCAACCAAT
ATAGTGACTCTGGCCGTTCTCCACAA
ATAGTGACTCTGGCTGTTCAACCAAT

Nr of selected repeats 9 Similarity 0.897436

Consensus:

ATAGTGACTCTGGCcGTTCaCCAAAt

>Cele-UNSB01_6:2093985-2094613 Satlength=629 Nr of Repeats=30 RepeatLength=19
seed=TAATATTTAT

TAATATTTATTTATTTAAA
TAATATTTATTTATTTAAC
TAATATTTATTTATTTATT
TAATATTTATTTATTTATT
TAAAATTTATTTATTTAAC
TAATAGTTATTTATTTATT
TAATATTTATTTATTTATT
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TAATATTTATTTATTTAAT
TAATATTTATTTATTTAAT
TAATATTTATTTATTTAAT

Nr of selected repeats 22 Similarity 0.883952

Consensus:

TAATATTTATTTATTTAaT

>Cele-UNSB01_6:2094704-2095024 Satlength=321 Nr of Repeats=8 RepeatLength=40
seed=TTCCAGAATT

TTCCAGAATTTTCTCTATTTTCTAGAAAGTTCTGGAAAA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCCGGAACA
TTCCAGAATTTTCTTGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TTCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA
TTCCAGAATTTTTTCGAAATTTCCAGAAAGTTCTGGAACA

Nr of selected repeats 6 Similarity 0.911111

Consensus:

TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACA

>Cele-UNSB01_6:2095079-2095359 Satlength=281 Nr of Repeats=7 RepeatLength=35
seed=CAGAAAATTT

CAGAAAATTTAAATTTCCCTCCAAAATTTTTATCTCAGAAATATTAAATTACCCGCCAAAATATTTTTCA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCT
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTTT
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTTT
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTTT
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTAA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCA

Nr of selected repeats 6 Similarity 0.903492

Consensus:

CAGAAAATTTAAATTTCCCGcCAAAATATTTTTtt

>Cele-UNSB01_6:2094705-2095572 Satlength=868 Nr of Repeats=10 RepeatLength=40
seed=TCCAGAATTT

TCCAGAATTTTCTCTATTTTCTAGAAAGTTCTGGAAAAT
TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTCTCGATTTTCTAGAAAGTTCCGGAACAT
TCCAGAATTTTCTTGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACATT
TCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT
TCCAGAATTTTTTCGAAATTTCCAGAAAGTTCTGGAACAT
TCCAGAATTTTTTCGAAATTTCCAGAAGATTCTAGATTTCCAGAATAGAATTTTCAGAAAATTTAAATTTCCC
TCCAAAATTTTTATCTCAGAAATATTAAATTACCCGCCAAAATATTTTTTCACAGAAAATTTAAATTTCCCGCCAAAATA
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GAAAATTTAAATTTCCCTCCAAAATATTTTTTTTTCAGAAAATTTAAATTTCCCGCCAAAATATTTTTTAACAGAAAATTTA
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ACGATGGCTCTCACCACGGTGGGTCTCGCCACGATGGGTCTCACCACGATGGGTCTTCCACGATGGGTCTCACCACGA
TGGGTCTCGCCACGATGGGTCTCGCCACGAAGATCTCGCAGCAACATTTTTTTAAATTTTCCAGAAGTTCTAGAACAA

Nr of selected repeats 6 Similarity 0.911111

Consensus:

TCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACAT

>Cele-UNSB01_6:2095085-2096434 Satlength=1350 Nr of Repeats=17 RepeatLength=35
seed=ATTTAAATTT

ATTTAAATTTCCCTCCAAAATTTTATCTCAGAAATATTAAATTACCCGCCAAAATATTTTTCACAGAAA
ATTTAAATTTCCCGCCAAAATATTTTCTCAGAAA
ATTTAAATTTCCCTCCAAAATATTTTTCAGAAA
ATTTAAATTTCCCTCCAAAATATTTTTCAGAAA
ATTTAAATTTCCCGCCAAAATATTTTAAACAGAAA
ATTTAAATTTCCCGCCAAAATATTTTTCACAGAAA
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ACGATGGGTCTCACCACGATGGGTCTTCCACGATGGGTCTCACCACGATGGGTCTCGCCACGATGGGTCTCGCCACGA
AGATCTCGCAGCAACATTTT
TTTTAAATTTCCAGAAGGTTCTAGAACAATCCAGAATTTTATTTATTTATTTAATTAATATTTATTTAATTTATTTAATT
AATATTTATTTATTTATTTAATTAATATTTATCTATTTAATTAATATTTATTTATCTAATGAATATTCATTTTTTTAAT
AAATATTTATTTATTTAATTAATATTTTTCATTT
ATTTAATATTTATTTATTTAATTAATATTTATTTATTTATTTAATTAATATTTATTTATTTAATTAATATTTATTTATT
TAATTAATATTTATTTATTTATTTAATTAATATTTATTTATTTAATTAACCAGCCGCTGACCGCGCTACGGCGCGGGC
AACAACTGGCACCATTAAGAAATTTGACACACATACACTTCCAGAATTTTCTCTATTTTCTAGAAAGTTCTGGAAAA
TTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCTCGATTTTCTAGAAAGTTCTGGAAC
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TTCCAGAATAGAATTTTCAGAAA
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ATTTAAATTTCCCTCCAAAATATTTTTCAGAAA
ATTTAAATTTCCCTCCAAAATATTTTTCAGAAA
ATTTAAATTTCCCTCCAAAATATTTTTCAGAAA
ATTTAAATTTCCCGCCAAAATATTTTAAACAGAAA
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Nr of selected repeats 12 Similarity 0.912266

Consensus:

ATTTAAATTTCCCGCCAAAATATTTTtCAGAAA

>Cele-UNSB01_6:2097795-2102366 Satlength=4572 Nr of Repeats=207 RepeatLength=19
seed=AATTAATATT

AATTAATATTTATTTATTT
AATTAATATTTATTTATTT
AATTTATATTTATTTATTTATTT
AATTAATATTTATTTACTT
AATTAATATTTATTTATTT
AATTAATATTTATTTATTTACCT
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AATTAATATTTATTTATTT
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Nr of selected repeats 127 Similarity 0.940253

Consensus:

AATTAATATTTATTTATTT

>Cele-UNSB01_6:2097795-2102461 Satlength=4667 Nr of Repeats=212 RepeatLength=19
seed=AATTAATATT

AATTAATATTTATTTATTT
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AATTAATTTTTATTTATTT

Nr of selected repeats 132 Similarity 0.937235

Consensus:

AATTAATATTTATTTATTT

>Cele-UNSB01_6:2109492-2110453 Satlength=962 Nr of Repeats=78 RepeatLength=12

seed=AATAAATAAT

AATAAATAATATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAATAAAT

AATAAATAAATA

AATAAATAATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAATA

AATAAAAATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAATA

AATAAATAAAA

AATAAAAATAAAT

AATAAATAAATA

AATAAATAAATAAT

AATAAATAATA

AATAAATAAATAAATA

Nr of selected repeats 54 Similarity 1.000000

Consensus:

AATAAATAAATA

>Cele-UNSB01_6:2154760-2154935 Satlength=176 Nr of Repeats=7 RepeatLength=25

seed=TATATTTTAC

TATATTTTACTATATGGCTTCCCAG

TATATTTTACTCTCTGGCATCACAC

TATATTTTACTCTCTGGCTTCACAT

TATATTTTACTCTCTGGCTTCACAT

TATATTTTACTCTCTGGCTTCACAC

TATATTTTACTCTCTGGCTTCACAG

TATAATTTACTATATGGCTTCCCAG

Nr of selected repeats 7 Similarity 0.852698

Consensus:

TATATTTTACTcTcTGGCTTCaCAn

>Cele-UNSB01_6:2156238-2156563 Satlength=326 Nr of Repeats=12 RepeatLength=25

seed=TCTGGCTTCA

TCTGGCTTCACATAATAATTTACTC

TCTGGCTTCACAGTAAAATTTACTA

TCTGGCTTCACACTATATTTTACTC

TCTGGCTTCACACTATATTTTACTC

TCTGGCTTCACACTATATTTTACTC

TCTGGCTTCACAGTATATTTTACTC

TCTGGCTTCACACTATTTTTTACTC

TCTGGCTTCACCCTATATTTTACTC

TCTGGCTTCACAGTATAATTTACTATATGGCTTCCCCTATATTTTACTC

TCTGGCTTCACACTATATTTTACTC

TCTGGCTTCACATAATAATTTACTC

TCTGGCTTCACAGTATATTTTACTC

Nr of selected repeats 11 Similarity 0.885576

Consensus:

TCTGGCTTCACAcTATAtTTTACTC

>Cele-UNSB01_6:2157154-2162472 Satlength=5319 Nr of Repeats=133 RepeatLength=40

seed=AAGTTCTGGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATATTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCTAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACACTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACGTTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAATACTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAATACTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCTAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACGTTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAATACTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AAGTTCTGGAACATTCCAGAATTTTCTCGATTTTTCTAGA

AGAATTTTCTCGATTTTCTAGAAAAGTTCTGGAACATTCC
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TGGGTCTCACCACGATGGGTCTCACCACGATGGGTATCACCTCGATGGGTCTCACCACGATGGGTCTCACCACGATGGG
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TCC
AGAATTTTTTTCGAATTTTCCAGAAGGTTCTGGAACATTCC
AGAATTTTCTAGAATCTTCCAGAAGGTTCTAAAGCTTTTT
AGAATTTTCCAGAAGGTTCTGGAACATTCT
AGAATTTTCCAGAAATTTCCAGAAGGTTCTGGAACATTTCCAGAAAAAAATTTAAATTTCCCGCCAAAATATTTTTTCC
AGAAAATTTAAATTTCCCGCCAAAATTTGGGTCTTACCACGGAGGGTCTCACTCACCACGACGGGTCTCACCACGA
CGGGTCTCACCACGATGGGTCTCACCACGATGGGTCTCCCCACGATGGGTCTCGCCACGAAGATCTCGCAGCAACATT
TTTAAATTTTCCAGAAGGTTCTAGAACAATCC
AGAATTTTTTTCGAATTTTCCAGAAGGTTCTGGAACATTCC
Nr of selected repeats 131 Similarity 0.954680
Consensus:

TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT ACCAGAGT CACTAT
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAT
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT ACCAGAGT TACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAT
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAT
TTTTAGTGAAGT GCCAGAGT CACTAT
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAA
TTTTAGTGAAGT GCCAGAGT CACTAT
TTTTAGTGAAGT GCCAGAGT CACTAT
TTTTAGTGAAGT ACCAGAGT TACTAT

Nr of selected repeats 55 Similarity 0.934801

Consensus:

TTTTAGTGAAGT GCCAGAGT cACTAA

>Cele-UNSB01_6:2669709-2669769 Satlength=61 Nr of Repeats=5 RepeatLength=12

seed=AGGCTTAGGC

AGGCTTAGGCTA

AGGCTTAGGCTT

AGGCTTAGGCTA

AGGCTTAGGCTT

AGGCTTAGGCAT

Nr of selected repeats 5 Similarity 0.888889

Consensus:

AATCTATTTTTTCGTGTAAC
AATCTATTTTTTTGTGTAAG
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTGTGTAAC
AATCTATTTTTTCGTGTAAC
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AATCTATTTTTTGTGTAAG
AATCTATTTTTTCGTGTAAC
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AATCTATTTTTTCGTGTAAC
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AATCTATTTTTTTGTGTAA
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AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC
AATCTATTTTTTCGTGTAAC

Nr of selected repeats 272 Similarity 0.892683

Consensus:

AATCTATTTTTTCGTGTAAC

>Cele-UNSB01_6:3190243-3190348 Satlength=106 Nr of Repeats=7 RepeatLength=15

seed=TCACCACGAT

TCACCACGATGGGTC

TCACCACGATTGGTC

TCACCACGATGGGTC

TCACCGCGATGGGTC

TCACCACGATGGGTC

TCACCACGATGGGTC

TCACCACGATGGGTT

Nr of selected repeats 7 Similarity 0.923810

Consensus:

TCACCACGATGGGTC

>Cele-UNSB01_6:3377659-3377780 Satlength=122 Nr of Repeats=11 RepeatLength=11

seed=AAAATGTGCT

AAAATGTGCTG

AAAATGTGCTA

AAAATGTGCTA

AAAATGTGCTA

AAAATGTGCTA

AAAATGTGCTTG

AAATGTGCTA

AAAATGTGCTAG

AAATGTGCTTG

AAATGTGCTA

AAAATGTGCTA

Nr of selected repeats 7 Similarity 0.826720

Consensus:

AAAATGTGCTa

>Cele-UNSB01_6:3455223-3455778 Satlength=556 Nr of Repeats=27 RepeatLength=18

seed=TTTTGTCAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGTGCTATAGTTCTTGCCAGTGCTATAGT

TTTTGTCAGTGCTATAGCTTTTGCCAGAGATATTGT

TTTTGTCATTGCTATAGTTGTTGTTTGTGCTATAGT

TTTTGTCAGTTCAATAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGTTCAATAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGTTCAATAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGAGATATTGT

TTTTGTCAGTGCTATAGTTCTTGCCAGTGCTATAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGTGCTGAAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGTGCTATAGT

TTTTGTCAGTGCTCTTAC

TTTGTGCTGCTATATT

TTTTGTCCGTGCAAAAG

TTTTGTCAGTGCTATTGT

TTTTGTCAGTGGTATAAT

TTTTGTCAGTGCAATAGT

TTTTATCAGTGATATTGT

TTTTGTCAGTGCTATAG

TTTTGTCAGTGCTATAGT

Nr of selected repeats 20 Similarity 0.766579

Consensus:

TTTTGTCAGTGCTATAGT

>Cele-UNSB01_6:3463610-3463814 Satlength=205 Nr of Repeats=10 RepeatLength=17
seed=TTTTAACGTG

TTTTAACGTGACCTAGT
TTTTAACGTGACCTACTATTCAACGTGACCTACT
TTTTAACGTGACCTAGG
TTTTAACGTGACTTAATTTTTTAAAATGACTTAAT
TTTTAACGTGACCTACT
TTTTAACGTGACCTAGT
TTTTAACGTGACCTATT
TTTTAACGTGACCTAAT
TTTTAACGTGACCTAGT
TTTTAACGTGGCCTACT

Nr of selected repeats 8 Similarity 0.901961

Consensus:

TTTTAACGTGACCTAgT

>Cele-UNSB01_6:3482169-3482345 Satlength=177 Nr of Repeats=12 RepeatLength=11
seed=TAGCTCAGCT

TAGCTCAGCTT
TAGCTCAGCTATGTCTCAGCTA
TAGCTCAGCTT
TAGCTCAGCTATGTCTCAGCTG
TAGCTCAGCTT
TAGCTCAGCTATGTCTCAGCTA
TAGCTCAGATATGTCCCAGCTA
TAGCTCAGCTA
TGGCTCAGCTA
TAGCTCAGCTA
TGGCTCAGCTA
TAGCTCAGCTA

Nr of selected repeats 8 Similarity 0.883117

Consensus:

TagCTCAGCTa

>Cele-UNSB01_6:3508288-3508508 Satlength=221 Nr of Repeats=10 RepeatLength=18
seed=TTGTCAGTGC

TTGTCAGTGCTATGGTTT
TTGTCAGTGCTATATTTT
TTGTCAGTGCTATATTTT
TTGTCAGTGCTATAGTTT
TTGTCAGTGCTATACTTTT
TTGTCAGTGCTTTTTTTTTTAATTTTTTAAATTCGGTTTCAAAAAATGGTAACTCAGTTT
TTGTCAGTGCTATAGTTA
TTGCCAGTGCTATAGTT
TTGCCAGTGCTATAGCTA
TTGTCAGTGCTATAGATT

Nr of selected repeats 7 Similarity 0.848325

Consensus:

TTGTCAGTGCTATAgTt

>Cele-UNSB01_6:3747622-3752392 Satlength=4771 Nr of Repeats=406 RepeatLength=11
seed=CAGTTGTCAC

CAGTTGTCACC
CAGTTGTCACAA
AGTTGTCACC
CAGTTGTCACAA
AGTTGTCACC

CAGTTGTCACT
CAGTTGTCACC
CAGTTGTCACC
CAGTTGTCACAA
AGTTGTCACC
CAGTTGTCACC
CAGTTATCACT
CAGTTGTCCCC
CAGTTGTCACT
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CAGTTGTCACCT
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CAGTTGTCACC
CAGTTATCACC
CAGTTGTCTCT
CAGTTGTCACC
CAGTTGTCACT
CAGTTGTCACCCAGGTGTTGTCACCCAGTTGTTGTCACC
CAGTTGTCACT
CAGTTGTCACC
CAGTTGTCACT
CAGTTGTCACC
CAGTTGTCACT
CAGTTGTTACC

Nr of selected repeats 340 Similarity 0.892175

Consensus:

CAGTTGTCACc

>Cele-UNSB01_6:3814487-3814588 Satlength=102 Nr of Repeats=5 RepeatLength=20
seed=TTTGGTCAGT

TTTGGTCAGTGCAATTACTAA
TTTGGTCAGTGCTTTTCGAC
TTTGGTCAGTGCTTTTCTAT
TTTGGTCAGTGCTTTTCTAT
TTTGGTCAGTGCTTTTCTAT

Nr of selected repeats 4 Similarity 0.933333

Consensus:

TTTGGTCAGTGCTTTTCTAt

>Cele-UNSB01_6:3834410-3834530 Satlength=121 Nr of Repeats=5 RepeatLength=20
seed=CCATGTAGCT

CCATGTAGCTTCAAAATTAC
CAATGTAGCTACATAGTTTC
CCATGTAGCTCCAAAAGATCCCATGCAGATCCACAGTTTC
CCATGTAGCTTCAAACTCT
CCATGTAGCCCCTAAATCTT

Nr of selected repeats 4 Similarity 0.561869

Consensus:

CcATGTAGCttCaaAatTnCt

>Cele-UNSB01_6:4047987-4048126 Satlength=140 Nr of Repeats=7 RepeatLength=20
seed=AAAATAGATT

AAAATAGATTGACATACCAA
AAAATAGATTGACATACCAG
AAAATAGATTGACATACCA
AAAATAGATTGGCATAACCAA
AAAATAGATTGACATACCAA
AAAATAGATTGACATACCAA

AAAATAGATTGACATACCAA

Nr of selected repeats 6 Similarity 0.955556

Consensus:

AAAATAGATTGACATACCAA

>Cele-UNSB01_6:4149433-4175058 Satlength=25626 Nr of Repeats=1025

RepeatLength=25 seed=AATGTTCTGC

AATGTTCTGCCAATTTATTTCTCC

AATGTTCTGCCAATTTATTTACTCC

AATGTTCTGCCAATTTATTTACTCT

AATGTTCTGCCAATTTATTTACTCT
AATGTTCTGCCAATTTATTTACTCT
AATGTTCTGCCAATTTATTTACTCT
AATGTTCTGCCAATTTATTTACTCT
AATGTTCTGCCAATTTATTTACTCT

Nr of selected repeats 1025 Similarity 0.999688

Consensus:

AATGTTCTGCCAATTTATTTACTCT

>Cele-UNSB01_6:4175079-4227144 Satlength=52066 Nr of Repeats=2000

RepeatLength=20 seed=CTATATCGTA

CTATATCGTATCGTAAATAG

Consensus :

TGTGGCTTCCCACTATATTTTACTCTC

>Cele-UNSB01_6:5352204-5352282 Satlength=79 Nr of Repeats=6 RepeatLength=13

seed=GCCATAGGCG

GCCATAGGCGTAA

GCCATAGGCGTAA

GCCATAGGCGTAA

GCCATAGGCGTAG

GCCATAGGCATAA

GCCATAGGCGTAA

Nr of selected repeats 6 Similarity 0.931624

Consensus :

GCCATAGGCGTAA

>Cele-UNSB01_6:5454734-5454854 Satlength=121 Nr of Repeats=8 RepeatLength=15

seed=TGGTGAGACC

TGGTGAGACCCGTGG

TGGTGAGACCCATCC

TGGTGAGACCTATCG

TGGTGAGACCTATCG

TGGTGAGACCCATCG

TGGTGAGACCCATCC

TGGTGAGACCCATCC

TGGTGAGACCTATCG

Nr of selected repeats 8 Similarity 0.860317

Consensus :

TGGTGAGACCcATCg

>Cele-UNSB01_6:5456252-5456359 Satlength=108 Nr of Repeats=5 RepeatLength=23

seed=AATAAATATT

AATAAATATTAAACAAATA

AATAAATATTAATTAATTAATG

AATAAATATTAAATAAATA

AATAAATATTAATTAATTAATA

AATAAATATTAATTAATTAATA

Nr of selected repeats 3 Similarity 0.922705

Consensus :

AATAAATATTAATTAATTAATA

>Cele-UNSB01_6:5456777-5457242 Satlength=466 Nr of Repeats=31 RepeatLength=15

seed=CCACGATGGG

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCACGACGGGTCTCA

CCACGGTGGGTCTCG

CCACAATGGGTCTCG

CCACGATGGTTCTTC

CCACGATGGGTCTCA

CCACGATGGGTCTCG

CCACGATGGGTCTTC

CCACGATGGGTCTCA

CCACGACGGGTCTCAA

CACGATGGGCCTCG

CCACGATGGGTCTCG

CCACGATGGGTCTCA

CCACGATGGGTCTCA

CCACGACGGGTCTCA

CCACGGTGGGTCTCG
CCACAATGGGTCTCG
CCACGATGGGTCTTC
CCACGATGGGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTTC
CCACGATGGGTCTCA
CCACGACGGGTCTCAA
CACGATGGGCCTCG
CCACGATGGGTCTCG
CCACGATGGGTCTCG
CCACGATGGGCCTTC
CCACGATGAGTCTCA
CCACGATGGGTCTCG
CCACGATGGGTCTTG

Nr of selected repeats 27 Similarity 0.802469

Consensus:

CCACGATGGGTCTCn

>Cele-UNSB01_6:5457466-5457723 Satlength=258 Nr of Repeats=10 RepeatLength=11

seed=CTACAGTACT

CTACAGTACTC

CTACAGTACTA

CTACAGTACCCCGACCATATTTCCACTGCTAACCGCAAACCTATATCTCTTCAAAGACAAAACTCAATTTTTCTTAA

CTACAGTAAATC

CTACAGTACTCCTAGAGTACCT

CTACAGTACTA

CTACAGTACCCCGACCATATCCCCTAATAACTCCAAACCTATATCTCTTCAAAGACAAAACTCAATTTTTCTTAA

CTACAGTAAATC

CTACCGTACTC

CTACAGTACTC

Nr of selected repeats 7 Similarity 0.849928

Consensus:

CTACAGTAcTc

>Cele-UNSB01_6:5769379-5769561 Satlength=183 Nr of Repeats=7 RepeatLength=26

seed=TAGTGACTCT

TAGTGACTCTGGCCGTTCACTATAAT

TAGTGACTCTGGCCGTTCAACATAAA

TAGTGACTCTGGCCGTTCAACCAAGAT

TAGTGACTCTGGCCGTTCAACAAAAA

TAGTGACTCTGGCCGTTCAACAAATA

TAGTGACTCTGGCCGTTCAACCAAGAT

TAGTGACTCTGACCGTTCAACATAAA

Nr of selected repeats 7 Similarity 0.836567

Consensus:

TAGTGACTCTGGCCGTTCAACAAaAt

>Cele-UNSB01_6:6133294-6134199 Satlength=906 Nr of Repeats=4 RepeatLength=226

seed=CAAGAAGCTT

CAAGAAGCTTCACGTAGTTACAGAAATAGTACATTTTCAGAGCTACCTTTTAGCGGTATTTTATTATTTAATGAAAAC

TACCATTTATAGGCAAAAATAGATAAATTTTCGAAACTTTGAAAATTCATAAATCTCTTCAATGTAACCTTTTTTTGAAA

TGTCTTTTCAGAAACTTTGTAGTAAATTTTAAGCTCTTTTGAATATACCAACAATACTCCAGTAGGTG

CAAGAAGCTTCACGTAGTTACAGAAATAGTACATTTTCAGCCCTACCTTTTAGTGCGTATTTTATTATTTAATGAAAAC

TACCATTTATAGGCAAAAATAGATGGATTTTCGTAATTTTGAACATCATAAATCTCTTCAAAGTAATTTTTTTGAAA

TGTCTTTTCAGAAACTTTGTAGTAAATTTTAAGCTCTTTCTGAATATATTAACAATATTTCCAGTAGGTA

TTCTAAATTTGCAACTTCATCTACCG
TTCTAAATTTGAAAATTCATCTACCG
TTCTAAATTTAAAAATTCATCTACCG
TTCTAAATTTGAAAATTTATCTACCG
TTCTAAATTTGCAACTTCATCTACCG
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TTCTAAATTTGAAAATTCATCTACCG
TTCTAAATTTGAAAATTCATCTACCG
TTCTAAATTTGAAAATTTATCTACCG
TTCTAAATTTGCAACTTCATCTACCA
TTCTAAATTTGAAAATTCATCTACCG
TTCTAAATTTGAAAATTCATCTACCG

Nr of selected repeats 329 Similarity 0.936466

Consensus:

TTCTAAATTTgAAAATTTcATCTACCG

>Cele-UNSB01_6:6343035-6343121 Satlength=87 Nr of Repeats=5 RepeatLength=17
seed=TAATTACTGG

TAATTACTGGAATAAAA
TAATTACTGGAATAAAA
TAATTACTGGAATAAAA
TAATTACTGGAATAAAAAC
TAATTACAGGAATAAAG

Nr of selected repeats 4 Similarity 0.921569

Consensus:

TAATTACTgGAATAAAAa

>Cele-UNSB01_6:6441827-6441956 Satlength=130 Nr of Repeats=8 RepeatLength=16
seed=GCACTGACAA

GCACTGACAATTTTTTA
GCACTGACAATTTTTTA
GCACTGACAATTTTTTA
GCACTGACAATTTTTTC
GCACTGACAATTTTTT
GCACTGACAATTTTTT
GCACTGACAAATTTTT
GCACTGACAAGTTATT

Nr of selected repeats 7 Similarity 0.876984

Consensus:

GCACTGACAAtTTTTt

>Cele-UNSB01_6:6516089-6517558 Satlength=1470 Nr of Repeats=50 RepeatLength=19
seed=GTCAGTGCAA

GTCAGTGCAACTTAAATTG
GTCAGTGCAACTGCAACTG
GTCAGTGCAACTAAAATTG
GTCAGTGCAACTGCAAGTG
GTCAGTGCAACTAAAATTG
GTCAGTGCAACTGTAAGTG
GTCAGTGCAACTAAAATTG
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GTCAGTGCAACTCCCCGGTTATAACTACACTTTTACCTCCATTCTCGTCTTTCTCCCCGTTTCACCTGTTCCCTATTA
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GTCAGTGCAAATGCAACTG
GTCAGTGCAACTAAAATTG
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TCAGTGCAACTGCAAGTG
GTCAGTGCAAATGCAAGTGA
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Nr of selected repeats 37 Similarity 0.811390
Consensus:
GTCAGTGCAAcTgcAAnTG
>Cele-UNSB01_6:7055357-7058647 Satlength=3291 Nr of Repeats=35 RepeatLength=94
seed=TGCCTTCAGA

TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTACATAGGGCATCGAAAAGCACTCAATATTTAGAGAACAGAA
GATTTTGAGAATTAC
TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTAGATAGGGCATCGAAAAGCACTTAATATTTAGAGAACAGAA
GATTTTGAGAATTAC
TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTACATAGGGCATCGAAAAGCACTCAATATTTAGAGAACAGAA
GATTTTGAGAATTAC
TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTACATAGGGCATCGAAAAGCACTCAATATTTAGAGAACAGAA
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TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTACATAGGGCATCGAAAAGCACTCAATATTTAGAGAACAGAA
GATTTTGAGAATTAC
TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTACAAAGGGCATCGAAAAGCACCCAATATTTAGAGGACAGAA
GATTTTGAGAATTAC
TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTACATAGGGCATCGAAAAGCACTCAATATTTAGAGAACAGAA
GATTTTGAGAATTAC
TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTACAAAGGGCATCGAAAAGCACCCAATATTTAGAGAACAGAA
GATTTTGAGAATTAC

Nr of selected repeats 35 Similarity 0.978211

Consensus:

TGCCTTCAGAAATTGACAATTTTCCCATTGATTTGTCTACAtAGGGCATCGAAAAGCACTCAATATTTAGAGAACAGAA
GATTTTGAGAATTAC

>Cele-UNSB01_6:7306204-7313772 Satlength=7569 Nr of Repeats=373 RepeatLength=20
seed=ATAGCTATGT

ATAGCTATGTTCGTGTCGTTT
ATAGCTATGTTCGTATCATAA
ATAGCTATGTTCGTGTCGTTTATAGCAGTGTTCGTGTCGTTT
ATAGCTATGTTCGTGTCGTTTATAGTTAAGTTCGTGTCGTTT
ATAGCTATGTTCGTATTGTAA
ATAGCTATGTTCGTGTCGTTT
ATAGCTATGTTCATGTCGTTT
ATAGCTATGTTCGTATCGTAA
ATAGCAATGTTCGTGTCGTTT
ATAGCTATGTTCGTGTCGTTT
ATAGCTATGTTCGTATCGTAA
ATAGCTATGTTCGTGTCGTTT
ATAGCTATGTTCGTATTGTAA
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ATAGCTATGTTCATGTCGTTT
ATAGCTATGTTCGTATCGTAA
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ATAGCTATGTTCATGTCGTTT
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ATAGCTATGTTCGTATTGTAA
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ATAGCTATGTTCGTGTCGTTT
ATAGCTATGTCATGTCGTTT
ATAGCTATGTTCGTATCGTAA
ATAGCTTTGTTCGTGTCGTTT
ATAGCTATGTTCGTATCGTAA
ATAGCTTTGTTCGTGTCGTTT

Nr of selected repeats 332 Similarity 0.894033

Consensus:

ATAGCTATGTTCGTgTCGTtt

>Cele-UNSB01_6:7315610-7315788 Satlength=179 Nr of Repeats=9 RepeatLength=20

seed=TTTTTCGTCT

TTTTTCGTCTGTCAATCTAT
TTTTTCGTCTGTCAACCTA
TTTTTCGTCTGTCAATCTAT
TTTTTCGTCTGTCAATCAAT
TTTTTCGTCTGCCAATCTA
TTTTTTGGTCTGTCAATCTAT
TTTTTCGTCTGTCAATCTAT
TTTTTCGTCTGTCAATCTAT
TTTTTCGTCTGTCAATCTAT

Nr of selected repeats 7 Similarity 0.961905

Consensus:

TTTTTCGTCTGTCAATCTAT

>Cele-UNSB01_6:7586233-7592821 Satlength=6589 Nr of Repeats=165 RepeatLength=40

seed=TTACCCTTAA

TTACCCTTAAATGGGCGCCGGTTTCTCTTTGAGCGATTCC
TTACCCTTAAATGGGCGCCGGTTTCGCTTTGAGCGATTCC
TTACCCTTAAATGGGCGCCGGTTTCGCTTAGAGCGATTCC
TTACCCTTAAATGGGCGCCGGTTTCGCTTAGAGCGATTCC
TTACCCTTAAATGGGCGCCGGTTTCGCTTAGAGCGATTCC
TTACCCTTAAATGGGCGCCGGTTTCTCTTTGAGCGATTCC
TTACCCTTAAATGGGCGCCGGTTTCGCTTAGAGCGATTCC
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TTACCCTTAAATGGGCGCCGGTTTCGCTTAGAGCGATTCC
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TTACCCTTAAATGGGCGCCGGTTTCGCTTAGAGCGATTCC

>Cele-UNSB01_6:7918402-7918617 Satlength=216 Nr of Repeats=6 RepeatLength=12
seed=TCTTCCTCCT
TCTTCCTCCTCT
TCTTCTTCCTCCTGAAAACATAGAAATCACCTTAAAACATTTTTTGGAAAGATTCATACCTCGAGCTCCTCT
TCTTCTTCCTCC
TCTTCCTCCTCC
TCTTCTTCCTCCTTCTCCTTGGCAGCTGGCTCCTCGATCTAGAATATCATCATAAAGTTGACATCGATTAATATTCCGT
TAAAACAAACCTTCTCC
TCTTCCTCCTCT
Nr of selected repeats 4 Similarity 0.870370
Consensus:
TCTTCcTCCTCc

>Cele-UNSB01_6:8111999-8112167 Satlength=169 Nr of Repeats=7 RepeatLength=24
seed=GGTGGCTGGT
GGTGGCTGGTCACAAAAGTAAGTT
GGTGGCTGGTCACAAAAGTAAGTT
GGTGGCTGGTCACAAAAGTAAGTT
GGTGGCTGGTCACAAAAGTAAGTT
GGTGGCTGGTCACAAAAGTAAGTT
GGTGGCTGGTCACAAAAGTAAGTT
GGTGGCTGGTCACAAAAGTAAGTT
GGTGGCTGGTCACAAAAGTAAGTT
Nr of selected repeats 7 Similarity 1.000000
Consensus:
GGTGGCTGGTCACAAAAGTAAGTT

>Cele-UNSB01_6:8127661-8127776 Satlength=116 Nr of Repeats=6 RepeatLength=19
seed=CAGACGAAAA
CAGACGAAAAATATATTGG
CAGACGACAAAATAGATTGA
CAGACGAAAAATATATTGG
CAGACGAAAAATAGATTGA
CAGACGAAAAATAGATTGA
CAGACGAAACATATATTGG
Nr of selected repeats 5 Similarity 0.887719
Consensus:
CAGACGAAAAaATAtATTGg

>Cele-UNSB01_6:8150139-8150195 Satlength=57 Nr of Repeats=4 RepeatLength=14
seed=TTACCAAAT
TTACCAAATGTAA
TTACCAAATCTAG
TTACCAAATCTAA
TTACCAAATCTAG
Nr of selected repeats 4 Similarity 0.888889
Consensus:
TTACCAAATcTAA

>Cele-UNSB01_6:8414337-8415392 Satlength=1056 Nr of Repeats=85 RepeatLength=11
seed=GAGCGGTTTT
GAGCGGTTTTG
GAGGGTTTTG
GAGCGGTCTTG
GAGCGGTTTTTG
GAGCGGTTTAG
GAGAGTTTTA
GAGCGGATTTG
GAGCGGTTTTG

GAGCGGTTTTG
GAGCGGTTTTT
GAGCGGTTTTT
GAGCGGTTTTG
GAGCGGTTTTG
GAGCGGTTTTTG
GAGCGGTTTTG
GAGCGGTTTTT
GAGCGGTTTTG
GAGCGGTTTTG
GAGCGGTTTTTG
GAGCGGTTTTG
GAGCGGTTTTTG
GAGCGGTTTAG
GAGAGGTTTTA
GAGCGGTTTTG
GAGCGGTTTTTG
GAGCGGTTTGG
GAGCGGTTTTG
GAGCGGTTTTG
GAGCGGTTTTA
GAGCGGTTTCTG
GAGCGGTTTTC

Nr of selected repeats 64 Similarity 0.790068

Consensus:

GAGCGGTTTTg

>Cele-UNSB01_6:8836090-8836155 Satlength=66 Nr of Repeats=5 RepeatLength=11
seed=GCAAAAAATG

GCAAAAAATGA
GCAAAAAATGT
GCAAAAAATGT
GCAAAGAATGT
GCAAAAAATGTGCGAAAATGT

Nr of selected repeats 4 Similarity 0.878788

Consensus:

GCAAAaAATGt

>Cele-UNSB01_6:8885720-8885804 Satlength=85 Nr of Repeats=5 RepeatLength=17
seed=AGGGGGCATC

AGGGGGCATCGAGAG
AGGGGGCATCGGTTCTA
AGGGGGCATTAGGTCAA
AGGGGGCATTGTTCGT
AGGGGGCATCCGTTTCAG

Nr of selected repeats 3 Similarity 0.686275

Consensus:

AGGGGGCATtnGtTCan

>Cele-UNSB01_6:8886112-8886213 Satlength=102 Nr of Repeats=6 RepeatLength=17
seed=GATGCCCCCT

GATGCCCCCTCTGAACG
GATGCCCCCTCTGAACG
GATGCCCCCTACGAACAA
ATGCCCCCTTTGACCTA
ATGCCCCCTTAGAACGC
GATGCCCCCTCTCTC

Nr of selected repeats 4 Similarity 0.722222

Consensus:

gATGCCCCCTctGAaCgn

>Cele-UNSB01_6:9243247-9243516 Satlength=270 Nr of Repeats=10 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGG

GTACTGTAGGGT

TACTGTAGGATTACTGTAGTTTTGGAAAAATTGACTTTTTGTCTTTTGAAGTGATATTGGTTTGGGTTAGTGGTGGGA
TATGGTCCGG

GTACTGTAGTA

GTACTGTAGTA

GTACTGTAGGA

GTACTGTAGGATTACTGTATTTTTGAAAAAAATTGGCTTTTCGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGTCCG
GATATGGTTGGG

GTACTGTAGTT

GTACTGTAGAG

GTACTGTAGGA

Nr of selected repeats 7 Similarity 0.832612

Consensus:

GTACTGTAGna

>Cele-UNSB01_6:9243610-9244090 Satlength=481 Nr of Repeats=12 RepeatLength=40
seed=CTTCTGGAAA

CTTCTGGAAAATTCGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATCCGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATTTGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATTTGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATTCGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATCCGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATTCGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATCCGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATTTGAGAAAATGCTGGAATGTTCCAGAAC

CTTCTGGAAAATTTGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATTCGAGAAAATTCGGAATGTTCCAGAAC

CTTCTGGAAAATTTGAGAAAATGCTGGAATGTTCCAGAAT

Nr of selected repeats 12 Similarity 0.953030

Consensus:

CTTCTGGAAAATtcGAGAAAATTCGGAATGTTCCAGAAC

>Cele-UNSB01_6:9244298-9244938 Satlength=641 Nr of Repeats=20 RepeatLength=32
seed=CGGGAATTCA

CGGGAATTCAAATTTCTGTGAAAAATTTTGG

CGGGAATTCAAATTTCTGTGAAAAATTTTGG

CGGGAATTCAAATTTCTGTGAAAAATTTTGG

CGGGAATTCAAATTTCTGTAAAAAAATTTGG

CGGGAATTCAAATTTCTGTGAAAAATTTTGG

CGGGAATTCAAAATTTCTATGAAAAATTTTGG
CGGGAATTCAAAATTTTCTGTGAAAAATTATAA
CGGGAATTCAAAGTTTTCTGTGAAAAATTTTGG
CGGGAATTCAAAATTTTCTGTGAAAAATTTTGG
CGGGAATTCAAAATTTCTTTGAAAAATTTTGG

Nr of selected repeats 20 Similarity 0.894298

Consensus:

CGGGAATTCAAAaTTTCTGTGAAAAaTTTgG

>Cele-UNSB01_6:9421607-9443178 Satlength=21572 Nr of Repeats=857

RepeatLength=25 seed=AGAGAGTAAA

AGAGAGTAAAATACACTGTGAAGCC

AGAGAGTAAACTATACTGTGAAGCC

AGAGAGTAAAATATACTGTGAAGCC

AGAGAGTAAAATATACTGTGAAGCC

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AGAGAGTAAAATATACTGTGAAGCC

AGAGAGTAAAATATACTGTGAAGCC
AGAGAGTAAAATAATCGGTGAAGCC
AGAGATTAAATTATTCTGTGAAGCC

Nr of selected repeats 649 Similarity 0.731868

Consensus:

AGAGAGTAAAATATACTGTGAAGCC

>Cele-UNSB01_6:9443244-9443487 Satlength=244 Nr of Repeats=7 RepeatLength=35
seed=AAAATTTGAA

AAAATTTGAAATTTCCCGCCAAAATATTTTTTCACTG
AAAATTTGAATTTCCCGCCAAAATTTTTTCACTG
AAAATTTGAATTTCCCGCCAAAATTTTTTACTG
AAAATTTGAATTTCCCGCCAAAATTTTTTACTG
AAAATTTGAATTTCCCGCCAAAATTTTTTCACTG
AAAATTTGAATTTCCCGCCGAAAATTTTTTCACTG
AAAATTTGAATTTCCCGCCAAAATTTTTTCACTT

Nr of selected repeats 5 Similarity 0.908571

Consensus:

AAAATTTGAAATTTCCCGCCaAAAAtTTTTTcACTg

>Cele-UNSB01_6:9866116-9867908 Satlength=1793 Nr of Repeats=48 RepeatLength=32
seed=TCCCGCCAAA

TCCCGCCAAATGTTTTCTCAGAAAATTTGAATT
TCCCGTCAAATCTTTTTCACTGAAAATTTGAATT
TCCCGCCAAATGTTTTTCACTGAAAATTTGAATT
TCCCGCCAAAATTTTTTCACTGAAAATTTGAATT
TCCCGCCAAATTTTTTCACTGAAAATTTGAATT
TCCCGCCAAAATGTGGGTCTCACCAGGAGGTCTCACCACGATGGGTCTCACCACGAAGGTCTCACCACGATGGGT
CTCACCACGATGGGTCTCACCACGAAGGTCTCACCACGATGGGTCTCAGACGAAGGTGACAGGCCCGCCACA
CTCACTGACTTTGGGTGTGACGTACAGACTACAAAGACTACATAGACTACAAACTATGGACAGACGA
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TCCCGCCAAAAATTTTGAAGAAAAATTTGAAC
TACCGCCAAAAATTTTTCACAGAAAAATTTGAAT
TCCCGCCAAAAATTTTCAAAGAAAAATTTAAAT

Nr of selected repeats 33 Similarity 0.845249

Consensus:

TCCCGCCAAAAatTTTcAaAGAAAAATTTgAAT

>Cele-UNSB01_6:9867922-9867997 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=ATGGGTCTCG

ATGGGTCTCGCCACG

ATGGGTCTCGCCACG

ATGGGTCTCGCCACG

ATGGGTCTCGCCACGA

AGGGTCTCGCAACG

Nr of selected repeats 3 Similarity 1.000000

Consensus:

ATGGGTCTCGCCACG

>Cele-UNSB01_6:10621309-10621525 Satlength=217 Nr of Repeats=4 RepeatLength=25

seed=ATTGGCAGAA

ATTGGCAGAACATTAGAGAGTGGTTTTTTTTAACTTTCATCTGCAAATTTGAAAGTTATCAAATTACCTGACTGCCAAT

ATATTTACTCTAATGTTCTGCCAATATATTTACTCTAATGTTCTGCCAATTAGAGTAATTAT

ATTGGCAGAACATTAGAGTAAATAT

ATTGGCAGAACATTAGAGTAAATAT

ATTGGCAGAACATTGGAGTAATAAA

Nr of selected repeats 3 Similarity 0.837607

Consensus:

ATTGGCAGAACATTaGAGTAAAtAt

>Cele-UNSB01_6:10621572-10641051 Satlength=19480 Nr of Repeats=772

RepeatLength=25 seed=CAGAGAGTAA

CAGAGAGTAAAATATGGTGGGAAGCCA

CAGAGAGTAAAATATAGTGGGAAGCCA

CAGAGAGTAAAATATAGTGGGAAGCCA

CAGAGAGTAAAATATAGTGGGAAGCCA

CAGAGAGTAAAATATGGTGGGAAGCCA

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CAGAGAGTAAAATATATGGTGAAGC

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CAGAGAGTAAAAAATATGGTGAAGC
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Nr of selected repeats 526 Similarity 0.847899

Consensus:

CAGAGAGTAAAAAtATttGGTGAAGC

>Cele-UNSB01_6:10641130-10642329 Satlength=1200 Nr of Repeats=107

RepeatLength=11 seed=TGGAGCGGTT

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TGGAGCGGTTA

TGGAGCGGTAT

TGGAACGGTTT

TGGAGCGGTTT

TGGAGCGGTTA

TGGAGCGGTTA

TGGAGCGGTTA

TGGAGCGGTTA

TGGAGCGGTTA

TGGAGCGGTTTTTGGAGCGGAAT

TGGAACGGTTT

TGGAGCGGTTT

TGGAGCGGTTA

TGGAGCGGTAT

TGGAGCGGTTT

TGGAGCGGTTA

TGGAGCGGTTT

TGGAGCGGTAT

TGGAACGGTTT

TGGAGCGGTTA

TGGAGCGGTAT

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TGGAGCGGTAT
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Nr of selected repeats 105 Similarity 0.866467

Consensus:

TGGAGCGGTtt

>Cele-UNSB01_6:11021354-11026794 Satlength=5441 Nr of Repeats=27

RepeatLength=214 seed=AAAACCTACA

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TTAACAACATCCCAGTAGGTGCCAGAAGCTCCGAGCAGTTACAG
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Nr of selected repeats 21 Similarity 0.959472

Consensus:

AAAACCTACAGTACCTTTGTGCGTATTTTATTATTAATGAAAACGACCATTTATAGGCAAAAATAGGTAAATTTATGAA
ACTTTGAAAATTCCCAAATCACTTCAAACCAACTTTTTTTgAAATTTCTTTCAGAAAACCTTGTGTGCAAATTTCCAAGCtT
TTTCAGAATTTACCAACAACATCCCAGTAGgtGCCAGAAGCTtcGAGCAGTTACAG

>Cele-UNSB01_6:11249167-11249852 Satlength=686 Nr of Repeats=21 RepeatLength=27
seed=CACTGACCAA

CACTGACCAAAAAAAAAATATTATACTTG
CACTGACCAAAAAAAAAATAATTAACGTGCACCTTATCAAAAAGGATTA AACACG
CACTGGCCAAAGAAAAAAAAATTACACGTG
CACTGACCAAAAGAAAAAAAAATTATACGTG
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CACTGACCAAAGAAAAGTATCAAGCTTC
CACTGACCAAAAAATAATTAACGTGCACCTTATCAAAAAAGATTAAACACG
CACTGGCCAAAGAAAAGATTGAACGTG

Nr of selected repeats 15 Similarity 0.793063

Consensus:

CACTGACCAAAGAAAatAtTAnaCgTg

>Cele-UNSB01_6:11535780-11535884 Satlength=105 Nr of Repeats=4 RepeatLength=26
seed=AAATTAATCT

AAATTAATCTGTCACTCTAACTTTTA
AAATTAATCTGTCTTCTAACTTGTT
AAATTAATATGTCTTCTAACTTTAT
AAATTAATCTGTCACTCTAAATTTT

Nr of selected repeats 4 Similarity 0.803419

Consensus:

AAATTAATcTGTCacTCTAAcTTttt

>Cele-UNSB01_6:11722389-11722452 Satlength=64 Nr of Repeats=4 RepeatLength=14
seed=CTATACGCTA

CTATACGCTATACG
CTATACGCTACACG
CTATACGCTATACG
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Nr of selected repeats 3 Similarity 0.936508

Consensus:

CTATACGCTAtACG

>Cele-UNSB01_6:11722486-11725761 Satlength=3276 Nr of Repeats=130
RepeatLength=25 seed=CTGCCGTAAT

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CTGCCGTAATGCCAATTTAAAGAAT
CTACCGTAATACCAATTTATAAAAT
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CTGCCGTAATGCCAATTTAAAGAAT
CTACCGTAATACCAATTTATAGAAT
CTGACGTAATGCCAATTCATAGAAT

Nr of selected repeats 129 Similarity 0.942132

Consensus:

CTGCCGTAATGCCAATTTATAGAAT

>Cele-UNSB01_6:11725790-11730325 Satlength=4536 Nr of Repeats=175

RepeatLength=26 seed=CGGCGGATTT

CGGCGGATTTTAGAAAAATGACATTG

CGGCGGATTTTAGAAAAATGGCATTG

CGGCGGATTTT CAGAAAAATGGCACTG
CGGCGGATTTT CAGAAAAATGGCACTG
CGGCGGATTTT CAGAAAAATGGCATTG
CGGCGGATTTT CAGAAAAATGGCATTG
CGGCGGATTTT TGAAAAATGGCATTG
CGGCGGATTTT TAGAAAAATGACATTG
CGACGGATTTT TAGAAAAATGACATTG
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CGGCGGATTTTTAGAAAAATGACATTG
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Nr of selected repeats 160 Similarity 0.928249

Consensus:

CGGCGGATTTtAGAAAAATGGCATTG

>Cele-UNSB01_6:11775904-11776150 Satlength=247 Nr of Repeats=7 RepeatLength=11
seed=TCCTACAGTA

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AATTTTTCCCAAACACTACAGTAA

TCCTACCGTAA

TCCTACAGTAC

TCCTACAGTAC

TACTACAGTACCCCGATCATATCCCTCCACTAACCCCAAAGCAATATCCCTTCAAAGACGAAAAGTGAATTTTTCCCA
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TCCTACCGTAA

TCCTACAGTAC

Nr of selected repeats 5 Similarity 0.854545

Consensus:

TCCTACaGTAc

>Cele-UNSB01_6:11975065-11975494 Satlength=430 Nr of Repeats=4 RepeatLength=108
seed=TTTCACGTTT

TTTCACGTTTTcAGGTGATTATCAAGGTCACAACTAATTTATTTTTGAAAATTGACCTGTGGACCTATAACTTTGGAGA
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TTTCACGTTTTcAGGTGATTATATAGGTCACGAACCTAATTTATTTTTGAAAATTGACCTGTGGACCTATAACTTTGGAGA
TATGGTAAATTGAGTATGGGCTTTTAGAT

TTTCACGTTTTTAGGTGATTATCTAGGTCACGAACCTAATTTATTTAGCAAGTTGGCCTGTTAGCCTATAACTTTGGGGA
TATGGGTAATCAAGTATGGGCTTTCAGAT

TTTCACGTTTTTACGCGTTATCTAGGTTACGAACCTAATTTAATTTGTAAATGAACTTGTGTGACTATAACTTTGGGGA
TATGTAATCAAGTATGGGATTCGGAA

Nr of selected repeats 3 Similarity 0.860082

Consensus:

TTTCACGTTTTcAGGTGATTATcTAgGTCACgAACTAATTTATTTtGaAAaTTGaCCTGTggaCCTATAACTTTGGaGA
TATGGgaAATtgAGTATGGGCTTTCAGAT

>Cele-UNSB01_6:12031687-12031907 Satlength=221 Nr of Repeats=10 RepeatLength=22
seed=TCAGTGCAAA

TCAGTGCAAAGTGTCACCTTTTG

TCAGTGCAAAGTGACAATTATG

TCAGTGCAAAGTTTCACGTTTG

TCAGTGCAAAGTGTCACCTTTTG
TCAGTGCAAAGTGACACTTTTG
TCAGTGCTAAGTGGCACTTTTGT
TAGTGCAAAGTGTCACCTTTTG
TCGGTGCAAAGTGACACTTTTG
TCAGTGCAAAGTGACAATTTTG
TCAGTGCAAATTGGCAGATTTA

Nr of selected repeats 8 Similarity 0.818182

Consensus:

TCAGTGCAAAGTGaCActTTTG

>Cele-UNSB01_6:12072301-12080487 Satlength=8187 Nr of Repeats=312

RepeatLength=26 seed=ATGACTCTAA

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ATGACTCTAACCATTACCTAAAAAT
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ATGACTCTAACCATTACCTAAAAATA
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ATGACTCTAACCATTACCTAAAAATA

Nr of selected repeats 264 Similarity 0.927423

Consensus:

ATGACTCTAACCATTTCACCTAAAATa

>Cele-UNSB01_6:12080509-12089472 Satlength=8964 Nr of Repeats=344

RepeatLength=26 seed=AAGTTAGACC

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AAGTTAGACATTAGATGAATTA

AATTAGACCATTAATGATTTATA

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CAAAAATGTTGTTGAAATCTTGAAATTAACGAGACGGGTTTGTAATACAAAAAAGTTAACGCAAGACTATTAGAGAG
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Nr of selected repeats 3 Similarity 0.901235

Consensus:

TGCAAgACTAaTAGGGAG

>Cele-UNSB01_6:12186349-12201499 Satlength=15151 Nr of Repeats=591

RepeatLength=25 seed=CTCTCTGGCT

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CTCTCTGGCTTCCCACCTATATTTTA

CTCTCTGGCTTCACCATGTTTTTTTA

CTCTCTGGCTTCGCCATATATTTTA

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Nr of selected repeats 490 Similarity 0.859225

Consensus:

CTCTCTGGCTTCACCATATATTTTA

>Cele-UNSB01_6:12201539-12202895 Satlength=1357 Nr of Repeats=6

RepeatLength=226 seed=TGTACTATTT

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Nr of selected repeats 6 Similarity 0.964602

Consensus:

TGTACTATTTCTGTAACCTACGTGAAGCTTCTTGTACCTACTGAAATATTGTTGGTATATTTCTAAAAGAGCTTAAAATTT
ACTACAAAGTTTCTaAAAgACATTTCaAAAAAAGTTACTTTGAAGAGATTTATGAATTTTCAAAGTTaCGAAAATTCGT
CTATTTTTGCCTATAAAATGGTAGTTTTTCATTAATAATAAAAATACGCAtTAtAAGGTAGGGCTGAAAA

>Cele-UNSB01_6:12589371-12589487 Satlength=117 Nr of Repeats=6 RepeatLength=19

seed=ATAGATTGTT

ATAGATTGTTACACGAAAA
ATAGATTGTTACACGAAAA
ATAGATTGTTACACGAAAA
ATAGATTGTTACACGAAAA
ATAGATTGTTACACGAAAA
ATAGATTGTTACACGAAAA

Nr of selected repeats 4 Similarity 1.000000

Consensus:

ATAGATTGTTACACGAAAA

>Cele-UNSB01_6:12589530-12590986 Satlength=1457 Nr of Repeats=71

RepeatLength=19 seed=TTAATTAATA

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Nr of selected repeats 50 Similarity 0.869728

Consensus:

TTAATTAATATTTATTTAT

>Cele-UNSB01_6:12591006-12601690 Satlength=10685 Nr of Repeats=320

RepeatLength=32 seed=GCTATTTGGT
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Nr of selected repeats 268 Similarity 0.880720

Consensus:

GCTATTTGGTGcTCCATcGGTGCTAcAtTGGT

>Cele-UNSB01_6:12591003-12604866 Satlength=13864 Nr of Repeats=415

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Nr of selected repeats 356 Similarity 0.868768

Consensus :

GGTGCTATTTGGTGcTCCATCGGTGCTAcAtT

>Cele-UNSB01_6:12827464-12828819 Satlength=1356 Nr of Repeats=70

RepeatLength=19 seed=AAAAATAGAT

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Nr of selected repeats 45 Similarity 0.943434

Consensus:

AAAAATAGATTGTTACACG

>Cele-UNSB01_6:12847168-12848031 Satlength=864 Nr of Repeats=10 RepeatLength=15
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GGGTCTCACCACGAT

GGGTCTCACCACGAA

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Nr of selected repeats 9 Similarity 0.920988

Consensus:

GGGTCTCACCACGAn

>Cele-UNSB01_6:12904034-12904836 Satlength=803 Nr of Repeats=12 RepeatLength=32
seed=CGACCTAGGT

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CGACCTAGGTTCGCGACGCGACCTAACCTCTAGGTTCGAGGT

Nr of selected repeats 8 Similarity 0.956845

Consensus:

CGACCTAGGTTCGCTTTGCGACCTGCGACCTAG

>Cele-UNSB01_6:12932636-12932914 Satlength=279 Nr of Repeats=9 RepeatLength=31
seed=TCGACAGAAG

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TCGGCAGAAGTTGTTCGGCCTACTACCTTTC
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TCGACAGAAGCTGTTCGGACATCACCTTTC
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Nr of selected repeats 8 Similarity 0.729437

Consensus:

TCGACAGAAGCTGTTCGGaCaTcACaCTTTCc

>Cele-UNSB01_6:12933662-12933969 Satlength=308 Nr of Repeats=5 RepeatLength=26
seed=AAAAATGGCA

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GTAGAATGAGGAGAAACAGGCGCCGAGCGCCCGGGGCGCTTGTTCGCGGCGAGACCCGTGCCGGAGGAAAATGCCTG
CGCCTTTAGTTTGTACTGTCTCTCTCTCACTCCGCTGTACCTC
AAAAATGGCATTGCGGCGGATTTTCAG
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Nr of selected repeats 4 Similarity 0.897436

Consensus:

AAAAATGGCATTGCGGCggATTTcaG

>Cele-UNSB01_6:13568461-13570473 Satlength=2013 Nr of Repeats=18
RepeatLength=108 seed=TTTCAGATTT

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TTTGAAGCTATGGGTAATTGAGTACGAGC

Nr of selected repeats 17 Similarity 0.875000

Consensus:

TTTCAGATTTTTCACaATTTTcACTTgAttATATAGGTCACGACCCAAATTATTTTGAAaAatTgAGCTAcAcGGcTgTAAC
TTTGgAgCTATGGGTAATCaAGTATGAGC

>Cele-UNSB01_6:13750177-13750509 Satlength=333 Nr of Repeats=8 RepeatLength=18
seed=TGCAAGACTA

TGCAAGACTAATAGAGAC

TGCAAGACTATTAAAGGC

TGCAAGACTAATTTTCGAAGATCCAATAGCTTTGCAAAATGGACCATTTCTTGTAAAACTTGTTTTGAAAAATATTAC
AAAATACATACTTTTAAATTATTTTATCAATTGTTTGAACACTTAAAATTTAATTTAGCTAAAAATGACGAATTTGTTG
AAGTTTCCACGAAATATTGCTAGCAGAAATAGGGG

TGCAAGACTATTAGAGAC

TGCAATACTAATAGAGGC

TGCAAGACTAATTTTCGATTGGCCCGTATGGG

TGCAAGACTAATAGGGG

TGCAAGACTAATAGAGGC

Nr of selected repeats 5 Similarity 0.851852

Consensus:

TGCAAgACTAaTAgAGgC

>Cele-UNSB01_6:13887397-13887577 Satlength=181 Nr of Repeats=11 RepeatLength=15
seed=TCGTGGTGAG

TCGTGGTGAGACCCG

TCGTGGTGAGACCCTTCGTGGAAAGACCCT

TCGTGGTGAGACCCT

TCGTGGTAAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACCCT

TCGTGGTGAGACCCA

TCGTGGTGAGACTTT
TCGTGGTAAGACCCA
TCGTGGTGAGACCTT
TCGTGGCGAGACCCA

Nr of selected repeats 10 Similarity 0.857778

Consensus:

TCGTGGTgAGACCCt

>Cele-UNSB01_6:14010915-14011665 Satlength=751 Nr of Repeats=7 RepeatLength=108
seed=TGGGTAATCA

TGGGTAATCAGGTACGGGCTTTCAGATTTTCAAGTTTTCAGGTGACTATCTAGGTCACGAGCCAATTTTCAGCCAGGAGT
GGGACTAGATATATGAATTTCTTGGGTTA

TGGGTAATCACGTACGGGCTTTCAGATTTTACGTTTTACGTGTAATATCTAGGTCACGAACCAATTTTGGTTAGGAGT
GGGAATCTTAAATTTTGGGTTG

TGGGTAATCAGGTGCGAGCTTTCAGATTTTTACGTTTTACGTGTAATATCTAGGTCACGAACCAATTTCTTTTCGGAAT
GGGACTAGGGACATGAAACTTTTGGTTTA

TGGGTAATCAGGTACGGGCTTTCAGATTTTCAAGTTTTCAGGTGACTATCTAGGTCACGAGCCAATTTTCAGCCAGGAGT
GGGACTAGATATATGAATTTCTTGGGTTA

TGGGTAATCAGGTGCGAGCTTTCAGATTTTTACGTTTTACGTGTAATATCTAGGTCACGAGCCAATTTCTTTTCGGAAT
GGGACTAGGGACATGAAACTTTTGGGTTA

TGGGTAATCAGGTACGGGCTTTCAGATTTTCAAGTTTTCAGGTGACTATCTAGGTCACGAGCCAATTTTCAGCCAGGAGT
GGGACTAGATATATGAATTTCTTGGGTTA

TGGGTAATCACGTACGGGATTTTCAGATTTTTACGTTTTACGTGTAATATCTAGGCCACGAGCCAATTTTGGTTAGGAGT
GGGACTAGGGATATGAAACTTTTGGGTTA

Nr of selected repeats 6 Similarity 0.845267

Consensus:

TGGGTAATCAGGTaCGgGCTTTCAGATTTTcAaGTTTTcAcGTGAaTATCTAGGTCACGAGCCAATTTcagccaGGAgT
GGGACTAGagAtATGAAacTcTTGGGTTA

>Cele-UNSB01_6:14101701-14101756 Satlength=56 Nr of Repeats=5 RepeatLength=11
seed=GTGCTTGGTC

GTGCTTGGTCA

GTGCTTGGTCA

GTGCTTGGTCA

GTGCTTGGTCT

GTGCTTGGTCA

Nr of selected repeats 5 Similarity 0.951515

Consensus:

GTGCTTGGTCa

>Cele-UNSB01_6:14121790-14122309 Satlength=520 Nr of Repeats=13 RepeatLength=40
seed=GAACATTCCA

GAACATTCCAGAATTTTATCGATTTTTCTAGAAAGTTCTG

GAACATTCCAGAAATTTCCCGATTTTTCTAGAAAGTTCTG

GAACATTCCAGAATTTTCTCGATTTTTTCTAGAAAGTTCTG

GAACATTCCAGAATTTTCTCGATTTTTCTAGAAAGCTCTT

GAACATTCCAGACTTTTCCCAATTTTTCTAGAAAGTTCTG

GAACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTG

GAACATTCCAGACTTTTCCCAATTTTTCTAGAAAGTTCTG

GAACATTCCAGAATTTTCTCGATTTTTCTAGAAAGCTCTT

GAACATTCCAGACTTTTCCCAATTTTTCTAGAAAGTTCTG

GAACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCT

GAACATTCCAGAATTTTCTCGATTTTTCTAGAAAGTTCTT

GAACATTCCAGAAATTTCCCGATTTTTCTAGAAAGTTCTG

GAACATTCCAGACTTTTCCCAATTTTTCTAGAAAGTTCTG

Nr of selected repeats 12 Similarity 0.904545

Consensus:

GAACATTCCAGAAATTTTCcCgATTTTTCTAGAAAGTTCTg

>Cele-UNSB01_6:14122412-14122622 Satlength=211 Nr of Repeats=6 RepeatLength=35
seed=CAGAAAATTT

CAGAAAATTTCAATTTCCCGCAAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTCT
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCA

Nr of selected repeats 6 Similarity 0.949206

Consensus:

CAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCA

>Cele-UNSB01_6:14122652-14123413 Satlength=762 Nr of Repeats=19 RepeatLength=15
seed=GGGTCTCACC

GGGTCTCACCACGGT
GGGTCTCACCACGAC
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCGCCACGAT

GGGTCTCACCACGATGGGTCTTTCCACGAT

GGGTCTCACCACGAT

GGGTCTCACCACGGT

GGGTCTCGCCACGAAGATCTCGCAGCAACATTTTTTTAATTTTCCAGAAGGTTCTAGAACAATCCAGAATTTTTTCGAA
TTTTCCAGAAGGTTCTGGAACATTCAGAATTTTCTAGAATTTTCCAGAACCTTATTTCCCGCCAAAATATTTTTTCACA
GAAAATTTAAATTTCCCGCCAAAATATTTTTTCACAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCACAGAAAATTTA
AATTTCCCGCCAAAATATTTTTTCACAGAAAATTTAAATTTCCCGCCAAAATATTTTTTCACAGAAAATTTAAATTTCCCT
CCAAAATATTTTTTCTCAGAAAATTTAAATATCCCGCCAAAATATTTTTTCACAGAAAATTTAAATTTCCCGCCAAAATAT
TTTTTCTCAGAAAATTTAAATTTCCCGCCAAAATTTGGGCCTTACCACGGT

GGGTCTCACCACGAC

GGGTCTCACCACGAT

GGGTCTCACCACGTT

GGGTCTCACCACGAT

GGGTCTCACCACGAT

GGGTCTCGCCACGAT

GGGTCTCGCCACGATGGGTCTCGCCACGAT

GGGTCTCACCACGATGGGTCTTTCCACGAT

Nr of selected repeats 15 Similarity 0.911958

Consensus:

GGGTCTCACCACGaT

>Cele-UNSB01_6:14123669-14124172 Satlength=504 Nr of Repeats=19 RepeatLength=11
seed=CTACAGTACT

CTACAGTACTC

CTACAGTACTA

CTACAGTACCCCGAACATATCCACTACTAACCGCAAACCTATATCTCTTCAAAAGACAAAAGCTCAATTTTTCTTAA

CTACAGTAATC

CTACAGTACTC

CTACAGTACCT

CTACAGTACTA

CTACAGTACCCCGACCATATCCCACCCTAACCCCAAACCTATATCTCTTCAAAAGACAAAAGCTCAATTTTTCTTAA

CTACAGTAATC

CTACAGTACTC

CTACAGTACCT

CTACAGTACTA
CTACAGTACCCCGACCATATCCCACCCTAACCCCAAACCTATATCTCTTCAAAAAGACAAAACTCAATTTTTCTCTAAA
CTACAGTAATC
CTACAGTACTCCTAAAGTACCT
CTACAGTACTACTGCAGTACCCCGACCATATCCCCTACTACTAACCTCAAACCTATATCTCTTCAAAAAGACAAAAACACAA
TTTTTCCCAA
CTACAGTAATC
CTACCGTACTC
CTACAGTACTC

Nr of selected repeats 14 Similarity 0.771368

Consensus:

CTACAGTAcTc

>Cele-UNSB01_6:14250466-14251066 Satlength=601 Nr of Repeats=4 RepeatLength=153
seed=TGAGGTGCAG

TGAGGTGCAGGACGTGATGAGCTTTGTTGAACTGGGAACTGTTGATTCCCGGAGCCGTGATTTCATAGATGAGTTGGAGG
GACCTGCTGTGGAACCTTGTTCACCTTGAGCAATTCCATGAGCCATCAAGAAGCTTTCCTGCAGACTGGGCAAC
TGAGGTGCAGGGCGTGATGAGCTCTGTCCCATTTCGGAACCTGTTGATTCCCGGAGCCGTGATTTCATAGATGAGTTGGAGG
GACCTGCTGTGGAACCTTGTTCGAACTTGAGAGAGTCCATGAGCCATCAAGAAGCTTTCGGCAGATTGGGCAAC
TGAGGTGCAGGGCGTGATGAGCTTTGTTGAACTGGGAACTGTTGATTCCCGGAGCCGTGATTTATGGAGGAATTGGAGG
GACCTGCTGGGGACCTTGTTCACCTTGACCAATTCCATGAGCCATCAGGAAGCTTTCGGCAGATTGGGCAAC
TGAGGTGCAGGGCCTGATGAGCTGTGGTTCATTTCGATTCCCGGAGCCGTGATTTCATTGCATTGAAAAGACCTGACAGAG
AACTCGTTGGAATTTGAGAGTTTGCATGAGCCATCAGGAATTTTCCGGAAGAGCAGGCAAT

Nr of selected repeats 3 Similarity 0.872186

Consensus:

TGAGGTGCAGGgCGTGATGAGCTtTGTTgaAcTgGGAACCTGTTGATTCCCGGAGCCGTGATTcATaGAtGAgTTGGAGG
GACCTGCTGtGGAaCTTGTTCaAcTTGAgcaAtTCCATGAGCCATCAaGAAGCTTTCcGcAGAtTGGGCAAC

>Cele-UNSB01_6:14307881-14308131 Satlength=251 Nr of Repeats=10 RepeatLength=25
seed=TCTCTGGCTT

TCTCTGGCTTCACAGAATATTTTAA
TCTCTGGCTTCACCGTATATTTTAC
TCTCTGGCTTCACAGAATATTTTAC
TCTCTGGCTTCGCAGAATATTTTAC
TCTCTGGCTTCACCGTATATTTTAC
TCTCTGGCTTCACCGTATATTTTAC
TCTCTGGCTTCACAGAATATTTTAC
TCTCTGGCTTCGCAGAATATTTTAC
TCTCTGGCTTCACCGTATATTTTAC
TCTCTGGCTTCACAGAATATTTTAC

Nr of selected repeats 10 Similarity 0.913481

Consensus:

TCTCTGGCTTCaCaGaATATTTTAC

>Cele-UNSB01_6:14447847-14448957 Satlength=1111 Nr of Repeats=73
RepeatLength=15 seed=TCGTGGTGAG

TCGTGGTGAGAACCA
TCGTGGTGAGAACTT
TCGTGGTGAGACCTT
TCGTGGAGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGAGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGTCCCA

TCATGGTGAGACCTT
TCGTGGAGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTA
TCGTGGTTAGACCTTG
CGTGGTGAGCCCCT
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGAGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTA
TCGTGGTTAGACCTT
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGACTTT
TCGTGGTGAGACACA
TCGTGGTTAGACCCA
TCATGGTGAGACCTT
TCGTGGAGAGGCCCA
TCGTGGTGAGACCAA
TCGTGGTGAGACCTT
TCGTGGTGAGACACA
TCGTGGTGAGACCTT
TCGTGGTGAGACACA
TCGTGGTTAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACTTA
TCGTGGTGAGACTTA
TCGTGGTGAGACGCA
TCGTGGTGAGACCCA
TCGTGGTGAGACCTT
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TCGTGGTGAGACCTT
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TCGTGGAGAGACCCA
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TCGTGGTGAGACCTT
TCGTGGTGAGACACA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT
TCGTGGTTAGACCCA
TCGTGGTGAGACCAATCGTGAAGAGACCCA
TCGTGGTGAGACCAA
TCGTGGTGAGACCTT
TCGTGGTGAGACCTT

TCGTGGAGAGACCCA
TCGTGGTGAGACCCA
TCGTGGTGAGACTTA
TCGTGGTGAGACTTA
TCGTGGTGAGACGCA
TCTTGGTGAGACCCA
TCGTGGTGAGACCTT
TCGTGGTGAGATCCA

Nr of selected repeats 70 Similarity 0.770484

Consensus:

TCGTGGTGAGACCa

>Cele-UNSB01_6:14452976-14453126 Satlength=151 Nr of Repeats=12 RepeatLength=12
seed=ATAGGCATAG

ATAGGCATAGGC
ATAGGCATAGGCATAGAC
AGAGGCATAGGC
ATAGGCATAGGC

Nr of selected repeats 11 Similarity 0.979798

Consensus:

ATAGGCATAGGC

>Cele-UNSB01_6:14480301-14480556 Satlength=256 Nr of Repeats=13 RepeatLength=20
seed=TAACAATCTA

TAACAATCTATTTTTTCGTG
TAACAATCTATTTTTTCGTG
TAACAATCTATTTTTTCGTG
TAACAATCTATTTTTTCGTG
TAACAATCTATTTTTTCGTT
TAACAATCTATTTTTTCGTG
TAACAATCTATTTTTTCGTG
TAACAATCTATTTTTTCGTG
TAACAATCTATTTTTTCGTG
TAACAATCTATTTTTTCGTA
TAACAATCTATTTTTTCGTG
TAACAATCTTTTTTTTTTCGTG

Nr of selected repeats 8 Similarity 0.966667

Consensus:

TAACAATCTATTTTTTCGTG

>Cele-UNSB01_6:14589132-14589372 Satlength=241 Nr of Repeats=5 RepeatLength=48
seed=GGAGGTGGAG

GGAGGTGGAGAAAGTGTAGTTCCCGGTGGTTGTGGTTCTTCCGAGGGT
GGAGGTGGAGAAAGTGTAGTTCCCGGTGGTCGCGGTTCTTTAGAGGGT
GGAGGTGGAGAAAGTGTAGTTCTTGGTGGTCGCGGCTCTGCAGAGGGT
GGAGGTGGAGCAAGTGTAGTTCCCGATGGTCGTGGCTCTTCCGACGGT
GGAGGTGGAGAAAGTGTGGTTCCCGGTGGTCGGGGCTCTTCTGATGGT

Nr of selected repeats 5 Similarity 0.841667

Consensus :

GGAGGTGGAGaAAGTGTaGTTCCcGgTGGTcGnGGcTCTtcnGAgGGT

>Cele-UNSB01_6:14650166-14651272 Satlength=1107 Nr of Repeats=10

RepeatLength=18 seed=TGCAAGACTA

TGCAAGACTAATAGAGAC

TGCAAGACTATTAGAGGC

TGCAAGACTGATTTTTCGAAGATCCAATAGCTTTGTAAAATTGACTATTTATCGTCAAAAACCTTGACTTGAAACAGTCTG

AATCATTCAAAATATATCATTTGTTAAATTATTTTATCAATATTTTGAACACGTATTTGGCTTTTAAAAAACCTTTATTT

AGCTAAAAATGACGAAATTGTTGAAGTTTTTCACGGAATATTGCTGGTCTGACAAAATGAAGGA

TGCAAGACTATTAAAGAC

TGCAAGACTAATTTTTCGATTGGTCCGTAGGGG

TGCAAGACTAATAAAGGC

TGCAAAACTAATAAAGGC

TGCAAAACTAATAAAGGC

TGCAAAACTAATAGAGGAAATACGGTTGATATTTTCAGCCTCACATAAAAAAGAAGAATCTAATGAAATAATTTAGTTC

CGAAATTTATATAATTTTTCCTAGAAAATCATGATTTTGAGTGACCGCAAAGCGTCATTTTCGCCATTCCCAAAGA

AAAAATTAACACAGCAACCGTACAAGAGGTTGACATAGAAAATATTTCTATGGGATTGCGACATTATTCATTATTATT

ATTCTTATAGTTATGATCACATCAAAACACAAAGAACGACGAAGGGGTAGGTGTTTGTTCGGCGGGCGACACCTCGCGGG

TTTGGCGCACCGCTGTAGTTTGTGTGGGGAAGCGGGGCATTACGATTTTTTTTTTACGATTTTCTAATGGCGAGGAGAG

AGATGTATGATTTTCTTTCAGTAAATGATTCGATATAATATTATTTGCAAATTTCTTGAAATTTTTTTTTTGAACGTGA

AGTACTAGATTTTTTTTGAATTTGTTTGAATTTGTATTGTGATCTCAAACCTTAAAACTTTTCCCTGTTGCAAATCA

TGCGACTATTTCTCAAAAATGCGATATTTCCCGCCATAAAAGCAATTTTTTAATGTAAATTTGCCCGTATTATACTT

TTTTTTCTCGAAAACGTGTTTGTTCAAAACCTAGATTGTGAATATTAACAAAATACTTTATTTCTCTATTAGTCTTG

CA

TGCAAGACTAATTTTTCAGTTAACCCGTAGGGG

Nr of selected repeats 6 Similarity 0.841975

Consensus :

TGCAAgACTAaTAaAGgC

>Cele-UNSB01_6:14688507-14688582 Satlength=76 Nr of Repeats=5 RepeatLength=15

seed=TCGTGGCGAG

TCGTGGCGAGACCCA

TCGTTGCGAGACCTT

TCGTGGCGAGACCCA

TCGTGGCGAGACCCA

TCGTGGCGAGACCCA

Nr of selected repeats 5 Similarity 0.928889

Consensus :

TCGTgGCGAGACCCa

>Cele-UNSB01_6:14688602-14689240 Satlength=639 Nr of Repeats=20 RepeatLength=32

seed=TTTGGCGGGA

TTTGGCGGGAATTTAAATTTTCTTCGAAATTT

TTTGGCGGGAATTCAAATTTTCTGTGAAAATTT

TTTGGCGGTTAGTTCAAATTTTCTTCAAAATTT

TTTGGCGGGAATTCAAATTTTCTTTGAAAATTT

TTTGGCGTGAATTCAAATTTTCTGAAACATT

TTTGGCGGGAATTCAAATTTTCTCTGAAAATTT

TTTGGCGGGAATTTAAATTTTCTTTAAAATTT

TTTGGCGGGAATTCAAATTTTCCGTGAAAATTT

TTTGGCGGGAATTCAAATTTTCTGAAAATTT

TTTGGCGGGAGTTCAAATTTTCTCTGAAAATTT

TTTGGCGGGAATTTAAATTTTCTTCAAAATTT

TTTGGCGGGAATTCAAATTTTCTTTGAAAATTT

TTTGGCGGGAATTCAAATTTTCTTTAAAATTT

TTTGGCGGGAATTCAAATTTTCTGTGAAAATTT

GGCAAATCAACAATTAATAATTCCTCATCCTCAGAAAAATATAAATTACG
GGCAAATCAACAATTAATAATTCCTCATCCTCAGAAAAATATAAATTACG

Nr of selected repeats 293 Similarity 0.961435

Consensus:

GGCAAATCAACAATTAATAATTCCTCATCCTCAGAAAAATATAAATTACG

>Cele-UNSB01_6:14983794-14983948 Satlength=155 Nr of Repeats=5 RepeatLength=22
seed=TTTGTGGGAG

TTTGTGGGAGGCGACCTACAACCTTCGTGGGATGCGACTTATAACC

TTTGTGGGAGTGAACCTTACACT

TTTGTGGGAGGCGACATATAACC

TTTGTGGGAGGCGACATATAACC

TTTGTGGGAGGCGACCTTTGTGAGCGGCGACCTACACC

Nr of selected repeats 3 Similarity 0.757576

Consensus:

TTTGTGGGAGGcgACaTAtACc

>Cele-UNSB01_6:15068529-15068945 Satlength=417 Nr of Repeats=13 RepeatLength=32
seed=TTGAATTCCC

TTGAATTCCCGCCAAAATTTTTCAAAGAAATT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAC

TTGAATTCCCGTTATAATTTTTCACAGAAAAT

TTGAATTCCCGCCAAAATTTTTCATAGAAAAT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

TTGAATTCCCGCTAAAAATTTTTCACAGAAAAT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

Nr of selected repeats 13 Similarity 0.927885

Consensus:

TTGAATTCCCGCCAAAATTTTTCACAGAAAAT

>Cele-UNSB01_6:15068534-15069086 Satlength=553 Nr of Repeats=16 RepeatLength=32
seed=TTCCCGCCAA

TTCCCGCCAAAATTTTTCAAAGAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTGAATTTCCCGTTATAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCATAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

TTCCCGCCAAAATTTTTCACAGAAAATTTGAAT

TTCCACCAAAAAGTTTTCTCAGTAAATTTGAAT

TTCCCGCCAAAATTTTTCTCAGAAAATTTGAAT

TTCCCGCCAAAATTTTTTATCAGAAAATTTGAAT

Nr of selected repeats 11 Similarity 0.947727

Consensus:

TTCCCGCCAAAATTTTTCACAGAAAATTTTGAA

>Cele-UNSB01_6:15068455-15069305 Satlength=851 Nr of Repeats=5 RepeatLength=40
seed=TTCTGGAACA
TTCTGGAACATTTCGAGAATTTTCCCGATTTTTCTAGAAAG
TTCTGGAATATTCCAGAATTTTTTTTCAGAAATTTTGAATTCCTCGCCAAAATTTTTCAAAGAAATTTTGAATTCCTCGCC
AAAATTTTTTCACAGAAAATTTGAATTCCTCGCCAAAATTTTTTCACAGAAAATTTGAATTCCTCGCCAAAATTTTTTCACAGA
AACTTGAATTCCTCGTTATAATTTTTTCACAGAAAATTTGAATTCCTCGCCAAAATTTTTTCATAGAAAATTTTGAATTCCTCG
CAAAATTTTTTCACAGAAAATTTGAATTCCTCGCCAAAATTTTTTCACAGAAAATTTGAATTCCTCGCCAAAATTTTTTCACA
GAAATTTTGAATTCCTCGCCAAAATTTTTTCACAGAAAATTTGAATTCCTCGCCAAAATTTTTTCACAGAAAATTTGAATTC
CGTAAAAATTTTTTCACAGAAAATTTGAATTCCTCGCCAAAATTTTTTCACAGAAAATTTGAATTCCTCGCCAAAATTTTTTC
CAGAAAATTTGAATTTCCACCAAAAAGTTTTTCTCAGTAAATTTGAATTTCCCGCCAAAATTTTTTCTCAGAAAATTT
GAATTTCCCGCCAAAATTTTTTATCAGAAAATTTGAATTTCCCGCCAAAATTTATGGGTCTCGCCAAGATGGGTCTCAC
CAGGAAGGTCTCACCACGAAGGTCTCACCACGAATTTTCTCGAATTTTCCAGAAGG
TTCTGGAACATTCCAGCATTTTCTCAAGTTTTCCAGAAGG
TTCTGGAACATTCCAGAATTTTCTCGAATTTTCCAGAAGG
TTCTGGAACATTCCAGAATTTTCTCAAATTTTCCAGAAGG
Nr of selected repeats 4 Similarity 0.866667

Consensus:
TTCTGGAACATTCCAGaATTTTCTCaAaTTTTTCcAGAAgG
>Cele-UNSB01_6:15069428-15069697 Satlength=270 Nr of Repeats=10 RepeatLength=11
seed=CCTACAGTAC
CCTACAGTACT
CCTACAGTACCT
CTACAGTACAA
CTACAGTACCCCAACCATATCCCGACACTAACCCCAAAGCAATATCACTTCAAAAAACGAAAAGCCAATTTTTTTTCAA
AATACAGTAAT
CCTACAGTACT
CCTACAGTATTA
CTACAGTACTA
CTACAGTACCCGACCATATCCCACCACTAACCTCAAACCAATATCACTTCAAAAAGACAAAAGTCAATTTTTTCCAAAA
CTACAGTAAC
CCTACAGTAAC
CCTACAGTACC
Nr of selected repeats 6 Similarity 0.738889

Consensus:
cCTACAGTACT
>Cele-UNSB01_6:15253053-15270737 Satlength=17685 Nr of Repeats=696
RepeatLength=25 seed=TGGCTTCACA
TGGCTTCACAATAAATTTTACTCTC
TGGCTTCACACTATATTTTACTCTG
TGGCTTCACAGTCTAATTTACTCTC
TGGCTTCACAGTATATTTTACTCTC
TGGCTTCACACTATATTTTACTCTG
TGGCTTCACAGTCTAATTTACTCTC
TGGCTTCACAGTATATTTTACTCTC
TGGCTTCACACTATATTTTACTCTC
TGGCTTCACAATATATTTTACTCTC
TGGCTTCACAAAATATTTTACTCTC
TGGCTTCACAATATATTTTACTCTC
TGGCTTCACAAAATATTTTACTCTC
TGGCTTCACAATATATTTTACTCTC
TGGCTTCACAAAATATTTTACTCTG
TGGCTTCACAATATATTTTACTCTC
TGGCTTCACACTATATTTTACTCTC

TGGCTTCACACTATATTTTACTCTG
TGGCTTCACAGTCTAATTTACTCTC
TGGCTTCACAGTATATTTTACTCTC
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TGGCTTCACAAAATATTTTACTCTC
TGGCTTCACAATATATTTTACTCTC
TGGCTTCACAAAATATTTTACTCTC
TGGCTTCACAATATATTTTACTCTC
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Nr of selected repeats 90 Similarity 0.968330

Consensus:

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Nr of selected repeats 9 Similarity 0.957672

Consensus:

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Consensus:

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Nr of selected repeats 5 Similarity 0.939048

Consensus:

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GTCTCACCACGATGG

Nr of selected repeats 92 Similarity 0.888135

Consensus:

GTCTCACCACGAaGG

>Cele-UNSB01_6:15876707-15876856 Satlength=150 Nr of Repeats=4 RepeatLength=21
seed=TGTCCTGAT

TGTCCGTGATCCTCATGGGAG

TGTCCGTGATGATCGTGAGCA

TGTCCGTGATGATGATCTTCTCCTCGTCACTAAAAATTGATAAGTTGCAGTAATTAACCTTTTTATTGAGAAATTCTTA
CTGGGAG

TGTCCATGATGATCATGTGCA

Nr of selected repeats 3 Similarity 0.666667

Consensus:

TGTCCgTGATgaTCaTGnGcA

>Cele-UNSB01_6:15966442-15966650 Satlength=209 Nr of Repeats=8 RepeatLength=26
seed=GGTCTAACTT

GGTCTAACTTTATAAAAAGGATCTGAC

GGTCTAACTTTATAAATGGATCTGAT

GGTCTAACTTTTTTAATGGATCTGAC

GGTCTAACTTTATAAAAAGGATCTGAC

GGTCTAACTTTATAAATGGATCTGAC

GGTCTAACTTTTTTAATGGATCTGAC

GGTCTAACTTCATAAATGGATCTGAC

GGTCTAACTTCATAAATGGATCTGAC

Nr of selected repeats 8 Similarity 0.899267

Consensus:

GGTCTAACTTtaTaAaTGGATCTGAC

>Cele-UNSB01_6:16004509-16004749 Satlength=241 Nr of Repeats=6 RepeatLength=40
seed=AAAGTTCTGG

AAAGTTCTGGAACATTCCAGACTTTTCCCAATTTTTCTAG

AAAGTTCTGGAACATTCCAGAATTTTCCCGATTTTTCTAA
AAAGTTCTGGAACATTCCAGACTTTTCCCATTTTTCTAG
AAAGTTCTGGAACATTCCAGACTATTCCAATTTTTCTAG
AAAGTTCTGGAACGTTCCAGAATTTTCTCGATTTTTCTAG
AAAGTTCTGGAACATTCCAGAATTTTCCCGATTTTTCTAG
Nr of selected repeats 6 Similarity 0.904444

Consensus:

AAAGTTCTGGAACATTCCAGAAaTTTTCCCaATTTTTCTAG

>Cele-UNSB01_6:16004822-16005172 Satlength=351 Nr of Repeats=10 RepeatLength=35
seed=CAGAAAATTT

CAGAAAATTTAAATTTCCCTCCAAACTTTTTTTCT
CAGAAAATTTAAATTACCCGCCAAAATATCTTTCA
CAGAAAATTTAAATTTCCCTCCAAAATTTTTTTCT
CAGAAAATTTAAATTACCCGCCAAAATATCTTTCA
CAGAAAATTTAAATTTCCCTCCAAAATTTTTTTCT
CAGAAAATTTAAATTACCCGCCAAAATATCTTTCA
CAGAAAATTTAAATTTCCCGCCAAAATATTTTTCT
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTT
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTT
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTT
CAGAAAATTTAAATTTCCCTCCAAAATATTTTTTT

Nr of selected repeats 10 Similarity 0.875556

Consensus:

CAGAAAATTTAAATTTtCCctCCAAAATaTtTTTTct

>Cele-UNSB01_6:16005217-16005457 Satlength=241 Nr of Repeats=15 RepeatLength=15
seed=GGGTCTCACC

GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTTTCACCACGAT
GGGTCTCACCACGAC
GGGTCTCACCACGGT
GGGTCTCACCACGAT
GGGTCTCACCACGAT
GGGTCTCACCTCGAT
GGGTCTCACCACGGT
GGGTCTCGCCACGAT
GGGTCTCACCACGAT
GGGTCTCACCACGGT
GGGTCTCGCCACGAT
GGGTCTCACCACGATGGGTCTTGCCACGAT

Nr of selected repeats 14 Similarity 0.906227

Consensus:

GGGTCTCACCACGaT

>Cele-UNSB01_6:16057246-16058243 Satlength=998 Nr of Repeats=38 RepeatLength=26
seed=AATTCATCTA

AATTCATCTAGTGGTCTAACTTTGGA
AATTCATCTAGTGGTCTAACTCTGGA
AATTCATCTAGTGGTCTAACTTTGGA
AATTCATCTACTGGTCTAACTTTGGA
AATTCATCTAGTGGTCTAACTCTGGA
AATTCATCTAGTGGTCTAACTTTGGA
AATTCATCTACTGGTCTAACTTTGGA
AATTCATCTACTGGTCTAACTTTGGG
AATTCATCTACTGGTCTAACTTTGGA

CATACCAAAAAATAGATTGG
CATACCAAAAAACAGATTGG
CATACCAAAAAATAGATTGG
CATACCAAAAAATAGATTGG
CATACCAAAAAATAGATTGG
CATACCAAAAAATAGATTGA
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CATACCAAAAAATAGATTGG
CATACCAAAAAACAGATTGG
CATACCAAAAAATAGATTGG
CATACCAAAAAACAGATTGG
CATACCAAAAAATAGATTGG
CATACCAAAAAATAGATTGA
CATACCAAAAAATAGATTGG

Nr of selected repeats 85 Similarity 0.936956

Consensus:

CATACCAAAAAAtAGATTGg

>Cele-UNSB01_6:16179578-16182464 Satlength=2887 Nr of Repeats=111

RepeatLength=26 seed=GTGAACGGCC

GTGAACGGCCAGAGTCACTAAATTTG
GTGAAGGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTATTTTTG
GAGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTATTTTTG
GAGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCATAGTCACTAAATTTG
GTAAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCATAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCATAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCATAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTAAATTTG

GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCAGAGTCACTATTTTTG
GTGAACGGCCATAGTCACTAAATTTG
GTGAACGGCCATAGTCACTAAATTTA
GTGAACGGCCATAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTATTTTTG
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GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG
GTGAACGGCCAGAGTCACTAAATTTG

Nr of selected repeats 111 Similarity 0.930666

Consensus:

GTGAACGGCCAGAGTCACTAttTTTTG

>Cele-UNSB01_6:16182513-16182592 Satlength=80 Nr of Repeats=4 RepeatLength=20
seed=TAACAATCTA

TAACAATCTATTTTTTTCGTG

TAACAATCTATTTTTTTCGTG

TAACAATCTATTTTTTTCGTG

TAACAATCTATTTTTTTCGTA

Nr of selected repeats 3 Similarity 0.955556

Consensus:

TAACAATCTATTTTTTTCGTg

>Cele-UNSB01_6:16300389-16301032 Satlength=644 Nr of Repeats=4 RepeatLength=158
seed=TATCAATTTT

TATCAATTTTCAGACGCGCTACAGGGGTTTTTGTCTTGAATTCCAATTTCAACAGGATTTACAGGCACAAAAAAAAACA
AAAATAAAATTTTTGGATTTTTGGAAAAGTTTTTATAGATTTGTATTCTAGATTGTTTAAAAATATTATTGGTACGTTT
TTGTACCAAAA

TATCAATTTTCAGACGCGCTACGGGGGTTTTTGTCTTGAATTCCAATTTCAACAGGCGCAAAAAACAAAAATAAAATT
TTTGGATTTTTGGAAAAGTTTTTATAGATTTGTATTCTAGATTGTTTAAAAATATTATTGGTACGTTTTTGGACCTATA
TATCAATTTTCAGACGCGCTACGGGGGTTTTTGTCTTGAATTCCAATTTCAACAGGCGCAAAAAACAAAAATAAAATT
TTTGGATTTTTGGAAAAGTTTTTATAGATTTCTATTCTAGATTGTTTAAAAATATTATTGTACGTTTTTGTACCAAGG
TATCAATTTTCAGACGCGCTAGAGGGGTTTTTGTGTCAAATTTCCAATTTCAACAGGCGCAAAAAACAAAAATAAAATT
TTTGGATTTTTGGAAAAGTTTTTATAGATTTCTATTCTAGATTGTTTAAAAATATTATTGGTATGTTTTTGTACCAAAA
Nr of selected repeats 3 Similarity 0.924051

Consensus:

TATCAATTTTCAGACGCGCTAcgGGGGTTTTTGTcTtgAATTCCAATTTCAACAGGCGCAAAAAACAAAAATAAAATT
TTTGGATTTTTGGAAAAGTTTTTATAGATTTcTATTCTAGATTGTTTaAAAAATATTATTgGTAcGTTTTTGTACCaAna
>Cele-UNSB01_6:16300466-16301134 Satlength=669 Nr of Repeats=4 RepeatLength=158
seed=CAAAAAATAAA

CAAAAATAAAATTTTTGGATTTTTGGAAAAGTTTTTATAGATTTGTATTCTAGATTGTTTAAAAATATTATTGGTACGT
TTTTGTACCAAAAATATCAATTTTCAGACGCGCTACGGGGGTTTTTGTCTTGAATTTCCAATTTCAACAGGCGCAAAAAA
CAAAAATAAAATTTTTGGATTTTTGGAAAAGTTTTTATAGATTTGTATTCTAGATTGTTTAAAAATATTATTGGTACGT
TTTTGGACCTATATATCAATTTTCAGACGCGCTACGGGGGTTTTTGTCTTGAATTTCCAATTTCAACAGGCGCAAAAAA
CAAAAATAAAATTTTTGGATTTTTGGAAAAGTTTTTATAGATTTCTATTCTAGATTGTTTAAAAATATTATTGTACGT
TTTTGTACCAAGGTATCAATTTTCAGACGCGCTAGAGGGGTTTTTGTGTCAAATTTCCAATTTCAACAGGCGCAAAAAA
CAAAAATAAAATTTTTGGATTTTTGGAAAAGTTTTTATAGATTTCTATTCTAGATTGTTTAAAAATATTATTGGTATGT
TTTTGTACCAAAAATATCAATTTTCAAACGCGCTACAAGGGTTTTTGTCTTGAATTTCCAATTTTTCAAAAATTCAAAAT
TCAAAAATTCAAAATTCAAAATTCAAAATTT

Nr of selected repeats 3 Similarity 0.935302

Consensus:

CAAAAATAAAATTTTTGGATTTTTGGAAAAGTTTTTATAGATTTgTATTCTAGATTGTTTAAAAATATTATTgGTACGT
TTTTTGTACCaAnaTATCAATTTTCAGACGCGCTAcgGGGGTTTTTGTcTtgAATTTCCAATTTCAACAGGCGCAAAAAA
>Cele-UNSB01_6:16421783-16421902 Satlength=120 Nr of Repeats=6 RepeatLength=20
seed=CCACCCTGTA

CCACCCTGTAATATAAGGGA
CACCTGTACAGTCAAAGA
CCACCCTGTAATATCATGGA
CCACCCTGTAATATCATTTG
CCACCTTGTAATAATCATCGA
CCACCCTGTAATAATCAAAGG

Nr of selected repeats 5 Similarity 0.706349

Consensus:

CCACCcTGTAAtATcAtgGa
>Cele-UNSB01_6:16471702-16471949 Satlength=248 Nr of Repeats=8 RepeatLength=11
seed=GTACTGTAGG

GTACTGTAGGGT
TACTGTAGGATTACTGTAGTTTTGGAAAAATTGACTTTTTGTCTTTTGAAGTGATATTGGTTTGGAGTTAGTGGTGGGA
TATGGTCGGG
GTACTGTAGTA
GTACTGTAGGA
GTACTGTAGGATTACTGTATTTTTGAAAAAAATTGGCTTTTCGTCTTTTGAAGTGATATTGCTTTGGGGTTAGTGTCCG
GATATGGTTGGG
GTACTGTAGTT
GTACTGTAGAG
GTACTGTAGGA

Nr of selected repeats 5 Similarity 0.755556

Consensus:

GTACTGTAGna
>Cele-UNSB01_6:16472035-16472475 Satlength=441 Nr of Repeats=11 RepeatLength=40
seed=TCCAGAACCT
TCCAGAACCTTCTGGAAAATTCGAGAAAATTCGGAATGT

TCCAGAACCTTCTGGAAAATCCGAGAAAATTCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGATAAAAATTCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTTCTGGAATGT
TCCAGAACCTTCTGGAAAATTCGAGAAAATTCTGGAATGT
TCCAGAACCTTCTGGAAAATCCGAGAAAATTCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATTCTGGAATGT
TCCAGAACCTTCTGGAAAATTCGAGAAAATTCTGGAATGT
TCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGAATGT
Nr of selected repeats 11 Similarity 0.950303

Consensus:

TCCAGAACCTTCTGGAAAATTTGAGAAAATTTCTGGAATGT
>Cele-UNSB01_6:16472071-16473145 Satlength=1075 Nr of Repeats=13
RepeatLength=40 seed=ATGTTCCAGA

ATGTTCCAGAACCTTCTGGAAAATCCGAGAAAATTCTGGA
ATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGA
ATGTTCCAGAACCTTCTGGAAAATTTGATAAAAATTCTGGA
ATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATTCTGGA
ATGTTCCAGAACCTTCTGGAAAATTCGAGAAAATTCTGGA
ATGTTCCAGAACCTTCTGGAAAATCCGAGAAAATTCTGGA
ATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGA
ATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATTCTGGA
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ATGTTCCAGAACCTTCTGGAAAATTTGAGAAAATGCTGGA
ATGTTCCAGAACCTTCTGGAAAATTCGAGAAAATTCGTGGTGAGACCCGTCTGGTGAGACCCCTTCGTGGTGAGACCCA
TCTTGGCGGAGACCCATAAGTTTTGGCGGGAATTCAAATTTTCTGATAAAAAATTTTGGCGGGAATTCAAATTTTCTG
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TGGCGGGAATTCAAATTTCTGTGAAAAAATTTGGCGGGAATTCAAATTTTCTGTGAAAAAATTTTGGCGGGAATTCAAA
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TTTAGCGGGAATTCAAATTTCTATGAAAAATTTGGCGGGAATTCAAATTTTCTGTGAAAAATTTATAACGGGAATTC
AGTTTTCTGTGAAAAAATTTGGCGGGAATTCAAATTTTCTGTGAAAAAATTTTGGCGGGAATTCAAATTTTCTTTGAAA
ATTTTGGCGGGAATTCAAATTTCTGAAAAAATTTCTGGA
ATGTTCCAGAAGTTTCTAGAAAATTCGAGAAAAGTCTGTG
ATGTTCCAGAACTTTCTAGAAAATTCGGGAAAATTCTCGA
Nr of selected repeats 12 Similarity 0.873676

Consensus:

ATGTTCCAGAACCTTCTGGAAAATTCGAGAAAATTTCTGGA
>Cele-UNSB01_6:16506358-16506686 Satlength=329 Nr of Repeats=5 RepeatLength=18
seed=ATTAGTTTTG

ATTAGTTTTGCACTCTCT
ATTAGTTTTGCACCCCTTCATTTGTTCCCTATTTTTAGGATTTCAAATTTGCATTATAAAATCGTTTTACAAATCAGG
AAAATTTCTTACAGACTTGGCATAACAAGTCAAATTTGGCAAATATGAGTACAACCTCGGACAGTTTTTGCATATCAGCC
TTAAAATTTGTCCATTTTGGTTCTACTGAAATGATGATATTTGCCATAACTTAATGGGAAACATGAGAAAAAACCTGT
TCGAAA
ATTAGTTTTGCACTCTCT
ATTAGTTTTGCACCCCTCT
ATTAGTTTTGCATAAAATTAGGTGTCCGAAA
Nr of selected repeats 3 Similarity 0.950617

Consensus:

ATTAGTTTTGCACTCTCT
>Cele-UNSB01_6:16529882-16530026 Satlength=145 Nr of Repeats=9 RepeatLength=14
seed=TACCATATAC
TACCATATACTATTTAAAACCATAT

TACCAAATACCATA
TACCATGTACCATA
TACCGTATACCGTA
TACCATATAACCATA
TACCATATAACCATA
TATCATATAACCATA
TACCATATGCCATATAGTATA
TACCATTTACCATA

Nr of selected repeats 7 Similarity 0.841270

Consensus:

TACCATaTACCATA

>Cele-UNSB01_6:16570815-16570983 Satlength=169 Nr of Repeats=12 RepeatLength=14

seed=CTTAGGGCTT

CTTAGGGCTTCGGG

CTTAGGGCTTCAGG

CTTAGGGCTTTGGG

CTTAGGGCTTAGGG

CTTAGGACTTAGGG

CTTAGGGCTTAGGG

CTTAGGGCTTAGGG

CTTAGGGCTTAGGG

CTTAGGGCTTAGGG

CTTGGGGCTTAGGG

CTTAGGGCTTAGGT

CTTAGGGCTTAGGG

CTTAGGGCTTAGGG

Nr of selected repeats 12 Similarity 0.894661

Consensus:

CTTAGGGCTTaGGG

>Cele-UNSB01_6:16657827-16657967 Satlength=141 Nr of Repeats=7 RepeatLength=20

seed=TACAGGGTGG

TACAGGGTGGTCCATTATTA

TACAGGGTGGCCATAATTA

TACAGGGTGGTCCATAACTA

TACAGGGTGGTCCATAATTA

TACAGGGTGGTCCATAATTGA

ACAGGGTGGTTCATAATTA

TACAGGGTGGTCCATAATTA

Nr of selected repeats 5 Similarity 0.920000

Consensus:

TACAGGGTGGtCCATaAtTA

>Cele-UNSB01_6:16744464-16744698 Satlength=235 Nr of Repeats=10 RepeatLength=16

seed=TTCCGGCAAT

TTCCGGCAATTGCCGGTTTTTTTTTTAAT

TTCCGGCAGTAGGCAAT

TTCCGGCAATTGCCGGTTTTCAACTAATCCAGCAACCGGCAATTCGACAATTGCCGGTTTTCAAAAT

TTCCGGCAATCGGCTA

TTCTGCAATTGCCAGTTTTCACAAT

TTCCGGCAATCGGCAA

TTCCGGCAATCGGCAA

TTCCGGCAATCGGCAA

TTCCGGCAATCGGCAA

TTCCGGCAATCGGCAA

Nr of selected repeats 6 Similarity 0.972222

Consensus:

TTCCGGCAATCGGCAA

>Cele-UNSB01_6:16876782-16877097 Satlength=316 Nr of Repeats=18 RepeatLength=15

seed=TCACCACGAA

TCACCACGAAGGGTC

TCACCACGAAGGGTC

TCGCCACGAAGGGTC

TCACCACGAAAGGTC

TCGCCACGAAGGGTC

TCACCACGAAGGGTC

TCACCACGAAGGGTC

TCACCACGAAGGGTCTCGCCACAATGGGTT

TCACCACGAAGGGTCTCGCCACAATGGGTC

TCACCACGAAAGGTC

TCACCACGAAGGGTC

TCACCACGAAGGGTC

TCACCACGAAGGGTC

TCACCACGAAGGGTC

TCACCACGAAGGGTC

TCACCACGAAGGGTC

TCACCACGAAGGGTCTCGCCACAATGGGTC

TCACCACGAAAGGTC

Nr of selected repeats 15 Similarity 0.947513

Consensus:

TCACCACGAAGGGTC

>Cele-UNSB01_6:17130007-17135013 Satlength=5007 Nr of Repeats=66

RepeatLength=76 seed=AGCATTAGAG

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTACCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCTACTTGCCCTTCGTGTACGGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCTACTTGCCCTTCGTGTACGGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTCCCTTCGTGCAAAGGAGTGTCTTCT

AGCATTAGAGCATGTACACAGACACCGACAACACCACAGTCTCTCCCACTTTCCCTTCGTGCAAAGGAGTGTCTTCT

TGGATCGGGA
TGGATTGGGATGGATGGCATCGGGTGTGGCGAGAACAACGACGACGACGACGACAACGACGACAACAACAAAGGATTG
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A
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TGGATCGGAATGGATCAGAATGGT
TGGATCGGGAGAAGGCGAGAACCACGGCAACGACGACGACGACGACGACGACGAGGAAGACAACAAAGGACCGGAATGG
TAAGGGAAGATTTAAATGACGCTTCAGTTAAACTGATTATTTACAGATCTACGATGAAAACGACGACGACGAACAGGAT
GGA
TGGATCGGAA
TGGATCGGAATGGATCAGAATGGT
TGGATCGGGAGAAGGCGAGAACCACGGCAACGACGACGACGACGACAACAAAGGACCGGAATGGTAAGGGAAGATTTAA
ATGACGCTTCAGTTAAACTGATTTTTTACAGATCTACGATGAAAACGACGACGACGAACAGGATGGA
TGGATCGGAA
TGGATCGGAATGGATCAGAATGGT
TGGATCGGGAGAAGGCGAGAACCACGGCAACGACGACGACGACGACAACGACGAGGACAACAAAGGACCGGAATGGTAA
GGGAAGATTTAAATGACGCTTCAGTTAAACTGATTTTTTACAGATCTACGATGAAAACGACGACGACGAACAGGATGGA
TGGATCAGAATGGATTGGAATGGATCAGAATGGT

Nr of selected repeats 23 Similarity 0.908300

Consensus:

TGGATCGGgA

>Cele-UNSB01_6:17259878-17260337 Satlength=460 Nr of Repeats=20 RepeatLength=14
seed=ATAGCGCATA

ATAGCGCATAGCGC

ATAGCGTATAGCGT

ATAGCGTATAGCGT

ATAGCGTATAGCGTATTTTTTTCCTTTTTTTTTTGACGAAAAAATTCGCAAAAAATTTCCCGTGTGGAGAGTTGAAC
TCAAATTTTCAAACCTAAAAAAGAAAAACAATAAAGAAATAAAGAATTTGGAATTTAAAAAACACACAAAAATCCC
AAAAATGAAAAAATTTCAAAT

ATAGCGTATAGCGC

ATAGCGCATAGCGT

ATAGCGTATAGCGTAAAGCGTATAGTGT

ATAGCGTATAGCGC

ATAGCGCATAGTGC

ATAGCGCATAGCAC

ATGGCGCATAGAGC

ATAGCGCATATCGC

ATATCGCATAGCGC

ATGGCGCATAGAGC

ATAGCGCATATCGC

ATATCGCATAGCGC

ATAGAGCATAGAGC

ATAGCGCATAGCGC

ATAGCGCATAGAGC

ATAGCGCATAGAGC

Nr of selected repeats 18 Similarity 0.808279

Consensus:

ATAGCGcATAGcGC

>Cele-UNSB01_6:17463543-17463648 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=GGTGGACCCA

GGTGGACCCACGGGTTTCCTAT
GGTGGATCCAGGGGTTTCCTAG
GGTGGACCCACGGGTTCCCAT
GGTGGATCCAGGGGTTTCCTAG
GGTGGACCCATGAGTTTCCTAG

Nr of selected repeats 5 Similarity 0.822222

Consensus:

GGTGGAcCCAnGgGTTCCtAg

>Cele-UNSB01_6:17501177-17501366 Satlength=190 Nr of Repeats=5 RepeatLength=38
seed=CCGTTTCGCC

CCGTTTCGCCTTGAGCGATTACCCCTTAAATGGGCCTC
CCGTTTCGCCTTGAGCGATGCACCCCTTAAATGGGCCTC
CCGTTTCGCCTTGAGCGATTACCCCTTAAATGGGCCTC
CCGTTTCGCCTTGAGCGATTACCCCTTAAATGGGCCTC
CCGTTTCGCCGTGAGCGATCCACCCCTGAATGGGCCG

Nr of selected repeats 4 Similarity 0.982456

Consensus:

CCGTTTCGCCTTGAGCGATtCACCCCTTAAATGGGCCTC

>Cele-UNSB01_6:17555071-17555695 Satlength=625 Nr of Repeats=16 RepeatLength=39
seed=ATTGATACTT

ATTGATACTTTGTTCGGGTTTAGATCATCGGCCGAGCTTC
ATTGATACTTTGTTCAGGTTTAGACCATCGGCCGAGCTTT
ATTGATACTTTGTTCGGATTAGACCATCGGCCGAGCTTC
ATTGATACTTTGTTCGGGTTTAGATCATCGGTCGAGCTTC
ATTGATACTTTGTTCGGGTTTAGACCATCGGCCGAGCTTC
ATTGATACTTTGTTCGGATTAGACCATTTGGGCCGAGCTTC
ATTGGTACTTTGTTCGGGTTTAGATCATCGGCCGAGCTTC
ATTGATACTTTGTTCGGGTTTAAACCATCGGCCGAGCTTC
ATTGATACTTTGCCGGGTTTAGACCATCGGCCGAGCTTC
ATTGATACTTTGTTCGGGTTTAGACCATCGGCCGAGCTTC
ATTGATACTTTGTTCGGGTTTAGACCATCGGCCGAGCTTC
ATTGATACTTTGTTCGGGTTTAGATCATCGCTCGAGCTTC
ATTGATACTTTGTTCGGATTAGACCATTTGGGCCGAGCTTC
ATTGATACTTTGTTCGGGTTTAGACCATCGGCCGAGCTTC
ATTGATACTTTGTTCGGGTTTAGACCATCGGCCGAGCTTC
ATTGATACTTTGTTCGGGTTTAGACCATCGGCCGAGCTTC

Nr of selected repeats 16 Similarity 0.929345

Consensus:

ATTGATACTTTGTTCGGGTTTAGAcCATCGGCCGAGCTTC

>Cele-UNSB01_6:17663802-17664403 Satlength=602 Nr of Repeats=6 RepeatLength=40
seed=TTTCTCGAAT

TTTCTCGAATTTTCCAGAAGGTTCTGGAACAGTCTAGAATTTTCCAGAAATTTTCATGAAACGTCTGGAACATTCAAGAA
CTTTCCTGATTTTCCAGAAGGTTCTTTCGGCGTTTTCCCGAACTTTTCAAATGTTTCTAGAACATTCCAGAGTTTTTC
CCAATTTTCCAGTTGGTTTTTCGATTATTCCAGAAT
TTTCTCGAATTTTCCAGAAGGTTCTAGAATATTCTAGAATTTTCTTGAAACTTCTGAAAGGTACTGAAACAAATAAAGT
TTCTCTAAAAATTTGAAGTTCCTCGTCAAAAGTCTTTTTTAGAAAAGTTGAAAATCCCGCTAAAATGCCTTTTCTCAGAA
AATTTAAACTTCCCGCAATTTTTTTAAACGACGTGTCTCATCACGATGGGTCTCACCACGATGGGTCTCGACACGAAC
ATTTCAAAT
TTTCTCGAATTTTCCAGAAGGTTCTAGAACATTCCAGAAA
TTTCTCGAATCTTCCAGAAGGTTCTGGAACATTCCAGAAT
TTTCTCGAATTTTCCAGAAGGTTCTAGAACATTCCAGAAT
TTTCTCGAGTCTTTCAAAGATTCTGGAACATTCCAGAAA

Nr of selected repeats 4 Similarity 0.866667

Consensus:

TTTCTCGAaTcTTcCAgAAGgTTCTaGAACATTCCAGAAa

>Cele-UNSB01_6:17686729-17686834 Satlength=106 Nr of Repeats=7 RepeatLength=15

seed=GAGACCCATC

GAGACCCATCGTGGC

GAGACCCATCATGGC

GAGACCCATCGTGGC

GAGGCCATCGTGGT

GAGACCCATCGTGGC

GAGACCCACCGTGGT

GAGACCCGTCGTGGT

Nr of selected repeats 7 Similarity 0.847619

Consensus:

GAGACCCATCGTGGc

>Cele-UNSB01_6:17686891-17687206 Satlength=316 Nr of Repeats=9 RepeatLength=35

seed=AAATTTTCTG

AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTT

AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTT

AAATTTTCTGTGAAAAATATTTTCGGCGGGAAATTC

AAATTTTCTGTGAAAAATATTTTGGCGGGAAATTT

AAATTTTCTGAAAAAAATATTTTGGAGGGAAATTT

AAATTTTCTGAAAAAAATATTTTGGAGGGAAATTTT

AATTTTCTGAGAAAAATATTTTGGAGGGAAATTT

AAATTTTCTGTGAAAAATATTTTGGCGGGTAATTT

AAATTTTCTGAGAAAAAAATTTTGGAGGGAAATTT

Nr of selected repeats 7 Similarity 0.909297

Consensus:

AAATTTTCTGtGAAAAATATTTTGGcGGGAAATTT

>Cele-UNSB01_6:17686552-17689936 Satlength=3385 Nr of Repeats=70

RepeatLength=40 seed=AATGTTCCAG

AATGTTCCAGAACCTTCTGGGAAATTTCTGAAAAATCTAG

AATGTTCCAGAACCTTCTGAAAAATCTAGAAAAATCTGG

AATGTTCCAGAACCTTCTGAAAAATTCGAAAAATCTGGATTGTTCTAGAACCTTCTGAAAAATTTTAAAAATGTTG

CTGCGAGATCTTTCGTGGCGAGACCCATCGTGGCGAGACCCATCATGGCGAGACCCATCGTGGCGAGGCCCATCGTGGT

AGACCCATCGTGGCGAGACCCACCGTGGTGGAGACCCGTCGTGGTGGAGACCCATCGTGGTGGAGACCCGTCGTGGTGGAGAC

CCAAAATTTTGGCGGGAAATTTAAATTTTCTGTGAAAAATATTTTGGCGGGAAATTTAAATTTTCTGTGAAAAATATTT

TGGCGGGAAATTTAAATTTTCTGTGAAAAATATTTTGGCGGGAAATTTCAAATTTTCTGTGAAAAATATTTTGGCGGGAA

ATTTAAATTTTCTGAAAAAAATATTTTGGAGGGAAATTTAAATTTTCTGAAAAAAATATTTTGGAGGGAAATTTAAAT

TTCTGAGAAAAATATTTTGGAGGGAAATTTAAATTTTCTGTGAAAAATATTTTGGCGGGTAATTTAAATTTTCTGAGAA

AAAAATTTTGGAGGGAAATTTAAATTTTCTGAAAATCTAAAATCTGAAAAATCTAGAAAGAAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGG

AATGTTCCAGAACCTTCTAGAAAAATGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATCGAGAAAATCTGA

AATGTTCCAGAACCTTCTAGAAAAATAGAGAAAATCTGA

Nr of selected repeats 69 Similarity 0.965771

Consensus:

AATGTTCCAGAACTTTCTAGAAAAATCGAGAAAATTCTGA

>Cele-UNSB01_6:17722232-17722379 Satlength=148 Nr of Repeats=8 RepeatLength=15

seed=GGGGGCAACA

GGGGGCAACATTTGAACTCTCCCT

GGGGGCAACAAATTA

GGGGGCAACATTTTCATAAAATGTA

GGGGGCAACAAAAA

GGGGGCAACAAAAA

GGGGGCAACATAATA

GGGGTCAACATTTGAACTCTCCCT

GGGGGCAACAAATTA

Nr of selected repeats 5 Similarity 0.822222

Consensus:

GGGGGCAaCAaAatA

>Cele-UNSB01_6:17820421-17836619 Satlength=16199 Nr of Repeats=357

RepeatLength=45 seed=CTCCATCCAC

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAACACTTCGA

CTCCATCCACCAGCACAGCTTCGAGTACCATAGAGAGCACTTCGA

CTCCATCCACCAGCACAGCTTCGAGTACCACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGTTTTCGAGTACGACAGAGAGCACTTCGA

CTCCATCCACCAGCACAGCTTCGAGTACCACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGTTTTCGAGTACGACAGAGAGCACTTCGA

CTCCATCCACCAGCACAGCTTCGAGTACCACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACAACAGAAAACACTTCGA

CTCCATCCACCAGCACTGTTTTCGAGTACGACAGAGAGCACTTCGA

CTCCATCCACCAGCACAGCTTCGAGTACCACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACAGCTTCGAGTACGACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGACTCGGTCCACCAGCACTGCTTCGAGTACGACAGA
AAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACAGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACAACAGAAAGCACTTCAA

CTCCATCCACCAGCACTGCTTCGAGTACAACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGGCTTTTCAGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACAACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGAGAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAGAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAACACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

CTCCATCCACCAGCACTGCTTCGAGTACAACAGAAGCACTTCGA

