

### Table S3. Alignment of satellites in families

Number of sequences=4066

There are 408 alignments:

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>Cele-UNSB01_Fam_1_12_169  Nr. of seq. 169 Alignment length(with gaps) =
14 Alignment score = 0.769097
Cele-UNSB01_3:2562874-2563954 Satlength=1081 Nr of Repeats=40
RepeatLength=10 seed=AGGCAGGCTT Num.seqs=27 Similarity=0.883001
0    AG-GC---AGGCTT
Rev.of_Cele-UNSB01_1:1-2668 Satlength=2668 Nr of Repeats=204
RepeatLength=12 seed=CTAAGCCTAA Num.seqs=173 Similarity=0.987409
2    AG-GCTT-AGGCTT
Rev.of_Cele-UNSB01_1:558852-559000 Satlength=149 Nr of Repeats=8
RepeatLength=12 seed=CTAAGCCTAA Num.seqs=5 Similarity=0.811111
2    AG-GCTT-AGGCTT
Cele-UNSB01_1:568805-568943 Satlength=139 Nr of Repeats=8 RepeatLength=12
seed=AGGCTTAGGC Num.seqs=5 Similarity=0.844444
12   AG-GCTT-AGGCTT
Rev.of_Cele-UNSB01_1:642767-642875 Satlength=109 Nr of Repeats=6
RepeatLength=12 seed=TAAGCCTAAG Num.seqs=4 Similarity=0.759259
13   AG-GCTT-AGGCTT
Cele-UNSB01_1:736250-736486 Satlength=237 Nr of Repeats=5 RepeatLength=12
seed=GCTTAGGCTT Num.seqs=3 Similarity=0.777778
2    AG-GCTT-AGGCTT
Rev.of_Cele-UNSB01_1:788353-788527 Satlength=175 Nr of Repeats=12
RepeatLength=12 seed=GCCTAAGCCT Num.seqs=10 Similarity=0.933333
10   AG-GCTT-AGGCTT
Rev.of_Cele-UNSB01_1:815618-815840 Satlength=223 Nr of Repeats=16
RepeatLength=12 seed=GCCTAAGCCT Num.seqs=10 Similarity=0.782716
10   AG-GCTT-AGGCTT
Cele-UNSB01_1:823660-823840 Satlength=181 Nr of Repeats=13
RepeatLength=12 seed=GCTTAGGCTT Num.seqs=9 Similarity=0.895062
2    AG-GCTT-AGGCTT
Cele-UNSB01_1:842713-843650 Satlength=938 Nr of Repeats=48
RepeatLength=12 seed=CTTAGGCTTA Num.seqs=32 Similarity=0.819668
9    AG-GCTT-AGGCTT
Cele-UNSB01_1:855372-855570 Satlength=199 Nr of Repeats=12
RepeatLength=12 seed=GCTTAGGCTT Num.seqs=8 Similarity=0.888889
2    AG-GCTT-AGGCTT
Rev.of_Cele-UNSB01_1:961004-961082 Satlength=79 Nr of Repeats=6
RepeatLength=12 seed=AGCCTAAGCC Num.seqs=5 Similarity=0.866667
11   AG-GCTT-AGGCTT
Rev.of_Cele-UNSB01_1:1018801-1019027 Satlength=227 Nr of Repeats=14
RepeatLength=12 seed=GCCTAAGCCT Num.seqs=9 Similarity=0.854938
10   AG-GCTT-AGGCTT
Rev.of_Cele-UNSB01_1:1149569-1149724 Satlength=156 Nr of Repeats=10
RepeatLength=12 seed=CCTAAGCCTA Num.seqs=6 Similarity=0.866667
9    AG-GCTT-AGGCTT
Cele-UNSB01_1:2301010-2301088 Satlength=79 Nr of Repeats=6
RepeatLength=12 seed=TAGGCTTAGG Num.seqs=5 Similarity=0.844444
11   AG-GCTT-AGGCTT
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Cele-UNSB01\_1:2308046-2308235 Satlength=190 Nr of Repeats=5  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=3 Similarity=0.703704  
 12 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:2402282-2402378 Satlength=97 Nr of Repeats=6  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=4 Similarity=0.839744  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:2881736-2881825 Satlength=90 Nr of Repeats=5  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=4 Similarity=0.833333  
 11 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:3158079-3158367 Satlength=289 Nr of Repeats=21  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=15 Similarity=0.766138  
 2 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:3325616-3325694 Satlength=79 Nr of Repeats=6  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=5 Similarity=0.888889  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:3430435-3430513 Satlength=79 Nr of Repeats=6  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=5 Similarity=0.788889  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:10588945-10589028 Satlength=84 Nr of Repeats=6  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=4 Similarity=0.777778  
 11 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:11661653-11661731 Satlength=79 Nr of Repeats=6  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=5 Similarity=1.000000  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:11662428-11662542 Satlength=115 Nr of Repeats=9  
 RepeatLength=12 seed=GCTTAGGCTT Num.seqs=8 Similarity=0.813492  
 2 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:11682141-11682225 Satlength=85 Nr of Repeats=7  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=7 Similarity=0.968254  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:12149612-12149804 Satlength=193 Nr of Repeats=15  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=11 Similarity=0.838695  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:12340678-12340816 Satlength=139 Nr of Repeats=10  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=6 Similarity=0.859259  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:12444291-12444339 Satlength=49 Nr of Repeats=4  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=4 Similarity=0.796296  
 10 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:12487096-12487168 Satlength=73 Nr of Repeats=5  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=4 Similarity=0.814815  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:14166580-14166640 Satlength=61 Nr of Repeats=5  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=5 Similarity=0.866667  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:2-3054 Satlength=3053 Nr of Repeats=243  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=197 Similarity=0.998872  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:577469-577719 Satlength=251 Nr of Repeats=20  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=18 Similarity=0.816993  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:2568294-2568366 Satlength=73 Nr of Repeats=6  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=6 Similarity=0.785185  
 10 AG-GCTT-AGGCTT

Rev.of\_Cele-UNSB01\_2:2659185-2659251 Satlength=67 Nr of Repeats=5  
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=4 Similarity=0.833333  
 9 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:2756689-2756749 Satlength=61 Nr of Repeats=4  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=3 Similarity=0.777778  
 10 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:3166478-3166668 Satlength=191 Nr of Repeats=8  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=6 Similarity=0.785185  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:4146856-4147072 Satlength=217 Nr of Repeats=14  
 RepeatLength=12 seed=CTTAGGCTTA Num.seqs=10 Similarity=0.748148  
 9 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:4380400-4380472 Satlength=73 Nr of Repeats=4  
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=3 Similarity=0.851852  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:11872286-11872364 Satlength=79 Nr of Repeats=6  
 RepeatLength=12 seed=CTTAGGCTTA Num.seqs=5 Similarity=0.844444  
 9 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:12045935-12046042 Satlength=108 Nr of Repeats=8  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=6 Similarity=0.748148  
 12 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:12070558-12070690 Satlength=133 Nr of Repeats=10  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=6 Similarity=0.792593  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:12072605-12072779 Satlength=175 Nr of Repeats=10  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=6 Similarity=0.822222  
 12 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:12388949-12389045 Satlength=97 Nr of Repeats=7  
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=5 Similarity=0.741026  
 9 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:12463695-12463773 Satlength=79 Nr of Repeats=5  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=4 Similarity=0.777778  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:12522288-12522472 Satlength=185 Nr of Repeats=13  
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=8 Similarity=0.884921  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:12608492-12608559 Satlength=68 Nr of Repeats=5  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=4 Similarity=0.944444  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:12968710-12969129 Satlength=420 Nr of Repeats=28  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=17 Similarity=0.799020  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:13813351-13813423 Satlength=73 Nr of Repeats=6  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=6 Similarity=0.962963  
 11 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:13878619-13878763 Satlength=145 Nr of Repeats=10  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=6 Similarity=0.725926  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:13968253-13968583 Satlength=331 Nr of Repeats=23  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=15 Similarity=0.803175  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:13977826-13977988 Satlength=163 Nr of Repeats=10  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=7 Similarity=0.798942  
 10 AG-GCTT-AGGCTT

Cele-UNSB01\_2:13981365-13981461 Satlength=97 Nr of Repeats=7  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=6 Similarity=0.755556  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:14106829-14106943 Satlength=115 Nr of Repeats=7  
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=5 Similarity=0.733333  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:14148276-14148504 Satlength=229 Nr of Repeats=14  
 RepeatLength=12 seed=GCTTAGGCTT Num.seqs=11 Similarity=0.711888  
 2 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:14195501-14195591 Satlength=91 Nr of Repeats=5  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=3 Similarity=0.851852  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:14213145-14213210 Satlength=66 Nr of Repeats=4  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=3 Similarity=0.925926  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:15121230-15121314 Satlength=85 Nr of Repeats=6  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=4 Similarity=0.814815  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_2:15182818-15182878 Satlength=61 Nr of Repeats=5  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=5 Similarity=0.888889  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_2:15522855-15525136 Satlength=2282 Nr of Repeats=188  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=173 Similarity=1.000000  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:11-3196 Satlength=3186 Nr of Repeats=261  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=239 Similarity=1.000000  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:119691-119763 Satlength=73 Nr of Repeats=5  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=3 Similarity=0.851852  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:214401-214633 Satlength=233 Nr of Repeats=8  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=5 Similarity=0.822222  
 12 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:1107553-1107733 Satlength=181 Nr of Repeats=10  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=7 Similarity=0.841270  
 12 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:1796051-1796519 Satlength=469 Nr of Repeats=35  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=27 Similarity=0.758492  
 2 AG-GCTT-AGGCTT  
 Cele-UNSB01\_3:2046603-2047209 Satlength=607 Nr of Repeats=30  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=18 Similarity=0.824256  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_3:3480039-3480224 Satlength=186 Nr of Repeats=12  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=9 Similarity=0.901235  
 11 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:3818464-3818544 Satlength=81 Nr of Repeats=5  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=3 Similarity=0.777778  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_3:11222702-11222792 Satlength=91 Nr of Repeats=6  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=5 Similarity=0.822222  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_3:11273157-11273241 Satlength=85 Nr of Repeats=5  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=3 Similarity=0.777778  
 13 AG-GCTT-AGGCTT

Cele-UNSB01\_3:11508351-11508507 Satlength=157 Nr of Repeats=10  
 RepeatLength=12 seed=GCTTAGGCTT Num.seqs=6 Similarity=0.755556  
 2 AG-GCTT-AGGCTT  
 Cele-UNSB01\_3:11725694-11725970 Satlength=277 Nr of Repeats=12  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=8 Similarity=0.916667  
 10 AG-GCTT-AGGCTT  
 Cele-UNSB01\_3:11779688-11779808 Satlength=121 Nr of Repeats=10  
 RepeatLength=12 seed=CTTAGGCTTA Num.seqs=8 Similarity=0.797619  
 9 AG-GCTT-AGGCTT  
 Cele-UNSB01\_3:12010851-12011440 Satlength=590 Nr of Repeats=30  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=20 Similarity=0.774854  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:12025839-12025976 Satlength=138 Nr of Repeats=8  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=5 Similarity=0.822222  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:12040777-12040867 Satlength=91 Nr of Repeats=6  
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=5 Similarity=0.833333  
 9 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:12088649-12088899 Satlength=251 Nr of Repeats=9  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=7 Similarity=0.936508  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:12433825-12433951 Satlength=127 Nr of Repeats=9  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=6 Similarity=0.814815  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_3:12447381-12447465 Satlength=85 Nr of Repeats=7  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=7 Similarity=0.968254  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_3:13248196-13248346 Satlength=151 Nr of Repeats=9  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=7 Similarity=0.830688  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_4:1-5637 Satlength=5637 Nr of Repeats=464  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=403 Similarity=0.920412  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_4:552425-552551 Satlength=127 Nr of Repeats=9 RepeatLength=12  
 seed=TAGGCTTAGG Num.seqs=7 Similarity=0.788360  
 11 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_4:1076311-1076365 Satlength=55 Nr of Repeats=4  
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=3 Similarity=0.851852  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_4:1078257-1078305 Satlength=49 Nr of Repeats=4  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.888889  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_4:1370044-1370460 Satlength=417 Nr of Repeats=8  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=5 Similarity=0.822222  
 11 AG-GCTT-AGGCTT  
 Cele-UNSB01\_4:1508767-1509123 Satlength=357 Nr of Repeats=5  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.740741  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_4:1643155-1643244 Satlength=90 Nr of Repeats=6  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=4 Similarity=0.888889  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_4:1703835-1704045 Satlength=211 Nr of Repeats=11  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=7 Similarity=0.777778  
 2 AG-GCTT-AGGCTT

Rev.of\_Cele-UNSB01\_4:1766949-1767039 Satlength=91 Nr of Repeats=5  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=4 Similarity=0.796296  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_4:3176916-3177039 Satlength=124 Nr of Repeats=7  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=5 Similarity=0.755556  
 11 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_4:4053946-4054647 Satlength=702 Nr of Repeats=6  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=4 Similarity=0.759259  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_4:17755008-17759186 Satlength=4179 Nr of Repeats=342  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=305 Similarity=1.000000  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:4-5075 Satlength=5072 Nr of Repeats=419  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=386 Similarity=0.918190  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_5:1161256-1161400 Satlength=145 Nr of Repeats=10  
 RepeatLength=12 seed=GGCTTAGGCT Num.seqs=7 Similarity=0.814815  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:1174135-1174237 Satlength=103 Nr of Repeats=5  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=3 Similarity=0.851852  
 2 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:1262246-1262294 Satlength=49 Nr of Repeats=4  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=4 Similarity=0.944444  
 12 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:1265623-1265875 Satlength=253 Nr of Repeats=19  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=14 Similarity=0.804640  
 12 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:1271695-1271973 Satlength=279 Nr of Repeats=15  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=9 Similarity=0.836420  
 2 AG-GCTT-AGGCTT  
 Cele-UNSB01\_5:1278621-1278717 Satlength=97 Nr of Repeats=7  
 RepeatLength=12 seed=CTTAGGCTTA Num.seqs=6 Similarity=0.822222  
 9 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:1379498-1379672 Satlength=175 Nr of Repeats=13  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=11 Similarity=0.826263  
 2 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:1461442-1461802 Satlength=361 Nr of Repeats=24  
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=17 Similarity=0.861928  
 9 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:1519749-1519965 Satlength=217 Nr of Repeats=10  
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=7 Similarity=0.788360  
 11 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:2527844-2527991 Satlength=148 Nr of Repeats=6  
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=4 Similarity=0.833333  
 9 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:2661964-2662120 Satlength=157 Nr of Repeats=13  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=13 Similarity=0.839031  
 2 AG-GCTT-AGGCTT  
 Cele-UNSB01\_5:15757927-15757998 Satlength=72 Nr of Repeats=5  
 RepeatLength=12 seed=CTTAGGCTTA Num.seqs=3 Similarity=0.925926  
 9 AG-GCTT-AGGCTT  
 Cele-UNSB01\_5:18824768-18825020 Satlength=253 Nr of Repeats=16  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=10 Similarity=0.935802  
 12 AG-GCTT-AGGCTT

Rev.of\_Cele-UNSB01\_5:18839756-18840116 Satlength=361 Nr of Repeats=22  
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=15 Similarity=0.860317  
 11 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:18846370-18846628 Satlength=259 Nr of Repeats=18  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=13 Similarity=0.874644  
 13 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:18874657-18874753 Satlength=97 Nr of Repeats=6  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=4 Similarity=0.888889  
 2 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:18891023-18891077 Satlength=55 Nr of Repeats=4  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=3 Similarity=0.851852  
 13 AG-GCTT-AGGCTT  
 Cele-UNSB01\_5:18898055-18898199 Satlength=145 Nr of Repeats=9  
 RepeatLength=12 seed=GCTTAGGCTT Num.seqs=6 Similarity=0.925926  
 2 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:19521326-19521536 Satlength=211 Nr of Repeats=15  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=11 Similarity=0.818182  
 10 AG-GCTT-AGGCTT  
 Cele-UNSB01\_5:19815492-19815850 Satlength=359 Nr of Repeats=22  
 RepeatLength=12 seed=CTTAGGCTTA Num.seqs=15 Similarity=0.813757  
 9 AG-GCTT-AGGCTT  
 Cele-UNSB01\_5:19826165-19826303 Satlength=139 Nr of Repeats=11  
 RepeatLength=12 seed=CTTAGGCTTA Num.seqs=10 Similarity=0.938272  
 9 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_5:20111577-20111694 Satlength=118 Nr of Repeats=5  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=3 Similarity=0.851852  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_5:21238953-21243221 Satlength=4269 Nr of Repeats=353  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=315 Similarity=0.999295  
 10 AG-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_6:1-2653 Satlength=2653 Nr of Repeats=219  
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=188 Similarity=0.920213  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_6:2669709-2669769 Satlength=61 Nr of Repeats=5  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=5 Similarity=0.888889  
 12 AG-GCTT-AGGCTT  
 Cele-UNSB01\_6:18106897-18110840 Satlength=3944 Nr of Repeats=258  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=218 Similarity=0.919666  
 10 AG-GCTT-AGGCTT  
 Cele-UNSB01\_1:479600-479769 Satlength=170 Nr of Repeats=13  
 RepeatLength=12 seed=TAGGCTTAGG Num.seqs=8 Similarity=0.813492  
 11 AG-GCNT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:1018800-1018890 Satlength=91 Nr of Repeats=5  
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=3 Similarity=0.740741  
 11 AG-GCNT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:12396670-12396802 Satlength=133 Nr of Repeats=9  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=7 Similarity=0.767196  
 10 AG-GCTT-AGGCNT  
 Rev.of\_Cele-UNSB01\_2:2842834-2842918 Satlength=85 Nr of Repeats=6  
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=4 Similarity=0.754274  
 21 AG-GCTT-AGGCGT  
 Rev.of\_Cele-UNSB01\_4:4525521-4525683 Satlength=163 Nr of Repeats=12  
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=11 Similarity=0.751515  
 22 AG-GCTT-AGGCGT

Cele-UNSB01\_2:1233155-1233235 Satlength=81 Nr of Repeats=5  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=3 Similarity=0.925926  
 10 AG-GCTT-AGGTTT  
 Cele-UNSB01\_4:3670951-3671065 Satlength=115 Nr of Repeats=7  
 RepeatLength=12 seed=TTAGGCTTAG Num.seqs=5 Similarity=0.866667  
 10 AG-GCTT-AGGATT  
 Cele-UNSB01\_4:1647487-1647595 Satlength=109 Nr of Repeats=9  
 RepeatLength=12 seed=CTTAAGCTTA Num.seqs=9 Similarity=0.975309  
 9 AA-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_4:1908625-1908709 Satlength=85 Nr of Repeats=5  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=3 Similarity=0.851852  
 13 AA-GCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_4:3517707-3518097 Satlength=391 Nr of Repeats=27  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=21 Similarity=0.808059  
 13 AA-GCTT-AGGCTT  
 Cele-UNSB01\_5:376477-376531 Satlength=55 Nr of Repeats=4 RepeatLength=12  
 seed=AGGCTTAGGC Num.seqs=3 Similarity=1.000000  
 12 AG-GCTT-AGGCTA  
 Rev.of\_Cele-UNSB01\_2:4433247-4433329 Satlength=83 Nr of Repeats=4  
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=3 Similarity=0.925926  
 13 AG-TCTT-AGGCTT  
 Cele-UNSB01\_2:12381269-12381383 Satlength=115 Nr of Repeats=7  
 RepeatLength=12 seed=TTAGTCTTAG Num.seqs=5 Similarity=0.833333  
 22 AG-TCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_6:1555230-1555302 Satlength=73 Nr of Repeats=5  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=4 Similarity=0.851852  
 14 AG-TCTT-TGGCTT  
 Rev.of\_Cele-UNSB01\_2:2657840-2658242 Satlength=403 Nr of Repeats=31  
 RepeatLength=13 seed=TAAGCCTAAG Num.seqs=28 Similarity=0.872449  
 14 AGAGCTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:12200484-12200598 Satlength=115 Nr of Repeats=7  
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=5 Similarity=0.766667  
 2 AG-GTTT-AGGCTT  
 Cele-UNSB01\_4:13187743-13188346 Satlength=604 Nr of Repeats=12  
 RepeatLength=12 seed=GCTTGGGTTT Num.seqs=9 Similarity=0.907407  
 8 GG-GTTT-AGGCTT  
 Cele-UNSB01\_4:13187743-13188478 Satlength=736 Nr of Repeats=17  
 RepeatLength=12 seed=GCTTGGGTTT Num.seqs=11 Similarity=0.903030  
 8 GG-GTTT-AGGCTT  
 Rev.of\_Cele-UNSB01\_1:1680231-1680351 Satlength=121 Nr of Repeats=7  
 RepeatLength=12 seed=AGCCTAAACC Num.seqs=5 Similarity=0.702564  
 11 AG-GTTT-AGGCTC  
 Cele-UNSB01\_3:1312329-1312425 Satlength=97 Nr of Repeats=5  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=3 Similarity=0.925926  
 12 AG-GCTT-AGGCTC  
 Cele-UNSB01\_3:1320709-1320805 Satlength=97 Nr of Repeats=5  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=3 Similarity=0.925926  
 12 AG-GCTT-AGGCTC  
 Cele-UNSB01\_3:1329089-1329185 Satlength=97 Nr of Repeats=5  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=3 Similarity=0.925926  
 12 AG-GCTT-AGGCTC  
 Cele-UNSB01\_3:1843958-1844048 Satlength=91 Nr of Repeats=6  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.668803  
 12 AG-GCTT-AGGCTC



Cele-UNSB01\_5:1343973-1344069 Satlength=97 Nr of Repeats=7  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=5 Similarity=1.000000  
 12 AG-GCTT-AGGCTC  
 Rev.of\_Cele-UNSB01\_5:1872631-1872733 Satlength=103 Nr of Repeats=7  
 RepeatLength=12 seed=AGCCTGAGCC Num.seqs=5 Similarity=0.955556  
 17 AG-GCTT-AGGCTC  
 Cele-UNSB01\_5:2444425-2444473 Satlength=49 Nr of Repeats=4  
 RepeatLength=12 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.870370  
 12 AG-GCTT-AGGCTC  
 Rev.of\_Cele-UNSB01\_5:18856264-18856396 Satlength=133 Nr of Repeats=9  
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=7 Similarity=0.841270  
 23 AG-GCTT-AGGCTC  
 Cele-UNSB01\_1:11868010-11868741 Satlength=732 Nr of Repeats=60  
 RepeatLength=12 seed=AGGCTCAGGC Num.seqs=57 Similarity=0.962545  
 18 AG-GCTC-AGGCTC  
 Cele-UNSB01\_2:649028-649082 Satlength=55 Nr of Repeats=4 RepeatLength=12  
 seed=GGCTCAGGCT Num.seqs=3 Similarity=1.000000  
 19 AG-GCTC-AGGCTC  
 Rev.of\_Cele-UNSB01\_3:1738456-1739086 Satlength=631 Nr of Repeats=52  
 RepeatLength=12 seed=TGAGCCTGAG Num.seqs=51 Similarity=0.969848  
 19 AG-GCTC-AGGCTC  
 Rev.of\_Cele-UNSB01\_3:12087067-12087157 Satlength=91 Nr of Repeats=4  
 RepeatLength=12 seed=AGCCTGAGCC Num.seqs=3 Similarity=0.851852  
 23 AG-GCTC-AGGCTC  
 Cele-UNSB01\_5:18937116-18937194 Satlength=79 Nr of Repeats=6  
 RepeatLength=12 seed=GGCTCAGGCT Num.seqs=5 Similarity=0.955556  
 19 AG-GCTC-AGGCTC  
 Rev.of\_Cele-UNSB01\_5:18982935-18983047 Satlength=113 Nr of Repeats=7  
 RepeatLength=12 seed=AGCCTGAGCC Num.seqs=6 Similarity=1.000000  
 23 AG-GCTC-AGGCTC  
 Rev.of\_Cele-UNSB01\_5:19004973-19005085 Satlength=113 Nr of Repeats=7  
 RepeatLength=12 seed=AGCCTGAGCC Num.seqs=6 Similarity=1.000000  
 23 AG-GCTC-AGGCTC  
 Cele-UNSB01\_5:19517858-19518362 Satlength=505 Nr of Repeats=37  
 RepeatLength=12 seed=AGGCTCAGGC Num.seqs=32 Similarity=0.903226  
 18 AG-GCTC-AGGCTC  
 Cele-UNSB01\_2:13509974-13510060 Satlength=87 Nr of Repeats=6  
 RepeatLength=12 seed=CTTAGGCTTA Num.seqs=4 Similarity=0.743590  
 10 AG-GCTTAAGNCTT  
 Cele-UNSB01\_4:1800043-1800133 Satlength=91 Nr of Repeats=7  
 RepeatLength=12 seed=TTAGGATTAG Num.seqs=6 Similarity=0.962963  
 10 AG-GATT-AGGATT  
 Rev.of\_Cele-UNSB01\_1:11752079-11752337 Satlength=259 Nr of Repeats=16  
 RepeatLength=12 seed=AAGCCAAAGC Num.seqs=13 Similarity=0.854701  
 12 TG-GCTT-TGGCTT  
 Cele-UNSB01\_2:14148263-14148341 Satlength=79 Nr of Repeats=6  
 RepeatLength=12 seed=GGCTTTGGCT Num.seqs=5 Similarity=1.000000  
 19 TG-GCTT-TGGCTT  
 Rev.of\_Cele-UNSB01\_3:2564180-2564252 Satlength=73 Nr of Repeats=5  
 RepeatLength=12 seed=CCAAGCCCAA Num.seqs=3 Similarity=0.851852  
 20 GG-GCTT-GGGCTT  
 Cele-UNSB01\_5:20312857-20314295 Satlength=1439 Nr of Repeats=50  
 RepeatLength=12 seed=GCTTGGGCTT Num.seqs=36 Similarity=0.903704  
 20 GG-GCTT-GGGCTT

Rev.of\_Cele-UNSB01\_5:3739928-3740028 Satlength=101 Nr of Repeats=6  
 RepeatLength=10 seed=TAGCCATGCC Num.seqs=4 Similarity=0.933333  
 1 AG-GCAT--GGC-T  
 Rev.of\_Cele-UNSB01\_1:11239237-11239369 Satlength=133 Nr of Repeats=12  
 RepeatLength=11 seed=TATGCCTAGC Num.seqs=12 Similarity=1.000000  
 7 AG-GCAT-AGGC-T  
 Rev.of\_Cele-UNSB01\_2:1258661-1259567 Satlength=907 Nr of Repeats=73  
 RepeatLength=12 seed=CTATGCCTAT Num.seqs=70 Similarity=0.936416  
 14 AG-GCAT-AGGCAT  
 Rev.of\_Cele-UNSB01\_2:1261170-1261684 Satlength=515 Nr of Repeats=42  
 RepeatLength=12 seed=CTATGCCTAT Num.seqs=38 Similarity=0.936621  
 14 AG-GCAT-AGGCAT  
 Rev.of\_Cele-UNSB01\_2:1429641-1430207 Satlength=567 Nr of Repeats=41  
 RepeatLength=12 seed=CCTATGCCTA Num.seqs=30 Similarity=0.874585  
 21 AG-GCAT-AGGCAT  
 Cele-UNSB01\_2:2986853-2986937 Satlength=85 Nr of Repeats=7  
 RepeatLength=12 seed=ATAGGCATAG Num.seqs=7 Similarity=1.000000  
 22 AG-GCAT-AGGCAT  
 Cele-UNSB01\_2:14355758-14355994 Satlength=237 Nr of Repeats=18  
 RepeatLength=12 seed=ATAGGCATAG Num.seqs=11 Similarity=0.834343  
 22 AG-GCAT-AGGCAT  
 Cele-UNSB01\_3:12605711-12605849 Satlength=139 Nr of Repeats=9  
 RepeatLength=12 seed=TAGGCATAGG Num.seqs=6 Similarity=0.829630  
 23 AG-GCAT-AGGCAT  
 Cele-UNSB01\_4:1444044-1444098 Satlength=55 Nr of Repeats=4  
 RepeatLength=12 seed=CATAGGCATA Num.seqs=3 Similarity=0.925926  
 21 AG-GCAT-AGGCAT  
 Cele-UNSB01\_6:14452976-14453126 Satlength=151 Nr of Repeats=12  
 RepeatLength=12 seed=ATAGGCATAG Num.seqs=11 Similarity=0.979798  
 22 AG-GCAT-AGGCAT

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Consensus:

AGGCTTAGGCTT

>Cele-UNSB01\_Fam\_2\_35\_166 Nr. of seq. 166 Alignment length(with gaps) =  
 46 Alignment score = 0.624350  
 Cele-UNSB01\_2:11799205-11799469 Satlength=265 Nr of Repeats=8  
 RepeatLength=33 seed=AATTGAAAAT Num.seqs=8 Similarity=0.834055  
 0 AATT--G-AAA--A---TCCGGCAAATG--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_1:3888641-3889727 Satlength=1087 Nr of Repeats=26  
 RepeatLength=34 seed=TGCCGGAATT Num.seqs=16 Similarity=0.878105  
 28 AATT--G--AA--A-TTTCCAGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_2:5722242-5722548 Satlength=307 Nr of Repeats=9  
 RepeatLength=34 seed=GGAATTGAAA Num.seqs=9 Similarity=0.831481  
 32 AATT--G--AA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_2:15432049-15432695 Satlength=647 Nr of Repeats=18  
 RepeatLength=34 seed=TTTCAATTCC Num.seqs=13 Similarity=0.912016  
 42 AATT--G--AA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:1833347-1833868 Satlength=522 Nr of Repeats=14  
 RepeatLength=34 seed=AATTGAAATT Num.seqs=9 Similarity=0.808279  
 34 AATT--G--AA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-

Rev.of\_Cele-UNSB01\_3:11800186-11800737 Satlength=552 Nr of Repeats=15  
 RepeatLength=34 seed=AAATTTCAAT Num.seqs=10 Similarity=0.841394  
 45 AATT--G--AA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:13415830-13416475 Satlength=646 Nr of Repeats=18  
 RepeatLength=34 seed=CGGAATTGAA Num.seqs=15 Similarity=0.854715  
 65 AATT--G--AA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:12889217-12889593 Satlength=377 Nr of Repeats=11  
 RepeatLength=34 seed=TTTCAATTCC Num.seqs=7 Similarity=0.788982  
 42 AATT--G--AA--A-TTTCGGTAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:15023397-15024044 Satlength=648 Nr of Repeats=19  
 RepeatLength=34 seed=CGGAAATTTTC Num.seqs=18 Similarity=0.965142  
 48 AATT--G--AA--A-TTTCGGCAAATC--GGC-AAATTGCTG-G-  
 Cele-UNSB01\_2:15097668-15098195 Satlength=528 Nr of Repeats=13  
 RepeatLength=35 seed=TTTCGGCAA Num.seqs=8 Similarity=0.791837  
 77 AATT--GA-AA--A-TTTCGGCAAATC--GGC-AAATTGCTG-G-  
 Rev.of\_Cele-UNSB01\_4:388221-388493 Satlength=273 Nr of Repeats=8  
 RepeatLength=34 seed=TTGCAGGAAA Num.seqs=8 Similarity=0.823529  
 52 AATT--G--AA--A-TTTCCTGCAAACC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:786342-786547 Satlength=206 Nr of Repeats=6  
 RepeatLength=34 seed=CAATTTGCCG Num.seqs=5 Similarity=0.788235  
 64 AATT--G--AA--A-TTTCGGCAAACC--GGC-AAATTGCCG-A-  
 Rev.of\_Cele-UNSB01\_2:13192718-13192854 Satlength=137 Nr of Repeats=4  
 RepeatLength=34 seed=TTCAATTCCG Num.seqs=4 Similarity=0.803922  
 41 AATT--G--AA--A-TTTCGGCAAATC--GAC-GAATTGCCG-G-  
 Cele-UNSB01\_1:11268535-11268966 Satlength=432 Nr of Repeats=11  
 RepeatLength=34 seed=TTCCGGCAAA Num.seqs=9 Similarity=0.844227  
 43 AATT--T--AA--A-TTTCGGCAAATC--GGA-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:1031726-1032601 Satlength=876 Nr of Repeats=25  
 RepeatLength=35 seed=ATTTTCAATT Num.seqs=25 Similarity=0.921397  
 44 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAACTGCCG-G-  
 Cele-UNSB01\_1:1591838-1592129 Satlength=292 Nr of Repeats=7  
 RepeatLength=35 seed=CGGCAAATCG Num.seqs=6 Similarity=0.895873  
 47 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:1632570-1633118 Satlength=549 Nr of Repeats=6  
 RepeatLength=35 seed=AAATTTTCAA Num.seqs=5 Similarity=0.878095  
 81 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:1976543-1977056 Satlength=514 Nr of Repeats=5  
 RepeatLength=35 seed=TTTGCCGAA Num.seqs=3 Similarity=0.759259  
 54 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_1:2850958-2851167 Satlength=210 Nr of Repeats=5  
 RepeatLength=35 seed=GGAATTGAAA Num.seqs=3 Similarity=0.898413  
 67 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:11183622-11184094 Satlength=473 Nr of Repeats=10  
 RepeatLength=35 seed=TTGCCGATTT Num.seqs=6 Similarity=0.702469  
 61 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_2:12914019-12914481 Satlength=463 Nr of Repeats=11  
 RepeatLength=35 seed=TCAATTCCGG Num.seqs=10 Similarity=0.869630  
 75 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_2:13551182-13551985 Satlength=804 Nr of Repeats=20  
 RepeatLength=35 seed=GATTTGCCGG Num.seqs=15 Similarity=0.816490  
 56 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_2:14428274-14428974 Satlength=701 Nr of Repeats=18  
 RepeatLength=35 seed=GCAAATCGGC Num.seqs=14 Similarity=0.835060  
 49 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-

Rev.of\_Cele-UNSB01\_2:15354583-15354863 Satlength=281 Nr of Repeats=8  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=8 Similarity=0.858503  
 54 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:1204553-1205580 Satlength=1028 Nr of Repeats=13  
 RepeatLength=35 seed=TTTAAAATTT Num.seqs=8 Similarity=0.863946  
 71 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:1395088-1395322 Satlength=235 Nr of Repeats=5  
 RepeatLength=35 seed=CAAATCGGCA Num.seqs=3 Similarity=0.695238  
 50 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:2665588-2665980 Satlength=393 Nr of Repeats=11  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=7 Similarity=0.807710  
 54 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:3795055-3795458 Satlength=404 Nr of Repeats=8  
 RepeatLength=35 seed=TTCCGGCAAA Num.seqs=5 Similarity=0.760000  
 79 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:12120993-12121420 Satlength=428 Nr of Repeats=12  
 RepeatLength=35 seed=AATTGCCGGA Num.seqs=10 Similarity=0.840847  
 60 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:12712606-12713078 Satlength=473 Nr of Repeats=10  
 RepeatLength=35 seed=GATTTGCCGG Num.seqs=7 Similarity=0.791446  
 56 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:4169850-4170172 Satlength=323 Nr of Repeats=8  
 RepeatLength=35 seed=TTTCAATTCC Num.seqs=7 Similarity=0.885714  
 77 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_5:4696924-4697115 Satlength=192 Nr of Repeats=5  
 RepeatLength=35 seed=CGGCAAATCG Num.seqs=3 Similarity=0.479798  
 47 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_1:13236201-13236854 Satlength=654 Nr of Repeats=16  
 RepeatLength=35 seed=ATTGCCGGAA Num.seqs=10 Similarity=0.780741  
 61 AATT--G-AAA--A-TTTCGGCAAATC--GGN-AAATTGCCG-G-  
 Cele-UNSB01\_2:236549-238078 Satlength=1530 Nr of Repeats=40  
 RepeatLength=35 seed=TTTCGGCAA Num.seqs=27 Similarity=0.708272  
 78 AATT--G-AAA--A-TTTCGGCAAATC--GGC-ANATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:11990778-11991299 Satlength=522 Nr of Repeats=14  
 RepeatLength=35 seed=CCGATTGGCC Num.seqs=10 Similarity=0.809053  
 58 AATT--G-AAA--A-TTTCNGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:1415140-1415840 Satlength=701 Nr of Repeats=21  
 RepeatLength=35 seed=ATTTTCAATT Num.seqs=15 Similarity=0.700680  
 79 AATT--G-AAA--A-TTTCNGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:2441369-2441565 Satlength=197 Nr of Repeats=4  
 RepeatLength=35 seed=AAATTTTCAA Num.seqs=3 Similarity=0.780864  
 81 AATT--G-AAA--A-TTTCGGCNAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_2:14453377-14453692 Satlength=316 Nr of Repeats=8  
 RepeatLength=35 seed=CGGCAAATCG Num.seqs=7 Similarity=0.780864  
 47 AATT--G-NAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:4698132-4698369 Satlength=238 Nr of Repeats=5  
 RepeatLength=35 seed=CAATTCCGGC Num.seqs=3 Similarity=0.873016  
 74 AATT--G-TAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:1840655-1841028 Satlength=374 Nr of Repeats=9  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=8 Similarity=0.766700  
 54 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_2:15290141-15290702 Satlength=562 Nr of Repeats=16  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=11 Similarity=0.731650  
 54 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-

Rev.of\_Cele-UNSB01\_1:2169410-2169690 Satlength=281 Nr of Repeats=8  
 RepeatLength=35 seed=CGGCAAATTG Num.seqs=5 Similarity=0.878095  
 68 AATT--G-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:2619946-2620165 Satlength=220 Nr of Repeats=6  
 RepeatLength=35 seed=GCCGGAAATT Num.seqs=4 Similarity=0.752381  
 51 AATT--G-AAA--A-TTTCCGGCAAATC--GGG-AAATTGCCG-G-  
 Cele-UNSB01\_1:11556393-11558176 Satlength=1784 Nr of Repeats=47  
 RepeatLength=35 seed=GGCAAATCAG Num.seqs=42 Similarity=0.911023  
 48 AATT--G-AAA--A-TTTCCGGCAAATC--AGC-AAATTGCCG-G-  
 Cele-UNSB01\_2:13754985-13755264 Satlength=280 Nr of Repeats=7  
 RepeatLength=35 seed=TTGCCGGAAT Num.seqs=6 Similarity=0.784127  
 62 AATT--G-AAT--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:3737155-3737311 Satlength=157 Nr of Repeats=4  
 RepeatLength=35 seed=TTGCCGATTT Num.seqs=3 Similarity=0.784127  
 96 AATT--G-AAT--N-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_2:15286316-15286491 Satlength=176 Nr of Repeats=5  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.771429  
 54 AATT--N-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCN-G-  
 Rev.of\_Cele-UNSB01\_2:15454038-15454614 Satlength=577 Nr of Repeats=12  
 RepeatLength=35 seed=CCGATTTGCC Num.seqs=11 Similarity=0.807446  
 58 AATT--C-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:12547936-12548181 Satlength=246 Nr of Repeats=7  
 RepeatLength=35 seed=AATTGCCGGA Num.seqs=7 Similarity=0.912925  
 60 AATT--C-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:2911307-2911655 Satlength=349 Nr of Repeats=10  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=8 Similarity=0.859864  
 89 AATT--A-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:13188476-13189044 Satlength=569 Nr of Repeats=13  
 RepeatLength=35 seed=TGCCGGAATT Num.seqs=8 Similarity=0.817687  
 63 AATT--T-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_5:2608578-2609028 Satlength=451 Nr of Repeats=10  
 RepeatLength=35 seed=TTTCCGGCAA Num.seqs=7 Similarity=0.807710  
 78 AATT--T-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:13199796-13200258 Satlength=463 Nr of Repeats=10  
 RepeatLength=35 seed=GCCGGAAATT Num.seqs=7 Similarity=0.776871  
 51 AATT--N-ANA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:2587851-2588904 Satlength=1054 Nr of Repeats=15  
 RepeatLength=35 seed=TCAATTCCGG Num.seqs=10 Similarity=0.832381  
 75 AATT--G-AGA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_1:1910732-1911187 Satlength=456 Nr of Repeats=11  
 RepeatLength=35 seed=AAATCGGCAA Num.seqs=8 Similarity=0.753742  
 51 AATT--G-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-A-  
 Rev.of\_Cele-UNSB01\_2:13911573-13912594 Satlength=1022 Nr of Repeats=28  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=18 Similarity=0.750016  
 54 AATT--C-AAA--A-TTTCCGGCAAATC--GGC-AAATTGCCG-A-  
 Cele-UNSB01\_2:14462473-14462688 Satlength=216 Nr of Repeats=5  
 RepeatLength=35 seed=CGGCAAATTG Num.seqs=3 Similarity=0.586563  
 55 AATT--G-AAA--A-TTTCCGNNAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_4:1946817-1947132 Satlength=316 Nr of Repeats=8  
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=7 Similarity=0.927438  
 82 AATT--G-AAA--A-TTTCCGTCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:2195476-2195914 Satlength=439 Nr of Repeats=10  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=6 Similarity=0.735873  
 54 AATT--C-AAA--A-TTTCCGGCAAATC--GGC-AAATTGTTCG-G-

Cele-UNSB01\_1:13683275-13683450 Satlength=176 Nr of Repeats=5  
 RepeatLength=35 seed=TGAAAATTTTC Num.seqs=5 Similarity=0.878095  
 72 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGTCG-G-  
 Cele-UNSB01\_1:14869199-14869444 Satlength=246 Nr of Repeats=6  
 RepeatLength=35 seed=CAAATCGGCA Num.seqs=4 Similarity=0.733333  
 85 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGTCG-G-  
 Rev.of\_Cele-UNSB01\_3:2149341-2150059 Satlength=719 Nr of Repeats=12  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=10 Similarity=0.926349  
 89 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGTCG-G-  
 Rev.of\_Cele-UNSB01\_5:5114820-5115220 Satlength=401 Nr of Repeats=8  
 RepeatLength=35 seed=TTGCCGATTT Num.seqs=5 Similarity=0.767619  
 61 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGNCG-G-  
 Cele-UNSB01\_2:14458676-14459058 Satlength=383 Nr of Repeats=11  
 RepeatLength=35 seed=CCGGCAAATC Num.seqs=8 Similarity=0.757275  
 81 AATT--G-AAA--C-TTTCGGCAAATC--GGC-AAATTGGCG-G-  
 Cele-UNSB01\_3:12309471-12309813 Satlength=343 Nr of Repeats=8  
 RepeatLength=35 seed=GGAATTGAAA Num.seqs=5 Similarity=0.843810  
 102 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGGCG-G-  
 Cele-UNSB01\_5:15289065-15289259 Satlength=195 Nr of Repeats=6  
 RepeatLength=35 seed=GGAATTGAAA Num.seqs=4 Similarity=0.904762  
 102 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGGCG-G-  
 Rev.of\_Cele-UNSB01\_5:1860337-1860547 Satlength=211 Nr of Repeats=7  
 RepeatLength=35 seed=TCCGGCAATT Num.seqs=5 Similarity=0.833333  
 70 ATTT--N-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:15094323-15094532 Satlength=210 Nr of Repeats=6  
 RepeatLength=35 seed=TTTCAATTCC Num.seqs=5 Similarity=0.878095  
 77 AATT--G-AAA--G-TTTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_4:2909681-2910188 Satlength=508 Nr of Repeats=14  
 RepeatLength=35 seed=ATTCCGGCAA Num.seqs=11 Similarity=0.820606  
 107 AATT--G-AAA--A-TTTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_1:14731269-14731934 Satlength=666 Nr of Repeats=19  
 RepeatLength=35 seed=GAAAATTTCC Num.seqs=19 Similarity=0.939850  
 73 AATT--G-AAA--A-TTTCGGCAAACC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:12934390-12934631 Satlength=242 Nr of Repeats=8  
 RepeatLength=35 seed=TTTTAATTCC Num.seqs=6 Similarity=0.888254  
 77 AATT--A-AAA--A-TTTCGGCAAACC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:12996870-12997291 Satlength=422 Nr of Repeats=8  
 RepeatLength=35 seed=GGAAATTTTA Num.seqs=5 Similarity=0.820952  
 83 AATT--T-AAA--A-TTTCGGCAAACC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:4165711-4166017 Satlength=307 Nr of Repeats=5  
 RepeatLength=35 seed=AATTTTCAAT Num.seqs=4 Similarity=0.847619  
 80 AATT--G-AAA--A-TTTCGGCAAACC--GGC-AAATTGCAG-G-  
 Cele-UNSB01\_5:786696-786877 Satlength=182 Nr of Repeats=5 RepeatLength=35  
 seed=TTTCGGCAA Num.seqs=3 Similarity=0.834921  
 78 AATT--G-AAG--A-TTTCGGCAAACC--GGC-NAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:2780250-2780460 Satlength=211 Nr of Repeats=6  
 RepeatLength=35 seed=AATTTCAATT Num.seqs=6 Similarity=0.860317  
 44 AATT--G-AAA--T-TTTCGGCAAATC--GGC-AAGTTGCCG-G-  
 Cele-UNSB01\_1:11199905-11200227 Satlength=323 Nr of Repeats=8  
 RepeatLength=35 seed=GCCGGAATTG Num.seqs=7 Similarity=0.829478  
 64 AATT--G-AAA--T-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_2:13805325-13805605 Satlength=281 Nr of Repeats=7  
 RepeatLength=35 seed=CTTGCCGATT Num.seqs=6 Similarity=0.862857  
 62 AATT--G-AAA--A-TTCTGGCAAATC--GGC-AAGTTGCCG-G-

Cele-UNSB01\_4:3371888-3372867 Satlength=980 Nr of Repeats=27  
 RepeatLength=35 seed=AATCGGCAAG Num.seqs=25 Similarity=0.852698  
 87 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTACCG-G-  
 Cele-UNSB01\_3:12834918-12835593 Satlength=676 Nr of Repeats=18  
 RepeatLength=35 seed=TTTCGGCAA Num.seqs=13 Similarity=0.878877  
 78 AATT--G-AAC--A-TTTCGGCAAATC--GGT-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_4:3192518-3194426 Satlength=1909 Nr of Repeats=53  
 RepeatLength=35 seed=CGGCAATTTG Num.seqs=43 Similarity=0.870738  
 103 AATT--G-AAC--A-TTTCGGCAAATN--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_1:1103105-1103421 Satlength=317 Nr of Repeats=8  
 RepeatLength=35 seed=CGGCAATTCG Num.seqs=7 Similarity=0.873016  
 47 AATT--G-AAA--A-TTTCGGCAAATC--GGC-ATTTTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:1423918-1424416 Satlength=499 Nr of Repeats=9  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=6 Similarity=0.779048  
 54 AATT--G-AAA--A-TTTCGGCAAATC--CGC-AATTTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:18206252-18206609 Satlength=358 Nr of Repeats=5  
 RepeatLength=35 seed=AATTCCGGCA Num.seqs=3 Similarity=0.822222  
 73 AATT--G-AAA--A-TTTCGGCAAAC--GGC-ATATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:14038349-14038662 Satlength=314 Nr of Repeats=9  
 RepeatLength=35 seed=AATTCCGGCA Num.seqs=7 Similarity=0.756173  
 73 AATT--T-AAA--T-TTTCGGCAAATN--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:3152376-3152920 Satlength=545 Nr of Repeats=14  
 RepeatLength=35 seed=AATTGCCGGA Num.seqs=11 Similarity=0.843463  
 95 AATT--T-AAA--A-TTTCGGCAAATT--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:11452503-11452739 Satlength=237 Nr of Repeats=6  
 RepeatLength=35 seed=AATTGCCGGA Num.seqs=4 Similarity=0.720635  
 95 AATT--A-AAA--A-TTTCGGCAAATT--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:12227970-12228196 Satlength=227 Nr of Repeats=6  
 RepeatLength=35 seed=TTCCGGCAAA Num.seqs=4 Similarity=0.676190  
 114 AATT--G-AAA--A-TTTCGGCAAATT--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:2602720-2603297 Satlength=578 Nr of Repeats=16  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=10 Similarity=0.790053  
 124 AATT--G-AAA--A-TTTCGGCAAATT--GGC-AAATTGNCG-G-  
 Rev.of\_Cele-UNSB01\_1:11636321-11636670 Satlength=350 Nr of Repeats=9  
 RepeatLength=35 seed=ATTCCGGCAA Num.seqs=6 Similarity=0.888254  
 72 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:15062491-15062841 Satlength=351 Nr of Repeats=10  
 RepeatLength=35 seed=AATTCCGGCA Num.seqs=10 Similarity=0.804115  
 73 AATT--G-AAA--A-TTTCAGGAAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_2:13932545-13934837 Satlength=2293 Nr of Repeats=68  
 RepeatLength=35 seed=CCGGAATTGA Num.seqs=48 Similarity=0.862310  
 100 AATT--G-AAA--A-TTTCAGGAAAATC--GAC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:12229422-12230200 Satlength=779 Nr of Repeats=21  
 RepeatLength=35 seed=TTCAATTCCG Num.seqs=15 Similarity=0.834492  
 111 AATT--G-AAA--A-TTTCAGGAAAATC--GAC-AAATTGCCG-G-  
 Cele-UNSB01\_3:3159908-3160529 Satlength=622 Nr of Repeats=13  
 RepeatLength=35 seed=AAATCGGCAA Num.seqs=8 Similarity=0.885714  
 86 AATT--G-AAA--A-TTTCAGGAAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:3676441-3676612 Satlength=172 Nr of Repeats=5  
 RepeatLength=34 seed=AATTGAAATT Num.seqs=4 Similarity=0.800794  
 34 AATT--G--AA--A-TTTCGGCAAAGC--GGC-AAATTGTTCG-G-  
 Rev.of\_Cele-UNSB01\_1:3650776-3650949 Satlength=174 Nr of Repeats=5  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.822222  
 54 AATT--G--AAC-A-TTTCGGCAAACC--GGC-AAATTGTTCG-G-

Cele-UNSB01\_1:11393763-11394894 Satlength=1132 Nr of Repeats=15  
 RepeatLength=35 seed=TTCCGGCAAA Num.seqs=9 Similarity=0.743915  
 44 AACT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCN-G-  
 Cele-UNSB01\_3:11851795-11852785 Satlength=991 Nr of Repeats=24  
 RepeatLength=35 seed=CGGCAAATCG Num.seqs=16 Similarity=0.809524  
 47 AACT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCA-A-  
 Cele-UNSB01\_2:4361834-4362159 Satlength=326 Nr of Repeats=8  
 RepeatLength=35 seed=TTCCGGCAAA Num.seqs=5 Similarity=0.790476  
 44 AATT--G-AAA--A-TTTCGGCAAAC--GGC-AAATTGCCA-A-  
 Cele-UNSB01\_3:12593157-12594697 Satlength=1541 Nr of Repeats=44  
 RepeatLength=35 seed=TTGCCAGAAT Num.seqs=44 Similarity=0.791362  
 62 AATT--G-AAA--A-ATTCCGNAAATC--GGC-AAATTGCCA-G-  
 Rev.of\_Cele-UNSB01\_2:12900948-12901228 Satlength=281 Nr of Repeats=8  
 RepeatLength=35 seed=ATTTCCAGGCA Num.seqs=8 Similarity=0.791832  
 73 AAAT--G-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCCT-G-  
 Cele-UNSB01\_3:12308090-12308555 Satlength=466 Nr of Repeats=12  
 RepeatLength=35 seed=AAAATTTCCG Num.seqs=9 Similarity=0.868783  
 74 AATT--G-AAA--A-TTTCGGCAAATCA-GCT-AA-TTGCCA-G-  
 Rev.of\_Cele-UNSB01\_5:1308044-1308391 Satlength=348 Nr of Repeats=8  
 RepeatLength=35 seed=AATTCTGGCA Num.seqs=7 Similarity=0.902041  
 108 AATT--G-AAA--A-TTTCGGCAAATC--GGT-AAATTGCCA-G-  
 Rev.of\_Cele-UNSB01\_2:14003653-14004477 Satlength=825 Nr of Repeats=18  
 RepeatLength=34 seed=AATTCCGGCA Num.seqs=12 Similarity=0.808081  
 38 AATT--G--AA--A-TTTCGGATAAATC--AGC-AAATTGCCG-G-  
 Cele-UNSB01\_2:15007973-15008319 Satlength=347 Nr of Repeats=4  
 RepeatLength=35 seed=TCCGGCAAAT Num.seqs=3 Similarity=0.586420  
 45 AATT--T-ANA--A-TNTCCGGCAAATC--GGC-AAATTGCCG-A-  
 Cele-UNSB01\_5:20109112-20109540 Satlength=429 Nr of Repeats=12  
 RepeatLength=35 seed=AATTTCCGGC Num.seqs=11 Similarity=0.926580  
 76 AATT--T-AAA--A-TTTCGGCAAATC--GGC-AAATAACCG-G-  
 Cele-UNSB01\_5:4664068-4664530 Satlength=463 Nr of Repeats=10  
 RepeatLength=35 seed=GCAAATCGGC Num.seqs=6 Similarity=0.837460  
 15 -ATTC-G-AAA--A-TGTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:15014974-15015203 Satlength=230 Nr of Repeats=5  
 RepeatLength=34 seed=GAAATTTCAA Num.seqs=4 Similarity=0.901961  
 12 AGTT--G--AA--A-TTTCGGCAAATT--GGC-TAATTGCCG-G-  
 Cele-UNSB01\_2:14326178-14326688 Satlength=511 Nr of Repeats=14  
 RepeatLength=34 seed=CGGAATTGAA Num.seqs=13 Similarity=0.833082  
 31 AATT--G--AA--A-TTTCGGCAAATT--GGT-AAAATGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:12836433-12837192 Satlength=760 Nr of Repeats=21  
 RepeatLength=34 seed=TTTCAATTCC Num.seqs=15 Similarity=0.747664  
 42 AATT--G--AA--A-NTTCCGGCAAATT--GGT-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:134796-135400 Satlength=605 Nr of Repeats=7  
 RepeatLength=34 seed=AATTCCGGCA Num.seqs=5 Similarity=0.976471  
 38 AATT--G--AA--A-TTTTTGGCAAATT--GGT-AAATTGCCG-G-  
 Cele-UNSB01\_4:1362949-1363282 Satlength=334 Nr of Repeats=9  
 RepeatLength=34 seed=ATTGCCGGAA Num.seqs=7 Similarity=0.886088  
 60 AATT--G--AA--A-TTTCGGCAAATT--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_3:10787273-10787444 Satlength=172 Nr of Repeats=5  
 RepeatLength=34 seed=TTTCGGCAA Num.seqs=4 Similarity=0.819841  
 42 AATC--A--AA--A-TTTCGGCAAATT--GAC-AAATTGCCG-G-  
 Cele-UNSB01\_5:3674779-3675094 Satlength=316 Nr of Repeats=9  
 RepeatLength=35 seed=AAAATTTCCG Num.seqs=9 Similarity=0.834921  
 5 AATT--G-AAA--A-TTTCGGCAAA-C-AGGC-AAATTTCTG-G-



Cele-UNSB01\_1:2599082-2599291 Satlength=210 Nr of Repeats=6  
 RepeatLength=35 seed=TTGCCGGAAT Num.seqs=5 Similarity=0.794286  
 28 AATT--G-AAA--A-TTTTTGGNAAATC--GGC-AATTTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:2886442-2886617 Satlength=176 Nr of Repeats=4  
 RepeatLength=35 seed=TTTGCCGATT Num.seqs=3 Similarity=0.733333  
 28 AATT--A-AAA--A-TTTTTGNCAAATC--GGC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:1274939-1275298 Satlength=360 Nr of Repeats=10  
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=8 Similarity=0.842177  
 48 AATT--G-AAA--A-TTCTGGCAATTT--GGC-AATTTGCCG-G-  
 Cele-UNSB01\_2:10844890-10845587 Satlength=698 Nr of Repeats=8  
 RepeatLength=35 seed=TTTCTGGCAA Num.seqs=5 Similarity=0.900952  
 44 AAAT--T-AAA--A-TTCTGGCAAACC--GGC-AATTTGCCG-A-  
 Cele-UNSB01\_3:12644803-12645326 Satlength=524 Nr of Repeats=7  
 RepeatLength=35 seed=TTGCCGGAAT Num.seqs=5 Similarity=0.729630  
 63 AATT--G-NAA--A-TTCTGGCAAACC--GGC-AATTTGCCG-G-  
 Cele-UNSB01\_2:15454990-15455468 Satlength=479 Nr of Repeats=9  
 RepeatLength=35 seed=TTGCCGGAAT Num.seqs=6 Similarity=0.740952  
 63 AATT--T-AAA--A-TTCTGGCAAACC--GCC-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:3070958-3071149 Satlength=192 Nr of Repeats=5  
 RepeatLength=35 seed=TTGCCGAAA Num.seqs=3 Similarity=0.808642  
 54 AATT-AC-AA---A-TTCCGGCAAATC--GGC-AATTTGTCTG-G-  
 Cele-UNSB01\_5:18261348-18261785 Satlength=438 Nr of Repeats=10  
 RepeatLength=35 seed=TTTCCGGCAA Num.seqs=6 Similarity=0.790432  
 80 AATT-TG-AA---AGTTTCCGGCAAATC--GGC-ATTTTGCCG-G-  
 Rev.of\_Cele-UNSB01\_1:3156606-3157000 Satlength=395 Nr of Repeats=8  
 RepeatLength=35 seed=CGATTTGCCG Num.seqs=6 Similarity=0.862857  
 58 AAAT--G-AAT--A-TTCCGGCAAATC--GGC-AGTTTGCCG-G-  
 Cele-UNSB01\_3:11614727-11615007 Satlength=281 Nr of Repeats=6  
 RepeatLength=35 seed=TTGCCGGATT Num.seqs=4 Similarity=0.815873  
 63 ATTG--G-AAT--A-TTTTCGGCAAATC--GGC-AATTTGCCG-G-  
 Rev.of\_Cele-UNSB01\_3:11612201-11612410 Satlength=210 Nr of Repeats=6  
 RepeatLength=35 seed=GATTTGCCGG Num.seqs=5 Similarity=0.850926  
 22 ATTT----TAA-TA-TTCCGGCAAATC--GAT-AAATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:4422681-4422875 Satlength=195 Nr of Repeats=5  
 RepeatLength=35 seed=ATTCCGGCAA Num.seqs=3 Similarity=0.822222  
 38 AATT----TAA-TA-GTTCCGGCAAATC--GGC-AAATTGCCG-G-  
 Cele-UNSB01\_5:20072393-20073779 Satlength=1387 Nr of Repeats=40  
 RepeatLength=35 seed=CCGGCAAATC Num.seqs=26 Similarity=0.887707  
 47 ATTT--G-TAA--A-TTCCGGCAAATC--GAN-AAATTACCG-G-  
 Rev.of\_Cele-UNSB01\_4:2889237-2889839 Satlength=603 Nr of Repeats=7  
 RepeatLength=35 seed=TTTTCAATTC Num.seqs=5 Similarity=0.801905  
 9 AATT--G-AAA--A-ATTCAGGCAAATC--TGC-AAATTGCTT-G-  
 Rev.of\_Cele-UNSB01\_5:3735730-3736160 Satlength=431 Nr of Repeats=4  
 RepeatLength=35 seed=GCCGATTTGC Num.seqs=3 Similarity=0.743827  
 25 ANTT--G-AAC--A-TTTCAGGCAAATC--GGC-AAATTGNCA-G-  
 Cele-UNSB01\_1:1234705-1235262 Satlength=558 Nr of Repeats=15  
 RepeatLength=35 seed=AAATCGGCAA Num.seqs=12 Similarity=0.802020  
 17 AAAT--G-AAA--G-ATTCCGGCAAATC--GGC-AATTTGCCN-A-  
 Rev.of\_Cele-UNSB01\_1:1946077-1948348 Satlength=2272 Nr of Repeats=60  
 RepeatLength=35 seed=TTGCCGATTT Num.seqs=44 Similarity=0.891070  
 27 AAAT--G-AAA--A-TTCCGGCAAATC--GGC-AATTTGCNA-A-  
 Cele-UNSB01\_5:4162356-4162767 Satlength=412 Nr of Repeats=11  
 RepeatLength=35 seed=TTCCGGCAAA Num.seqs=7 Similarity=0.865760  
 45 AAAT--G-AAA--A-TTCCGGCAAACC--GGC-AATTTGCCA-A-

Rev.of\_Cele-UNSB01\_3:11723112-11723392 Satlength=281 Nr of Repeats=6  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=4 Similarity=0.790476  
 55 AAAT--C-AAA--A-TTTCGGCAAATC--GGC-AATTTGCCA-G-  
 Cele-UNSB01\_3:13127780-13127920 Satlength=141 Nr of Repeats=4  
 RepeatLength=35 seed=CGGCAATTTG Num.seqs=4 Similarity=0.936508  
 56 AAAT--C-AAA--A-TTTCGGCAAATC--GGC-AATTTGCCA-A-  
 Rev.of\_Cele-UNSB01\_5:1427061-1427411 Satlength=351 Nr of Repeats=8  
 RepeatLength=35 seed=TGCCGGAAAT Num.seqs=5 Similarity=0.790476  
 88 AAAT--C-AAA--A-TTTCGGCAAATC--GGC-AATTTGCCA-A-  
 Rev.of\_Cele-UNSB01\_3:13026111-13026534 Satlength=424 Nr of Repeats=13  
 RepeatLength=35 seed=AAATTTTGAT Num.seqs=9 Similarity=0.900529  
 82 AAAT--C-AAA--A-TTTCGGCAAATC--GGC-AAATTGCCA-A-  
 Cele-UNSB01\_4:1669669-1669879 Satlength=211 Nr of Repeats=6  
 RepeatLength=35 seed=ATTTCCGGCA Num.seqs=6 Similarity=0.819683  
 43 AAAT--G-AAA--A-TTTCGGCAAATC--GGC-AATATGCCG-A-  
 Cele-UNSB01\_4:16653889-16654239 Satlength=351 Nr of Repeats=10  
 RepeatLength=35 seed=CAAATCGGCA Num.seqs=8 Similarity=0.824490  
 51 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AATATGCCA-A-  
 Cele-UNSB01\_4:16659843-16660088 Satlength=246 Nr of Repeats=7  
 RepeatLength=35 seed=GCAAATCGGC Num.seqs=7 Similarity=0.842177  
 85 AATT--G-AAA--A-TTTCGGCAAATC--GGC-AATATGCCA-A-  
 Rev.of\_Cele-UNSB01\_4:16658516-16659248 Satlength=733 Nr of Repeats=21  
 RepeatLength=35 seed=TTTGGCATAT Num.seqs=16 Similarity=0.860000  
 71 AATT--G-AAA--T-TTTCGGCAAATC--GGC-AATATGCCA-A-  
 Rev.of\_Cele-UNSB01\_5:5204356-5204779 Satlength=424 Nr of Repeats=9  
 RepeatLength=35 seed=CGATTTGCCG Num.seqs=6 Similarity=0.576768  
 58 AAAT--A-AAA--A-TTTCGGCAAATC--GGC-AATTTGCC-GA-  
 Cele-UNSB01\_6:229151-229455 Satlength=305 Nr of Repeats=8 RepeatLength=36  
 seed=ATAAAAAATTT Num.seqs=7 Similarity=0.865961  
 73 AAAT--A-AAA--A-TTTCGGCAAATC--GGC-AATTTGCCAGA-  
 Rev.of\_Cele-UNSB01\_4:1309063-1309423 Satlength=361 Nr of Repeats=9  
 RepeatLength=36 seed=TTATTTTCTG Num.seqs=8 Similarity=0.838624  
 77 AAAT--A-AAA--A-TTTCGGCAAATG--GGC-AATTTGTCAGA-  
 Rev.of\_Cele-UNSB01\_4:1313914-1314237 Satlength=324 Nr of Repeats=8  
 RepeatLength=36 seed=TTTGCCGGAA Num.seqs=5 Similarity=0.859259  
 91 AAAT--A-AAA--A-TTTCGGCAAATC--GGC-AATTTGTCAGA-  
 Rev.of\_Cele-UNSB01\_1:1961569-1963172 Satlength=1604 Nr of Repeats=40  
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=33 Similarity=0.890620  
 48 AACT--G-AAA--A-TTTCGGCAAATC--GGC-AATTTGCCG-A-  
 Rev.of\_Cele-UNSB01\_1:1961569-1964216 Satlength=2648 Nr of Repeats=64  
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=47 Similarity=0.883388  
 48 AACT--G-AAA--A-TTTCGGCAAATC--GGC-AATTTGCCG-A-  
 Rev.of\_Cele-UNSB01\_1:1961569-1966139 Satlength=4571 Nr of Repeats=108  
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=73 Similarity=0.839524  
 48 AACT--G-AAA--A-TTTCNGGCAAATC--GGC-AATTTGCCG-A-  
 Rev.of\_Cele-UNSB01\_1:1961569-1968269 Satlength=6701 Nr of Repeats=154  
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=94 Similarity=0.828463  
 48 AACT--G-AAA--A-TTTCGGCAAATC--GGC-AATTTGCCG-A-  
 Rev.of\_Cele-UNSB01\_1:1980049-1980327 Satlength=279 Nr of Repeats=8  
 RepeatLength=35 seed=TTGCCGGAAA Num.seqs=6 Similarity=0.654655  
 54 AATT--G-AAC--A-TTTCGGCAAATC--GGC-AATTTGCCG-A-  
 Cele-UNSB01\_1:14694045-14694325 Satlength=281 Nr of Repeats=8  
 RepeatLength=35 seed=AAAATTTCCG Num.seqs=8 Similarity=0.952381  
 75 AAGT--G-AAA--A-TTTCGGCAAATC--GGC-AATTTACCG-A-

Rev.of\_Cele-UNSB01\_1:14697056-14704541 Satlength=7486 Nr of Repeats=214  
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=213 Similarity=0.929447  
 83 AAGT--G-AAA--A-TTTCCGGCAAATC--GGC-AATTTACCG-A-  
 Cele-UNSB01\_5:1987432-1987712 Satlength=281 Nr of Repeats=8  
 RepeatLength=35 seed=GGCAAATCGG Num.seqs=8 Similarity=0.914286  
 84 AAAT--G-AAA--A-TTTCCGGCAAATC--GGC-AATTTTCCG-A-  
 Rev.of\_Cele-UNSB01\_2:4637434-4637644 Satlength=211 Nr of Repeats=5  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=4 Similarity=0.757716  
 55 AAAT--G-AAA--T-TTTCCGGCAAATC--GGT-AATTTGCCG-A-  
 Rev.of\_Cele-UNSB01\_5:20105608-20107135 Satlength=1528 Nr of Repeats=40  
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=29 Similarity=0.756979  
 83 AAAT--G-AAA--A-TTTCCGGCAAATC--NGT-AATTTGCCG-A-  
 Rev.of\_Cele-UNSB01\_5:4118450-4118598 Satlength=149 Nr of Repeats=4  
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.682540  
 55 AAAT--N-AAA--A-TTTCCGGCAAAAC--GGC-AATTTACCA-A-  
 Cele-UNSB01\_1:11398081-11398840 Satlength=760 Nr of Repeats=4  
 RepeatLength=35 seed=TCGGCAAATT Num.seqs=3 Similarity=1.000000  
 20 AAAT--G-AAA--A-TTTCCGGCAAATC--GGC-AAATTACGG-A-  
 Rev.of\_Cele-UNSB01\_2:2547654-2548528 Satlength=875 Nr of Repeats=24  
 RepeatLength=35 seed=CCGGAAATTT Num.seqs=16 Similarity=0.798413  
 51 AAAT--G-AAA--A-TTTCCGGCAAATC--GGC-AAATCGCCG-A-  
 Rev.of\_Cele-UNSB01\_5:978655-978943 Satlength=289 Nr of Repeats=7  
 RepeatLength=35 seed=TGCCGATTG Num.seqs=5 Similarity=0.809524  
 26 AAAT--G-AAC--A-TTTCCGGCAAATC--GGC-AAATTCTCG-A-  
 Rev.of\_Cele-UNSB01\_2:13579229-13580664 Satlength=1436 Nr of Repeats=41  
 RepeatLength=35 seed=GAATTTTTGA Num.seqs=41 Similarity=0.852172  
 48 AAAT--C-AAA--A-ATTCCGGCAAATC--GGC-AAATTGCCG-A-  
 Rev.of\_Cele-UNSB01\_3:13035804-13036305 Satlength=502 Nr of Repeats=16  
 RepeatLength=35 seed=ATTTGCCGGA Num.seqs=10 Similarity=0.867936  
 56 AAAT--C-AAA--A-TTTCCGGCAAATC--GGC-ATATTGCCG-G-  
 Rev.of\_Cele-UNSB01\_5:5106861-5107246 Satlength=386 Nr of Repeats=10  
 RepeatLength=35 seed=TGCCGGAAAT Num.seqs=6 Similarity=0.730794  
 88 AAAT--C-AAA--A-TTTCCGGCAAATC--GGC-ATTTTGCCG-G-  
 Cele-UNSB01\_4:4418485-4418703 Satlength=219 Nr of Repeats=5  
 RepeatLength=35 seed=TTCCGGCAAA Num.seqs=3 Similarity=0.675676  
 45 AAAT--C-AGA--G-TTTCCGGCAAATC--GAC-AATTTGCCG-A-  
 Cele-UNSB01\_2:13844810-13844989 Satlength=180 Nr of Repeats=5  
 RepeatLength=36 seed=TTGCCTAAAA Num.seqs=4 Similarity=0.938272  
 29 AAAT--T-AAA--A-TTTCCGGCAAATC--AGCAAATTTGCCT-A-  
 Rev.of\_Cele-UNSB01\_4:1949645-1950620 Satlength=976 Nr of Repeats=28  
 RepeatLength=35 seed=CATTTTCGCC Num.seqs=22 Similarity=0.945083  
 40 AAAT--G-GAA--A-TTTCCGGCAAACC--GGC-AATTCGGCG-A-  
 Cele-UNSB01\_1:3506179-3506592 Satlength=414 Nr of Repeats=8  
 RepeatLength=35 seed=TCCGGCAAAT Num.seqs=5 Similarity=0.939048  
 46 AAGT--C-AAA--A-ATTCCGGCAAATC--GGA-AATCTGCCG-G-  
 Rev.of\_Cele-UNSB01\_4:4858228-4858874 Satlength=647 Nr of Repeats=17  
 RepeatLength=35 seed=TTGCCGGAAA Num.seqs=13 Similarity=0.909646  
 54 AAAC--C-AAA--A-TTTCCGGCAAATC--GGA-AACTTGCCG-G-  
 Cele-UNSB01\_1:2141918-2142329 Satlength=412 Nr of Repeats=7  
 RepeatLength=35 seed=CAAACCGGCA Num.seqs=5 Similarity=0.675926  
 15 AATT----AAC--A-TTTNGAGCAAACC--GGC-AANTTGCCG-AA

\* \*  
 Consensus:

AAATgAAAAATTTCCGGCAAATCGGCAAaTTGCCGg

>Cele-UNSB01\_Fam\_3\_15\_146 Nr. of seq. 146 Alignment length(with gaps) =  
15 Alignment score = 0.943142  
Cele-UNSB01\_1:224582-224687 Satlength=106 Nr of Repeats=5 RepeatLength=15  
seed=AGACCCATCG Num.seqs=4 Similarity=0.911111  
0 AGACCCATCGTGGTG  
Cele-UNSB01\_1:283314-284124 Satlength=811 Nr of Repeats=52  
RepeatLength=15 seed=TCGTGGTGAG Num.seqs=48 Similarity=0.862569  
7 AGACCCATCGTGGTG  
Cele-UNSB01\_1:698928-699108 Satlength=181 Nr of Repeats=12  
RepeatLength=15 seed=GGTGAGACCC Num.seqs=12 Similarity=0.900337  
11 AGACCCATCGTGGTG  
Rev.of\_Cele-UNSB01\_1:4695896-4696451 Satlength=556 Nr of Repeats=34  
RepeatLength=15 seed=GGGTCTCACC Num.seqs=31 Similarity=0.896583  
6 AGACCCATCGTGGTG  
Cele-UNSB01\_1:8014213-8014468 Satlength=256 Nr of Repeats=17  
RepeatLength=15 seed=ACCCATCGTG Num.seqs=17 Similarity=0.847712  
2 AGACCCATCGTGGTG  
Rev.of\_Cele-UNSB01\_1:9977112-9977772 Satlength=661 Nr of Repeats=41  
RepeatLength=15 seed=CACGATGGGT Num.seqs=38 Similarity=0.852821  
12 AGACCCATCGTGGTG  
Cele-UNSB01\_1:11351419-11351614 Satlength=196 Nr of Repeats=13  
RepeatLength=15 seed=TCGTGGTGAG Num.seqs=13 Similarity=0.842735  
7 AGACCCATCGTGGTG  
Cele-UNSB01\_1:11691383-11691503 Satlength=121 Nr of Repeats=8  
RepeatLength=15 seed=TCGTGGTGAG Num.seqs=8 Similarity=0.930159  
7 AGACCCATCGTGGTG  
Rev.of\_Cele-UNSB01\_2:454595-455440 Satlength=846 Nr of Repeats=32  
RepeatLength=15 seed=TCTCACCACG Num.seqs=30 Similarity=0.884138  
3 AGACCCATCGTGGTG  
Rev.of\_Cele-UNSB01\_2:636908-637328 Satlength=421 Nr of Repeats=27  
RepeatLength=15 seed=GGGTCTCACC Num.seqs=26 Similarity=0.898256  
6 AGACCCATCGTGGTG  
Cele-UNSB01\_2:698255-706115 Satlength=7861 Nr of Repeats=432  
RepeatLength=15 seed=GGTGAGACCC Num.seqs=346 Similarity=0.920561  
11 AGACCCATCGTGGTG  
Cele-UNSB01\_2:698255-706481 Satlength=8227 Nr of Repeats=433  
RepeatLength=15 seed=GGTGAGACCC Num.seqs=346 Similarity=0.920561  
11 AGACCCATCGTGGTG  
Cele-UNSB01\_2:1044642-1047492 Satlength=2851 Nr of Repeats=181  
RepeatLength=15 seed=TCGTGGTGAG Num.seqs=173 Similarity=0.911565  
7 AGACCCATCGTGGTG  
Cele-UNSB01\_2:3406743-3406803 Satlength=61 Nr of Repeats=4  
RepeatLength=15 seed=GGTGAGACCC Num.seqs=4 Similarity=0.911111  
11 AGACCCATCGTGGTG  
Cele-UNSB01\_2:4751413-4751956 Satlength=544 Nr of Repeats=21  
RepeatLength=15 seed=TGGTGAGACC Num.seqs=13 Similarity=0.879202  
10 AGACCCATCGTGGTG  
Rev.of\_Cele-UNSB01\_2:8586336-8586411 Satlength=76 Nr of Repeats=4  
RepeatLength=15 seed=GGGTCTCACC Num.seqs=3 Similarity=0.822222  
6 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_2:9765369-9765639 Satlength=271 Nr of Repeats=17  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=16 Similarity=0.891852  
 13 AGACCCATCGTGGTG  
 Cele-UNSB01\_2:12792220-12794215 Satlength=1996 Nr of Repeats=131  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=129 Similarity=0.876421  
 7 AGACCCATCGTGGTG  
 Cele-UNSB01\_2:15064232-15064367 Satlength=136 Nr of Repeats=9  
 RepeatLength=15 seed=AGACCCATCG Num.seqs=9 Similarity=0.881481  
 0 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_2:15106134-15106254 Satlength=121 Nr of Repeats=7  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=6 Similarity=0.881481  
 13 AGACCCATCGTGGTG  
 Cele-UNSB01\_2:15221118-15221238 Satlength=121 Nr of Repeats=8  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=8 Similarity=0.926984  
 11 AGACCCATCGTGGTG  
 Cele-UNSB01\_2:15224452-15224572 Satlength=121 Nr of Repeats=8  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=8 Similarity=0.926984  
 11 AGACCCATCGTGGTG  
 Cele-UNSB01\_2:15229801-15229921 Satlength=121 Nr of Repeats=8  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=8 Similarity=0.926984  
 11 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_3:2621291-2621771 Satlength=481 Nr of Repeats=29  
 RepeatLength=15 seed=GGTCTCACCA Num.seqs=26 Similarity=0.920957  
 5 AGACCCATCGTGGTG  
 Cele-UNSB01\_3:4030293-4031043 Satlength=751 Nr of Repeats=50  
 RepeatLength=15 seed=CGTGGTGAGA Num.seqs=50 Similarity=0.939483  
 8 AGACCCATCGTGGTG  
 Cele-UNSB01\_3:8580701-8581151 Satlength=451 Nr of Repeats=29  
 RepeatLength=15 seed=ACCCATCGTG Num.seqs=28 Similarity=0.904762  
 2 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_3:13765752-13765977 Satlength=226 Nr of Repeats=15  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=15 Similarity=0.930582  
 13 AGACCCATCGTGGTG  
 Cele-UNSB01\_3:14063373-14064273 Satlength=901 Nr of Repeats=60  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=60 Similarity=0.880778  
 7 AGACCCATCGTGGTG  
 Cele-UNSB01\_4:287372-287852 Satlength=481 Nr of Repeats=32  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=32 Similarity=0.882258  
 7 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:1161180-1161420 Satlength=241 Nr of Repeats=16  
 RepeatLength=15 seed=GGTCTCACCA Num.seqs=16 Similarity=0.880741  
 5 AGACCCATCGTGGTG  
 Cele-UNSB01\_4:1454445-1454610 Satlength=166 Nr of Repeats=11  
 RepeatLength=15 seed=AGACCCATCG Num.seqs=11 Similarity=0.880404  
 0 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:2119001-2119076 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=5 Similarity=0.840000  
 6 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:2267683-2267908 Satlength=226 Nr of Repeats=15  
 RepeatLength=15 seed=CGATGGGTCT Num.seqs=15 Similarity=0.914497  
 10 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:3090317-3090467 Satlength=151 Nr of Repeats=8  
 RepeatLength=15 seed=CACGATGGGT Num.seqs=7 Similarity=0.843386  
 12 AGACCCATCGTGGTG

Cele-UNSB01\_4:3733029-3733089 Satlength=61 Nr of Repeats=4  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=4 Similarity=0.940741  
 7 AGACCCATCGTGGTG

Cele-UNSB01\_4:4963981-4964546 Satlength=566 Nr of Repeats=18  
 RepeatLength=15 seed=GAGACCCATC Num.seqs=15 Similarity=0.903492  
 14 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:4987504-4988044 Satlength=541 Nr of Repeats=32  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=28 Similarity=0.940506  
 6 AGACCCATCGTGGTG

Cele-UNSB01\_4:4988071-4988281 Satlength=211 Nr of Repeats=14  
 RepeatLength=15 seed=ACCCATCGTG Num.seqs=14 Similarity=0.916972  
 2 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:4987504-4989222 Satlength=1719 Nr of Repeats=80  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=69 Similarity=0.943090  
 6 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:4990696-4991348 Satlength=653 Nr of Repeats=40  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=33 Similarity=0.951515  
 6 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:5521070-5521205 Satlength=136 Nr of Repeats=9  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=7 Similarity=0.898413  
 13 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:8107145-8107415 Satlength=271 Nr of Repeats=18  
 RepeatLength=15 seed=CTCACCACGA Num.seqs=18 Similarity=0.902977  
 2 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:8504495-8505035 Satlength=541 Nr of Repeats=35  
 RepeatLength=15 seed=TCTCACCACG Num.seqs=34 Similarity=0.956744  
 3 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:9125039-9126314 Satlength=1276 Nr of Repeats=76  
 RepeatLength=15 seed=CTCACCACGA Num.seqs=55 Similarity=0.889240  
 2 AGACCCATCGTGGTG

Cele-UNSB01\_4:10323949-10324337 Satlength=389 Nr of Repeats=26  
 RepeatLength=15 seed=GACCCATCGT Num.seqs=25 Similarity=0.898074  
 1 AGACCCATCGTGGTG

Cele-UNSB01\_4:13645449-13645792 Satlength=344 Nr of Repeats=22  
 RepeatLength=15 seed=ACCCATCGTG Num.seqs=19 Similarity=0.894997  
 2 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:14068578-14068998 Satlength=421 Nr of Repeats=24  
 RepeatLength=15 seed=ACGATGGGTC Num.seqs=21 Similarity=0.916191  
 11 AGACCCATCGTGGTG

Cele-UNSB01\_4:14106973-14107062 Satlength=90 Nr of Repeats=6  
 RepeatLength=15 seed=ACCCATCGTG Num.seqs=5 Similarity=0.946667  
 2 AGACCCATCGTGGTG

Cele-UNSB01\_4:14678232-14682258 Satlength=4027 Nr of Repeats=80  
 RepeatLength=15 seed=CGTGGTGAGA Num.seqs=64 Similarity=0.890917  
 8 AGACCCATCGTGGTG

Cele-UNSB01\_4:15313710-15313830 Satlength=121 Nr of Repeats=8  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=8 Similarity=0.930159  
 7 AGACCCATCGTGGTG

Cele-UNSB01\_4:15421750-15421870 Satlength=121 Nr of Repeats=8  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=8 Similarity=0.926984  
 11 AGACCCATCGTGGTG

Cele-UNSB01\_4:15554617-15554707 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=6 Similarity=0.887407  
 7 AGACCCATCGTGGTG

Rev.of\_Cele-UNSB01\_4:15608407-15609476 Satlength=1070 Nr of Repeats=51  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=44 Similarity=0.911299  
 13 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:16000962-16001082 Satlength=121 Nr of Repeats=8  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=8 Similarity=0.939683  
 6 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:16000985-16001240 Satlength=256 Nr of Repeats=17  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=17 Similarity=0.875163  
 13 AGACCCATCGTGGTG  
 Cele-UNSB01\_4:16061332-16061647 Satlength=316 Nr of Repeats=21  
 RepeatLength=15 seed=CCCATCGTGG Num.seqs=21 Similarity=0.916191  
 3 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:16220033-16221319 Satlength=1287 Nr of Repeats=15  
 RepeatLength=15 seed=CACGATGGGT Num.seqs=13 Similarity=0.863248  
 12 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:16709008-16709188 Satlength=181 Nr of Repeats=10  
 RepeatLength=15 seed=TGGGTCTCAC Num.seqs=8 Similarity=0.895238  
 7 AGACCCATCGTGGTG  
 Cele-UNSB01\_4:17138861-17138981 Satlength=121 Nr of Repeats=8  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=8 Similarity=0.866667  
 7 AGACCCATCGTGGTG  
 Cele-UNSB01\_4:17168764-17168899 Satlength=136 Nr of Repeats=9  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=9 Similarity=0.980247  
 7 AGACCCATCGTGGTG  
 Cele-UNSB01\_4:17401416-17402316 Satlength=901 Nr of Repeats=60  
 RepeatLength=15 seed=ACCCATCGTG Num.seqs=60 Similarity=0.889768  
 2 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:17408961-17409411 Satlength=451 Nr of Repeats=28  
 RepeatLength=15 seed=TCTCACCACG Num.seqs=25 Similarity=0.847111  
 3 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:1441948-1442263 Satlength=316 Nr of Repeats=21  
 RepeatLength=15 seed=CGATGGGTCT Num.seqs=21 Similarity=0.927196  
 10 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:2625951-2626161 Satlength=211 Nr of Repeats=14  
 RepeatLength=15 seed=CTCACCACGA Num.seqs=14 Similarity=0.840316  
 2 AGACCCATCGTGGTG  
 Cele-UNSB01\_5:3593686-3593761 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=CGTGGTGAGA Num.seqs=5 Similarity=0.840000  
 8 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:4989154-4989259 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=7 Similarity=0.898413  
 6 AGACCCATCGTGGTG  
 Cele-UNSB01\_5:6073958-6074258 Satlength=301 Nr of Repeats=20  
 RepeatLength=15 seed=ACCCATCGTG Num.seqs=20 Similarity=0.901287  
 2 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:6314778-6314883 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=7 Similarity=0.881481  
 6 AGACCCATCGTGGTG  
 Cele-UNSB01\_5:6605586-6605676 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=6 Similarity=0.917037  
 11 AGACCCATCGTGGTG  
 Cele-UNSB01\_5:6963686-6964031 Satlength=346 Nr of Repeats=23  
 RepeatLength=15 seed=AGACCCATCG Num.seqs=23 Similarity=0.901625  
 0 AGACCCATCGTGGTG

Cele-UNSB01\_5:6966476-6966776 Satlength=301 Nr of Repeats=20  
 RepeatLength=15 seed=AGACCCATCG Num.seqs=20 Similarity=0.894269  
 0 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:7958037-7958202 Satlength=166 Nr of Repeats=11  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=11 Similarity=0.877172  
 13 AGACCCATCGTGGTG  
 Cele-UNSB01\_5:7959905-7960085 Satlength=181 Nr of Repeats=11  
 RepeatLength=15 seed=ACCCATCGTG Num.seqs=10 Similarity=0.907161  
 2 AGACCCATCGTGGTG  
 Cele-UNSB01\_5:8372367-8372880 Satlength=514 Nr of Repeats=17  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=16 Similarity=0.932593  
 11 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:9479685-9479850 Satlength=166 Nr of Repeats=11  
 RepeatLength=15 seed=CGATGGGTCT Num.seqs=11 Similarity=0.899798  
 10 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:15445975-15447055 Satlength=1081 Nr of Repeats=72  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=70 Similarity=0.859308  
 13 AGACCCATCGTGGTG  
 Cele-UNSB01\_5:15725489-15725564 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=AGACCCATCG Num.seqs=5 Similarity=0.928889  
 0 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:180452-180557 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=GTCTCACCAC Num.seqs=7 Similarity=0.932275  
 4 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:188088-188493 Satlength=406 Nr of Repeats=27  
 RepeatLength=15 seed=ACGATGGGTC Num.seqs=27 Similarity=0.913897  
 11 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:983566-988244 Satlength=4679 Nr of Repeats=290  
 RepeatLength=15 seed=CACGATGGGT Num.seqs=284 Similarity=0.839014  
 12 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:1421556-1421900 Satlength=345 Nr of Repeats=23  
 RepeatLength=15 seed=CGATGGGTCT Num.seqs=22 Similarity=0.845695  
 10 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:2088902-2090459 Satlength=1558 Nr of Repeats=79  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=73 Similarity=0.860748  
 13 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:2088902-2090835 Satlength=1934 Nr of Repeats=85  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=78 Similarity=0.862715  
 13 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:3190243-3190348 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=TCACCACGAT Num.seqs=7 Similarity=0.923810  
 1 AGACCCATCGTGGTG  
 Cele-UNSB01\_6:5454734-5454854 Satlength=121 Nr of Repeats=8  
 RepeatLength=15 seed=TGGTGAGACC Num.seqs=8 Similarity=0.860317  
 10 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:14122652-14123413 Satlength=762 Nr of Repeats=19  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=15 Similarity=0.911958  
 6 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:16005217-16005457 Satlength=241 Nr of Repeats=15  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=14 Similarity=0.906227  
 6 AGACCCATCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:17225477-17225567 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=6 Similarity=0.922963  
 6 AGACCCATCGTGGTG



Rev.of\_Cele-UNSB01\_1:3435421-3440265 Satlength=4845 Nr of Repeats=323  
 RepeatLength=15 seed=CTCACCACGA Num.seqs=294 Similarity=0.881418  
 2 AGACCCNTCGTGGTG  
 Rev.of\_Cele-UNSB01\_2:15381973-15383739 Satlength=1767 Nr of Repeats=38  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=35 Similarity=0.915593  
 6 AGACCCNTCGTGGTG  
 Cele-UNSB01\_5:16414904-16415369 Satlength=466 Nr of Repeats=31  
 RepeatLength=15 seed=TGGTGAGACC Num.seqs=31 Similarity=0.865806  
 10 AGACCCNTCGTGGTG  
 Rev.of\_Cele-UNSB01\_6:12847168-12848031 Satlength=864 Nr of Repeats=10  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=9 Similarity=0.920988  
 6 AGACCCNTCGTGGTG  
 Cele-UNSB01\_1:6785229-6785394 Satlength=166 Nr of Repeats=11  
 RepeatLength=15 seed=GAGACCCATC Num.seqs=11 Similarity=0.883636  
 14 AGACCCATCGTGGCG  
 Rev.of\_Cele-UNSB01\_2:865003-865078 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=ATGGGTCTCG Num.seqs=3 Similarity=1.000000  
 23 AGACCCATCGTGGCG  
 Cele-UNSB01\_2:2017071-2017146 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCGTGGCGAG Num.seqs=5 Similarity=0.928889  
 22 AGACCCATCGTGGCG  
 Cele-UNSB01\_2:2403604-2403679 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCGTGGCGAG Num.seqs=5 Similarity=0.928889  
 22 AGACCCATCGTGGCG  
 Cele-UNSB01\_2:4751417-4751507 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=GAGACCCATC Num.seqs=6 Similarity=0.899259  
 14 AGACCCATCGTGGCG  
 Cele-UNSB01\_2:15219171-15219261 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=TCGTGGCGAG Num.seqs=6 Similarity=0.940741  
 22 AGACCCATCGTGGCG  
 Cele-UNSB01\_2:15242777-15242951 Satlength=175 Nr of Repeats=9  
 RepeatLength=15 seed=AGACCCATCG Num.seqs=8 Similarity=0.895238  
 15 AGACCCATCGTGGCG  
 Cele-UNSB01\_4:14030460-14031210 Satlength=751 Nr of Repeats=45  
 RepeatLength=15 seed=CCCATCGTGG Num.seqs=40 Similarity=0.901766  
 18 AGACCCATCGTGGCG  
 Cele-UNSB01\_4:15399620-15399800 Satlength=181 Nr of Repeats=11  
 RepeatLength=15 seed=GAGACCCATC Num.seqs=10 Similarity=0.917037  
 14 AGACCCATCGTGGCG  
 Cele-UNSB01\_5:6969386-6969716 Satlength=331 Nr of Repeats=22  
 RepeatLength=15 seed=AGACCCATCG Num.seqs=22 Similarity=0.899182  
 15 AGACCCATCGTGGCG  
 Rev.of\_Cele-UNSB01\_6:9867922-9867997 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=ATGGGTCTCG Num.seqs=3 Similarity=1.000000  
 23 AGACCCATCGTGGCG  
 Cele-UNSB01\_6:14688507-14688582 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCGTGGCGAG Num.seqs=5 Similarity=0.928889  
 22 AGACCCATCGTGGCG  
 Cele-UNSB01\_6:17686729-17686834 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=GAGACCCATC Num.seqs=7 Similarity=0.847619  
 14 AGACCCATCGTGGCG  
 Rev.of\_Cele-UNSB01\_4:1359612-1359777 Satlength=166 Nr of Repeats=11  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=11 Similarity=0.880404  
 28 AGACCCATCGTGGNG

Rev.of\_Cele-UNSB01\_4:9469814-9470654 Satlength=841 Nr of Repeats=56  
 RepeatLength=15 seed=ACGATGGGTC Num.seqs=56 Similarity=0.902684  
 26 AGACCCATCGTGGNG  
 Rev.of\_Cele-UNSB01\_4:13647491-13647701 Satlength=211 Nr of Repeats=14  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=14 Similarity=0.902320  
 28 AGACCCATCGTGGNG  
 Cele-UNSB01\_4:14678240-14678405 Satlength=166 Nr of Repeats=11  
 RepeatLength=15 seed=GACCCATCGT Num.seqs=11 Similarity=0.878788  
 16 AGACCCATCGTGGNG  
 Rev.of\_Cele-UNSB01\_6:556288-556934 Satlength=647 Nr of Repeats=15  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=14 Similarity=0.873016  
 28 AGACCCATCGTGGNG  
 Rev.of\_Cele-UNSB01\_6:5456777-5457242 Satlength=466 Nr of Repeats=31  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=27 Similarity=0.802469  
 28 AGACCCATCGTGGNG  
 Rev.of\_Cele-UNSB01\_1:14918515-14918575 Satlength=61 Nr of Repeats=4  
 RepeatLength=15 seed=CCACGATGGG Num.seqs=4 Similarity=0.881481  
 28 AGACCCATCGTGGAG  
 Cele-UNSB01\_1:4033028-4033133 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=7 Similarity=0.949206  
 7 AGACCCTTCGTGGTG  
 Cele-UNSB01\_1:5266039-5266863 Satlength=825 Nr of Repeats=51  
 RepeatLength=15 seed=CGTGGTGAGA Num.seqs=47 Similarity=0.827485  
 8 AGACCCTTCGTGGTG  
 Cele-UNSB01\_1:7886332-7886407 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=5 Similarity=0.911111  
 7 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_2:4325748-4326453 Satlength=706 Nr of Repeats=45  
 RepeatLength=15 seed=CTCACCACGA Num.seqs=40 Similarity=0.798251  
 17 AGACCCTTCGTGGTG  
 Cele-UNSB01\_2:9328143-9328548 Satlength=406 Nr of Repeats=27  
 RepeatLength=15 seed=TGGTGAGACC Num.seqs=25 Similarity=0.902519  
 10 AGACCCTTCGTGGTG  
 Cele-UNSB01\_2:15221118-15221591 Satlength=474 Nr of Repeats=14  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=12 Similarity=0.916498  
 11 AGACCCTTCGTGGTG  
 Cele-UNSB01\_2:15224452-15225368 Satlength=917 Nr of Repeats=26  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=22 Similarity=0.913805  
 11 AGACCCTTCGTGGTG  
 Cele-UNSB01\_2:15229801-15230289 Satlength=489 Nr of Repeats=15  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=13 Similarity=0.913390  
 11 AGACCCTTCGTGGTG  
 Cele-UNSB01\_2:15235758-15235848 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=6 Similarity=0.905185  
 11 AGACCCTTCGTGGTG  
 Cele-UNSB01\_3:1400275-1400335 Satlength=61 Nr of Repeats=4  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=4 Similarity=0.955556  
 7 AGACCCTTCGTGGTG  
 Cele-UNSB01\_3:3579672-3580411 Satlength=740 Nr of Repeats=47  
 RepeatLength=15 seed=GTGGTGAGAC Num.seqs=44 Similarity=0.837350  
 9 AGACCCTTCGTGGTG  
 Cele-UNSB01\_3:14059760-14060650 Satlength=891 Nr of Repeats=57  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=54 Similarity=0.868872  
 7 AGACCCTTCGTGGTG

Rev.of\_Cele-UNSB01\_4:1492099-1492204 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=CTCACCACGA Num.seqs=7 Similarity=0.873016  
 17 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:14417295-14419575 Satlength=2281 Nr of Repeats=148  
 RepeatLength=15 seed=CTCACCACGA Num.seqs=134 Similarity=0.914962  
 17 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:15284214-15284904 Satlength=691 Nr of Repeats=39  
 RepeatLength=15 seed=GGTCTCACC Num.seqs=32 Similarity=0.917921  
 20 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:15313385-15313490 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=7 Similarity=0.949206  
 21 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:16376935-16378753 Satlength=1819 Nr of Repeats=17  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=11 Similarity=0.935354  
 21 AGACCCTTCGTGGTG  
 Cele-UNSB01\_4:16402456-16402561 Satlength=106 Nr of Repeats=7  
 RepeatLength=15 seed=GTGGTGAGAC Num.seqs=7 Similarity=0.898413  
 9 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_4:16472875-16473271 Satlength=397 Nr of Repeats=25  
 RepeatLength=15 seed=TCTCACCACG Num.seqs=21 Similarity=0.820106  
 18 AGACCCTTCGTGGTG  
 Cele-UNSB01\_5:1289399-1289474 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=5 Similarity=0.911111  
 7 AGACCCTTCGTGGTG  
 Cele-UNSB01\_5:1289402-1291686 Satlength=2285 Nr of Repeats=44  
 RepeatLength=15 seed=TGGTGAGACC Num.seqs=41 Similarity=0.901138  
 10 AGACCCTTCGTGGTG  
 Cele-UNSB01\_5:4984650-4985356 Satlength=707 Nr of Repeats=46  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=38 Similarity=0.852948  
 7 AGACCCTTCGTGGTG  
 Cele-UNSB01\_5:5638035-5638095 Satlength=61 Nr of Repeats=4  
 RepeatLength=15 seed=CGTGGTGAGA Num.seqs=4 Similarity=0.911111  
 8 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:7764570-7764720 Satlength=151 Nr of Repeats=10  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=10 Similarity=0.934815  
 21 AGACCCTTCGTGGTG  
 Cele-UNSB01\_5:9642570-9642900 Satlength=331 Nr of Repeats=22  
 RepeatLength=15 seed=GGTGAGACCC Num.seqs=22 Similarity=0.929582  
 11 AGACCCTTCGTGGTG  
 Cele-UNSB01\_5:13979410-13979500 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=6 Similarity=0.857778  
 7 AGACCCTTCGTGGTG  
 Cele-UNSB01\_5:14226001-14226091 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=CGTGGTGAGA Num.seqs=6 Similarity=0.893333  
 8 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:14260478-14260568 Satlength=91 Nr of Repeats=6  
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=6 Similarity=0.917037  
 21 AGACCCTTCGTGGTG  
 Rev.of\_Cele-UNSB01\_5:15415879-15416665 Satlength=787 Nr of Repeats=8  
 RepeatLength=15 seed=TCTCACCACG Num.seqs=7 Similarity=0.923810  
 18 AGACCCTTCGTGGTG  
 Cele-UNSB01\_6:13887397-13887577 Satlength=181 Nr of Repeats=11  
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=10 Similarity=0.857778  
 7 AGACCCTTCGTGGTG

Rev.of\_Cele-UNSB01\_6:15851847-15853377 Satlength=1531 Nr of Repeats=97  
RepeatLength=15 seed=GTCTCACCAC Num.seqs=92 Similarity=0.888135  
19 AGACCCCTTCGTGGTG  
Rev.of\_Cele-UNSB01\_6:16876782-16877097 Satlength=316 Nr of Repeats=18  
RepeatLength=15 seed=TCACCACGAA Num.seqs=15 Similarity=0.947513  
16 AGACCCCTTCGTGGTG  
Cele-UNSB01\_6:14447847-14448957 Satlength=1111 Nr of Repeats=73  
RepeatLength=15 seed=TCGTGGTGAG Num.seqs=70 Similarity=0.770484  
7 AGACCTATCGTGGTG  
Cele-UNSB01\_1:309874-309994 Satlength=121 Nr of Repeats=7 RepeatLength=15  
seed=GAGACCCATC Num.seqs=6 Similarity=0.764583  
14 AGACCCATCGTGACG

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Consensus:

AGACCCaTCGTGGTG

>Cele-UNSB01\_Fam\_4\_35\_122 Nr. of seq. 122 Alignment length(with gaps) =  
43 Alignment score = 0.628454  
Cele-UNSB01\_1:1158888-1159076 Satlength=189 Nr of Repeats=5  
RepeatLength=31 seed=ATTCCCGCCA Num.seqs=3 Similarity=0.628472  
0 ATT--CCCGCC--AATT-----TTTT-CTCAGGAAATTTGA-  
Rev.of\_Cele-UNSB01\_3:1400394-1400521 Satlength=128 Nr of Repeats=4  
RepeatLength=31 seed=AATTCAAATT Num.seqs=3 Similarity=0.885305  
3 ATT--CCCGCC--AAAA-----TTTT-TTGAAGAAATTTGA-  
Cele-UNSB01\_4:6734929-6735237 Satlength=309 Nr of Repeats=9  
RepeatLength=31 seed=CCCGCCAAAA Num.seqs=7 Similarity=0.897593  
3 ATT--CCCGCC--AAAA-----TTTT-TTGAAAAAATTTGA-  
Rev.of\_Cele-UNSB01\_4:13661650-13661868 Satlength=219 Nr of Repeats=6  
RepeatLength=31 seed=AATTCAAATT Num.seqs=4 Similarity=0.942652  
3 ATT--CCCGCC--AAAA-----TTTT-TTGAGGAAATTTGA-  
Rev.of\_Cele-UNSB01\_5:19338537-19338764 Satlength=228 Nr of Repeats=7  
RepeatLength=33 seed=GGAATTCAAA Num.seqs=5 Similarity=0.967677  
6 AT-T-CCCGCC--AAAATT----TTTT-TTGAATAAATTTGA-  
Rev.of\_Cele-UNSB01\_3:12445241-12445717 Satlength=477 Nr of Repeats=10  
RepeatLength=32 seed=ATTCAAATTT Num.seqs=6 Similarity=0.602694  
34 ATT--TTCGCC--AAAA-N----TTTT-CTGAAGAAATTTGA-  
Cele-UNSB01\_4:17523613-17523740 Satlength=128 Nr of Repeats=4  
RepeatLength=32 seed=GAAGAAATTT Num.seqs=3 Similarity=0.861111  
52 ATT--TGCACC--AAAA-T----TTTT-CTGAAGAAATTTGA-  
Rev.of\_Cele-UNSB01\_1:671513-680928 Satlength=9416 Nr of Repeats=294  
RepeatLength=32 seed=GAATTCAAAT Num.seqs=192 Similarity=0.889807  
4 ATT-C-CCGCC--AAAA-T----TTTT-CTCAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_1:1386048-1386208 Satlength=161 Nr of Repeats=5  
RepeatLength=32 seed=AAAATTTTGG Num.seqs=5 Similarity=0.983333  
17 ATT-C-CCGCC--AAAA-T----TTTT-CTCAGAAAATTTGA-  
Cele-UNSB01\_4:15943206-15943656 Satlength=451 Nr of Repeats=14  
RepeatLength=32 seed=TTGAATTCCC Num.seqs=13 Similarity=0.905983  
28 ATT-C-CCGCC--AAAA-T----TTTT-CACAGAAAATTTGA-  
Cele-UNSB01\_5:4025406-4025890 Satlength=485 Nr of Repeats=15  
RepeatLength=32 seed=TTTCACAGAA Num.seqs=11 Similarity=0.921212  
47 ATT-C-CCGCC--AAAA-T----TTTT-CACAGAAAATTTGA-

Cele-UNSB01\_6:15068529-15068945 Satlength=417 Nr of Repeats=13  
RepeatLength=32 seed=TTGAATTCCC Num.seqs=13 Similarity=0.927885  
28 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Cele-UNSB01\_5:20304611-20305126 Satlength=516 Nr of Repeats=14  
RepeatLength=32 seed=AAATTTGAAT Num.seqs=9 Similarity=0.806958  
24 ATT-T-CCGCC--AAAA-T---TTTT-CTCAGAAAATTTGA-  
Cele-UNSB01\_1:13840435-13852243 Satlength=11809 Nr of Repeats=369  
RepeatLength=32 seed=TGAATTCCCG Num.seqs=365 Similarity=0.924622  
29 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_2:4623470-4624110 Satlength=641 Nr of Repeats=20  
RepeatLength=32 seed=CGGGAATTCA Num.seqs=20 Similarity=0.921491  
39 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_3:11461401-11461721 Satlength=321 Nr of Repeats=10  
RepeatLength=32 seed=TTTCTGTGAA Num.seqs=10 Similarity=0.896296  
58 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Cele-UNSB01\_4:8500583-8501255 Satlength=673 Nr of Repeats=21  
RepeatLength=32 seed=TTTTTCACAGA Num.seqs=21 Similarity=0.903571  
46 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_4:12150586-12159522 Satlength=8937 Nr of Repeats=274  
RepeatLength=32 seed=CGGGAATTCA Num.seqs=262 Similarity=0.923743  
39 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_5:3493344-3494338 Satlength=995 Nr of Repeats=31  
RepeatLength=32 seed=CGGGAATTCA Num.seqs=29 Similarity=0.920874  
39 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_6:9244298-9244938 Satlength=641 Nr of Repeats=20  
RepeatLength=32 seed=CGGGAATTCA Num.seqs=20 Similarity=0.894298  
39 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Cele-UNSB01\_6:15068534-15069086 Satlength=553 Nr of Repeats=16  
RepeatLength=32 seed=TTCCCGCCAA Num.seqs=11 Similarity=0.947727  
33 ATT-C-CCGCC--AAAA-T---TTTT-CACAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_5:7024350-7024712 Satlength=363 Nr of Repeats=11  
RepeatLength=32 seed=AATTCAAATT Num.seqs=7 Similarity=0.908730  
35 ATT-C-CCGCC--AAAA-T---TTTT-CACAAAAAATTTGA-  
Cele-UNSB01\_2:863874-864986 Satlength=1113 Nr of Repeats=34  
RepeatLength=32 seed=AATTCCCGCC Num.seqs=26 Similarity=0.854615  
31 ATT-C-CCGCC--AAAA-A---TTTT-CAAAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_2:2017169-2017519 Satlength=351 Nr of Repeats=10  
RepeatLength=32 seed=GGCGGGAATT Num.seqs=7 Similarity=0.843675  
41 ATT-C-CCGCC--AAAA-A---TTTT-CAAAGAAAATTTGA-  
Cele-UNSB01\_6:9866116-9867908 Satlength=1793 Nr of Repeats=48  
RepeatLength=32 seed=TCCCGCCAAA Num.seqs=33 Similarity=0.845249  
34 ATT-C-CCGCC--AAAA-A---TTTT-CAAAGAAAATTTGA-  
Cele-UNSB01\_2:1991206-1991967 Satlength=762 Nr of Repeats=23  
RepeatLength=32 seed=AATTCCCGCC Num.seqs=16 Similarity=0.855208  
31 ATT-C-CCGCC--AAAA-A---TTTT-CANAGAAAATTTGA-  
Cele-UNSB01\_2:2000093-2000918 Satlength=826 Nr of Repeats=25  
RepeatLength=32 seed=AATTCCCGCC Num.seqs=18 Similarity=0.865196  
31 ATT-C-CCGCC--AAAA-A---TTTT-CANAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_2:15219280-15219502 Satlength=223 Nr of Repeats=7  
RepeatLength=32 seed=TTTTGGCGGG Num.seqs=5 Similarity=0.841667  
45 ATT-C-CCGCC--AAAA-A---TTTT-CANAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_2:15221267-15222837 Satlength=1571 Nr of Repeats=42  
RepeatLength=32 seed=TTTTGGCGGG Num.seqs=27 Similarity=0.855679  
45 ATT-C-CCGCC--AAAA-A---TTTT-CANAGAAAATTTGA-

Rev.of\_Cele-UNSB01\_2:15224601-15228185 Satlength=3585 Nr of Repeats=96  
 RepeatLength=32 seed=TTTTGGCGGG Num.seqs=67 Similarity=0.850591  
 45 ATT-C-CCGCC--AAAA-A---TTTT-CANAGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_2:15229950-15234144 Satlength=4195 Nr of Repeats=125  
 RepeatLength=32 seed=TTTTGGCGGG Num.seqs=93 Similarity=0.859221  
 45 ATT-C-CCGCC--AAAA-A---TTTT-CANAGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_6:14688602-14689240 Satlength=639 Nr of Repeats=20  
 RepeatLength=32 seed=TTTGGCGGGA Num.seqs=15 Similarity=0.817027  
 44 ATT-C-CCGCC--AAAA-A---TTTT-CANAGAAAATTTGA-  
 Cele-UNSB01\_2:6532865-6533025 Satlength=161 Nr of Repeats=5  
 RepeatLength=32 seed=AAAAATTTTC Num.seqs=5 Similarity=0.916667  
 41 ATT-C-CCGCC--AAAA-A---TTTT-CACAGAAAATTTGA-  
 Cele-UNSB01\_2:6532865-6533618 Satlength=754 Nr of Repeats=6  
 RepeatLength=32 seed=AAAAATTTTC Num.seqs=5 Similarity=0.916667  
 41 ATT-C-CCGCC--AAAA-A---TTTT-CACAGAAAATTTGA-  
 Cele-UNSB01\_2:2625510-2625733 Satlength=224 Nr of Repeats=7  
 RepeatLength=32 seed=AATTCCCGCC Num.seqs=6 Similarity=0.855556  
 31 ATT-C-CCGCC--AAAA-A---ATTT-CAAAGAAAATTTAA-  
 Cele-UNSB01\_2:2625547-2626102 Satlength=556 Nr of Repeats=7  
 RepeatLength=32 seed=CCGCCAAAAA Num.seqs=5 Similarity=0.866667  
 36 ATT-C-CCGCC--AAAA-A---ATTT-CAAAGAAAATTTAA-  
 Cele-UNSB01\_1:927465-927693 Satlength=229 Nr of Repeats=6 RepeatLength=32  
 seed=GAAAATTTGA Num.seqs=4 Similarity=0.727941  
 22 ATT-C-CCGCC--AAAA-T---TTTT-CTTTGAAAATTTGA-  
 Cele-UNSB01\_5:20786599-20786882 Satlength=284 Nr of Repeats=9  
 RepeatLength=32 seed=CCGCCAAAAT Num.seqs=7 Similarity=0.853175  
 36 ATT-C-CCGCC--AAAA-T---TTTT-CTTTGAAAATTTGA-  
 Cele-UNSB01\_1:1012680-1013098 Satlength=419 Nr of Repeats=4  
 RepeatLength=32 seed=CAAAATTTTT Num.seqs=3 Similarity=0.888889  
 9 A-T-CGCCGCC--AAAA-T---TTTT-CTCAGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_5:18728400-18728559 Satlength=160 Nr of Repeats=4  
 RepeatLength=32 seed=GAATTCAAAT Num.seqs=3 Similarity=0.888889  
 4 ATT-C-ACGCC--AAAA-A---TTTT-TTCAGAAAATTTGA-  
 Cele-UNSB01\_2:14078695-14078860 Satlength=166 Nr of Repeats=5  
 RepeatLength=33 seed=AAAATTTGAA Num.seqs=5 Similarity=0.749495  
 24 ATT-TCCCGCC--AAAA-T---T-TTT-CTCAGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_5:1406535-1406737 Satlength=203 Nr of Repeats=6  
 RepeatLength=34 seed=AAATTCAAAT Num.seqs=5 Similarity=0.823529  
 37 ATT-TCCCGCC--AAAA-T---TATTT-CTCAGAAAATTTGA-  
 Cele-UNSB01\_1:768290-768741 Satlength=452 Nr of Repeats=13  
 RepeatLength=34 seed=TTTCTCAGAA Num.seqs=8 Similarity=0.787245  
 50 ATT-TCCCACC--AAAA-T---TTTTT-CTCAGAAAATTTGA-  
 Cele-UNSB01\_5:2665615-2665738 Satlength=124 Nr of Repeats=4  
 RepeatLength=35 seed=TTTCTCAGAA Num.seqs=3 Similarity=0.923810  
 51 ATT-TCCCGCC--AAAA-TG--TTTTT-CTCAGAAAATTTGA-  
 Cele-UNSB01\_3:12784240-12784411 Satlength=172 Nr of Repeats=5  
 RepeatLength=35 seed=AATTTGAATT Num.seqs=3 Similarity=0.923810  
 26 ATT-TCCCGCC--AAAA-T-CAT-TTT-CTGAGAAAATTTGA-  
 Cele-UNSB01\_2:1815608-1815814 Satlength=207 Nr of Repeats=6  
 RepeatLength=34 seed=ATTTGAATTT Num.seqs=4 Similarity=0.980392  
 27 ATT-TCCCGCC--AAAA---TTTTTT-CACTGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_2:1818966-1819342 Satlength=377 Nr of Repeats=11  
 RepeatLength=34 seed=CGGGAAATTC Num.seqs=9 Similarity=0.956427  
 41 ATT-TCCCGCC--AAAA---TTTTTT-CACTGAAAATTTGA-

Rev.of\_Cele-UNSB01\_2:15235864-15236243 Satlength=380 Nr of Repeats=11  
 RepeatLength=34 seed=TTGGCGGGAA Num.seqs=7 Similarity=0.880511  
 45 ATT-TCCCGCC--AAAA---TTTTTT-CACTGAAAATTGA-  
 Cele-UNSB01\_4:1358775-1359527 Satlength=753 Nr of Repeats=22  
 RepeatLength=34 seed=ATTTCCCGCC Num.seqs=18 Similarity=0.995643  
 33 ATT-TCCCGCC--AAAA---TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_4:15421887-15425906 Satlength=4020 Nr of Repeats=116  
 RepeatLength=34 seed=TGGCGGGAAA Num.seqs=83 Similarity=0.986125  
 44 ATT-TCCCGCC--AAAA---TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_5:10311486-10312622 Satlength=1137 Nr of Repeats=33  
 RepeatLength=34 seed=TTGGCGGGAA Num.seqs=20 Similarity=0.915765  
 45 ATT-TCCCGCC--AAAA---TTTTTT-CACTGAAAATTGA-  
 Cele-UNSB01\_1:1456315-1457241 Satlength=927 Nr of Repeats=24  
 RepeatLength=35 seed=AAATTTGAAT Num.seqs=15 Similarity=0.827628  
 60 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_1:7886430-7887346 Satlength=917 Nr of Repeats=26  
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=17 Similarity=0.870370  
 77 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_1:11691539-11692754 Satlength=1216 Nr of Repeats=24  
 RepeatLength=35 seed=TGGCGGGAAA Num.seqs=17 Similarity=0.860771  
 79 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_2:9328575-9329101 Satlength=527 Nr of Repeats=15  
 RepeatLength=35 seed=ATTCAAATTT Num.seqs=10 Similarity=0.900952  
 70 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_2:9328566-9329542 Satlength=977 Nr of Repeats=16  
 RepeatLength=35 seed=TGGCGGGAAA Num.seqs=10 Similarity=0.909418  
 79 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_4:1490085-1491772 Satlength=1688 Nr of Repeats=46  
 RepeatLength=35 seed=AAAAATTTT Num.seqs=30 Similarity=0.963442  
 88 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Cele-UNSB01\_4:1491894-1492067 Satlength=174 Nr of Repeats=5  
 RepeatLength=35 seed=GAAAATTGA Num.seqs=3 Similarity=0.949206  
 93 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_4:10324370-10326780 Satlength=2411 Nr of Repeats=67  
 RepeatLength=35 seed=GAAATTCAAA Num.seqs=43 Similarity=0.847276  
 73 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Cele-UNSB01\_4:12289740-12290350 Satlength=611 Nr of Repeats=8  
 RepeatLength=35 seed=AAATTTGAAT Num.seqs=5 Similarity=0.847619  
 60 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_4:15554734-15555678 Satlength=945 Nr of Repeats=27  
 RepeatLength=35 seed=GAAATTCAAA Num.seqs=18 Similarity=0.936508  
 73 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Cele-UNSB01\_4:16219937-16221099 Satlength=1163 Nr of Repeats=29  
 RepeatLength=35 seed=TTCCCGCCAA Num.seqs=20 Similarity=0.896341  
 70 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Rev.of\_Cele-UNSB01\_5:1289520-1292435 Satlength=2916 Nr of Repeats=32  
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=20 Similarity=0.939850  
 77 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Cele-UNSB01\_5:6307822-6308103 Satlength=282 Nr of Repeats=8  
 RepeatLength=35 seed=AATTTCCCGC Num.seqs=7 Similarity=0.909297  
 67 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-  
 Cele-UNSB01\_5:6309373-6309654 Satlength=282 Nr of Repeats=8  
 RepeatLength=35 seed=AATTTCCCGC Num.seqs=7 Similarity=0.909297  
 67 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTGA-

Cele-UNSB01\_5:6310933-6311214 Satlength=282 Nr of Repeats=8  
 RepeatLength=35 seed=AATTTCCCGC Num.seqs=7 Similarity=0.909297  
 67 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_5:9642989-9644244 Satlength=1256 Nr of Repeats=36  
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=25 Similarity=0.936127  
 77 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_5:13979523-13981831 Satlength=2309 Nr of Repeats=66  
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=50 Similarity=0.968964  
 77 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_5:13979521-13982440 Satlength=2920 Nr of Repeats=68  
 RepeatLength=35 seed=TGGCGGGAAA Num.seqs=50 Similarity=0.947124  
 79 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_5:14226151-14226968 Satlength=818 Nr of Repeats=21  
 RepeatLength=35 seed=GGAAATTCAA Num.seqs=14 Similarity=0.922554  
 74 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_5:15725600-15726976 Satlength=1377 Nr of Repeats=36  
 RepeatLength=35 seed=TTCAAATTTT Num.seqs=30 Similarity=0.828501  
 69 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTTGA-  
 Cele-UNSB01\_6:9443244-9443487 Satlength=244 Nr of Repeats=7  
 RepeatLength=35 seed=AAAATTTGAA Num.seqs=5 Similarity=0.908571  
 94 ATT-TCCCGCC--AAAA-T--TTTTTT-CACTGAAAATTTGA-  
 Cele-UNSB01\_3:10975904-10976322 Satlength=419 Nr of Repeats=11  
 RepeatLength=35 seed=CCGCCAAAAT Num.seqs=10 Similarity=0.943280  
 38 ATT-TCCCGCC--AAAA-T--ATTTTT-CACTAAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_3:10980699-10982201 Satlength=1503 Nr of Repeats=43  
 RepeatLength=35 seed=AAATTCAAAT Num.seqs=40 Similarity=0.893520  
 72 ATT-TCCCGCC--AAAA-T--ATTTTT-CACTAAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_4:15436315-15436698 Satlength=384 Nr of Repeats=11  
 RepeatLength=35 seed=GGGAAATTCA Num.seqs=7 Similarity=0.941950  
 40 ATT-TCCCGCC--AAAA-T--ATTTTT-TACTAAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_4:15436367-15437145 Satlength=779 Nr of Repeats=9  
 RepeatLength=35 seed=GTAAAAATA Num.seqs=7 Similarity=0.929252  
 57 ATT-TCCCGCC--AAAA-T--ATTTTT-TACTAAAAATTTGA-  
 Rev.of\_Cele-UNSB01\_1:8014573-8014958 Satlength=386 Nr of Repeats=11  
 RepeatLength=35 seed=GGGAAATTTA Num.seqs=11 Similarity=0.944589  
 40 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Cele-UNSB01\_2:15105694-15106081 Satlength=388 Nr of Repeats=11  
 RepeatLength=35 seed=CAGAAAATTT Num.seqs=9 Similarity=0.949206  
 56 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_4:13645884-13646555 Satlength=672 Nr of Repeats=18  
 RepeatLength=35 seed=GAAATTTAAA Num.seqs=15 Similarity=0.948481  
 73 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_4:13645885-13647427 Satlength=1543 Nr of Repeats=25  
 RepeatLength=35 seed=AAATTTAAAT Num.seqs=19 Similarity=0.791694  
 72 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_4:14107092-14108860 Satlength=1769 Nr of Repeats=51  
 RepeatLength=35 seed=GGGAAATTTA Num.seqs=34 Similarity=0.943706  
 40 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_4:14107092-14111107 Satlength=4016 Nr of Repeats=106  
 RepeatLength=35 seed=GGGAAATTTA Num.seqs=73 Similarity=0.941958  
 40 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_4:14107093-14113320 Satlength=6228 Nr of Repeats=160  
 RepeatLength=35 seed=GGAAATTTAA Num.seqs=111 Similarity=0.941169  
 74 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-



Rev.of\_Cele-UNSB01\_4:15399887-15400027 Satlength=141 Nr of Repeats=4  
 RepeatLength=35 seed=AAATTTTCTG Num.seqs=4 Similarity=0.904762  
 66 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_4:17168941-17169150 Satlength=210 Nr of Repeats=6  
 RepeatLength=35 seed=GAAATTTAAA Num.seqs=5 Similarity=0.900952  
 73 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_4:17402400-17402610 Satlength=211 Nr of Repeats=6  
 RepeatLength=35 seed=AAATTTTCTG Num.seqs=6 Similarity=0.928889  
 66 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_5:6074295-6074435 Satlength=141 Nr of Repeats=4  
 RepeatLength=35 seed=ATTTTGGCGG Num.seqs=4 Similarity=0.961905  
 48 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Cele-UNSB01\_5:7957689-7957969 Satlength=281 Nr of Repeats=8  
 RepeatLength=35 seed=CAGAAAATTT Num.seqs=8 Similarity=0.964626  
 56 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Cele-UNSB01\_6:1420856-1421521 Satlength=666 Nr of Repeats=19  
 RepeatLength=35 seed=CCCGCCAAAA Num.seqs=19 Similarity=0.932275  
 72 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Cele-UNSB01\_6:14122412-14122622 Satlength=211 Nr of Repeats=6  
 RepeatLength=35 seed=CAGAAAATTT Num.seqs=6 Similarity=0.949206  
 56 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Cele-UNSB01\_6:15851631-15851806 Satlength=176 Nr of Repeats=5  
 RepeatLength=35 seed=ATTTAAATTT Num.seqs=5 Similarity=0.939048  
 62 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_6:17686891-17687206 Satlength=316 Nr of Repeats=9  
 RepeatLength=35 seed=AAATTTTCTG Num.seqs=7 Similarity=0.909297  
 66 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_4:16061680-16061959 Satlength=280 Nr of Repeats=8  
 RepeatLength=35 seed=AATTTAAATT Num.seqs=7 Similarity=0.896599  
 71 ATT-TCCCGCC--AAAA-T--ATTTTT-CNCAGAAAATTTAA-  
 Cele-UNSB01\_2:635957-636850 Satlength=894 Nr of Repeats=4 RepeatLength=35  
 seed=GAAAATTTAA Num.seqs=3 Similarity=0.923810  
 58 ATT-TCCCTCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_2:15064421-15065299 Satlength=879 Nr of Repeats=25  
 RepeatLength=35 seed=TTAAATTTTC Num.seqs=22 Similarity=0.939312  
 68 ATT-TCCCTCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_3:8581179-8581353 Satlength=175 Nr of Repeats=5  
 RepeatLength=35 seed=GGGAAATTTA Num.seqs=4 Similarity=0.974603  
 75 ATT-TCCCTCC--AAAA-T--ATTTTT-CACAGAAAATTTAA-  
 Rev.of\_Cele-UNSB01\_5:6964092-6964484 Satlength=393 Nr of Repeats=9  
 RepeatLength=35 seed=CGGGAAATTT Num.seqs=6 Similarity=0.921270  
 41 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAAATTTCAA-  
 Rev.of\_Cele-UNSB01\_1:14648049-14648258 Satlength=210 Nr of Repeats=6  
 RepeatLength=35 seed=AATTTAAATT Num.seqs=5 Similarity=0.859048  
 71 ATT-TCCCGCC--AAAA-T--ATTTTT-CTCAGAAAATTTAA-  
 Cele-UNSB01\_4:7464933-7465143 Satlength=211 Nr of Repeats=6  
 RepeatLength=35 seed=CAGAAAATTT Num.seqs=6 Similarity=0.926349  
 91 ATT-TCCCGCC--AAAA-T--ATTTTT-CTCAGAAAATTTAA-  
 Cele-UNSB01\_4:16144580-16144720 Satlength=141 Nr of Repeats=4  
 RepeatLength=35 seed=CCAAAATATT Num.seqs=4 Similarity=0.892063  
 76 ATT-TCCCGCC--AAAA-T--ATTTTT-CTCAGAAAATTTAA-  
 Cele-UNSB01\_5:9479420-9479630 Satlength=211 Nr of Repeats=6  
 RepeatLength=35 seed=AGAAAATTTA Num.seqs=6 Similarity=0.888254  
 92 ATT-TCCCGCC--AAAA-T--ATTTTT-CTCAGAAAATTTAA-

Cele-UNSB01\_5:19059372-19059511 Satlength=140 Nr of Repeats=4  
RepeatLength=35 seed=TCAGAAATT Num.seqs=3 Similarity=0.923810  
90 ATT-TCCCGCC--AAAA-T--ATTTTT-CTCAGAAATTTAA-  
Cele-UNSB01\_6:15298701-15298945 Satlength=245 Nr of Repeats=7  
RepeatLength=35 seed=CAGAAATTT Num.seqs=6 Similarity=0.893333  
91 ATT-TCCCGCC--AAAA-T--ATTTTT-CTCAGAAATTTAA-  
Cele-UNSB01\_4:8504239-8504449 Satlength=211 Nr of Repeats=6  
RepeatLength=35 seed=GAAATTTAA Num.seqs=6 Similarity=0.898413  
93 ATT-TCCCTCC--AAAA-T--ATTTTT-CTCAGAAATTTAA-  
Cele-UNSB01\_6:16004822-16005172 Satlength=351 Nr of Repeats=10  
RepeatLength=35 seed=CAGAAATTT Num.seqs=10 Similarity=0.875556  
126 ATT-TCCCTCC--AAAA-T--ATTTTT-CTCAGAAATTTAA-  
Cele-UNSB01\_4:15999976-16000920 Satlength=945 Nr of Repeats=8  
RepeatLength=35 seed=AAAATTTAAA Num.seqs=7 Similarity=0.883900  
94 ATT-TCCCNCC--AAAA-T--ATTTTT-CTCAGAAATTTAA-  
Rev.of\_Cele-UNSB01\_2:15242891-15243160 Satlength=270 Nr of Repeats=5  
RepeatLength=35 seed=ATTTTGGCGG Num.seqs=4 Similarity=0.904762  
83 ATT-TCCCGCC--AAAA-T--ATTTTT-CTCCGAAATTTAA-  
Cele-UNSB01\_4:16926416-16926623 Satlength=208 Nr of Repeats=6  
RepeatLength=35 seed=TTGAATTTCC Num.seqs=4 Similarity=0.917460  
64 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAGAAATTTGA-  
Rev.of\_Cele-UNSB01\_6:161019-161648 Satlength=630 Nr of Repeats=17  
RepeatLength=35 seed=GGGAAATTCa Num.seqs=14 Similarity=0.796654  
75 ATT-TCCCGCC--AAAA-T--ATTTTT-CACAAAAATTTGA-  
Cele-UNSB01\_2:9764656-9765286 Satlength=631 Nr of Repeats=18  
RepeatLength=35 seed=CCAAATATT Num.seqs=18 Similarity=0.925801  
41 ATT-TCCCTCC--AAAA-T--ATTTTT-TTCAGAAATTTAA-  
Cele-UNSB01\_4:1160589-1161121 Satlength=533 Nr of Repeats=4  
RepeatLength=35 seed=AAAATATTTT Num.seqs=3 Similarity=0.898413  
43 ATT-TCCCTCC--AAAA-T--ATTTTT-TTCAGAAATTTAA-  
Rev.of\_Cele-UNSB01\_3:4031086-4031330 Satlength=245 Nr of Repeats=7  
RepeatLength=35 seed=AATTTAAATT Num.seqs=6 Similarity=0.890794  
71 ATT-TCCCGCC--AAAA-T--ATTTTT-TTCAGAAATTTAA-  
Cele-UNSB01\_6:2095079-2095359 Satlength=281 Nr of Repeats=7  
RepeatLength=35 seed=CAGAAATTT Num.seqs=6 Similarity=0.903492  
91 ATT-TCCCGCC--AAAA-T--ATTTTT-TTCAGAAATTTAA-  
Cele-UNSB01\_6:2095085-2096434 Satlength=1350 Nr of Repeats=17  
RepeatLength=35 seed=ATTTAAATTT Num.seqs=12 Similarity=0.912266  
97 ATT-TCCCGCC--AAAA-T--ATTTTT-TTCAGAAATTTAA-  
Cele-UNSB01\_4:4986914-4987437 Satlength=524 Nr of Repeats=15  
RepeatLength=35 seed=TTTTTCAGAAA Num.seqs=13 Similarity=0.973626  
52 ATT-TCCCTCC--AAAA-T--ATTTTT-TTCAGAAATTTAAA-  
Cele-UNSB01\_4:4990413-4990623 Satlength=211 Nr of Repeats=6  
RepeatLength=35 seed=AATATTTTTT Num.seqs=6 Similarity=0.964444  
80 ATT-TCCCTCC--AAAA-T--ATTTTT-TTCAGAAATTTAAA-  
Rev.of\_Cele-UNSB01\_3:12788650-12788963 Satlength=314 Nr of Repeats=8  
RepeatLength=35 seed=TTCAAATTTT Num.seqs=5 Similarity=0.658559  
34 ATT-TNCCGCC--AAAA-T--GTCTTT-CACAGAAATTTGA-  
Cele-UNSB01\_5:20176707-20177444 Satlength=738 Nr of Repeats=21  
RepeatLength=33 seed=TTTGAATTTT Num.seqs=17 Similarity=0.722086  
26 -TT-TCCACC--AAAA-T---TTTC--TCAAAAAATTTGAA  
Cele-UNSB01\_5:20065513-20066023 Satlength=511 Nr of Repeats=14  
RepeatLength=34 seed=TTTCCGCCA Num.seqs=12 Similarity=0.859774  
32 -TT-TCCCGCC--AAAA-T---ATTCACTCNAAAAAATTTGAA

Rev.of\_Cele-UNSB01\_3:13065987-13066581 Satlength=595 Nr of Repeats=17  
RepeatLength=35 seed=AAATTCAAAT Num.seqs=16 Similarity=0.851746  
35 -TT-TCCCGCCATAAAA-T---ATTT-CTCAAATAATTTGAA  
Rev.of\_Cele-UNSB01\_5:18032604-18033134 Satlength=531 Nr of Repeats=13  
RepeatLength=34 seed=TCAAATTTTC Num.seqs=8 Similarity=0.860204  
0 ATT-T-CCGCC--AAAG-T--TTTTTT-AAAAGAAAATTTGA-  
Rev.of\_Cele-UNSB01\_1:3453387-3453600 Satlength=214 Nr of Repeats=5  
RepeatLength=32 seed=AATTCAAATT Num.seqs=3 Similarity=0.602694  
2 -TT-TTCCACC--TAAA-T---TATT-CT-TGAAAATTTGAA

\* \*\* \* \* \* \*

Consensus:

ATTtcCCGCCAAAAtntTTTTCaCaGAAAATTTgA

>Cele-UNSB01\_Fam\_5\_40\_94 Nr. of seq. 94 Alignment length(with gaps) = 41  
Alignment score = 0.668259  
Cele-UNSB01\_1:336527-337247 Satlength=721 Nr of Repeats=18  
RepeatLength=40 seed=AATTTTCTCG Num.seqs=18 Similarity=0.920044  
0 AATTTTCTCGAAATTTCCAAAAGGTTCTAGAACATTTC-A-G  
Rev.of\_Cele-UNSB01\_5:1390382-1390822 Satlength=441 Nr of Repeats=9  
RepeatLength=40 seed=AATGTTCTAG Num.seqs=6 Similarity=0.738753  
36 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTTC-A-G  
Cele-UNSB01\_1:13852339-13853459 Satlength=1121 Nr of Repeats=28  
RepeatLength=40 seed=GAATTTTCTC Num.seqs=28 Similarity=0.956702  
39 AATTTTCTCGAATTTTCCAGAAGGTTCTGGAGCATTTCCA-G  
Rev.of\_Cele-UNSB01\_6:16472071-16473145 Satlength=1075 Nr of Repeats=13  
RepeatLength=40 seed=ATGTTCCAGA Num.seqs=12 Similarity=0.873676  
75 AATTTTCTCGAATTTTCCAGAAGGTTCTGGAACATTTC-A-G  
Cele-UNSB01\_4:2158460-2158710 Satlength=251 Nr of Repeats=6  
RepeatLength=40 seed=TTCCAGAATT Num.seqs=5 Similarity=0.866667  
74 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTTC-A-G  
Rev.of\_Cele-UNSB01\_4:13851511-13852113 Satlength=603 Nr of Repeats=12  
RepeatLength=40 seed=AAAATTCTGG Num.seqs=9 Similarity=0.870370  
86 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTTC-A-G  
Rev.of\_Cele-UNSB01\_6:483296-484174 Satlength=879 Nr of Repeats=19  
RepeatLength=40 seed=AAAATTCTGG Num.seqs=12 Similarity=0.943434  
86 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTTC-A-G  
Rev.of\_Cele-UNSB01\_4:14046107-14046777 Satlength=671 Nr of Repeats=11  
RepeatLength=40 seed=CTGGAATGTT Num.seqs=9 Similarity=0.940741  
40 AATTTTCTCAAATTTTCCAGAAGGTTCTGGAACATTTC-A-G  
Rev.of\_Cele-UNSB01\_5:17207041-17207511 Satlength=471 Nr of Repeats=12  
RepeatLength=40 seed=AAAATTCTGG Num.seqs=11 Similarity=0.899394  
6 AATTTTCTCAAATTTTCCAAAAGGCTCTAGAACATTTC-A-G  
Cele-UNSB01\_6:17663802-17664403 Satlength=602 Nr of Repeats=6  
RepeatLength=40 seed=TTTCTCGAAT Num.seqs=4 Similarity=0.866667  
43 AAATTTCTCGAATCTTCCAGAAGGTTCTAGAACATTTC-A-G  
Cele-UNSB01\_4:2721172-2721362 Satlength=191 Nr of Repeats=5  
RepeatLength=40 seed=GAATTTTCCA Num.seqs=4 Similarity=0.822222  
9 AATTTTTTCTGAATTTTCCAGAAAGTTCTAGAAAATTTC-A-G  
Cele-UNSB01\_1:4694849-4695647 Satlength=799 Nr of Repeats=20  
RepeatLength=40 seed=CATTCCAGAA Num.seqs=18 Similarity=0.964052  
22 ATTTTCTAGAAAGTTCTGGAACATTCCAGAAATTTTCCC-G

Cele-UNSB01\_2:9763711-9764616 Satlength=906 Nr of Repeats=23  
 RepeatLength=40 seed=TTCCAGAATT Num.seqs=22 Similarity=0.947763  
 24 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G  
 Cele-UNSB01\_3:2620888-2621068 Satlength=181 Nr of Repeats=5  
 RepeatLength=40 seed=TTCCAGAATT Num.seqs=4 Similarity=0.966667  
 24 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G  
 Cele-UNSB01\_4:16000310-16000589 Satlength=280 Nr of Repeats=6  
 RepeatLength=40 seed=GATTTTCTA Num.seqs=4 Similarity=0.911111  
 39 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G  
 Rev.of\_Cele-UNSB01\_5:13535913-13536380 Satlength=468 Nr of Repeats=12  
 RepeatLength=40 seed=TCTGGAATGT Num.seqs=11 Similarity=0.922424  
 31 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G  
 Rev.of\_Cele-UNSB01\_6:161741-162501 Satlength=761 Nr of Repeats=19  
 RepeatLength=40 seed=GAAAATTCTG Num.seqs=19 Similarity=0.974269  
 37 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G  
 Cele-UNSB01\_6:14121790-14122309 Satlength=520 Nr of Repeats=13  
 RepeatLength=40 seed=GAACATTCCA Num.seqs=12 Similarity=0.904545  
 59 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G  
 Cele-UNSB01\_4:16130574-16144444 Satlength=13871 Nr of Repeats=346  
 RepeatLength=40 seed=TTTTCTAGA Num.seqs=331 Similarity=0.987691  
 41 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G  
 Rev.of\_Cele-UNSB01\_4:17169175-17169333 Satlength=159 Nr of Repeats=4  
 RepeatLength=40 seed=AAAATTCTGG Num.seqs=3 Similarity=0.977778  
 76 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G  
 Cele-UNSB01\_5:15441112-15445831 Satlength=4720 Nr of Repeats=118  
 RepeatLength=40 seed=ATTTTCTAG Num.seqs=117 Similarity=0.948354  
 80 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G  
 Cele-UNSB01\_6:1420400-1420757 Satlength=358 Nr of Repeats=9  
 RepeatLength=40 seed=ATTTTCTAG Num.seqs=6 Similarity=0.937778  
 80 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G  
 Rev.of\_Cele-UNSB01\_3:8581474-8581754 Satlength=281 Nr of Repeats=7  
 RepeatLength=40 seed=TCTGGAATGT Num.seqs=7 Similarity=0.971429  
 31 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTCCC-A  
 Rev.of\_Cele-UNSB01\_3:8589669-8589949 Satlength=281 Nr of Repeats=7  
 RepeatLength=40 seed=TCTGGAATGT Num.seqs=7 Similarity=0.971429  
 31 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTCCC-A  
 Rev.of\_Cele-UNSB01\_3:8597864-8598144 Satlength=281 Nr of Repeats=7  
 RepeatLength=40 seed=TCTGGAATGT Num.seqs=7 Similarity=0.971429  
 31 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTCCC-A  
 Rev.of\_Cele-UNSB01\_3:8606059-8606339 Satlength=281 Nr of Repeats=7  
 RepeatLength=40 seed=TCTGGAATGT Num.seqs=7 Similarity=0.971429  
 31 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTCCC-A  
 Cele-UNSB01\_4:1160688-1160967 Satlength=280 Nr of Repeats=7  
 RepeatLength=40 seed=ATTTTCTAG Num.seqs=6 Similarity=0.911111  
 40 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTCCC-A  
 Cele-UNSB01\_4:1160701-1161595 Satlength=895 Nr of Repeats=10  
 RepeatLength=40 seed=GTTCTGGAAC Num.seqs=7 Similarity=0.844444  
 53 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTCCC-A  
 Cele-UNSB01\_5:1441594-1441873 Satlength=280 Nr of Repeats=7  
 RepeatLength=40 seed=ATTTTCTAG Num.seqs=6 Similarity=0.880000  
 40 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTCCC-A  
 Rev.of\_Cele-UNSB01\_1:6785543-6785983 Satlength=441 Nr of Repeats=11  
 RepeatLength=40 seed=TTCTGGAATG Num.seqs=11 Similarity=0.960000  
 32 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G

Rev.of\_Cele-UNSB01\_1:8015067-8016984 Satlength=1918 Nr of Repeats=48  
 RepeatLength=40 seed=GAATGTTCCA Num.seqs=45 Similarity=0.944512  
 67 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_3:438790-441355 Satlength=2566 Nr of Repeats=43  
 RepeatLength=40 seed=ACATTCCAGA Num.seqs=41 Similarity=0.892358  
 61 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Rev.of\_Cele-UNSB01\_3:4031404-4032964 Satlength=1561 Nr of Repeats=39  
 RepeatLength=40 seed=GTTCAGAAC Num.seqs=39 Similarity=0.942330  
 63 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_4:7464716-7464914 Satlength=199 Nr of Repeats=5  
 RepeatLength=40 seed=TCCAGAATTT Num.seqs=4 Similarity=0.966667  
 65 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_4:7464716-7465331 Satlength=616 Nr of Repeats=6  
 RepeatLength=40 seed=TCCAGAATTT Num.seqs=4 Similarity=0.966667  
 65 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Rev.of\_Cele-UNSB01\_4:14031556-14031756 Satlength=201 Nr of Repeats=5  
 RepeatLength=40 seed=AATGTTCCAG Num.seqs=5 Similarity=0.973333  
 66 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Rev.of\_Cele-UNSB01\_4:15400092-15400412 Satlength=321 Nr of Repeats=8  
 RepeatLength=40 seed=GAATGTTCCA Num.seqs=8 Similarity=0.897619  
 67 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_4:16708641-16708839 Satlength=199 Nr of Repeats=5  
 RepeatLength=40 seed=TTCCAGAATT Num.seqs=4 Similarity=0.966667  
 64 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_6:187518-187756 Satlength=239 Nr of Repeats=6 RepeatLength=40  
 seed=TTCCAGAATT Num.seqs=5 Similarity=0.986667  
 64 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_6:2087511-2088871 Satlength=1361 Nr of Repeats=34  
 RepeatLength=40 seed=GAATTTTCTC Num.seqs=34 Similarity=0.961200  
 69 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_6:2094704-2095024 Satlength=321 Nr of Repeats=8  
 RepeatLength=40 seed=TTCCAGAATT Num.seqs=6 Similarity=0.911111  
 64 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_6:2094705-2095572 Satlength=868 Nr of Repeats=10  
 RepeatLength=40 seed=TCCAGAATTT Num.seqs=6 Similarity=0.911111  
 65 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Cele-UNSB01\_6:2157131-2163386 Satlength=6256 Nr of Repeats=140  
 RepeatLength=40 seed=AGAATTTTCT Num.seqs=131 Similarity=0.954680  
 68 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G  
 Rev.of\_Cele-UNSB01\_1:13456767-13461871 Satlength=5105 Nr of Repeats=124  
 RepeatLength=40 seed=AATGTTCCAG Num.seqs=118 Similarity=0.974311  
 66 ATTTTCTAGAAAGTTCTGGAACATTTTCAGAATTTTCTC-G  
 Rev.of\_Cele-UNSB01\_6:17686552-17689936 Satlength=3385 Nr of Repeats=70  
 RepeatLength=40 seed=AATGTTCCAG Num.seqs=69 Similarity=0.965771  
 66 ATTTTCTAGAAAGTTCTGGAACATTTTCAGAATTTTCTC-G  
 Cele-UNSB01\_4:16926190-16926350 Satlength=161 Nr of Repeats=4  
 RepeatLength=40 seed=TTCCAGAATT Num.seqs=4 Similarity=0.950000  
 64 ATTTTCTAGAAAGTTCTGGAACGTTCCAGAATTTTCCC-G  
 Cele-UNSB01\_5:4024546-4025389 Satlength=844 Nr of Repeats=21  
 RepeatLength=40 seed=CTAGAAAGTT Num.seqs=18 Similarity=0.796514  
 46 AATTTCCTAGAAAGTTCTGGAACATTCCAGAATTTTCTT-G  
 Rev.of\_Cele-UNSB01\_1:787252-787531 Satlength=280 Nr of Repeats=6  
 RepeatLength=40 seed=GAACCTTCTG Num.seqs=4 Similarity=0.850000  
 7 AAGGTTCTAGAACATTCCAGAATTTTCTCAAATTTTCCA-G

Rev.of\_Cele-UNSB01\_2:4622617-4623337 Satlength=721 Nr of Repeats=18  
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=18 Similarity=0.957734  
 11 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G  
 Cele-UNSB01\_4:8501471-8501871 Satlength=401 Nr of Repeats=10  
 RepeatLength=40 seed=AGAAGGTTCT Num.seqs=10 Similarity=0.953333  
 38 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G  
 Cele-UNSB01\_4:15944034-15944234 Satlength=201 Nr of Repeats=5  
 RepeatLength=40 seed=ATTTTCCAGA Num.seqs=5 Similarity=0.920000  
 31 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G  
 Cele-UNSB01\_6:15068455-15069305 Satlength=851 Nr of Repeats=5  
 RepeatLength=40 seed=TTCTGGAACA Num.seqs=4 Similarity=0.866667  
 44 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_6:16472035-16472475 Satlength=441 Nr of Repeats=11  
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=11 Similarity=0.950303  
 11 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G  
 Cele-UNSB01\_5:7485041-7485201 Satlength=161 Nr of Repeats=4  
 RepeatLength=40 seed=GAAGGTTCTA Num.seqs=4 Similarity=0.794444  
 39 AAGGTTCTAGAACATTCCAGAATTTTCTNAAAATTTCCA-G  
 Cele-UNSB01\_1:14918627-14918817 Satlength=191 Nr of Repeats=5  
 RepeatLength=40 seed=CCAGAAGGTT Num.seqs=4 Similarity=0.800000  
 36 AAGGTTCTAGAACATCCAGAATTTTCTCGAATTTTCCA-G  
 Cele-UNSB01\_2:637418-637568 Satlength=151 Nr of Repeats=4 RepeatLength=40  
 seed=CAGAAGGTTTC Num.seqs=3 Similarity=0.800000  
 37 AAGGTTCTGGAACATTCCAGAATTTTCTAGAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_3:4029920-4030220 Satlength=301 Nr of Repeats=8  
 RepeatLength=40 seed=AGAACCTTCT Num.seqs=6 Similarity=0.824444  
 48 AAGGTTCTGGAACATTCCAGAATTTTCTAGAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_3:9810383-9810703 Satlength=321 Nr of Repeats=8  
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=8 Similarity=0.945238  
 51 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_3:9810418-9811039 Satlength=622 Nr of Repeats=9  
 RepeatLength=40 seed=AATGTTCCAG Num.seqs=8 Similarity=0.903571  
 56 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_4:12150067-12150386 Satlength=320 Nr of Repeats=8  
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=7 Similarity=0.946032  
 51 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_4:14046078-14046558 Satlength=481 Nr of Repeats=12  
 RepeatLength=40 seed=CAGAACCTTC Num.seqs=12 Similarity=0.914646  
 89 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_5:3492923-3493163 Satlength=241 Nr of Repeats=6  
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=6 Similarity=0.931111  
 51 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_6:9243610-9244090 Satlength=481 Nr of Repeats=12  
 RepeatLength=40 seed=CTTCTGGAAA Num.seqs=12 Similarity=0.953030  
 83 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G  
 Cele-UNSB01\_1:789928-790208 Satlength=281 Nr of Repeats=7 RepeatLength=40  
 seed=TCTAGAACAT Num.seqs=7 Similarity=0.838095  
 45 AAGGTTCTAGAACATTCCAGAATTTTCTCGAATTTTCCA-A  
 Cele-UNSB01\_5:1393460-1393720 Satlength=261 Nr of Repeats=6  
 RepeatLength=40 seed=CTAGAACATT Num.seqs=5 Similarity=0.712195  
 46 AANGTTCTAGAACATTCCAGAATTTTCTCGAATTTTCCA-G  
 Rev.of\_Cele-UNSB01\_1:14275073-14275913 Satlength=841 Nr of Repeats=24  
 RepeatLength=40 seed=TTCTGGAAAA Num.seqs=18 Similarity=0.755338  
 82 AAGGTTCTAGAACATTCCAGAATTTTATCGAATTTTCCA-G

Rev.of\_Cele-UNSB01\_5:4022711-4023271 Satlength=561 Nr of Repeats=14  
RepeatLength=40 seed=GAACCTTCTG Num.seqs=12 Similarity=0.857071  
47 AAGGTTCAAAAACATTCCAGAATTTTCTCGAATTTTCCA-G  
Cele-UNSB01\_5:1568984-1569144 Satlength=161 Nr of Repeats=4  
RepeatLength=40 seed=GTTCTAGAAC Num.seqs=4 Similarity=0.875339  
84 AAGGTTCTAGAACATTCCAGAATTTTCTCGAATTTACCAGG  
Rev.of\_Cele-UNSB01\_3:11461018-11461218 Satlength=201 Nr of Repeats=5  
RepeatLength=40 seed=TCCAGAACCT Num.seqs=5 Similarity=0.960000  
11 AAGGTTCTGGAACATTCCAGCATTTTCTCAAATTTTCCA-G  
Rev.of\_Cele-UNSB01\_5:16694107-16694865 Satlength=759 Nr of Repeats=17  
RepeatLength=40 seed=CTGGAATGTT Num.seqs=13 Similarity=0.950427  
20 AAGGTTCTGGAACATTCCAGCATTTTCTCAAATTTTCCA-G  
Rev.of\_Cele-UNSB01\_5:16694107-16695183 Satlength=1077 Nr of Repeats=18  
RepeatLength=40 seed=CTGGAATGTT Num.seqs=13 Similarity=0.950427  
20 AAGGTTCTGGAACATTCCAGCATTTTCTCAAATTTTCCA-G  
Cele-UNSB01\_3:12305276-12305678 Satlength=403 Nr of Repeats=10  
RepeatLength=40 seed=ATTCCAGAAT Num.seqs=8 Similarity=0.860714  
13 AAGGTTCTAGAACATTCCAGAATTTTTTAAAATTTTCCA-G  
Rev.of\_Cele-UNSB01\_1:4033525-4033725 Satlength=201 Nr of Repeats=6  
RepeatLength=40 seed=TTTCTAGAAA Num.seqs=4 Similarity=0.816667  
43 AAAATTCTGGACCATTCCGGAATTTTCTCGAATTTTCTA-G  
Rev.of\_Cele-UNSB01\_4:3733495-3734015 Satlength=521 Nr of Repeats=15  
RepeatLength=40 seed=TTTCTAGAAA Num.seqs=11 Similarity=0.820606  
43 AAAATTCTGGACCATTCCNGAATTTTCTCGAATTTTCTA-G  
Rev.of\_Cele-UNSB01\_1:7887436-7887916 Satlength=481 Nr of Repeats=13  
RepeatLength=40 seed=TTTCTAGAAA Num.seqs=11 Similarity=0.818182  
43 AAANTTCTGGAACATTCCAGANTTTTCCCGAATTTTCTA-G  
Cele-UNSB01\_4:14942266-14942426 Satlength=161 Nr of Repeats=5  
RepeatLength=40 seed=TTTTCTAGAA Num.seqs=3 Similarity=0.755556  
72 AAAGTTCTGGAACATTCCAGAATTTTCCCGAATTTTCTA-G  
Cele-UNSB01\_6:17224721-17225161 Satlength=441 Nr of Repeats=13  
RepeatLength=40 seed=TTTCTAGAAA Num.seqs=9 Similarity=0.814815  
73 AAANTTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G  
Cele-UNSB01\_1:14936456-14937856 Satlength=1401 Nr of Repeats=35  
RepeatLength=40 seed=TTTCTAGAAA Num.seqs=35 Similarity=0.907675  
73 AAAGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G  
Cele-UNSB01\_4:8501476-8504168 Satlength=2693 Nr of Repeats=54  
RepeatLength=40 seed=GTTCTGGAAC Num.seqs=51 Similarity=0.884078  
83 AAAGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G  
Cele-UNSB01\_4:13646820-13647869 Satlength=1050 Nr of Repeats=12  
RepeatLength=40 seed=GTTCTGGAAC Num.seqs=10 Similarity=0.891111  
83 AAAGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G  
Cele-UNSB01\_4:16130581-16145036 Satlength=14456 Nr of Repeats=348  
RepeatLength=40 seed=AGAAAGTTCT Num.seqs=328 Similarity=0.988340  
78 AAAGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G  
Cele-UNSB01\_6:2157154-2162472 Satlength=5319 Nr of Repeats=133  
RepeatLength=40 seed=AAGTTCTGGA Num.seqs=127 Similarity=0.964104  
81 AAAGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G  
Cele-UNSB01\_3:438816-440336 Satlength=1521 Nr of Repeats=38  
RepeatLength=40 seed=TAGAAAGTTC Num.seqs=38 Similarity=0.903556  
77 AAAGTTCTGGAACATTCCAGAATTTTCCCGAATTTTCTA-G  
Cele-UNSB01\_4:15280499-15283896 Satlength=3398 Nr of Repeats=88  
RepeatLength=40 seed=AGAAAGTTCT Num.seqs=79 Similarity=0.897220  
78 AAAGTTCTGGAACATTCCAGAATTTTCCCGAATTTTCTA-G

Rev.of\_Cele-UNSB01\_4:16061215-16062273 Satlength=1059 Nr of Repeats=8  
RepeatLength=40 seed=GTTCAGAAC Num.seqs=7 Similarity=0.814286  
93 AAAGTTCTGGAACATTCCAGAATTTTCCCGATTTTCTA-G  
Rev.of\_Cele-UNSB01\_5:6074472-6074951 Satlength=480 Nr of Repeats=12  
RepeatLength=40 seed=TTCCAGAACT Num.seqs=11 Similarity=0.960000  
92 AAAGTTCTGGAACATTCCAGAATTTTCCCGATTTTCTA-G  
Cele-UNSB01\_4:4986658-4986858 Satlength=201 Nr of Repeats=5  
RepeatLength=40 seed=TTCTAGAAAG Num.seqs=5 Similarity=0.913333  
114 AAAGTTCTGGAACATTCCAGAATTTTCCCGATTTTCTA-G  
Cele-UNSB01\_2:636344-636664 Satlength=321 Nr of Repeats=8 RepeatLength=40  
seed=TTTCTAGAAA Num.seqs=8 Similarity=0.917857  
73 AAAATTCTGGAACATTCCAGAATTTTCCCGATTTTCTA-G  
Cele-UNSB01\_2:8585644-8586044 Satlength=401 Nr of Repeats=10  
RepeatLength=40 seed=AAAGTTCTGG Num.seqs=10 Similarity=0.901482  
80 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G  
Cele-UNSB01\_3:13762939-13765339 Satlength=2401 Nr of Repeats=60  
RepeatLength=40 seed=ATTTTCTAG Num.seqs=60 Similarity=0.908418  
110 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G  
Cele-UNSB01\_4:15607346-15608026 Satlength=681 Nr of Repeats=17  
RepeatLength=40 seed=GAACATTCCA Num.seqs=17 Similarity=0.919608  
89 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G  
Cele-UNSB01\_5:7956964-7957604 Satlength=641 Nr of Repeats=16  
RepeatLength=40 seed=TCTGGAACAT Num.seqs=16 Similarity=0.859790  
85 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G  
Cele-UNSB01\_6:16004509-16004749 Satlength=241 Nr of Repeats=6  
RepeatLength=40 seed=AAAGTTCTGG Num.seqs=6 Similarity=0.904444  
80 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G  
Rev.of\_Cele-UNSB01\_5:9644299-9645659 Satlength=1361 Nr of Repeats=40  
RepeatLength=40 seed=TTTCTAGAAA Num.seqs=28 Similarity=0.851676  
83 AAANTTCTGGAATATTCCAGAATTTTCCCGAATTTTCTA-G

\* \* \* \*\* \* \* \*

Consensus:

AantTTCTnGAAnaTTCcaGAAttTTCcaGAaTTTTTcCaG

>Cele-UNSB01\_Fam\_6\_11\_76 Nr. of seq. 76 Alignment length(with gaps) = 12  
Alignment score = 0.808392  
Cele-UNSB01\_1:564264-564319 Satlength=56 Nr of Repeats=5 RepeatLength=11  
seed=GTACTCCTAC Num.seqs=5 Similarity=0.830303  
0 GTACTC-CTACC  
Rev.of\_Cele-UNSB01\_1:1236946-1237103 Satlength=158 Nr of Repeats=7  
RepeatLength=11 seed=GTACTGTAGG Num.seqs=6 Similarity=0.870707  
4 GTACTC-CTACA  
Rev.of\_Cele-UNSB01\_1:13456302-13456675 Satlength=374 Nr of Repeats=12  
RepeatLength=11 seed=GTACTGTAGG Num.seqs=9 Similarity=0.952862  
4 GTACTC-CTACA  
Rev.of\_Cele-UNSB01\_1:14647518-14647641 Satlength=124 Nr of Repeats=4  
RepeatLength=11 seed=GTACTGTAGG Num.seqs=3 Similarity=0.919192  
4 GTACTC-CTACA  
Cele-UNSB01\_2:637664-637798 Satlength=135 Nr of Repeats=4 RepeatLength=11  
seed=GTACTCCTAC Num.seqs=3 Similarity=0.838384  
11 GTACTC-CTACA



Cele-UNSB01\_2:9765885-9766019 Satlength=135 Nr of Repeats=5  
 RepeatLength=11 seed=GTACTCCTAC Num.seqs=4 Similarity=0.878788  
 11 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_2:14178132-14178499 Satlength=368 Nr of Repeats=11  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=8 Similarity=0.878788  
 4 GTACTC-CTACA  
 Cele-UNSB01\_3:441483-441987 Satlength=505 Nr of Repeats=18  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=12 Similarity=0.773779  
 6 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_3:1399964-1400110 Satlength=147 Nr of Repeats=5  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=3 Similarity=0.919192  
 4 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_3:9809905-9810297 Satlength=393 Nr of Repeats=13  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=8 Similarity=0.796537  
 4 GTACTC-CTACA  
 Cele-UNSB01\_4:1161685-1161942 Satlength=258 Nr of Repeats=8  
 RepeatLength=11 seed=GTACTCCTAC Num.seqs=5 Similarity=0.854545  
 11 GTACTC-CTACA  
 Cele-UNSB01\_4:2268162-2268293 Satlength=132 Nr of Repeats=4  
 RepeatLength=11 seed=GTACTCCTAC Num.seqs=3 Similarity=0.838384  
 11 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_4:2780831-2781210 Satlength=380 Nr of Repeats=12  
 RepeatLength=11 seed=TACTGTAGGA Num.seqs=8 Similarity=0.787698  
 14 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_4:4368763-4369020 Satlength=258 Nr of Repeats=5  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=3 Similarity=1.000000  
 4 GTACTC-CTACA  
 Cele-UNSB01\_4:4388126-4388633 Satlength=508 Nr of Repeats=13  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=9 Similarity=0.878788  
 6 GTACTC-CTACA  
 Cele-UNSB01\_4:4620647-4621153 Satlength=507 Nr of Repeats=13  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=9 Similarity=0.878788  
 6 GTACTC-CTACA  
 Cele-UNSB01\_4:9470964-9471243 Satlength=280 Nr of Repeats=10  
 RepeatLength=11 seed=GTACTCCTAC Num.seqs=8 Similarity=0.883117  
 11 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_4:14030114-14030248 Satlength=135 Nr of Repeats=6  
 RepeatLength=11 seed=AGTACTGTAG Num.seqs=4 Similarity=0.939394  
 5 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_4:14106561-14106695 Satlength=135 Nr of Repeats=6  
 RepeatLength=11 seed=AGTACTGTAG Num.seqs=4 Similarity=0.939394  
 5 GTACTC-CTACA  
 Cele-UNSB01\_4:16001468-16002088 Satlength=621 Nr of Repeats=19  
 RepeatLength=11 seed=GTACTCCTAC Num.seqs=13 Similarity=0.888112  
 11 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_4:16343642-16344390 Satlength=749 Nr of Repeats=18  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=12 Similarity=0.878788  
 4 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_4:17168442-17168576 Satlength=135 Nr of Repeats=6  
 RepeatLength=11 seed=AGTACTGTAG Num.seqs=4 Similarity=0.939394  
 5 GTACTC-CTACA  
 Cele-UNSB01\_4:17337235-17337502 Satlength=268 Nr of Repeats=10  
 RepeatLength=11 seed=CCTACAGTAC Num.seqs=6 Similarity=0.716667  
 5 GTACTC-CTACA

Rev.of\_Cele-UNSB01\_5:3492580-3492838 Satlength=259 Nr of Repeats=7  
 RepeatLength=11 seed=TACTGTAGGA Num.seqs=5 Similarity=0.763889  
 14 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_5:4982997-4984483 Satlength=1487 Nr of Repeats=35  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=22 Similarity=0.888233  
 4 GTACTC-CTACA  
 Cele-UNSB01\_5:9480075-9480332 Satlength=258 Nr of Repeats=8  
 RepeatLength=11 seed=GTACTCCTAC Num.seqs=6 Similarity=0.870707  
 11 GTACTC-CTACA  
 Cele-UNSB01\_5:15447313-15447447 Satlength=135 Nr of Repeats=5  
 RepeatLength=11 seed=GTACTCCTAC Num.seqs=4 Similarity=0.878788  
 11 GTACTC-CTACA  
 Rev.of\_Cele-UNSB01\_5:16693408-16693990 Satlength=583 Nr of Repeats=10  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=6 Similarity=0.846465  
 4 GTACTC-CTACA  
 Cele-UNSB01\_5:17709602-17709736 Satlength=135 Nr of Repeats=5  
 RepeatLength=11 seed=CCTACAGTAC Num.seqs=3 Similarity=0.919192  
 5 GTACTC-CTACA  
 Cele-UNSB01\_5:20903761-20903966 Satlength=206 Nr of Repeats=5  
 RepeatLength=11 seed=CCTACAGTAC Num.seqs=3 Similarity=1.000000  
 5 GTACTC-CTACA  
 Cele-UNSB01\_6:1422210-1422590 Satlength=381 Nr of Repeats=13  
 RepeatLength=11 seed=GTACTCCTAC Num.seqs=10 Similarity=0.886869  
 11 GTACTC-CTACA  
 Cele-UNSB01\_6:5457466-5457723 Satlength=258 Nr of Repeats=10  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=7 Similarity=0.849928  
 6 GTACTC-CTACA  
 Cele-UNSB01\_6:11775904-11776150 Satlength=247 Nr of Repeats=7  
 RepeatLength=11 seed=TCCTACAGTA Num.seqs=5 Similarity=0.854545  
 4 GTACTC-CTACA  
 Cele-UNSB01\_6:14123669-14124172 Satlength=504 Nr of Repeats=19  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=14 Similarity=0.771368  
 6 GTACTC-CTACA  
 Cele-UNSB01\_6:15069428-15069697 Satlength=270 Nr of Repeats=10  
 RepeatLength=11 seed=CCTACAGTAC Num.seqs=6 Similarity=0.738889  
 5 GTACTC-CTACA  
 Cele-UNSB01\_1:1457508-1457876 Satlength=369 Nr of Repeats=14  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=10 Similarity=0.753704  
 6 GTACTN-CTACA  
 Rev.of\_Cele-UNSB01\_2:1043954-1044457 Satlength=504 Nr of Repeats=17  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=11 Similarity=0.819284  
 4 GTACTN-CTACA  
 Cele-UNSB01\_2:2366031-2366422 Satlength=392 Nr of Repeats=13  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=9 Similarity=0.763889  
 6 GTACTN-CTACA  
 Cele-UNSB01\_2:12843731-12843956 Satlength=226 Nr of Repeats=7  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=5 Similarity=0.775000  
 6 GTACTN-CTACA  
 Cele-UNSB01\_4:8600392-8600896 Satlength=505 Nr of Repeats=13  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=9 Similarity=0.865320  
 6 GTACTN-CTACA  
 Rev.of\_Cele-UNSB01\_4:12149712-12149981 Satlength=270 Nr of Repeats=10  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=7 Similarity=0.832612  
 4 GTACTN-CTACA

Cele-UNSB01\_4:16762223-16763229 Satlength=1007 Nr of Repeats=39  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=30 Similarity=0.778225  
 6 GTACTN-CTACA  
 Cele-UNSB01\_5:1958361-1958506 Satlength=146 Nr of Repeats=7  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=6 Similarity=0.723148  
 6 GTACTN-CTACA  
 Cele-UNSB01\_5:17041242-17041488 Satlength=247 Nr of Repeats=7  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=5 Similarity=0.786111  
 6 GTACTN-CTACA  
 Cele-UNSB01\_5:20572226-20572853 Satlength=628 Nr of Repeats=16  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=11 Similarity=0.854545  
 6 GTACTN-CTACA  
 Cele-UNSB01\_6:988331-988610 Satlength=280 Nr of Repeats=13  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=11 Similarity=0.823691  
 6 GTACTN-CTACA  
 Rev.of\_Cele-UNSB01\_6:1657466-1657754 Satlength=289 Nr of Repeats=10  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=6 Similarity=0.790741  
 4 GTACTN-CTACA  
 Rev.of\_Cele-UNSB01\_6:9243247-9243516 Satlength=270 Nr of Repeats=10  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=7 Similarity=0.832612  
 4 GTACTN-CTACA  
 Rev.of\_Cele-UNSB01\_6:16471702-16471949 Satlength=248 Nr of Repeats=8  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=5 Similarity=0.755556  
 4 GTACTN-CTACA  
 Rev.of\_Cele-UNSB01\_2:10964073-10965096 Satlength=1024 Nr of Repeats=24  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=16 Similarity=0.896970  
 4 GTACTA-CTACA  
 Rev.of\_Cele-UNSB01\_3:6746945-6756350 Satlength=9406 Nr of Repeats=204  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=123 Similarity=0.909143  
 4 GTACTA-CTACA  
 Cele-UNSB01\_5:1442495-1442763 Satlength=269 Nr of Repeats=8  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=6 Similarity=0.798148  
 6 GTACTA-CTACA  
 Rev.of\_Cele-UNSB01\_6:40792-40926 Satlength=135 Nr of Repeats=5  
 RepeatLength=11 seed=GTACTGTAGT Num.seqs=3 Similarity=1.000000  
 4 GTACTA-CTACA  
 Rev.of\_Cele-UNSB01\_1:11631541-11632264 Satlength=724 Nr of Repeats=15  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=9 Similarity=0.841751  
 4 GTACCC-CTACA  
 Rev.of\_Cele-UNSB01\_2:889690-889842 Satlength=153 Nr of Repeats=5  
 RepeatLength=11 seed=TGTAGGGGTA Num.seqs=3 Similarity=1.000000  
 11 GTACCC-CTACA  
 Cele-UNSB01\_2:12492091-12492147 Satlength=57 Nr of Repeats=5  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=4 Similarity=0.919192  
 6 GTACCC-CTACA  
 Cele-UNSB01\_2:13571681-13571955 Satlength=275 Nr of Repeats=20  
 RepeatLength=11 seed=CCTACAGTAC Num.seqs=12 Similarity=0.853076  
 5 GTACCC-CTACA  
 Cele-UNSB01\_3:265034-265468 Satlength=435 Nr of Repeats=11  
 RepeatLength=11 seed=CCTACAGTAC Num.seqs=7 Similarity=0.965368  
 5 GTACCC-CTACA  
 Rev.of\_Cele-UNSB01\_3:1406406-1406896 Satlength=491 Nr of Repeats=33  
 RepeatLength=11 seed=GGTACTGTAG Num.seqs=21 Similarity=0.844156  
 5 GTACCC-CTACA

Rev.of\_Cele-UNSB01\_3:1715361-1716220 Satlength=860 Nr of Repeats=41  
 RepeatLength=11 seed=TACTGTAGGG Num.seqs=30 Similarity=0.811076  
 14 GTACCC-CTACA  
 Cele-UNSB01\_4:9493015-9493149 Satlength=135 Nr of Repeats=4  
 RepeatLength=11 seed=CCCTACAGTA Num.seqs=3 Similarity=0.919192  
 4 GTACCC-CTACA  
 Cele-UNSB01\_4:16773369-16773770 Satlength=402 Nr of Repeats=28  
 RepeatLength=11 seed=CCCCTACAGT Num.seqs=17 Similarity=0.887701  
 14 GTACCC-CTACA  
 Cele-UNSB01\_5:14159253-14159397 Satlength=145 Nr of Repeats=6  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=4 Similarity=0.818182  
 6 GTACCC-CTACA  
 Rev.of\_Cele-UNSB01\_5:15966117-15966182 Satlength=66 Nr of Repeats=4  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=3 Similarity=0.919192  
 4 GTACCC-CTACA  
 Cele-UNSB01\_5:17834079-17834336 Satlength=258 Nr of Repeats=8  
 RepeatLength=11 seed=CCTACAGTAC Num.seqs=6 Similarity=0.886869  
 5 GTACCC-CTACA  
 Rev.of\_Cele-UNSB01\_2:4159337-4159593 Satlength=257 Nr of Repeats=13  
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=9 Similarity=0.735043  
 4 GTACNC-CTACA  
 Cele-UNSB01\_3:546017-546152 Satlength=136 Nr of Repeats=6 RepeatLength=11  
 seed=CTACAGTACC Num.seqs=4 Similarity=0.858586  
 6 GTACCA-CTACA  
 Cele-UNSB01\_3:2118334-2118593 Satlength=260 Nr of Repeats=20  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=14 Similarity=0.795788  
 6 GTACCN-CTACA  
 Cele-UNSB01\_5:2189835-2190349 Satlength=515 Nr of Repeats=18  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=14 Similarity=0.742063  
 6 GTACCN-CTACA  
 Rev.of\_Cele-UNSB01\_4:10086561-10087053 Satlength=493 Nr of Repeats=10  
 RepeatLength=11 seed=TACTGTAGGG Num.seqs=6 Similarity=0.935354  
 14 GTAACC-CTACA  
 Rev.of\_Cele-UNSB01\_5:3703054-3703534 Satlength=481 Nr of Repeats=23  
 RepeatLength=11 seed=AGGATTACTG Num.seqs=15 Similarity=0.843001  
 19 GTAATC-CTACA  
 Cele-UNSB01\_3:11631810-11631935 Satlength=126 Nr of Repeats=4  
 RepeatLength=11 seed=CTACAGTACT Num.seqs=3 Similarity=0.838384  
 6 GTACTT-CTACA  
 Rev.of\_Cele-UNSB01\_3:12003957-12004292 Satlength=336 Nr of Repeats=7  
 RepeatLength=11 seed=GTACTGTAGA Num.seqs=5 Similarity=0.854545  
 15 GTACNT-CTACA  
 Cele-UNSB01\_5:7485330-7487566 Satlength=2237 Nr of Repeats=74  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=56 Similarity=0.675400  
 6 GTACCT-CTACA  
 Cele-UNSB01\_4:2158825-2158968 Satlength=144 Nr of Repeats=5  
 RepeatLength=11 seed=CTACAGTACC Num.seqs=4 Similarity=0.796296  
 6 GTACCTACTACA  
 Rev.of\_Cele-UNSB01\_1:11979429-11979575 Satlength=147 Nr of Repeats=6  
 RepeatLength=11 seed=AGTACTGTAG Num.seqs=4 Similarity=0.731481  
 16 GTACTNACTACA

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Consensus:

GTACTcCTACA

>Cele-UNSB01\_Fam\_7\_15\_70 Nr. of seq. 70 Alignment length(with gaps) = 15  
Alignment score = 0.830265  
Cele-UNSB01\_1:911764-911915 Satlength=152 Nr of Repeats=8 RepeatLength=15  
seed=ATCTTCTTTT Num.seqs=5 Similarity=0.911111  
0 ATCTTCTTTTCGTAG  
Cele-UNSB01\_1:2174082-2174248 Satlength=167 Nr of Repeats=10  
RepeatLength=15 seed=AGATCTTGTT Num.seqs=8 Similarity=0.831746  
13 ATCTTGTTTTTCGTAG  
Rev.of\_Cele-UNSB01\_2:12142720-12142795 Satlength=76 Nr of Repeats=4  
RepeatLength=15 seed=AAAACAAGAT Num.seqs=3 Similarity=0.792593  
25 ATCTTGTTTTTNGTAG  
Cele-UNSB01\_2:694600-694660 Satlength=61 Nr of Repeats=4 RepeatLength=15  
seed=GTAGATCTTG Num.seqs=4 Similarity=0.675347  
26 ATCTTGTTTTGGTAG  
Cele-UNSB01\_2:7594307-7594367 Satlength=61 Nr of Repeats=4  
RepeatLength=15 seed=GTAGATCTTG Num.seqs=4 Similarity=0.675347  
26 ATCTTGTTTTGGTAG  
Cele-UNSB01\_4:17545983-17546043 Satlength=61 Nr of Repeats=4  
RepeatLength=15 seed=GTAGATCTTG Num.seqs=4 Similarity=0.675347  
26 ATCTTGTTTTGGTAG  
Rev.of\_Cele-UNSB01\_5:105361-105451 Satlength=91 Nr of Repeats=6  
RepeatLength=15 seed=AAAAGGAGAA Num.seqs=6 Similarity=0.822222  
10 TTCTCCTTTTCGTNG  
Cele-UNSB01\_5:105684-105774 Satlength=91 Nr of Repeats=6 RepeatLength=15  
seed=TTCTCCTTTT Num.seqs=6 Similarity=0.792593  
15 TTCTCCTTTTCGTNG  
Rev.of\_Cele-UNSB01\_1:5080040-5080117 Satlength=78 Nr of Repeats=5  
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.807407  
12 CTCCCCTTTTCGTAT  
Cele-UNSB01\_1:5080289-5080381 Satlength=93 Nr of Repeats=5  
RepeatLength=15 seed=CTCCCCTTTT Num.seqs=3 Similarity=0.847222  
15 CTCCCCTTTTCGTAT  
Cele-UNSB01\_1:5082880-5082987 Satlength=108 Nr of Repeats=6  
RepeatLength=15 seed=CTCCCCTTTT Num.seqs=4 Similarity=0.869792  
15 CTCCCCTTTTCGTAT  
Rev.of\_Cele-UNSB01\_2:1142725-1142802 Satlength=78 Nr of Repeats=5  
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.777778  
12 CTCCCCTTTTCGTAT  
Rev.of\_Cele-UNSB01\_3:6731291-6731428 Satlength=138 Nr of Repeats=9  
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=8 Similarity=0.847619  
12 CTCCCCTTTTCGTAT  
Rev.of\_Cele-UNSB01\_3:13181955-13182047 Satlength=93 Nr of Repeats=5  
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.881481  
12 CTCCCCTTTTCGTAT  
Cele-UNSB01\_4:1461281-1461373 Satlength=93 Nr of Repeats=6  
RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.840000  
16 CTCCCCTTTTCGTAT  
Rev.of\_Cele-UNSB01\_4:4768182-4768259 Satlength=78 Nr of Repeats=5  
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.777778  
12 CTCCCCTTTTCGTAT

Cele-UNSB01\_4:12770991-12771083 Satlength=93 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=3 Similarity=0.881481  
 16 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_1:5313372-5313447 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAT  
 Rev.of\_Cele-UNSB01\_1:10660173-10660265 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_1:10660440-10660532 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_2:1142992-1143084 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAT  
 Rev.of\_Cele-UNSB01\_2:8013550-8013642 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_2:8013818-8013910 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CCCCTTTTCG Num.seqs=5 Similarity=0.733333  
 17 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_2:10367690-10367782 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.733333  
 16 CTCCCCTTTTCGTAT  
 Rev.of\_Cele-UNSB01\_2:11673801-11673893 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_2:11674068-11674143 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAT  
 Rev.of\_Cele-UNSB01\_2:14573634-14573711 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148  
 27 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_3:7953695-7953787 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAT  
 Rev.of\_Cele-UNSB01\_3:10399868-10399945 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148  
 27 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_3:10733861-10733953 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_4:634851-634943 Satlength=93 Nr of Repeats=6 RepeatLength=15  
 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAT  
 Rev.of\_Cele-UNSB01\_4:3087838-3087930 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.760000  
 27 CTCCCCTTTTCGTAT  
 Cele-UNSB01\_4:3088105-3088197 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAT  
 Rev.of\_Cele-UNSB01\_4:4464716-4464793 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148  
 27 CTCCCCTTTTCGTAT

Cele-UNSB01\_4:4768434-4768526 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAG  
 Rev.of\_Cele-UNSB01\_4:8048486-8048578 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAG  
 Cele-UNSB01\_4:8048753-8048845 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAG  
 Rev.of\_Cele-UNSB01\_4:11302758-11302850 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAG  
 Rev.of\_Cele-UNSB01\_4:12770724-12770816 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAG  
 Rev.of\_Cele-UNSB01\_4:15434528-15434620 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAG  
 Rev.of\_Cele-UNSB01\_5:1229040-1229117 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148  
 27 CTCCCCTTTTCGTAG  
 Cele-UNSB01\_5:1229292-1229367 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAG  
 Rev.of\_Cele-UNSB01\_5:5757268-5757343 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAG  
 Cele-UNSB01\_5:5757528-5757620 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.733333  
 16 CTCCCCTTTTCGTAG  
 Cele-UNSB01\_5:14550286-14550378 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 CTCCCCTTTTCGTAG  
 Rev.of\_Cele-UNSB01\_5:15913508-15913600 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889  
 27 CTCCCCTTTTCGTAG  
 Rev.of\_Cele-UNSB01\_5:16699381-16699441 Satlength=61 Nr of Repeats=4  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148  
 27 CTCCCCTTTTCGTAG  
 Cele-UNSB01\_4:17606143-17606220 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=TTCCCCTTTT Num.seqs=4 Similarity=0.866667  
 15 TTCCCCTTTTCGTAT  
 Cele-UNSB01\_1:5758991-5759083 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_2:14573886-14573978 Satlength=93 Nr of Repeats=6  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889  
 16 ATCCCCTTTTCGCAG  
 Rev.of\_Cele-UNSB01\_3:6192343-6192405 Satlength=63 Nr of Repeats=4  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.762963  
 27 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_3:6192580-6192657 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.748148  
 16 ATCCCCTTTTCGCAG

Cele-UNSB01\_3:6731603-6731679 Satlength=77 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.748148  
 16 ATCCCCTTTTCGCAG  
 Rev.of\_Cele-UNSB01\_3:7953449-7953511 Satlength=63 Nr of Repeats=4  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.762963  
 27 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_3:10400120-10400212 Satlength=93 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=3 Similarity=0.762963  
 16 ATCCCCTTTTCGCAG  
 Rev.of\_Cele-UNSB01\_3:10733639-10733701 Satlength=63 Nr of Repeats=4  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.762963  
 27 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_3:11109268-11109343 Satlength=76 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.751111  
 16 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_3:13182222-13182299 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.777778  
 16 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_4:391568-391630 Satlength=63 Nr of Repeats=4 RepeatLength=15  
 seed=TCCCCTTTTC Num.seqs=3 Similarity=0.762963  
 16 ATCCCCTTTTCGCAG  
 Rev.of\_Cele-UNSB01\_4:1729821-1729883 Satlength=63 Nr of Repeats=4  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.703704  
 27 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_4:11303025-11303087 Satlength=63 Nr of Repeats=4  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=3 Similarity=0.762963  
 16 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_4:15434795-15434872 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.748148  
 16 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_5:4531686-4531763 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=CCCCTTTTCG Num.seqs=4 Similarity=0.748148  
 17 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_5:16699651-16699786 Satlength=136 Nr of Repeats=7  
 RepeatLength=15 seed=GCAGATCCCC Num.seqs=6 Similarity=0.946667  
 26 ATCCCCTTTTCGCAG  
 Rev.of\_Cele-UNSB01\_5:21154449-21154526 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.822222  
 27 ATCCCCTTTTCGCAG  
 Cele-UNSB01\_5:21154702-21154779 Satlength=78 Nr of Repeats=5  
 RepeatLength=15 seed=CCCCTTTTCG Num.seqs=4 Similarity=0.748148  
 17 ATCCCCTTTTCGCAG  
 Rev.of\_Cele-UNSB01\_6:276570-276632 Satlength=63 Nr of Repeats=4  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.762963  
 27 ATCCCCTTTTCGCAG  
 Rev.of\_Cele-UNSB01\_1:7149236-7149296 Satlength=61 Nr of Repeats=4  
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.807407  
 27 ATCCCCTTTTCGCTG  
 Rev.of\_Cele-UNSB01\_1:13121380-13121635 Satlength=256 Nr of Repeats=17  
 RepeatLength=15 seed=AAAAGGGGAT Num.seqs=15 Similarity=0.935661  
 25 ATCCCCTTTTTCGAG  
 Cele-UNSB01\_6:276806-276883 Satlength=78 Nr of Repeats=5 RepeatLength=15  
 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.762963  
 16 ATCCCCTTTTCGTAG



\*\*      \*\*\*\* \*

Consensus:

cTCCCCTTTTCGtAG

>Cele-UNSB01\_Fam\_8\_16\_50 Nr. of seq. 50 Alignment length(with gaps) = 16  
Alignment score = 0.867364

Cele-UNSB01\_1:11481110-11481222 Satlength=113 Nr of Repeats=7  
RepeatLength=16 seed=CTACATGCCT Num.seqs=7 Similarity=0.805556  
0 CTACATGCCTACATGC

Cele-UNSB01\_1:11481110-11482230 Satlength=1121 Nr of Repeats=68  
RepeatLength=16 seed=CTACATGCCT Num.seqs=64 Similarity=0.868304  
0 CTACATGCCTACATGC

Rev.of\_Cele-UNSB01\_1:11869240-11870103 Satlength=864 Nr of Repeats=53  
RepeatLength=16 seed=GCATGTAGGC Num.seqs=50 Similarity=0.957891  
0 CTACATGCCTACATGC

Cele-UNSB01\_2:13133064-13133208 Satlength=145 Nr of Repeats=9  
RepeatLength=16 seed=GCCTACATGC Num.seqs=7 Similarity=0.861111  
6 CTACATGCCTACATGC

Rev.of\_Cele-UNSB01\_2:13460078-13460334 Satlength=257 Nr of Repeats=15  
RepeatLength=16 seed=GGCATGTAGG Num.seqs=13 Similarity=0.840812  
1 CTACATGCCTACATGC

Rev.of\_Cele-UNSB01\_2:13465788-13466109 Satlength=322 Nr of Repeats=20  
RepeatLength=16 seed=GGCATGTAGG Num.seqs=19 Similarity=0.773879  
1 CTACATGCCTACATGC

Cele-UNSB01\_2:13663688-13663784 Satlength=97 Nr of Repeats=6  
RepeatLength=16 seed=ACATGCCTAC Num.seqs=6 Similarity=0.888889  
2 CTACATGCCTACATGC

Cele-UNSB01\_2:13794379-13794568 Satlength=190 Nr of Repeats=10  
RepeatLength=16 seed=CCTACATGCC Num.seqs=7 Similarity=0.976190  
7 CTACATGCCTACATGC

Rev.of\_Cele-UNSB01\_3:3880760-3880928 Satlength=169 Nr of Repeats=10  
RepeatLength=16 seed=TAGGCATGTA Num.seqs=9 Similarity=0.912037  
3 CTACATGCCTACATGC

Rev.of\_Cele-UNSB01\_4:600866-601084 Satlength=219 Nr of Repeats=10  
RepeatLength=16 seed=AGGCATGTAG Num.seqs=9 Similarity=0.796296  
2 CTACATGCCTACATGC

Rev.of\_Cele-UNSB01\_4:2990271-2990613 Satlength=343 Nr of Repeats=19  
RepeatLength=16 seed=TAGGCATGTA Num.seqs=16 Similarity=0.859028  
3 CTACATGCCTACATGC

Cele-UNSB01\_4:3222029-3222419 Satlength=391 Nr of Repeats=5  
RepeatLength=16 seed=TACATGCCTA Num.seqs=4 Similarity=0.958333  
1 CTACATGCCTACATGC

Cele-UNSB01\_4:3226485-3226669 Satlength=185 Nr of Repeats=11  
RepeatLength=16 seed=CATGCCTACA Num.seqs=10 Similarity=0.816667  
3 CTACATGCCTACATGC

Cele-UNSB01\_4:3230422-3232144 Satlength=1723 Nr of Repeats=67  
RepeatLength=16 seed=ATGCCTACAT Num.seqs=46 Similarity=0.819565  
4 CTACATGCCTACATGC

Rev.of\_Cele-UNSB01\_4:3274030-3274126 Satlength=97 Nr of Repeats=6  
RepeatLength=16 seed=AGGCATGTAG Num.seqs=6 Similarity=0.872222  
2 CTACATGCCTACATGC

Cele-UNSB01\_4:3630301-3630781 Satlength=481 Nr of Repeats=28  
 RepeatLength=16 seed=TGCCTACATG Num.seqs=23 Similarity=0.914032  
 5 CTACATGCCTACATGC  
 Rev.of\_Cele-UNSB01\_4:3888107-3888300 Satlength=194 Nr of Repeats=12  
 RepeatLength=16 seed=TAGGCATGTA Num.seqs=9 Similarity=0.981481  
 3 CTACATGCCTACATGC  
 Cele-UNSB01\_5:345871-345991 Satlength=121 Nr of Repeats=7 RepeatLength=16  
 seed=CATGCCTACA Num.seqs=6 Similarity=0.972222  
 3 CTACATGCCTACATGC  
 Rev.of\_Cele-UNSB01\_5:353635-353859 Satlength=225 Nr of Repeats=14  
 RepeatLength=16 seed=GGCATGTAGG Num.seqs=14 Similarity=0.928571  
 1 CTACATGCCTACATGC  
 Cele-UNSB01\_5:788141-788221 Satlength=81 Nr of Repeats=5 RepeatLength=16  
 seed=CTACATGCCT Num.seqs=5 Similarity=0.933333  
 0 CTACATGCCTACATGC  
 Rev.of\_Cele-UNSB01\_5:788660-789185 Satlength=526 Nr of Repeats=12  
 RepeatLength=16 seed=AGGCATGTAG Num.seqs=9 Similarity=0.907407  
 2 CTACATGCCTACATGC  
 Rev.of\_Cele-UNSB01\_5:790113-790281 Satlength=169 Nr of Repeats=10  
 RepeatLength=16 seed=AGGCATGTAG Num.seqs=9 Similarity=0.944444  
 2 CTACATGCCTACATGC  
 Cele-UNSB01\_5:896085-896285 Satlength=201 Nr of Repeats=12  
 RepeatLength=16 seed=ATGCCTACAT Num.seqs=11 Similarity=0.956061  
 4 CTACATGCCTACATGC  
 Cele-UNSB01\_5:2213030-2213142 Satlength=113 Nr of Repeats=6  
 RepeatLength=16 seed=ATGCCTACAT Num.seqs=4 Similarity=0.875000  
 4 CTACATGCCTACATGC  
 Rev.of\_Cele-UNSB01\_5:4763134-4763326 Satlength=193 Nr of Repeats=11  
 RepeatLength=16 seed=TAGGCATGTA Num.seqs=9 Similarity=0.944444  
 3 CTACATGCCTACATGC  
 Rev.of\_Cele-UNSB01\_5:3035465-3035958 Satlength=494 Nr of Repeats=4  
 RepeatLength=16 seed=GCATGTAGGC Num.seqs=3 Similarity=0.944444  
 0 CTACAAGCCTACATGC  
 Cele-UNSB01\_3:11779996-11780140 Satlength=145 Nr of Repeats=7  
 RepeatLength=16 seed=TACAAGCCTA Num.seqs=5 Similarity=0.866667  
 1 CTACAAGCCTACAAGC  
 Cele-UNSB01\_2:677942-678110 Satlength=169 Nr of Repeats=9 RepeatLength=16  
 seed=CCTACGTGCC Num.seqs=6 Similarity=0.844444  
 7 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_2:2787652-2787836 Satlength=185 Nr of Repeats=11  
 RepeatLength=16 seed=CACGTAGGCA Num.seqs=10 Similarity=0.966667  
 7 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_2:3154398-3154558 Satlength=161 Nr of Repeats=9  
 RepeatLength=16 seed=TAGGCACGTA Num.seqs=7 Similarity=0.849206  
 11 CTACGTGCCTACGTGC  
 Cele-UNSB01\_2:3155808-3156160 Satlength=353 Nr of Repeats=18  
 RepeatLength=16 seed=TACGTGCCTA Num.seqs=12 Similarity=0.845960  
 9 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_2:3220556-3221123 Satlength=568 Nr of Repeats=21  
 RepeatLength=16 seed=GTAGGCACGT Num.seqs=18 Similarity=0.936819  
 12 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_2:3312389-3313069 Satlength=681 Nr of Repeats=42  
 RepeatLength=16 seed=CGTAGGCACG Num.seqs=39 Similarity=0.967611  
 13 CTACGTGCCTACGTGC

Rev.of\_Cele-UNSB01\_2:3460910-3461075 Satlength=166 Nr of Repeats=5  
 RepeatLength=16 seed=GCACGTAGGC Num.seqs=3 Similarity=0.944444  
 8 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_2:3557247-3557399 Satlength=153 Nr of Repeats=9  
 RepeatLength=16 seed=GTAGGCACGT Num.seqs=8 Similarity=0.958333  
 12 CTACGTGCCTACGTGC  
 Cele-UNSB01\_2:4095823-4096643 Satlength=821 Nr of Repeats=4  
 RepeatLength=16 seed=TGCCTACGTG Num.seqs=3 Similarity=1.000000  
 13 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_2:13216705-13216849 Satlength=145 Nr of Repeats=8  
 RepeatLength=16 seed=TAGGCACGTA Num.seqs=6 Similarity=0.916667  
 11 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_3:8579889-8580089 Satlength=201 Nr of Repeats=12  
 RepeatLength=16 seed=AGGCACGTAG Num.seqs=11 Similarity=0.887879  
 10 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_3:10778310-10778713 Satlength=404 Nr of Repeats=14  
 RepeatLength=16 seed=GTAGGCACGT Num.seqs=9 Similarity=0.981481  
 12 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_3:12493882-12494280 Satlength=399 Nr of Repeats=13  
 RepeatLength=16 seed=ACGTAGGCAC Num.seqs=10 Similarity=0.916667  
 14 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_4:1777357-1777453 Satlength=97 Nr of Repeats=5  
 RepeatLength=16 seed=CACGTAGGCA Num.seqs=4 Similarity=0.916667  
 7 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_4:1802551-1803063 Satlength=513 Nr of Repeats=30  
 RepeatLength=16 seed=TAGGCACGTA Num.seqs=26 Similarity=0.962564  
 11 CTACGTGCCTACGTGC  
 Cele-UNSB01\_4:5124505-5124705 Satlength=201 Nr of Repeats=12  
 RepeatLength=16 seed=CTACGTGCCT Num.seqs=11 Similarity=0.969697  
 8 CTACGTGCCTACGTGC  
 Cele-UNSB01\_4:12476016-12476336 Satlength=321 Nr of Repeats=18  
 RepeatLength=16 seed=GTGCCTACGT Num.seqs=14 Similarity=0.887363  
 12 CTACGTGCCTACGTGC  
 Rev.of\_Cele-UNSB01\_2:3182927-3183063 Satlength=137 Nr of Repeats=8  
 RepeatLength=16 seed=AGGCACGTAG Num.seqs=7 Similarity=0.853175  
 10 CTACGTGCCTACNTGC  
 Rev.of\_Cele-UNSB01\_2:14297875-14298051 Satlength=177 Nr of Repeats=10  
 RepeatLength=16 seed=TAGGCATATA Num.seqs=9 Similarity=0.842593  
 3 CTATATGCCTATATGC  
 Cele-UNSB01\_3:3780853-3780925 Satlength=73 Nr of Repeats=4  
 RepeatLength=16 seed=CCTACATACC Num.seqs=3 Similarity=0.888889  
 7 CTACATACCTACATAC  
 Cele-UNSB01\_5:16845717-16846129 Satlength=413 Nr of Repeats=25  
 RepeatLength=16 seed=ACATACCTAC Num.seqs=22 Similarity=0.969697  
 10 CTACATACCTACATAC  
 Rev.of\_Cele-UNSB01\_3:211856-211976 Satlength=121 Nr of Repeats=7  
 RepeatLength=16 seed=TAGGCATCTA Num.seqs=6 Similarity=0.827778  
 3 CTAGGTGCATAGATGC  
 Rev.of\_Cele-UNSB01\_4:3018891-3018971 Satlength=81 Nr of Repeats=4  
 RepeatLength=16 seed=AGGTAGGAAG Num.seqs=3 Similarity=0.722222  
 2 CTACCTACCTTCCTAC

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Consensus:

CTACaTGCCTACaTGC

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>Cele-UNSB01_Fam_9_20_48 Nr. of seq. 48 Alignment length(with gaps) = 20
Alignment score = 0.805585
Cele-UNSB01_1:2574462-2585290 Satlength=10829 Nr of Repeats=565
RepeatLength=19 seed=TACACGAAAA Num.seqs=539 Similarity=0.979754
0 TACACG-AAAAATAGATTGT
Rev.of_Cele-UNSB01_1:4530676-4530829 Satlength=154 Nr of Repeats=8
RepeatLength=19 seed=TTTTTCGTGT Num.seqs=7 Similarity=0.900000
11 TACACG-AAAAATAGATTGT
Cele-UNSB01_3:4122367-4122965 Satlength=599 Nr of Repeats=31
RepeatLength=19 seed=AAAAATAGAT Num.seqs=22 Similarity=1.000000
6 TACACG-AAAAATAGATTGT
Cele-UNSB01_3:6364525-6365839 Satlength=1315 Nr of Repeats=65
RepeatLength=19 seed=AAAAATAGAT Num.seqs=61 Similarity=0.968479
6 TACACG-AAAAATAGATTGT
Rev.of_Cele-UNSB01_3:7913456-7913988 Satlength=533 Nr of Repeats=28
RepeatLength=19 seed=AATCTATTTT Num.seqs=28 Similarity=0.920040
17 TACACG-AAAAATAGATTGT
Rev.of_Cele-UNSB01_3:7922958-7923224 Satlength=267 Nr of Repeats=14
RepeatLength=19 seed=CAATCTATTT Num.seqs=14 Similarity=0.974552
18 TACACG-AAAAATAGATTGT
Cele-UNSB01_3:13559329-13561136 Satlength=1808 Nr of Repeats=95
RepeatLength=19 seed=AAAAATAGAT Num.seqs=93 Similarity=0.940307
6 TACACG-AAAAATAGATTGT
Cele-UNSB01_4:10751931-10752311 Satlength=381 Nr of Repeats=20
RepeatLength=19 seed=ATTGTTACAC Num.seqs=20 Similarity=0.967867
14 TACACG-AAAAATAGATTGT
Cele-UNSB01_4:17223540-17224619 Satlength=1080 Nr of Repeats=56
RepeatLength=19 seed=AAAAATAGAT Num.seqs=41 Similarity=0.957039
6 TACACG-AAAAATAGATTGT
Rev.of_Cele-UNSB01_5:6955453-6955644 Satlength=192 Nr of Repeats=10
RepeatLength=19 seed=AACAATCTAT Num.seqs=9 Similarity=1.000000
1 TACACG-AAAAATAGATTGT
Rev.of_Cele-UNSB01_5:9977175-9978242 Satlength=1068 Nr of Repeats=56
RepeatLength=19 seed=TGTAACAATC Num.seqs=53 Similarity=0.979833
4 TACACG-AAAAATAGATTGT
Cele-UNSB01_5:13457267-13457761 Satlength=495 Nr of Repeats=26
RepeatLength=19 seed=GTTACACGAA Num.seqs=26 Similarity=0.979703
17 TACACG-AAAAATAGATTGT
Cele-UNSB01_5:13461673-13462167 Satlength=495 Nr of Repeats=26
RepeatLength=19 seed=GTTACACGAA Num.seqs=26 Similarity=0.979703
17 TACACG-AAAAATAGATTGT
Rev.of_Cele-UNSB01_5:17626210-17626494 Satlength=285 Nr of Repeats=15
RepeatLength=19 seed=TTTTTCGTGTA Num.seqs=14 Similarity=0.934452
10 TACACG-AAAAATAGATTGT
Rev.of_Cele-UNSB01_6:3115311-3123060 Satlength=7750 Nr of Repeats=398
RepeatLength=19 seed=AATCTATTTT Num.seqs=272 Similarity=0.892683
17 TACACG-AAAAATAGATTGT
Cele-UNSB01_6:12589371-12589487 Satlength=117 Nr of Repeats=6
RepeatLength=19 seed=ATAGATTGTT Num.seqs=4 Similarity=1.000000
10 TACACG-AAAAATAGATTGT
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Cele-UNSB01\_6:12827464-12828819 Satlength=1356 Nr of Repeats=70  
 RepeatLength=19 seed=AAAAATAGAT Num.seqs=45 Similarity=0.943434  
 6 TACACG-AAAAATAGATTGT  
 Cele-UNSB01\_4:16493225-16495520 Satlength=2296 Nr of Repeats=119  
 RepeatLength=19 seed=AAATAGATTG Num.seqs=85 Similarity=0.941540  
 8 TACACG-GAAAATAGATTGT  
 Rev.of\_Cele-UNSB01\_1:11564527-11564628 Satlength=102 Nr of Repeats=5  
 RepeatLength=20 seed=TGTAACAATC Num.seqs=4 Similarity=0.933333  
 4 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_1:13507191-13507550 Satlength=360 Nr of Repeats=18  
 RepeatLength=20 seed=AAAATAGATT Num.seqs=17 Similarity=0.992157  
 8 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_3:11094399-11094498 Satlength=100 Nr of Repeats=5  
 RepeatLength=20 seed=GTTACACGAA Num.seqs=4 Similarity=1.000000  
 18 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_4:16093909-16094066 Satlength=158 Nr of Repeats=8  
 RepeatLength=20 seed=TGTTACACGA Num.seqs=5 Similarity=1.000000  
 17 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_5:1308547-1312321 Satlength=3775 Nr of Repeats=192  
 RepeatLength=20 seed=AAAATAGATT Num.seqs=127 Similarity=0.995817  
 8 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_5:18642200-18655941 Satlength=13742 Nr of Repeats=679  
 RepeatLength=20 seed=ACACGAAAAA Num.seqs=525 Similarity=0.915785  
 21 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_5:19009672-19010877 Satlength=1206 Nr of Repeats=61  
 RepeatLength=20 seed=AAAAATAGAT Num.seqs=52 Similarity=1.000000  
 7 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_6:2020674-2021510 Satlength=837 Nr of Repeats=42  
 RepeatLength=20 seed=GTTACACGAA Num.seqs=38 Similarity=1.000000  
 18 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_6:2029404-2030161 Satlength=758 Nr of Repeats=38  
 RepeatLength=20 seed=ACACGAAAAA Num.seqs=33 Similarity=1.000000  
 21 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_6:2038051-2039066 Satlength=1016 Nr of Repeats=51  
 RepeatLength=20 seed=GTTACACGAA Num.seqs=46 Similarity=1.000000  
 18 TACACGAAAAAATAGATTGT  
 Rev.of\_Cele-UNSB01\_6:14480301-14480556 Satlength=256 Nr of Repeats=13  
 RepeatLength=20 seed=TAACAATCTA Num.seqs=8 Similarity=0.966667  
 22 TACACGAAAAAATAGATTGT  
 Rev.of\_Cele-UNSB01\_6:16182513-16182592 Satlength=80 Nr of Repeats=4  
 RepeatLength=20 seed=TAACAATCTA Num.seqs=3 Similarity=0.955556  
 22 TACACGAAAAAATAGATTGT  
 Cele-UNSB01\_2:4043072-4059727 Satlength=16656 Nr of Repeats=833  
 RepeatLength=20 seed=ATTGTTACAC Num.seqs=812 Similarity=0.960325  
 15 TACACTAAAAAATAGATTGT  
 Cele-UNSB01\_4:6277867-6278002 Satlength=136 Nr of Repeats=7  
 RepeatLength=19 seed=ATTGACAGAC Num.seqs=5 Similarity=0.971930  
 14 CAGACG-AAAAATAGATTGA  
 Cele-UNSB01\_4:12734217-12734312 Satlength=96 Nr of Repeats=5  
 RepeatLength=19 seed=AAAAATAGAT Num.seqs=5 Similarity=0.971930  
 25 CAGACG-AAAAATAGATTGA  
 Cele-UNSB01\_5:5649265-5649420 Satlength=156 Nr of Repeats=8  
 RepeatLength=19 seed=AAAAATAGAT Num.seqs=5 Similarity=1.000000  
 25 CAGACG-AAAAATAGATTGG

Cele-UNSB01\_3:1307999-1309276 Satlength=1278 Nr of Repeats=65  
RepeatLength=20 seed=AAAAATAGAT Num.seqs=40 Similarity=0.893203  
26 CAGACGAAAAAATAGATTGA  
Cele-UNSB01\_3:12312970-12313186 Satlength=217 Nr of Repeats=11  
RepeatLength=20 seed=AAATAGATTG Num.seqs=7 Similarity=0.904762  
28 CAGACGAAAAAATAGATTGA  
Cele-UNSB01\_6:4456017-4456156 Satlength=140 Nr of Repeats=7  
RepeatLength=20 seed=ACAGACGAAA Num.seqs=6 Similarity=0.937778  
38 CAGACGAAAAAATAGATTGA  
Rev.of\_Cele-UNSB01\_6:7315610-7315788 Satlength=179 Nr of Repeats=9  
RepeatLength=20 seed=TTTTTCGTCT Num.seqs=7 Similarity=0.961905  
30 CAGACGAAAAAATAGATTGA  
Cele-UNSB01\_6:8127661-8127776 Satlength=116 Nr of Repeats=6  
RepeatLength=19 seed=CAGACGAAAA Num.seqs=5 Similarity=0.887719  
19 CAGACG-AAAAATATATTGG  
Cele-UNSB01\_1:3532132-3534432 Satlength=2301 Nr of Repeats=115  
RepeatLength=20 seed=AAAAATAGA Num.seqs=115 Similarity=0.971320  
25 CATACCAAAAAATAGATTGA  
Cele-UNSB01\_1:14164675-14164835 Satlength=161 Nr of Repeats=8  
RepeatLength=20 seed=AAAAATAGA Num.seqs=8 Similarity=0.900000  
25 CATACCAAAAAATAGATTGA  
Cele-UNSB01\_3:10216874-10217114 Satlength=241 Nr of Repeats=12  
RepeatLength=20 seed=AAAAATAGAT Num.seqs=8 Similarity=0.950000  
26 CATACCAAAAAATAGATTGA  
Rev.of\_Cele-UNSB01\_3:11302620-11306800 Satlength=4181 Nr of Repeats=209  
RepeatLength=20 seed=TCTATTTTTT Num.seqs=209 Similarity=0.952647  
35 CATACCAAAAAATAGATTGA  
Cele-UNSB01\_6:4047987-4048126 Satlength=140 Nr of Repeats=7  
RepeatLength=20 seed=AAAATAGATT Num.seqs=6 Similarity=0.955556  
27 CATACCAAAAAATAGATTGA  
Rev.of\_Cele-UNSB01\_2:894739-894896 Satlength=158 Nr of Repeats=8  
RepeatLength=20 seed=CAATCTATTT Num.seqs=6 Similarity=0.902222  
38 CATACCAAAAAATAGATTGN  
Cele-UNSB01\_6:16177777-16179557 Satlength=1781 Nr of Repeats=89  
RepeatLength=20 seed=CATACCAAAA Num.seqs=85 Similarity=0.936956  
39 CATACCAAAAAATAGATTGG  
Cele-UNSB01\_2:11560093-11560292 Satlength=200 Nr of Repeats=9  
RepeatLength=20 seed=AAAAATAGA Num.seqs=8 Similarity=0.892857  
25 CATACGAAAAAATAGATTGG  
Cele-UNSB01\_1:14566637-14566717 Satlength=81 Nr of Repeats=4  
RepeatLength=20 seed=ATATCAAAAA Num.seqs=4 Similarity=0.855556  
40 CATATCAAAAAATAAATTGG

\* \* \* \* \*

Consensus:

tAcACGaAAAAAATAGATTGt

>Cele-UNSB01\_Fam\_10\_25\_41 Nr. of seq. 41 Alignment length(with gaps) =  
27 Alignment score = 0.791177  
Cele-UNSB01\_1:3815334-3818659 Satlength=3326 Nr of Repeats=133  
RepeatLength=25 seed=TTTACTCTCT Num.seqs=133 Similarity=0.898680  
0 TTTACTCTC--TGGCTTCACCAATAT

Rev.of\_Cele-UNSB01\_6:10621572-10641051 Satlength=19480 Nr of Repeats=772  
 RepeatLength=25 seed=CAGAGAGTAA Num.seqs=526 Similarity=0.847899  
 11 TTTACTCTC--TGGCTTCACCAAATAT  
 Rev.of\_Cele-UNSB01\_2:5217526-5241162 Satlength=23637 Nr of Repeats=927  
 RepeatLength=25 seed=AGCCAGAGAG Num.seqs=627 Similarity=0.736670  
 14 TTTACTCTC--TGGCTTCACCAATTAT  
 Rev.of\_Cele-UNSB01\_3:1364177-1382615 Satlength=18439 Nr of Repeats=734  
 RepeatLength=25 seed=CAGAGAGTAA Num.seqs=587 Similarity=0.896061  
 36 TTTACTCTC--TGGCTTCACCAATTAT  
 Rev.of\_Cele-UNSB01\_2:5217429-5217681 Satlength=253 Nr of Repeats=9  
 RepeatLength=25 seed=AGAGTAAAAT Num.seqs=6 Similarity=0.823932  
 8 TTTACTCTC--TGGCTTTCCCAATTAT  
 Rev.of\_Cele-UNSB01\_1:6909627-6919602 Satlength=9976 Nr of Repeats=399  
 RepeatLength=25 seed=GAAGCCAGAG Num.seqs=399 Similarity=0.903264  
 16 TTTACTCTC--TGGCTTCACAGTATAT  
 Cele-UNSB01\_2:9530992-9537371 Satlength=6380 Nr of Repeats=247  
 RepeatLength=25 seed=CTCTCTGGCT Num.seqs=194 Similarity=0.906588  
 29 TTTACTCTC--TGGCTTCACAGTATAT  
 Cele-UNSB01\_4:5363528-5363903 Satlength=376 Nr of Repeats=15  
 RepeatLength=25 seed=TTTACTCTCT Num.seqs=15 Similarity=0.890286  
 25 TTTACTCTC--TGGCTTCACAGTATAT  
 Cele-UNSB01\_5:10495318-10500018 Satlength=4701 Nr of Repeats=187  
 RepeatLength=25 seed=TTTACTCTCT Num.seqs=186 Similarity=0.897636  
 25 TTTACTCTC--TGGCTTCACAGTATAT  
 Rev.of\_Cele-UNSB01\_6:9421607-9443178 Satlength=21572 Nr of Repeats=857  
 RepeatLength=25 seed=AGAGAGTAAA Num.seqs=649 Similarity=0.731868  
 35 TTTACTCTC--TGGCTTCACAGTATAT  
 Cele-UNSB01\_6:2154760-2154935 Satlength=176 Nr of Repeats=7  
 RepeatLength=25 seed=TATATTTTAC Num.seqs=7 Similarity=0.852698  
 20 TTTACTCTC--TGGCTTCACANTATAT  
 Cele-UNSB01\_6:2156238-2156563 Satlength=326 Nr of Repeats=12  
 RepeatLength=25 seed=TCTGGCTTCA Num.seqs=11 Similarity=0.885576  
 32 TTTACTCTC--TGGCTTCACACTATAT  
 Cele-UNSB01\_6:15253053-15270737 Satlength=17685 Nr of Repeats=696  
 RepeatLength=25 seed=TGGCTTCACA Num.seqs=628 Similarity=0.913347  
 34 TTTACTCTC--TGGCTTCACAATATAT  
 Rev.of\_Cele-UNSB01\_5:8047889-8048164 Satlength=276 Nr of Repeats=11  
 RepeatLength=25 seed=CCAGAGAGTA Num.seqs=11 Similarity=0.870061  
 37 TTTACTCTC--TGGCTTCACAGTATAA  
 Rev.of\_Cele-UNSB01\_2:4325046-4325721 Satlength=676 Nr of Repeats=27  
 RepeatLength=25 seed=GAGAGTAAAA Num.seqs=27 Similarity=0.936486  
 34 TTTACTCTC--TGGCTTCACCGTATAT  
 Rev.of\_Cele-UNSB01\_4:17753355-17753780 Satlength=426 Nr of Repeats=17  
 RepeatLength=25 seed=AGCCAGAGAG Num.seqs=17 Similarity=0.890980  
 39 TTTACTCTC--TGGCTTCACCGTATAT  
 Cele-UNSB01\_4:17753798-17754998 Satlength=1201 Nr of Repeats=48  
 RepeatLength=25 seed=ACTCTCTGGC Num.seqs=48 Similarity=0.888227  
 53 TTTACTCTC--TGGCTTCACCGTATAT  
 Rev.of\_Cele-UNSB01\_3:2604631-2620875 Satlength=16245 Nr of Repeats=650  
 RepeatLength=25 seed=AGAGAGTAAA Num.seqs=546 Similarity=0.862999  
 35 TTTACTCTC--TGGCTTCACCATATAT  
 Cele-UNSB01\_6:12186349-12201499 Satlength=15151 Nr of Repeats=591  
 RepeatLength=25 seed=CTCTCTGGCT Num.seqs=490 Similarity=0.859225  
 54 TTTACTCTC--TGGCTTCACCATATAT

Cele-UNSB01\_4:6158202-6158352 Satlength=151 Nr of Repeats=6  
 RepeatLength=25 seed=TTTACTCTCT Num.seqs=6 Similarity=0.882667  
 25 TTTACTCTC--TGGCTTCACAGAATAA  
 Rev.of\_Cele-UNSB01\_5:14856483-14857645 Satlength=1163 Nr of Repeats=45  
 RepeatLength=25 seed=TGTGAAGCCA Num.seqs=41 Similarity=0.923265  
 44 TTTACTCTC--TGGCTTCACAGAATAA  
 Cele-UNSB01\_4:13540735-13544977 Satlength=4243 Nr of Repeats=166  
 RepeatLength=25 seed=TTTACTCTCT Num.seqs=131 Similarity=0.786650  
 25 TTTACTCTC--TGGCTTCACAGAATAT  
 Rev.of\_Cele-UNSB01\_5:4305444-4315394 Satlength=9951 Nr of Repeats=398  
 RepeatLength=25 seed=AGTAAAATAT Num.seqs=346 Similarity=0.935129  
 31 TTTACTCTC--TGGCTTCACAGAATAT  
 Cele-UNSB01\_6:14307881-14308131 Satlength=251 Nr of Repeats=10  
 RepeatLength=25 seed=TCTCTGGCTT Num.seqs=10 Similarity=0.913481  
 30 TTTACTCTC--TGGCTTCACAGAATAT  
 Rev.of\_Cele-UNSB01\_4:5945791-5945941 Satlength=151 Nr of Repeats=6  
 RepeatLength=25 seed=CCAGAGAGTA Num.seqs=6 Similarity=0.875556  
 37 TTTACTCTC--TGGTTTCCAGTATAT  
 Cele-UNSB01\_3:3456392-3470370 Satlength=13979 Nr of Repeats=556  
 RepeatLength=25 seed=ACTCTCTGGC Num.seqs=537 Similarity=0.870368  
 28 TTTACTCTC--TGGCTTCCCATCATAT  
 Cele-UNSB01\_2:12990090-13000798 Satlength=10709 Nr of Repeats=416  
 RepeatLength=25 seed=TGGCTTCCCA Num.seqs=292 Similarity=0.913730  
 9 TTTACTCTC--TGGCTTCCCACTATAT  
 Cele-UNSB01\_1:943054-953346 Satlength=10293 Nr of Repeats=369  
 RepeatLength=27 seed=TTTTACTCTC Num.seqs=309 Similarity=0.884164  
 24 TTTACTCTCTGTGGCTTCCCACTATAT  
 Cele-UNSB01\_1:4635066-4668893 Satlength=33828 Nr of Repeats=1253  
 RepeatLength=27 seed=TGGCTTCCCA Num.seqs=1251 Similarity=1.000000  
 36 TTTACTCTCTGTGGCTTCCCACTATAT  
 Cele-UNSB01\_2:3331473-3331608 Satlength=136 Nr of Repeats=5  
 RepeatLength=27 seed=TTTACTCTCT Num.seqs=5 Similarity=1.000000  
 25 TTTACTCTCTGTGGCTTCCCACTATAT  
 Cele-UNSB01\_2:14535014-14566604 Satlength=31591 Nr of Repeats=1170  
 RepeatLength=27 seed=TGTGGCTTCC Num.seqs=1170 Similarity=0.999916  
 34 TTTACTCTCTGTGGCTTCCCACTATAT  
 Rev.of\_Cele-UNSB01\_3:958162-973687 Satlength=15526 Nr of Repeats=569  
 RepeatLength=27 seed=TGGGAAGCCA Num.seqs=519 Similarity=0.929610  
 46 TTTACTCTCTGTGGCTTCCCACTATAT  
 Rev.of\_Cele-UNSB01\_3:7587437-7632311 Satlength=44875 Nr of Repeats=1482  
 RepeatLength=27 seed=GTGGGAAGCC Num.seqs=1481 Similarity=0.999867  
 47 TTTACTCTCTGTGGCTTCCCACTATAT  
 Rev.of\_Cele-UNSB01\_4:9095021-9107795 Satlength=12775 Nr of Repeats=451  
 RepeatLength=27 seed=ATAGTGGGAA Num.seqs=334 Similarity=0.885216  
 50 TTTACTCTCTGTGGCTTCCCACTATAT  
 Rev.of\_Cele-UNSB01\_6:122121-133095 Satlength=10975 Nr of Repeats=405  
 RepeatLength=27 seed=ACAGAGAGTA Num.seqs=396 Similarity=0.948514  
 37 TTTACTCTCTGTGGCTTCCCACTATAT  
 Cele-UNSB01\_6:5238384-5284176 Satlength=45793 Nr of Repeats=1482  
 RepeatLength=27 seed=TGTGGCTTCC Num.seqs=1481 Similarity=1.000000  
 34 TTTACTCTCTGTGGCTTCCCACTATAT  
 Rev.of\_Cele-UNSB01\_5:14878525-14883699 Satlength=5175 Nr of Repeats=182  
 RepeatLength=27 seed=GGAAGCCACA Num.seqs=139 Similarity=0.948635  
 44 TTTACTCTCTGTGGCTTCCCACTATAT



Cele-UNSB01\_6:1814276-1830201 Satlength=15926 Nr of Repeats=595  
RepeatLength=27 seed=TTACTCTCTG Num.seqs=528 Similarity=0.899607  
53 TTTACTCTCTGTGGCTTCCCACCATAT  
Rev.of\_Cele-UNSB01\_2:12988123-12990065 Satlength=1943 Nr of Repeats=72  
RepeatLength=27 seed=GTGGGAAGCC Num.seqs=71 Similarity=0.975358  
47 TTTACTCTCTATGGCTTCCCACATAT  
Rev.of\_Cele-UNSB01\_3:958146-965823 Satlength=7678 Nr of Repeats=284  
RepeatLength=27 seed=AGAGAGTAAA Num.seqs=246 Similarity=0.923613  
35 TTTACTCTCTGTGGCTTCCCACATAT  
Cele-UNSB01\_5:1115366-1136806 Satlength=21441 Nr of Repeats=722  
RepeatLength=27 seed=TCTGTGGCTT Num.seqs=708 Similarity=0.928835  
32 TTTACTCTCTGTGGCTTCACAGTATAT

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Consensus:

TTTACTCTCTGGCTTCaCantATAT

>Cele-UNSB01\_Fam\_11\_45\_30 Nr. of seq. 30 Alignment length(with gaps) =  
46 Alignment score = 0.806030  
Cele-UNSB01\_2:11366885-11367108 Satlength=224 Nr of Repeats=5  
RepeatLength=44 seed=AAGGATCAGA Num.seqs=3 Similarity=0.696296  
0 AAGGATCAGAACATCA-GGAAG-AGCCTCGTGATCCTTTGGAGCTG  
Rev.of\_Cele-UNSB01\_1:3600639-3600909 Satlength=271 Nr of Repeats=6  
RepeatLength=45 seed=CTGAATCTTC Num.seqs=6 Similarity=0.990123  
9 AAGATTCAGATCATAAAGGAGG-ATCCTTGTGATCCTTTGGAGCTG  
Cele-UNSB01\_5:18556604-18557205 Satlength=602 Nr of Repeats=6  
RepeatLength=45 seed=GGGGGACCCT Num.seqs=5 Similarity=0.940741  
17 AAGATTCAGTTCATAAGGGGGG-ACCCTTATGATCCTTTGGAGCTG  
Rev.of\_Cele-UNSB01\_1:685710-685978 Satlength=269 Nr of Repeats=6  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=4 Similarity=0.792593  
10 AAGGATCAGACCATCA-GGAGGTACCCTTGTGATCCTTCTTATCTG  
Rev.of\_Cele-UNSB01\_3:7846966-7847368 Satlength=403 Nr of Repeats=9  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=6 Similarity=0.857778  
10 AAGGATCAGACCATCA-GGAGGTACCCTTGTGATCCTTCTTATCTG  
Cele-UNSB01\_1:6114632-6114855 Satlength=224 Nr of Repeats=5  
RepeatLength=45 seed=AAGGATCAGA Num.seqs=3 Similarity=0.841975  
45 AAGGATCAGACCATCA-GAAGGTACCCTTACGATCCTTCTTATCTG  
Rev.of\_Cele-UNSB01\_5:11176286-11176509 Satlength=224 Nr of Repeats=5  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=3 Similarity=0.822222  
55 AAGGATCAGACCATCA-GGAGGTACCCTTACGATTCTTCTTATCTG  
Rev.of\_Cele-UNSB01\_1:1691009-1691188 Satlength=180 Nr of Repeats=4  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=3 Similarity=0.743210  
10 AAGGATCAGAACATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG  
Rev.of\_Cele-UNSB01\_5:14452450-14453298 Satlength=849 Nr of Repeats=19  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=12 Similarity=0.868013  
10 AAGGATCAGAACATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG  
Rev.of\_Cele-UNSB01\_1:3798271-3798674 Satlength=404 Nr of Repeats=9  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=7 Similarity=0.825044  
10 AAGGATCAGANCATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG  
Cele-UNSB01\_1:3799094-3799407 Satlength=314 Nr of Repeats=7  
RepeatLength=45 seed=CTGAAGGATC Num.seqs=5 Similarity=0.792593  
42 AAGGATCAGANCATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG

Cele-UNSB01\_2:11667411-11669597 Satlength=2187 Nr of Repeats=49  
RepeatLength=45 seed=GAAGGATCAG Num.seqs=30 Similarity=0.857233  
44 AAGGATCAGANCATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG  
Rev.of\_Cele-UNSB01\_1:6112428-6113232 Satlength=805 Nr of Repeats=18  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=12 Similarity=0.835690  
10 AAGGATCAGAACATCA-GAAGGTACCCTTGTGATCCTTCGGATCTG  
Rev.of\_Cele-UNSB01\_2:11664501-11665796 Satlength=1296 Nr of Repeats=29  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=19 Similarity=0.857050  
10 AAGGATCAGANCATCA-GAAGGTACCCATGTGATCCTTCGGATCTG  
Cele-UNSB01\_2:6176621-6177425 Satlength=805 Nr of Repeats=18  
RepeatLength=45 seed=CTGAAGGATC Num.seqs=12 Similarity=0.850954  
42 AAGGATCAGAACATCA-GAAGGTACCCATACGATCCTTCGGAGCTG  
Cele-UNSB01\_5:11176622-11177248 Satlength=627 Nr of Repeats=14  
RepeatLength=45 seed=CTGAAGGATC Num.seqs=10 Similarity=0.868313  
42 AAGGATCAGAACATCA-GAAGGTACCCATACGATCCTTCGGAGCTG  
Cele-UNSB01\_5:14454544-14454902 Satlength=359 Nr of Repeats=8  
RepeatLength=45 seed=AAGGATCAGA Num.seqs=6 Similarity=0.857778  
45 AAGGATCAGAACATCA-GAAGGTACCCATACGATCCTTCGGAGCTG  
Rev.of\_Cele-UNSB01\_3:2604301-2604569 Satlength=269 Nr of Repeats=6  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=4 Similarity=0.802469  
10 AAGGATCAGACCATCA-GGAGGTACCCATGTGATCCTTCGGATCTG  
Cele-UNSB01\_3:7847664-7848155 Satlength=492 Nr of Repeats=11  
RepeatLength=45 seed=GAAGGATCAG Num.seqs=7 Similarity=0.820811  
44 AAGGATCAGANCATCA-GGAGGTACCCATGTGATCCTTCGGATCTG  
Rev.of\_Cele-UNSB01\_3:11090269-11090626 Satlength=358 Nr of Repeats=8  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=5 Similarity=0.801481  
10 AAGGATCAGANCATCA-GGAGGTACCCATGTGATCCTTCGGATCTG  
Cele-UNSB01\_4:355820-356311 Satlength=492 Nr of Repeats=11  
RepeatLength=45 seed=GAAGGATCAG Num.seqs=7 Similarity=0.826455  
44 AAGGATCAGANCATCA-GGAGGTACCCATGTGATCCTTCGGATCTG  
Rev.of\_Cele-UNSB01\_4:8289359-8289627 Satlength=269 Nr of Repeats=6  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=4 Similarity=0.851852  
10 AAGGATCAGACCATCA-GGAGGTACCCTTACGATCCTTCGGAGCTG  
Cele-UNSB01\_2:3989433-3989722 Satlength=290 Nr of Repeats=6  
RepeatLength=45 seed=AAGGATCAGA Num.seqs=5 Similarity=0.643210  
45 AAGGATCAGATCANCA-GGAGGTACCCTTCTGATCCTTCGGAGCTG  
Rev.of\_Cele-UNSB01\_2:12892893-12893074 Satlength=182 Nr of Repeats=4  
RepeatLength=45 seed=ATCTGATCCT Num.seqs=3 Similarity=0.950617  
56 AAGGATCAGATCACCA-GGAGGTACCCTTNTGATCCTTCGGAGCTG  
Cele-UNSB01\_4:3428944-3430273 Satlength=1330 Nr of Repeats=24  
RepeatLength=45 seed=TCTGATCCTT Num.seqs=17 Similarity=0.598811  
72 AAGGATCAGATCANCA-GGAGGTACCCTTCTGATCCTTCGNAGCTG  
Rev.of\_Cele-UNSB01\_4:9825630-9825857 Satlength=228 Nr of Repeats=5  
RepeatLength=45 seed=GGGTACCTCC Num.seqs=3 Similarity=0.920988  
71 AAGGATCAGATCACCA-GGAGGTACCCTTCTGATCCTTCGGAGCTG  
Rev.of\_Cele-UNSB01\_4:11013752-11031328 Satlength=17577 Nr of Repeats=392  
RepeatLength=45 seed=TCCTGGTGAT Num.seqs=347 Similarity=0.928761  
64 AAGGATCAGATCACCA-GGAGGTACCCTTCTGATCCTTCGGAGCTT  
Cele-UNSB01\_4:11032975-11034460 Satlength=1486 Nr of Repeats=33  
RepeatLength=45 seed=TCACCAGGAG Num.seqs=33 Similarity=0.911616  
100 AAGGATCAGATCACCA-GGAGGTACCCTTCTGATCCTTCGGAGCTT  
Cele-UNSB01\_2:13755448-13762935 Satlength=7488 Nr of Repeats=166  
RepeatLength=45 seed=ACCAGGAGGT Num.seqs=165 Similarity=0.932682  
57 AATGATCAGATCACCA-GGAGGTACCCTTCTTATCCTTCGGAGCTG

Rev.of\_Cele-UNSB01\_1:10648848-10654019 Satlength=5172 Nr of Repeats=115  
RepeatLength=45 seed=AAGGATCACA Num.seqs=114 Similarity=0.941734  
37 AAGGATCAGATCATCA-GAAACTACCCTTGTGATCCTTCGAAGCTG

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Consensus:

AAGGATCAGAnCAcAGgAGGTACCcTtgtGATCCTTCGgAgCTG

>Cele-UNSB01\_Fam\_12\_20\_29 Nr. of seq. 29 Alignment length(with gaps) =  
25 Alignment score = 0.605057

Cele-UNSB01\_1:356425-357011 Satlength=587 Nr of Repeats=29  
RepeatLength=19 seed=TATCGATTTT Num.seqs=25 Similarity=0.914854  
0 TATCGATTTTT-C---TG-G-AATT

Rev.of\_Cele-UNSB01\_5:19313130-19313974 Satlength=845 Nr of Repeats=33  
RepeatLength=20 seed=AAAATCGATA Num.seqs=22 Similarity=0.814643

10 TATCGATTTTT-C---TG-GAAATT  
Cele-UNSB01\_5:19270843-19271693 Satlength=851 Nr of Repeats=31  
RepeatLength=20 seed=ATTTATTGAT Num.seqs=20 Similarity=0.886667  
17 TATCGATTTTT-C---TG-GAAATT

Cele-UNSB01\_5:19398669-19400674 Satlength=2006 Nr of Repeats=80  
RepeatLength=20 seed=TATCGATTTT Num.seqs=72 Similarity=0.876291  
20 TATCGATTTTT-C---TG-GAAATT

Cele-UNSB01\_5:19279992-19280235 Satlength=244 Nr of Repeats=8  
RepeatLength=20 seed=TATCGATTTT Num.seqs=5 Similarity=0.900000  
20 TATCGATTTTT-C---TG-CAAATT

Cele-UNSB01\_5:20220047-20220618 Satlength=572 Nr of Repeats=12  
RepeatLength=20 seed=TTATTGATTT Num.seqs=8 Similarity=0.876190  
19 TATTGATTTTT-A---TG-GAAATT

Rev.of\_Cele-UNSB01\_1:1841619-1842039 Satlength=421 Nr of Repeats=18  
RepeatLength=19 seed=AAAATCAATA Num.seqs=14 Similarity=0.796414  
10 TATTGATTTTT-C---TT-AGAATT

Rev.of\_Cele-UNSB01\_1:1841619-1843394 Satlength=1776 Nr of Repeats=44  
RepeatLength=19 seed=AAAATCAATA Num.seqs=32 Similarity=0.769949  
10 TATTGATTTTT-C---TN-NGAATT

Rev.of\_Cele-UNSB01\_4:1755267-1755667 Satlength=401 Nr of Repeats=20  
RepeatLength=20 seed=CAGAAAAATC Num.seqs=20 Similarity=0.835088  
14 TATTGATTTTT-C---TG-AGAATT

Cele-UNSB01\_5:18890478-18890638 Satlength=161 Nr of Repeats=8  
RepeatLength=20 seed=GATTTTTCTG Num.seqs=8 Similarity=0.871429  
24 TATTGATTTTT-C---TG-AAAATT

Rev.of\_Cele-UNSB01\_5:18933758-18934184 Satlength=427 Nr of Repeats=12  
RepeatLength=20 seed=AGAAAAATCA Num.seqs=8 Similarity=0.902381  
33 TATTGATTTTT-C---TG-AAAATT

Rev.of\_Cele-UNSB01\_5:19272660-19272781 Satlength=122 Nr of Repeats=6  
RepeatLength=20 seed=ATAAATTTTC Num.seqs=5 Similarity=0.960000  
43 TATTGATTTTT-C---TG-AAAATT

Rev.of\_Cele-UNSB01\_5:19385136-19386466 Satlength=1331 Nr of Repeats=44  
RepeatLength=20 seed=AAAAATCAAT Num.seqs=31 Similarity=0.770186  
31 TATTGATTTTT-C---TG-AAAATT

Cele-UNSB01\_5:19386514-19386960 Satlength=447 Nr of Repeats=10  
RepeatLength=20 seed=ATTGATTTTT Num.seqs=8 Similarity=0.861905  
41 TATTGATTTTT-C---TG-AAAATT

Cele-UNSB01\_5:19416239-19417040 Satlength=802 Nr of Repeats=34  
RepeatLength=20 seed=GATTTTTCTG Num.seqs=28 Similarity=0.875661  
24 TATTGATTTTT-C---TG-AAAATT  
Rev.of\_Cele-UNSB01\_5:19387732-19388133 Satlength=402 Nr of Repeats=17  
RepeatLength=20 seed=CAGAAAAATC Num.seqs=12 Similarity=0.905051  
14 TATTGATTTTT-C---TG-GAAATT  
Cele-UNSB01\_5:20212391-20212631 Satlength=241 Nr of Repeats=10  
RepeatLength=20 seed=TTATTGATTT Num.seqs=8 Similarity=0.866667  
19 TATTGATTTTT-C---TG-GAAATT  
Rev.of\_Cele-UNSB01\_5:20217981-20218181 Satlength=201 Nr of Repeats=9  
RepeatLength=20 seed=CAGAAAAATC Num.seqs=8 Similarity=0.873810  
14 TATTGATTTTT-C---TG-GAAATT  
Cele-UNSB01\_5:19407563-19408121 Satlength=559 Nr of Repeats=25  
RepeatLength=20 seed=AATTTATTGA Num.seqs=16 Similarity=0.823333  
16 TATTGATTTTT-T---TG-GAAATT  
Rev.of\_Cele-UNSB01\_6:210105-210613 Satlength=509 Nr of Repeats=10  
RepeatLength=20 seed=AAAAATCAAT Num.seqs=9 Similarity=0.907407  
31 TATTGATTTTT-N---TG-GAAATT  
Rev.of\_Cele-UNSB01\_1:11696998-11697105 Satlength=108 Nr of Repeats=5  
RepeatLength=19 seed=TCAAAAATCA Num.seqs=4 Similarity=0.873611  
12 -ATTGATTTTT-GA--TG--AAATT  
Rev.of\_Cele-UNSB01\_1:11591612-11591946 Satlength=335 Nr of Repeats=14  
RepeatLength=20 seed=AAAAATCAAT Num.seqs=11 Similarity=0.883636  
29 -ATTGATTTTTCGA--TG--AAATT  
Rev.of\_Cele-UNSB01\_1:11696961-11698223 Satlength=1263 Nr of Repeats=20  
RepeatLength=19 seed=AAAAATCGAT Num.seqs=12 Similarity=0.725830  
29 -ATCGATTTTT-GA--NG--AAATT  
Rev.of\_Cele-UNSB01\_2:2648748-2648862 Satlength=115 Nr of Repeats=6  
RepeatLength=19 seed=AAAATCGATA Num.seqs=6 Similarity=0.601058  
47 -ATCGATTTTC-GA--TG--AAATT  
Rev.of\_Cele-UNSB01\_1:11744458-11744933 Satlength=476 Nr of Repeats=17  
RepeatLength=19 seed=TTTCACAAAA Num.seqs=12 Similarity=0.943647  
17 -ATTGATTTTT-G---TGA-AAATT  
Rev.of\_Cele-UNSB01\_1:11743735-11745857 Satlength=2123 Nr of Repeats=45  
RepeatLength=19 seed=AAAATCGATA Num.seqs=29 Similarity=0.730706  
29 -ATCGATTTTT-N---TGA-AAATT  
Rev.of\_Cele-UNSB01\_4:984710-985413 Satlength=704 Nr of Repeats=35  
RepeatLength=19 seed=CAATAATTTTC Num.seqs=27 Similarity=0.905233  
24 -ATTGATTTTT-T-G-GG--AAATT  
Cele-UNSB01\_1:11592271-11597890 Satlength=5620 Nr of Repeats=277  
RepeatLength=20 seed=ATTGATTTTT Num.seqs=273 Similarity=0.884518  
40 -ATTGATTTTT-T-GAGG--AAATT  
Cele-UNSB01\_1:2396315-2396849 Satlength=535 Nr of Repeats=20  
RepeatLength=20 seed=TTATTGATTT Num.seqs=12 Similarity=0.816162  
38 -ATTGATTTTT-C-TAGG--ACATT

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Consensus:

tATtGATTTTTtTcTnAAATT

>Cele-UNSB01\_Fam\_13\_31\_27 Nr. of seq. 27 Alignment length(with gaps) =  
32 Alignment score = 0.817159

Cele-UNSB01\_3:81693-82933 Satlength=1241 Nr of Repeats=39 RepeatLength=31  
seed=TAAATAATTA Num.seqs=38 Similarity=0.865584  
0 TAAATAATTAGCAGA-CCAAAGTTGGGTCTGC

Cele-UNSB01\_3:88388-88698 Satlength=311 Nr of Repeats=9 RepeatLength=31  
seed=TGCTAAATAA Num.seqs=8 Similarity=0.907834  
28 TAAATAATTAGCAGA-CCAAAGTTGGGTATGC

Rev.of\_Cele-UNSB01\_3:523916-525062 Satlength=1147 Nr of Repeats=37  
RepeatLength=31 seed=GGTCTGCTAA Num.seqs=31 Similarity=0.865048  
48 TAAATAATTAGCAGA-CCAAAGTTGGGTATGC

Cele-UNSB01\_3:614340-614495 Satlength=156 Nr of Repeats=5 RepeatLength=31  
seed=TGGGTATGCT Num.seqs=5 Similarity=1.000000  
53 TAAATAATTAGCAGA-CCAAAGTTGGGTATGC

Rev.of\_Cele-UNSB01\_3:611245-611586 Satlength=342 Nr of Repeats=11  
RepeatLength=31 seed=GGTCTGCTAA Num.seqs=11 Similarity=0.968719  
17 TAAATAATTAGCAGA-CCGAAGTTGGGTATGC

Rev.of\_Cele-UNSB01\_3:344303-344830 Satlength=528 Nr of Repeats=17  
RepeatLength=31 seed=TGGTCTGCTA Num.seqs=15 Similarity=0.868920  
18 TAAATATTTAGCAGA-CCAAAGTTGGGTATGC

Cele-UNSB01\_3:356762-357146 Satlength=385 Nr of Repeats=13  
RepeatLength=31 seed=TTAGCAGACC Num.seqs=11 Similarity=0.960899  
38 TAAATATTTAGCAGA-CCAAAGTTGGGTATGC

Cele-UNSB01\_3:495426-496459 Satlength=1034 Nr of Repeats=16  
RepeatLength=31 seed=TTTAGCAGAC Num.seqs=10 Similarity=0.931183  
37 TAAATATTTAGCAGA-CCAAAGTTGGGTATGC

Cele-UNSB01\_3:503013-503261 Satlength=249 Nr of Repeats=8 RepeatLength=31  
seed=TTGGGTATGC Num.seqs=8 Similarity=0.970814  
21 TAAATATTTAGCAGA-CCAAAGTTGGGTATGC

Cele-UNSB01\_3:506857-507105 Satlength=249 Nr of Repeats=8 RepeatLength=31  
seed=GTATGCTAAA Num.seqs=8 Similarity=0.967742  
25 TAAATATTTAGCAGA-CCAAAGTTGGGTATGC

Rev.of\_Cele-UNSB01\_3:516006-516440 Satlength=435 Nr of Repeats=14  
RepeatLength=31 seed=GGTCTGCTAA Num.seqs=14 Similarity=0.954626  
48 TAAATATTTAGCAGA-CCAAAGTTGGGTATGC

Cele-UNSB01\_3:517798-519152 Satlength=1355 Nr of Repeats=34  
RepeatLength=31 seed=TTAGCAGACC Num.seqs=25 Similarity=0.924301  
38 TAAATATTTAGCAGA-CCAAAGATGGGTATGC

Cele-UNSB01\_3:882434-882682 Satlength=249 Nr of Repeats=7 RepeatLength=31  
seed=TAAATATTTA Num.seqs=6 Similarity=0.862366  
31 TAAATATTTAGCAGA-CCAAAGTTAGGTATGC

Rev.of\_Cele-UNSB01\_3:192738-193322 Satlength=585 Nr of Repeats=4  
RepeatLength=31 seed=TTAGCAGACC Num.seqs=3 Similarity=0.942652  
3 TAAATAATTAGCAGA-CCATAGTTGGGTCTGC

Cele-UNSB01\_3:421701-421887 Satlength=187 Nr of Repeats=6 RepeatLength=31  
seed=TTGGGTCTGC Num.seqs=6 Similarity=0.868100  
21 TAAATAATTAGCAGA-CCATAATTGGGTCTGC

Rev.of\_Cele-UNSB01\_3:437143-437747 Satlength=605 Nr of Repeats=6  
RepeatLength=31 seed=TATTTAGCAG Num.seqs=5 Similarity=0.901075  
37 TAAATAATTAGCAGA-CCATAATTGGGTCTGC

Rev.of\_Cele-UNSB01\_3:194647-195253 Satlength=607 Nr of Repeats=5  
RepeatLength=31 seed=TTAGCAGACC Num.seqs=3 Similarity=0.971326  
3 TAATTATTTAGCAGA-CCATACTTGGGTCTGC

Rev.of\_Cele-UNSB01\_3:196367-196735 Satlength=369 Nr of Repeats=7  
RepeatLength=31 seed=GGTCTGCTAA Num.seqs=6 Similarity=0.868100  
17 TAAATATTTAGCAGA-CCATACTTGGGTCTGC

Rev.of\_Cele-UNSB01\_3:198288-198567 Satlength=280 Nr of Repeats=9  
RepeatLength=31 seed=ACCCAAGTAT Num.seqs=9 Similarity=0.906810  
27 TAAACATTTAGCAGA-CCATACTTGGGTCTGC  
Cele-UNSB01\_3:10130069-10130193 Satlength=125 Nr of Repeats=4  
RepeatLength=31 seed=TCTGCTAAAT Num.seqs=4 Similarity=0.878136  
26 TAAATAATTAGCAGA-CCATACTTGATTCTGC  
Cele-UNSB01\_3:347263-347821 Satlength=559 Nr of Repeats=17  
RepeatLength=31 seed=TATGCTAAAT Num.seqs=16 Similarity=0.883154  
26 TAAATATTTAGCAGA-CCAAAAGTAGGTATGC  
Cele-UNSB01\_3:350896-352295 Satlength=1400 Nr of Repeats=23  
RepeatLength=31 seed=TTAGCAGACC Num.seqs=22 Similarity=0.867430  
38 TAAATATTTAGCAGA-CCAAAANTAGGTATGC  
Rev.of\_Cele-UNSB01\_3:355335-355552 Satlength=218 Nr of Repeats=7  
RepeatLength=31 seed=CTGCTAAATA Num.seqs=7 Similarity=0.938556  
45 TAAATATTTAGCAGA-CCCAAAGTTGGTATGC  
Rev.of\_Cele-UNSB01\_3:665955-666358 Satlength=404 Nr of Repeats=13  
RepeatLength=31 seed=TGGGTCTGCT Num.seqs=13 Similarity=0.912876  
50 TAAATATTTAGCAGA-CCCACAGTTGGTCTGC  
Rev.of\_Cele-UNSB01\_3:10214948-10215134 Satlength=187 Nr of Repeats=6  
RepeatLength=31 seed=TCTGCTAAAT Num.seqs=6 Similarity=0.962724  
46 TAAATATTTAGCAGA-CCCAATGTGGGTATGC  
Cele-UNSB01\_3:10234987-10235185 Satlength=199 Nr of Repeats=4  
RepeatLength=31 seed=TATGCTAAAT Num.seqs=3 Similarity=0.812500  
57 TAAATATTTAGCAGA-CCCAANGTGGNTATGC  
Cele-UNSB01\_3:660202-660394 Satlength=193 Nr of Repeats=6 RepeatLength=31  
seed=TTAGCAGACC Num.seqs=4 Similarity=0.781250  
7 TAAATAATTAGCAGACCCATAGGTAGGTATGC

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Consensus:

TAAATATTTAGCAGACCAaAgtTgGGTaTGC

>Cele-UNSB01\_Fam\_14\_43\_26 Nr. of seq. 26 Alignment length(with gaps) =  
46 Alignment score = 0.721271  
Cele-UNSB01\_1:1346901-1347222 Satlength=322 Nr of Repeats=5  
RepeatLength=42 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.705426  
0 TTTGCCGGAAATT-TTCATTTCCGGCAA-ATTGCCGATTTGNCG--  
Cele-UNSB01\_2:13106081-13106253 Satlength=173 Nr of Repeats=4  
RepeatLength=43 seed=CGGCAAATTA Num.seqs=4 Similarity=0.803618  
21 TTTGCCGGAAATT-TTCATTTCCGGCAA-ATTACCAATTTGCCGA-  
Rev.of\_Cele-UNSB01\_1:1822719-1823169 Satlength=451 Nr of Repeats=9  
RepeatLength=43 seed=AAATCGGCAA Num.seqs=7 Similarity=0.793282  
3 TTTGCCGGAAATT-TTCAATTCGGCAA-ATTGCCGGTTTGCCGA-  
Cele-UNSB01\_2:13060029-13060418 Satlength=390 Nr of Repeats=5  
RepeatLength=43 seed=GATTTGCCGG Num.seqs=3 Similarity=0.875969  
41 TTTGCCGGAAATT-TTCAATCCCGGCAA-ATTGCAGGTTTGCCGA-  
Cele-UNSB01\_4:2163715-2164250 Satlength=536 Nr of Repeats=8  
RepeatLength=43 seed=TTGCCGGAAA Num.seqs=5 Similarity=0.868148  
44 TTTGCCGGAAATT-TTCAATCCCGGCAT-TTTGCCGGTTTGCCGA-  
Rev.of\_Cele-UNSB01\_1:3471234-3471484 Satlength=251 Nr of Repeats=6  
RepeatLength=43 seed=TTGAAAATTT Num.seqs=5 Similarity=0.810853  
18 TTTGCCGGAAATT-TTCAATTCGGCAA-TTTGCCGGTTTGCCGA-

Rev.of\_Cele-UNSB01\_2:3141695-3142468 Satlength=774 Nr of Repeats=16  
 RepeatLength=43 seed=TTGCCGGAAT Num.seqs=13 Similarity=0.825084  
 27 TTTACAGGAAATT-TTCAATTCGGCAA-GTTGCCGGTTTGCCGA-  
 Rev.of\_Cele-UNSB01\_4:3002005-3002220 Satlength=216 Nr of Repeats=4  
 RepeatLength=43 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.739899  
 28 TTTNCAGGAAATT-TTCAATTCGGCAA-ACTGCCGGTTTGCCGA-  
 Rev.of\_Cele-UNSB01\_1:2293586-2294094 Satlength=509 Nr of Repeats=12  
 RepeatLength=43 seed=AATTTCCGGC Num.seqs=11 Similarity=0.790839  
 13 TTTGCCGGAAATT-TTTATTTTCGGCAA-NTTGCCGGTTTGCCGA-  
 Rev.of\_Cele-UNSB01\_1:11685636-11685851 Satlength=216 Nr of Repeats=5  
 RepeatLength=43 seed=CGGCAAATCG Num.seqs=5 Similarity=0.801550  
 50 TTTGCCGGAAATT-TTCATTTTCGGCAA-NTTGCCGGTTTGCCGA-  
 Rev.of\_Cele-UNSB01\_2:12544046-12545336 Satlength=1291 Nr of Repeats=30  
 RepeatLength=43 seed=TTTCCGGCAA Num.seqs=30 Similarity=0.867914  
 54 TTTGCCGGAAATT-TTCATTTTCGGCAA-ATTGCCGGTTTGCCGA-  
 Cele-UNSB01\_3:12321003-12321555 Satlength=553 Nr of Repeats=10  
 RepeatLength=43 seed=AATTGCCGGT Num.seqs=7 Similarity=0.748854  
 69 TTTGCCGGAAAT-TTCATTTTCGGCAA-ATTGCCGGTTTGCCGA-  
 Cele-UNSB01\_3:13409998-13411238 Satlength=1241 Nr of Repeats=25  
 RepeatLength=43 seed=CGGAAATTTT Num.seqs=17 Similarity=0.776106  
 48 TTTGCCGGAAATT-TTNATTTTCGGCAA-TTGCCNGTTTGCCGA-  
 Cele-UNSB01\_2:12862834-12863019 Satlength=186 Nr of Repeats=5  
 RepeatLength=43 seed=TATTTTCATT Num.seqs=3 Similarity=0.979328  
 52 TTTGCCGGGTATT-TTCATTTTCGGCAA-ATTGCCGGTTTGCCGA-  
 Cele-UNSB01\_1:696260-697073 Satlength=814 Nr of Repeats=14  
 RepeatLength=44 seed=TTTGCCGGTT Num.seqs=9 Similarity=0.920875  
 28 TTTGCCCGAAATTTTCAATTTTCGGCAA-TTTGCCGGTTTGCCGA-  
 Rev.of\_Cele-UNSB01\_1:1824052-1824465 Satlength=414 Nr of Repeats=9  
 RepeatLength=43 seed=GCCGGAATTG Num.seqs=7 Similarity=0.864157  
 25 TTTGCCAGAAATT-TTCAATTCGGCTA-TGTGCCGGTTTGCCGA-  
 Cele-UNSB01\_1:2859395-2859671 Satlength=277 Nr of Repeats=5  
 RepeatLength=43 seed=TTGCCGATTT Num.seqs=3 Similarity=0.834625  
 29 TTTGCCGGAAATT-TACAATTCC-ACTATTTTGCCGGTTTGCCGA-  
 Rev.of\_Cele-UNSB01\_1:1232170-1233535 Satlength=1366 Nr of Repeats=32  
 RepeatLength=43 seed=CCAGAAATTA Num.seqs=22 Similarity=0.892211  
 24 TTTGCCGAAATT-CTAATTTCTGGCAA-TTGCCGGTTTGCTGA-  
 Rev.of\_Cele-UNSB01\_1:2899706-2899878 Satlength=173 Nr of Repeats=4  
 RepeatLength=43 seed=AAATCGGCAA Num.seqs=4 Similarity=0.906977  
 46 TTTGCCGGGAATT-TTCATTTTTTGCAA-TTGCCGGATTGCCGA-  
 Rev.of\_Cele-UNSB01\_3:12885748-12886017 Satlength=270 Nr of Repeats=5  
 RepeatLength=43 seed=GGCAAATCGG Num.seqs=3 Similarity=0.689394  
 49 TTTGCCGGAAATT-TTNATATTTNACAA-ATTGCCGGTTTGCCGA-  
 Cele-UNSB01\_1:2695367-2695539 Satlength=173 Nr of Repeats=4  
 RepeatLength=43 seed=TTGCCGATTT Num.seqs=4 Similarity=0.798450  
 36 TTTGCCGGAAATG-TTTATTTCCGACAA-TTGGCAGATTGCCGA-  
 Cele-UNSB01\_1:14804070-14804449 Satlength=380 Nr of Repeats=9  
 RepeatLength=43 seed=TTTGCCGGTT Num.seqs=8 Similarity=0.931340  
 27 TTCGACGGAAATT-TTTATTTTCGGCAC-TTGCCGGTTTGCCGG-  
 Rev.of\_Cele-UNSB01\_5:3651691-3651860 Satlength=170 Nr of Repeats=4  
 RepeatLength=42 seed=TTTCCAGCAA Num.seqs=3 Similarity=0.767196  
 11 TTTGCTGGAAT-T-CTCAATTCGGCAA-TTCGCTGATTGCCGA-  
 Rev.of\_Cele-UNSB01\_1:2263475-2263726 Satlength=252 Nr of Repeats=6  
 RepeatLength=43 seed=CAAATCGGCA Num.seqs=5 Similarity=0.782946  
 47 TTTGCTGGAATT-TTAATTTCGGAAA-TTGCCGAGTTGCCGA-

Cele-UNSB01\_5:18100660-18102309 Satlength=1650 Nr of Repeats=32  
RepeatLength=44 seed=TTGCCGGAAA Num.seqs=27 Similarity=0.807908  
1 TTTGCCGGAAATA-TTCAATTTTGGCAA-ATTGNCGGTTTGCTGAA  
Cele-UNSB01\_1:11320046-11320214 Satlength=169 Nr of Repeats=4  
RepeatLength=42 seed=TGCCGGAAAT Num.seqs=4 Similarity=0.788360  
2 GCTGCCGGAAATT--TCAAACCCGGCAA-TTGCCCATTGCCGA-

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Consensus:

TTTGCCGGAAATTTTcAaTTcCGGCAAtTTGCCGgTTTGCCGA

>Cele-UNSB01\_Fam\_15\_26\_22 Nr. of seq. 22 Alignment length(with gaps) =  
26 Alignment score = 0.774226  
Cele-UNSB01\_1:3213789-3217715 Satlength=3927 Nr of Repeats=151  
RepeatLength=26 seed=CAGAGTCACT Num.seqs=151 Similarity=0.930474  
0 CAGAGTCACTATTTTTGGGGAACGGC  
Cele-UNSB01\_4:15642758-15643070 Satlength=313 Nr of Repeats=12  
RepeatLength=26 seed=CAGAGTCACT Num.seqs=12 Similarity=0.943279  
0 CAGAGTCACTATTTTTGGTGAACGGC  
Cele-UNSB01\_6:16179578-16182464 Satlength=2887 Nr of Repeats=111  
RepeatLength=26 seed=GTGAACGGCC Num.seqs=111 Similarity=0.930666  
17 CAGAGTCACTATTTTTGGTGAACGGC  
Rev.of\_Cele-UNSB01\_2:3110-3266 Satlength=157 Nr of Repeats=6  
RepeatLength=26 seed=GTTCACCAA Num.seqs=6 Similarity=0.921368  
23 CAGAGTCACTATTTTTGGTGAACGGT  
Cele-UNSB01\_6:1682621-1693139 Satlength=10519 Nr of Repeats=404  
RepeatLength=26 seed=AACGGTCAGA Num.seqs=393 Similarity=0.943434  
46 CAGAGTCACTATTTTTGGTGAACGGT  
Rev.of\_Cele-UNSB01\_4:11073363-11083545 Satlength=10183 Nr of Repeats=395  
RepeatLength=26 seed=GTTCACCAA Num.seqs=331 Similarity=0.919481  
23 CAGAGTCACTAAATTTGGTGAACGGC  
Cele-UNSB01\_5:5272176-5275211 Satlength=3036 Nr of Repeats=112  
RepeatLength=26 seed=CAGAGTCACT Num.seqs=99 Similarity=0.819649  
26 CAGAGTCACTAATTTTGGTGAACGGC  
Rev.of\_Cele-UNSB01\_6:5769379-5769561 Satlength=183 Nr of Repeats=7  
RepeatLength=26 seed=TAGTGACTCT Num.seqs=7 Similarity=0.836567  
37 CAGAGTCACTAATTTTGGTGAACGGC  
Cele-UNSB01\_5:10490005-10492889 Satlength=2885 Nr of Repeats=111  
RepeatLength=26 seed=CCAGAGTCAC Num.seqs=109 Similarity=0.974141  
25 CAGAGTCACTATATTTGGTGAACGGC  
Rev.of\_Cele-UNSB01\_6:2093711-2093945 Satlength=235 Nr of Repeats=9  
RepeatLength=26 seed=ATAGTGACTC Num.seqs=9 Similarity=0.897436  
38 CAGAGTCACTATATTTGGTGAACGGC  
Cele-UNSB01\_3:958005-958109 Satlength=105 Nr of Repeats=4 RepeatLength=26  
seed=CGGCCAGAGT Num.seqs=4 Similarity=0.863248  
22 CAGAGTCACTACTTATGGTGAACGGC  
Rev.of\_Cele-UNSB01\_1:13507576-13507758 Satlength=183 Nr of Repeats=7  
RepeatLength=26 seed=CTCTGGCAGT Num.seqs=7 Similarity=0.941392  
5 CAGAGCCACTTATTTTAGTGAAGTGC  
Cele-UNSB01\_4:11084695-11084799 Satlength=105 Nr of Repeats=4  
RepeatLength=26 seed=CCAGAGTCAC Num.seqs=4 Similarity=0.863248  
25 CAGAGTCACTATTTTAGTGAAGTGC



Cele-UNSB01\_6:2485227-2486657 Satlength=1431 Nr of Repeats=55  
RepeatLength=26 seed=TTTTAGTGAA Num.seqs=55 Similarity=0.934801  
38 CAGAGTCACTAATTTTAGTGAAGTGC  
Cele-UNSB01\_1:3711978-3718275 Satlength=6298 Nr of Repeats=242  
RepeatLength=26 seed=ATGGTTAGAG Num.seqs=238 Similarity=0.970067  
21 TAGAGTCATATTTTAGGTGAATGGT  
Rev.of\_Cele-UNSB01\_6:1697161-1700255 Satlength=3095 Nr of Repeats=119  
RepeatLength=26 seed=GACTCTAACC Num.seqs=119 Similarity=0.954495  
33 TAGAGTCATATTTTAGGTGAATGGT  
Cele-UNSB01\_1:13634561-13638668 Satlength=4108 Nr of Repeats=158  
RepeatLength=26 seed=TTTTAGGTGA Num.seqs=157 Similarity=0.972948  
37 TAGAGTCATAATTTTAGGTGAATGGT  
Cele-UNSB01\_3:5494321-5534864 Satlength=40544 Nr of Repeats=1542  
RepeatLength=26 seed=GTAGAGTCA Num.seqs=1416 Similarity=0.990443  
24 TAGAGTCATTATTTTAGGTGAATGGT  
Rev.of\_Cele-UNSB01\_3:5534873-5535003 Satlength=131 Nr of Repeats=5  
RepeatLength=26 seed=ACCATTCCACC Num.seqs=5 Similarity=0.917949  
26 TAGAGTCATTATTTTAGGTGAATGGT  
Cele-UNSB01\_4:15002663-15002793 Satlength=131 Nr of Repeats=5  
RepeatLength=26 seed=TGGTTAGAGT Num.seqs=5 Similarity=0.958974  
48 TAGAGTCATTATTTTAGGTGAATGGT  
Rev.of\_Cele-UNSB01\_5:15290454-15290610 Satlength=157 Nr of Repeats=6  
RepeatLength=26 seed=TTCACCTAAA Num.seqs=6 Similarity=0.846154  
48 TAGAGTCATTATTTTAGGTGAATGGT  
Rev.of\_Cele-UNSB01\_6:12072301-12080487 Satlength=8187 Nr of Repeats=312  
RepeatLength=26 seed=ATGACTCTAA Num.seqs=264 Similarity=0.927423  
35 TAGAGTCATTATTTTAGGTGAATGGT

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Consensus:

cAGAGTCACtAtTTTTtGGTGAAcGGc

>Cele-UNSB01\_Fam\_16\_11\_21 Nr. of seq. 21 Alignment length(with gaps) =  
11 Alignment score = 0.924964  
Cele-UNSB01\_1:11907174-11907313 Satlength=140 Nr of Repeats=13  
RepeatLength=11 seed=TTTTGCACAT Num.seqs=9 Similarity=0.838384  
0 TTTTGCACATT  
Cele-UNSB01\_1:12310642-12315079 Satlength=4438 Nr of Repeats=373  
RepeatLength=11 seed=CACATTTTTT Num.seqs=292 Similarity=0.843776  
5 TTTTGCACATT  
Cele-UNSB01\_1:12350087-12350549 Satlength=463 Nr of Repeats=41  
RepeatLength=11 seed=TTGCACATTT Num.seqs=31 Similarity=0.961681  
2 TTTTGCACATT  
Cele-UNSB01\_2:4510577-4510967 Satlength=391 Nr of Repeats=36  
RepeatLength=11 seed=TGCACATTTT Num.seqs=30 Similarity=0.991919  
3 TTTTGCACATT  
Cele-UNSB01\_3:1301641-1302992 Satlength=1352 Nr of Repeats=116  
RepeatLength=11 seed=TTTTTGCA Num.seqs=73 Similarity=0.910060  
10 TTTTGCACATT  
Rev.of\_Cele-UNSB01\_3:1753459-1753580 Satlength=122 Nr of Repeats=11  
RepeatLength=11 seed=GCAAAAAATG Num.seqs=11 Similarity=0.960331  
6 TTTTGCACATT

Cele-UNSB01\_3:1891974-1892414 Satlength=441 Nr of Repeats=36  
RepeatLength=11 seed=ATTTTGTGCA Num.seqs=32 Similarity=0.920088  
8 TTTTGCACATT  
Rev.of\_Cele-UNSB01\_3:2068206-2068691 Satlength=486 Nr of Repeats=44  
RepeatLength=11 seed=TGTGCAAAAA Num.seqs=31 Similarity=0.939785  
9 TTTTGCACATT  
Cele-UNSB01\_3:12475925-12476790 Satlength=866 Nr of Repeats=62  
RepeatLength=11 seed=TTTTTGCACA Num.seqs=46 Similarity=1.000000  
10 TTTTGCACATT  
Rev.of\_Cele-UNSB01\_3:13432209-13432275 Satlength=67 Nr of Repeats=5  
RepeatLength=11 seed=AAAAATGTGC Num.seqs=4 Similarity=1.000000  
3 TTTTGCACATT  
Cele-UNSB01\_4:15883454-15883531 Satlength=78 Nr of Repeats=6  
RepeatLength=11 seed=TGCACATTTT Num.seqs=5 Similarity=0.903030  
3 TTTTGCACATT  
Rev.of\_Cele-UNSB01\_5:3602166-3602210 Satlength=45 Nr of Repeats=4  
RepeatLength=11 seed=CAAAAAATGT Num.seqs=4 Similarity=0.878788  
5 TTTTGCACATT  
Cele-UNSB01\_5:11125880-11126094 Satlength=215 Nr of Repeats=10  
RepeatLength=11 seed=CACATTTTTT Num.seqs=9 Similarity=0.946128  
5 TTTTGCACATT  
Rev.of\_Cele-UNSB01\_6:8836090-8836155 Satlength=66 Nr of Repeats=5  
RepeatLength=11 seed=GCAAAAAATG Num.seqs=4 Similarity=0.878788  
6 TTTTGCACATT  
Cele-UNSB01\_3:12166501-12166666 Satlength=166 Nr of Repeats=15  
RepeatLength=11 seed=ACATTTTTTTG Num.seqs=13 Similarity=0.919192  
6 TTTTGNACATT  
Rev.of\_Cele-UNSB01\_1:12056400-12056477 Satlength=78 Nr of Repeats=7  
RepeatLength=11 seed=CAAAAAATGT Num.seqs=7 Similarity=0.942280  
5 TTTTGGACATT  
Cele-UNSB01\_4:13730774-13730818 Satlength=45 Nr of Repeats=4  
RepeatLength=11 seed=CACATTTTTT Num.seqs=4 Similarity=0.919192  
5 TTTTCCACATT  
Rev.of\_Cele-UNSB01\_4:15255716-15255837 Satlength=122 Nr of Repeats=9  
RepeatLength=11 seed=TGTGCAAAAA Num.seqs=7 Similarity=0.838384  
9 TTTTGCACAAT  
Cele-UNSB01\_4:13759189-13759529 Satlength=341 Nr of Repeats=30  
RepeatLength=11 seed=GCACATTTTT Num.seqs=22 Similarity=0.772787  
4 TTTAGCACATT  
Rev.of\_Cele-UNSB01\_6:3377659-3377780 Satlength=122 Nr of Repeats=11  
RepeatLength=11 seed=AAAATGTGCT Num.seqs=7 Similarity=0.826720  
13 TTTAGCACATT  
Cele-UNSB01\_5:2836474-2836692 Satlength=219 Nr of Repeats=20  
RepeatLength=11 seed=GCACATTTTT Num.seqs=18 Similarity=0.909685  
4 TTTCGCACATT

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Consensus:

TTTTGCACATT

>Cele-UNSB01\_Fam\_17\_37\_19 Nr. of seq. 19 Alignment length(with gaps) =  
44 Alignment score = 0.712431

Cele-UNSB01\_5:16414638-16414819 Satlength=182 Nr of Repeats=5  
RepeatLength=36 seed=GGGAATTCAA Num.seqs=4 Similarity=0.962963  
0 GGGAA-TTCAAATTTT--AA--TTTTTGAAAAC-ATTTTGGC-  
Cele-UNSB01\_1:1341786-1343571 Satlength=1786 Nr of Repeats=47  
RepeatLength=38 seed=GGGAATTCAA Num.seqs=46 Similarity=0.937825  
0 GGGAA-TTCAAATTTT--AATTTTTTTGAAAAC-ATTTTGGC-  
Cele-UNSB01\_3:3145893-3146730 Satlength=838 Nr of Repeats=18  
RepeatLength=37 seed=ATTTTGGCGG Num.seqs=16 Similarity=0.920120  
29 GGGAA-TTCAAATTTT--AA-TTTTTCGAAAAC-ATTTTGGC-  
Cele-UNSB01\_5:17487338-17487635 Satlength=298 Nr of Repeats=8  
RepeatLength=37 seed=AAAACATTTT Num.seqs=5 Similarity=0.894737  
61 GGGAA-TTCAAATTTT--AA-TTTTTTGAAAAC-ATTTTGGC-  
Cele-UNSB01\_4:3135501-3135649 Satlength=149 Nr of Repeats=4  
RepeatLength=37 seed=TGGCGGGAAT Num.seqs=4 Similarity=0.867868  
33 GGGAA-TTCAAATTTT--AA-TTTTCCGAAAAC-ATTTTGGC-  
Cele-UNSB01\_2:12791702-12792113 Satlength=412 Nr of Repeats=11  
RepeatLength=37 seed=ATTTTGGCGG Num.seqs=7 Similarity=0.951952  
29 GGGAA-TTCAAATTTT--AA-TTTTTTGAAAAT-ATTTTGGC-  
Cele-UNSB01\_3:11241850-11242636 Satlength=787 Nr of Repeats=15  
RepeatLength=37 seed=TTGGCGGGAA Num.seqs=10 Similarity=0.935135  
32 GGGAA-TTCAAATTTT--AA-TTTTTTGAAAAT-ATTTTGGC-  
Cele-UNSB01\_4:286805-287284 Satlength=480 Nr of Repeats=13  
RepeatLength=37 seed=TTGGCGGGAA Num.seqs=9 Similarity=0.933934  
32 GGGAA-TTCAAATTTT--AA-TTTTTTGAAAAT-ATTTTGGC-  
Rev.of\_Cele-UNSB01\_4:17408894-17409724 Satlength=831 Nr of Repeats=9  
RepeatLength=37 seed=ATTCCCGCCA Num.seqs=6 Similarity=0.896697  
43 GGGAA-TTCAAATTTT--AA-TTTTTTGAAAAT-ATTTTGGC-  
Rev.of\_Cele-UNSB01\_4:1695920-1696142 Satlength=223 Nr of Repeats=6  
RepeatLength=37 seed=CGCCAAAATG Num.seqs=6 Similarity=0.894294  
38 GGGAA-TTCAAATTTT--AA-TTTTTTGAAAAC-ATTTTGGC-  
Cele-UNSB01\_4:16721546-16722348 Satlength=803 Nr of Repeats=4  
RepeatLength=37 seed=ATTCAAATTT Num.seqs=3 Similarity=0.951952  
41 GGGAA-TTCAAATTTT--AA-TTTTTTGAAAAT-ACTTTGGC-  
Cele-UNSB01\_3:13002319-13002507 Satlength=189 Nr of Repeats=5  
RepeatLength=38 seed=TTTTGGCGGG Num.seqs=3 Similarity=0.811966  
30 GGGAA-TTCAAATTTT--AA-TTTTTTGAAAAT-ATTTTGGC-  
Rev.of\_Cele-UNSB01\_5:20465532-20465791 Satlength=260 Nr of Repeats=7  
RepeatLength=37 seed=AATTTGAATT Num.seqs=7 Similarity=0.941656  
50 GGGAA-TTCAAATTTT--AA-TTTTTTCAAAAAT-ATTTTGGC-  
Cele-UNSB01\_4:16077133-16078206 Satlength=1074 Nr of Repeats=16  
RepeatLength=37 seed=CGGGAATTCA Num.seqs=13 Similarity=0.831370  
36 GGGAA-TTCAAATTTT--AA-TTTTTTG-AAATCATTTTGGC-  
Cele-UNSB01\_5:16082522-16083430 Satlength=909 Nr of Repeats=7  
RepeatLength=37 seed=GCGGGAATTC Num.seqs=5 Similarity=0.877477  
72 GGGAA-TTCAAATTTT--AA-TTATTTG-AAATCATTTTGGC-  
Cele-UNSB01\_1:282371-283239 Satlength=869 Nr of Repeats=23  
RepeatLength=38 seed=AAATTTTAAT Num.seqs=17 Similarity=0.995872  
9 GGGAAATTTAAATTTT--AA-TTTTTTGAAAAT-ATTTTGGC-  
Cele-UNSB01\_3:2214780-2216279 Satlength=1500 Nr of Repeats=39  
RepeatLength=39 seed=TTTTTGGCGG Num.seqs=29 Similarity=0.914530  
30 GGAAA-TTCAAAAATT-CAAA--TTTTCAAATAT-TTTTGGCG  
Cele-UNSB01\_3:2219970-2221469 Satlength=1500 Nr of Repeats=39  
RepeatLength=39 seed=TTTTTGGCGG Num.seqs=29 Similarity=0.914530  
30 GGAAA-TTCAAAAATT-CAAA--TTTTCAAATAT-TTTTGGCG

Rev.of\_Cele-UNSB01\_3:2223808-2223967 Satlength=160 Nr of Repeats=4  
RepeatLength=40 seed=TCCCGCCAAA Num.seqs=3 Similarity=0.866667  
42 GGAAA-TTCAAAAATT-TAAA-TTTTTTGAATAT-TTTTGGCG

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Consensus:

GGGAATTCAAATTTTAATTTTTtGAAAAtATTTTGGC

>Cele-UNSB01\_Fam\_18\_19\_18 Nr. of seq. 18 Alignment length(with gaps) =  
19 Alignment score = 0.859420

Cele-UNSB01\_1:13177981-13178228 Satlength=248 Nr of Repeats=13  
RepeatLength=19 seed=CAAGGCACTA Num.seqs=13 Similarity=0.816464  
0 CAAGGCACTAGAAATGCGC

Rev.of\_Cele-UNSB01\_5:18833669-18833973 Satlength=305 Nr of Repeats=15  
RepeatLength=19 seed=TAGTGCCTTG Num.seqs=12 Similarity=0.808612

10 CAAGGCACTAGAATTGCGC

Rev.of\_Cele-UNSB01\_5:18944459-18944687 Satlength=229 Nr of Repeats=8  
RepeatLength=19 seed=TTCTAGTGCC Num.seqs=5 Similarity=0.817544

13 CAAGGCACTAGAATTGCGC

Cele-UNSB01\_5:19667001-19667210 Satlength=210 Nr of Repeats=9  
RepeatLength=19 seed=TTGCGCCAAG Num.seqs=7 Similarity=0.744444

13 CAAGGCACTAGAATTGCGC

Rev.of\_Cele-UNSB01\_3:3356021-3356788 Satlength=768 Nr of Repeats=13  
RepeatLength=19 seed=CTTGCGCAA Num.seqs=8 Similarity=0.764411

4 CAAGGCACGAGAATTGCGC

Cele-UNSB01\_5:19673680-19673832 Satlength=153 Nr of Repeats=5  
RepeatLength=19 seed=AGAATTGCGC Num.seqs=3 Similarity=0.859649

9 CAAGGCACGAGAATTGCGC

Rev.of\_Cele-UNSB01\_5:19434732-19435093 Satlength=362 Nr of Repeats=16  
RepeatLength=19 seed=TGGCGCATTT Num.seqs=14 Similarity=0.787160

21 CAAGGCACGAGAAATGCGC

Rev.of\_Cele-UNSB01\_5:18413578-18417093 Satlength=3516 Nr of Repeats=121  
RepeatLength=19 seed=TTGACGCAAT Num.seqs=77 Similarity=0.809381

3 CAAGNCACTAGAATTGCGT

Rev.of\_Cele-UNSB01\_5:18631640-18632148 Satlength=509 Nr of Repeats=18  
RepeatLength=19 seed=TGACGCAATT Num.seqs=14 Similarity=0.787931

21 CAAGGCACTAGAATTGCGT

Rev.of\_Cele-UNSB01\_5:18934684-18935273 Satlength=590 Nr of Repeats=23  
RepeatLength=19 seed=TGACGCAATT Num.seqs=15 Similarity=0.830476

21 CAAGGCACTAGAATTGCGT

Cele-UNSB01\_5:18935616-18936186 Satlength=571 Nr of Repeats=26  
RepeatLength=19 seed=ACTAGAATTG Num.seqs=23 Similarity=0.820539

25 CAAGGCACTAGAATTGCGT

Rev.of\_Cele-UNSB01\_5:19673879-19674316 Satlength=438 Nr of Repeats=16  
RepeatLength=19 seed=GCCTTGACGC Num.seqs=11 Similarity=0.888995

25 CAAGGCACTAGAATTGCGT

Rev.of\_Cele-UNSB01\_5:20131328-20132164 Satlength=837 Nr of Repeats=37  
RepeatLength=19 seed=TAGTGCCTTG Num.seqs=30 Similarity=0.844807

29 CAAGGCACTAGAATTGCGT

Cele-UNSB01\_5:18630095-18630532 Satlength=438 Nr of Repeats=22  
RepeatLength=19 seed=CAAGGCACTA Num.seqs=21 Similarity=0.750042

19 CAAGGCACTANAATTGCGT

Rev.of\_Cele-UNSB01\_5:18831834-18832119 Satlength=286 Nr of Repeats=11  
RepeatLength=19 seed=TTGACGCAAT Num.seqs=9 Similarity=0.666667  
3 CAANGCACTAGAAATTGCGT  
Rev.of\_Cele-UNSB01\_5:18877478-18878086 Satlength=609 Nr of Repeats=29  
RepeatLength=19 seed=GTGCCTTGAC Num.seqs=26 Similarity=0.876923  
8 CAAGGCACTAGAAANTGCGT  
Cele-UNSB01\_2:3065991-3066701 Satlength=711 Nr of Repeats=18  
RepeatLength=19 seed=GCCAAGGCAC Num.seqs=11 Similarity=0.680606  
17 CAAGGCACTNGAAANGCGC  
Rev.of\_Cele-UNSB01\_5:19309007-19310074 Satlength=1068 Nr of Repeats=10  
RepeatLength=19 seed=TGGCGCATTT Num.seqs=6 Similarity=0.714620  
2 CAACTCACCAAATTGCGC

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Consensus:

CAAGGCACTAGAAATGCGC

>Cele-UNSB01\_Fam\_19\_14\_17 Nr. of seq. 17 Alignment length(with gaps) =  
14 Alignment score = 0.892682  
Cele-UNSB01\_2:11443617-11443668 Satlength=52 Nr of Repeats=4  
RepeatLength=12 seed=ACTATAACTA Num.seqs=3 Similarity=0.851852  
0 ACTATA-ACTACA-  
Cele-UNSB01\_1:11361560-11361658 Satlength=99 Nr of Repeats=7  
RepeatLength=14 seed=AACTACTAAC Num.seqs=7 Similarity=0.803175  
6 ACTACTAACTACTA  
Rev.of\_Cele-UNSB01\_1:13241763-13242154 Satlength=392 Nr of Repeats=8  
RepeatLength=14 seed=AGTTTGTAGT Num.seqs=5 Similarity=0.885714  
10 ACTACAAACTACAA  
Rev.of\_Cele-UNSB01\_1:13729567-13730578 Satlength=1012 Nr of Repeats=11  
RepeatLength=14 seed=TAGTTTGTAG Num.seqs=7 Similarity=0.845805  
18 ACTACAAACTACAA  
Cele-UNSB01\_1:13730896-13731271 Satlength=376 Nr of Repeats=11  
RepeatLength=14 seed=TACAAACTAC Num.seqs=7 Similarity=0.918367  
23 ACTACAAACTACAA  
Rev.of\_Cele-UNSB01\_1:14568940-14569168 Satlength=229 Nr of Repeats=4  
RepeatLength=14 seed=TGTAGTTTGT Num.seqs=3 Similarity=0.936508  
20 ACTACAAACTACAA  
Cele-UNSB01\_2:2655599-2656120 Satlength=522 Nr of Repeats=10  
RepeatLength=14 seed=CTACAAACTA Num.seqs=6 Similarity=0.796825  
22 ACTACAAACTACAA  
Cele-UNSB01\_2:12905171-12905894 Satlength=724 Nr of Repeats=9  
RepeatLength=14 seed=AACTACAAAC Num.seqs=7 Similarity=0.845805  
20 ACTACAAACTACAA  
Rev.of\_Cele-UNSB01\_2:13459229-13459607 Satlength=379 Nr of Repeats=13  
RepeatLength=14 seed=TAGTTTGTAG Num.seqs=8 Similarity=0.829932  
18 ACTACAAACTACAA  
Cele-UNSB01\_2:14136989-14138428 Satlength=1440 Nr of Repeats=41  
RepeatLength=14 seed=TACAAACTAC Num.seqs=27 Similarity=0.871659  
23 ACTACAAACTACAA  
Rev.of\_Cele-UNSB01\_2:14194765-14194942 Satlength=178 Nr of Repeats=5  
RepeatLength=14 seed=GTAGTTTGTGTA Num.seqs=3 Similarity=0.809524  
19 ACTACAAACTACAA

Rev.of\_Cele-UNSB01\_4:15529257-15530020 Satlength=764 Nr of Repeats=4  
RepeatLength=14 seed=TTGTAGTTTG Num.seqs=3 Similarity=0.936508  
21 ACTACAAACTACAA  
Cele-UNSB01\_5:18596071-18596370 Satlength=300 Nr of Repeats=14  
RepeatLength=14 seed=ACAAACTACA Num.seqs=10 Similarity=0.942857  
10 ACTACAAACTACAA  
Rev.of\_Cele-UNSB01\_5:19848468-19849404 Satlength=937 Nr of Repeats=7  
RepeatLength=14 seed=TTTGTAGTTT Num.seqs=5 Similarity=0.804444  
22 ACTACAAACTACAA  
Cele-UNSB01\_5:19849444-19849810 Satlength=367 Nr of Repeats=11  
RepeatLength=14 seed=ACAAACTACA Num.seqs=7 Similarity=0.931973  
10 ACTACANACTACAA  
Rev.of\_Cele-UNSB01\_1:13831060-13832042 Satlength=983 Nr of Repeats=52  
RepeatLength=14 seed=TGTAGTATGT Num.seqs=44 Similarity=0.966375  
20 ACTACATACTACAT  
Cele-UNSB01\_4:1639262-1639353 Satlength=92 Nr of Repeats=6  
RepeatLength=14 seed=ACTACACACT Num.seqs=5 Similarity=1.000000  
21 ACTACACACTACAC

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Consensus:

ACTACAaACTACAA

>Cele-UNSB01\_Fam\_20\_12\_15 Nr. of seq. 15 Alignment length(with gaps) =  
14 Alignment score = 0.745805  
Cele-UNSB01\_4:15644313-15644403 Satlength=91 Nr of Repeats=8  
RepeatLength=10 seed=TGTTATGATA Num.seqs=5 Similarity=0.763636  
0 TG-T-TATG--ATA  
Rev.of\_Cele-UNSB01\_1:11352081-11352141 Satlength=61 Nr of Repeats=5  
RepeatLength=12 seed=TATACATATA Num.seqs=5 Similarity=1.000000  
0 TG-TATATG-TATA  
Cele-UNSB01\_1:11550058-11550130 Satlength=73 Nr of Repeats=6  
RepeatLength=12 seed=TATATGTATA Num.seqs=6 Similarity=1.000000  
8 TG-TATATG-TATA  
Cele-UNSB01\_1:14674978-14675094 Satlength=117 Nr of Repeats=10  
RepeatLength=12 seed=ATATGTATAT Num.seqs=6 Similarity=0.888889  
9 TG-TATATG-TATA  
Cele-UNSB01\_2:2015956-2016256 Satlength=301 Nr of Repeats=25  
RepeatLength=12 seed=ATGTATATGT Num.seqs=25 Similarity=0.948889  
11 TG-TATATG-TATA  
Rev.of\_Cele-UNSB01\_2:3515774-3515844 Satlength=71 Nr of Repeats=4  
RepeatLength=12 seed=ATACATATAC Num.seqs=3 Similarity=1.000000  
11 TG-TATATG-TATA  
Rev.of\_Cele-UNSB01\_3:12842209-12842347 Satlength=139 Nr of Repeats=11  
RepeatLength=12 seed=TATACATATA Num.seqs=10 Similarity=1.000000  
0 TG-TATATG-TATA  
Cele-UNSB01\_4:1452742-1452796 Satlength=55 Nr of Repeats=4  
RepeatLength=12 seed=TATATGTATA Num.seqs=3 Similarity=1.000000  
8 TG-TATATG-TATA  
Cele-UNSB01\_5:18730021-18731423 Satlength=1403 Nr of Repeats=114  
RepeatLength=12 seed=GTATATGTAT Num.seqs=110 Similarity=0.972866  
7 TG-TATATG-TATA

Rev.of\_Cele-UNSB01\_5:19325271-19325379 Satlength=109 Nr of Repeats=9  
 RepeatLength=12 seed=ATACATATAC Num.seqs=9 Similarity=0.975309  
 11 TG-TATATG-TATA  
 Cele-UNSB01\_5:20269010-20269323 Satlength=314 Nr of Repeats=8  
 RepeatLength=12 seed=TATGTATATG Num.seqs=6 Similarity=1.000000  
 10 TG-TATATG-TATA  
 Rev.of\_Cele-UNSB01\_5:20277753-20277891 Satlength=139 Nr of Repeats=11  
 RepeatLength=12 seed=ATATACATAT Num.seqs=10 Similarity=1.000000  
 7 TG-TATATG-TATA  
 Cele-UNSB01\_5:19329973-19330169 Satlength=197 Nr of Repeats=8  
 RepeatLength=12 seed=ATATGTATAT Num.seqs=5 Similarity=0.777778  
 11 TA-TNTATA-TNTA  
 Cele-UNSB01\_5:19334298-19334625 Satlength=328 Nr of Repeats=23  
 RepeatLength=14 seed=TATATGTTAT Num.seqs=20 Similarity=0.980952  
 10 TGTTATATGTTATA  
 Rev.of\_Cele-UNSB01\_6:16529882-16530026 Satlength=145 Nr of Repeats=9  
 RepeatLength=14 seed=TACCATATAC Num.seqs=7 Similarity=0.841270  
 12 TGGTATATGGTATA

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Consensus:

TGTATATGTATA

>Cele-UNSB01\_Fam\_21\_18\_14 Nr. of seq. 14 Alignment length(with gaps) =  
 18 Alignment score = 0.786121  
 Cele-UNSB01\_2:4275898-4276001 Satlength=104 Nr of Repeats=5  
 RepeatLength=18 seed=TGCAAGACTA Num.seqs=3 Similarity=0.950617  
 0 TGCAAGACTAATAGAGAC  
 Cele-UNSB01\_3:949283-949630 Satlength=348 Nr of Repeats=8 RepeatLength=18  
 seed=TGCAAGACTA Num.seqs=5 Similarity=0.822222  
 0 TGCAAGACTAATAGAGAC  
 Rev.of\_Cele-UNSB01\_2:14582719-14582837 Satlength=119 Nr of Repeats=5  
 RepeatLength=18 seed=TAGTCTTGCA Num.seqs=3 Similarity=0.901235  
 10 TGCAAGACTAATAGAGGC  
 Cele-UNSB01\_6:13750177-13750509 Satlength=333 Nr of Repeats=8  
 RepeatLength=18 seed=TGCAAGACTA Num.seqs=5 Similarity=0.851852  
 18 TGCAAGACTAATAGAGGC  
 Cele-UNSB01\_5:3289995-3290260 Satlength=266 Nr of Repeats=4  
 RepeatLength=18 seed=TGCAAGACTA Num.seqs=3 Similarity=0.876543  
 18 TGCAAGACTANTAGAGGC  
 Rev.of\_Cele-UNSB01\_6:7806159-7806450 Satlength=292 Nr of Repeats=5  
 RepeatLength=18 seed=TAGTCTTGCA Num.seqs=3 Similarity=0.901235  
 10 TGCAAGACTATTAGAGGC  
 Cele-UNSB01\_6:14650166-14651272 Satlength=1107 Nr of Repeats=10  
 RepeatLength=18 seed=TGCAAGACTA Num.seqs=6 Similarity=0.841975  
 0 TGCAAGACTAATAAAGGC  
 Rev.of\_Cele-UNSB01\_4:3896416-3896737 Satlength=322 Nr of Repeats=5  
 RepeatLength=18 seed=ATTAGTATTG Num.seqs=3 Similarity=0.802469  
 12 TGCAATACTAATAGGGAG  
 Cele-UNSB01\_6:12159416-12159737 Satlength=322 Nr of Repeats=5  
 RepeatLength=18 seed=TGCAATACTA Num.seqs=3 Similarity=0.901235  
 18 TGCAAGACTAATAGGGAG

Rev.of\_Cele-UNSB01\_4:17395956-17396303 Satlength=348 Nr of Repeats=5  
RepeatLength=18 seed=GCACTCCCTA Num.seqs=3 Similarity=0.950617  
21 TGCAAGACTATTAGGGAG  
Rev.of\_Cele-UNSB01\_5:12442637-12442985 Satlength=349 Nr of Repeats=5  
RepeatLength=18 seed=GCACTCCCTA Num.seqs=3 Similarity=0.950617  
21 TGCAAGACTATTAGGGAG  
Rev.of\_Cele-UNSB01\_6:16506358-16506686 Satlength=329 Nr of Repeats=5  
RepeatLength=18 seed=ATTAGTTTTG Num.seqs=3 Similarity=0.950617  
12 TGCAAACTAATAGAGAG  
Rev.of\_Cele-UNSB01\_3:949715-950024 Satlength=310 Nr of Repeats=5  
RepeatLength=18 seed=TAGTGCTGCA Num.seqs=3 Similarity=0.777778  
10 TGCAGCACTANTAGAGAC  
Cele-UNSB01\_3:3928597-3928907 Satlength=311 Nr of Repeats=5  
RepeatLength=18 seed=TGCAGCACTA Num.seqs=3 Similarity=0.851852  
18 TGCAGCACTATTAGAGAC

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Consensus:

TGCAAGACTAaTAGaGac

>Cele-UNSB01\_Fam\_22\_59\_13 Nr. of seq. 13 Alignment length(with gaps) =  
60 Alignment score = 0.818661  
Cele-UNSB01\_1:4042754-4055380 Satlength=12627 Nr of Repeats=214  
RepeatLength=59 seed=AAAACCAAGTG Num.seqs=214 Similarity=0.852508  
0 AAAACCAAGTGACATTTGAAATT-TTATATTCTCCATAATTCTCGGTTTTAAATATTTTG  
Rev.of\_Cele-UNSB01\_2:898652-902061 Satlength=3410 Nr of Repeats=58  
RepeatLength=59 seed=TATGGAAAAT Num.seqs=56 Similarity=0.981848  
37 AAAACCAAGTGACATTTAAAAAT-CCATATTTTCCATAATTCTCAGTTTAAAAAATTTTG  
Rev.of\_Cele-UNSB01\_3:1059346-1075750 Satlength=16405 Nr of Repeats=279  
RepeatLength=59 seed=AACTGAGAAT Num.seqs=241 Similarity=0.923220  
47 AAAACCAAGTGACATTTAAATTT-CCATATTCTCCATAATTCTCAGTTTAAAAAATTTTG  
Rev.of\_Cele-UNSB01\_5:17588702-17608641 Satlength=19940 Nr of Repeats=337  
RepeatLength=59 seed=TTATGGTGAA Num.seqs=283 Similarity=0.948621  
97 AAAACCAAGTGACATTTGAATTT-CCATATTCACATAATTCTCGGTTTTAAAAAATTTTG  
Rev.of\_Cele-UNSB01\_3:9234667-9236218 Satlength=1552 Nr of Repeats=21  
RepeatLength=59 seed=TTCAAACTT Num.seqs=20 Similarity=0.972643  
61 AAAACCAAGTGACATTTGAAATT-CCATATTCTCCATAAATCTCAGTTTAAAAAGTTTTG  
Rev.of\_Cele-UNSB01\_5:6230981-6231799 Satlength=819 Nr of Repeats=13  
RepeatLength=59 seed=ATGTGCACTG Num.seqs=10 Similarity=0.954300  
74 AAAACCAAGTGACATTTGAAATT-CCATATTCTCCATTATTCTCAGTTTAAAAATTTTGT  
Rev.of\_Cele-UNSB01\_5:3006278-3006868 Satlength=591 Nr of Repeats=10  
RepeatLength=59 seed=AATTTCAAAT Num.seqs=10 Similarity=0.895123  
82 AAAACCAAGTGACATTTGAAATTNCCATATTTTCCATAATTCTCAGTTTAAAAATTTTGT  
Cele-UNSB01\_4:12303349-12310067 Satlength=6719 Nr of Repeats=128  
RepeatLength=59 seed=TCCATAATTC Num.seqs=91 Similarity=0.837481  
31 AAAACCAAGTGAAGTCTTGATATT-CCATATTTTCCATAATTCTCAGTTTAAAAATTTTGT  
Rev.of\_Cele-UNSB01\_5:6963271-6963507 Satlength=237 Nr of Repeats=4  
RepeatLength=59 seed=TGGAAATTCA Num.seqs=4 Similarity=0.951036  
85 AAAACCAAGTGAAGTCTTGAATTT-CCATTTTCCCATAATTCTCGGTTTTAAAAATTTTGT  
Rev.of\_Cele-UNSB01\_5:6966002-6966297 Satlength=296 Nr of Repeats=5  
RepeatLength=59 seed=TGGAAATTCA Num.seqs=5 Similarity=0.941243  
85 AAAACCAAGTGAAGTCTTGAATTT-CCATATTTCCCATAATTCTCGGTTTTAAAAATTTTGT



Rev.of\_Cele-UNSB01\_5:6971634-6982576 Satlength=10943 Nr of Repeats=186  
RepeatLength=59 seed=ATGGAAATTC Num.seqs=182 Similarity=0.914233  
86 AAAACCAAGTGAAGTCTTGAATTT-CCATATTCCCATAATTCTCGGTTTTAAANATTTTG  
Cele-UNSB01\_5:6964823-6965938 Satlength=1116 Nr of Repeats=19  
RepeatLength=59 seed=ACCAGTGAAG Num.seqs=13 Similarity=0.950167  
121 AAAACCAAGTGAAGTCTTGAATTT-CCATATTCCCATAATTCTCGGTTTTAAATTTTTTG  
Cele-UNSB01\_5:6967498-6969084 Satlength=1587 Nr of Repeats=27  
RepeatLength=59 seed=ACCAGTGAAG Num.seqs=20 Similarity=0.961939  
121 AAAACCAAGTGAAGTCTTGAATTT-CCATATTCCCATAATTCTCGGTTTTAAATTTTTTG

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Consensus:

AAAACCAAGTGcAcatTTGAAtTTCCATATTctCCATAATTCTCgGTTTTAAAaaTTTTG

>Cele-UNSB01\_Fam\_23\_20\_12 Nr. of seq. 12 Alignment length(with gaps) =  
21 Alignment score = 0.831890  
Cele-UNSB01\_1:1878816-1878916 Satlength=101 Nr of Repeats=5  
RepeatLength=20 seed=CTAGGCAGAC Num.seqs=5 Similarity=1.000000  
0 CTAGGCAG-ACCTAGCCTACC  
Cele-UNSB01\_1:3474380-3475480 Satlength=1101 Nr of Repeats=54  
RepeatLength=20 seed=CTAGGCAGAC Num.seqs=53 Similarity=0.846734  
0 CTAGGCAG-ACCTAGCCTACC  
Cele-UNSB01\_1:3474383-3476103 Satlength=1721 Nr of Repeats=83  
RepeatLength=20 seed=GGCAGACCTA Num.seqs=80 Similarity=0.844789  
3 CTAGGCAG-ACCTAGCCTACC  
Rev.of\_Cele-UNSB01\_3:5426163-5426753 Satlength=591 Nr of Repeats=28  
RepeatLength=20 seed=CTAGGTCTGC Num.seqs=25 Similarity=0.872444  
14 CTAGGCAG-ACCTAGCCTACC  
Rev.of\_Cele-UNSB01\_3:5426187-5427065 Satlength=879 Nr of Repeats=40  
RepeatLength=20 seed=GGTAGGCTAG Num.seqs=28 Similarity=0.844293  
0 CTAGGCAG-ACCTAGCCTACC  
Cele-UNSB01\_6:1553970-1554390 Satlength=421 Nr of Repeats=18  
RepeatLength=20 seed=AGGCAGACCT Num.seqs=16 Similarity=0.885556  
2 CTAGGCAG-ACCTAGCCTACC  
Cele-UNSB01\_5:915226-915380 Satlength=155 Nr of Repeats=8 RepeatLength=20  
seed=GGCAGACCTA Num.seqs=7 Similarity=0.809524  
3 CTAGGCAG-ACCTAGTCTACC  
Cele-UNSB01\_3:2578277-2578816 Satlength=540 Nr of Repeats=27  
RepeatLength=20 seed=GACCCAGCCT Num.seqs=26 Similarity=0.985026  
7 CCAGGCAG-ACCCAGCCTACC  
Cele-UNSB01\_3:2578282-2579101 Satlength=820 Nr of Repeats=41  
RepeatLength=20 seed=AGCCTACCCC Num.seqs=40 Similarity=0.907436  
12 CCAGGCAG-ACCCAGCCTACC  
Cele-UNSB01\_5:915117-915271 Satlength=155 Nr of Repeats=7 RepeatLength=20  
seed=CCTACCCAG Num.seqs=6 Similarity=0.871111  
14 CCAGGCAG-ACCTAGCCTACC  
Cele-UNSB01\_1:1878726-1878810 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=CCTACTCTAG Num.seqs=4 Similarity=1.000000  
15 CTAGGCAGCCCCTAGCCTACT  
Rev.of\_Cele-UNSB01\_6:16108332-16108500 Satlength=169 Nr of Repeats=8  
RepeatLength=21 seed=GGCTGCCGAG Num.seqs=8 Similarity=0.916100  
31 CTCGGCAGCCCCTAGCCTACC

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Consensus:

CtAGGCAGACCTAGCCTACC

>Cele-UNSB01\_Fam\_24\_32\_11   Nr. of seq. 11 Alignment length(with gaps) =  
34 Alignment score = 0.834759

Cele-UNSB01\_5:20579964-20580501 Satlength=538 Nr of Repeats=15  
RepeatLength=31 seed=CTACAAACTA   Num.seqs=9 Similarity=0.899642  
0   CTACAAACTACG-AG-TTTTGGGCGCTGCTAAG-

Cele-UNSB01\_5:20584979-20587201 Satlength=2223 Nr of Repeats=68  
RepeatLength=31 seed=GGCGCTGCTA   Num.seqs=43 Similarity=0.966992  
19   CTACAAACTACA-AG-ATTTGGGCGCTGCTAA-A

Rev.of\_Cele-UNSB01\_5:20575835-20576061 Satlength=227 Nr of Repeats=7  
RepeatLength=32 seed=TTAGCAGCGC   Num.seqs=5 Similarity=0.931313  
30   CTACAAACTACA-AGTTTTTGGGCGCTGCTAA-A

Rev.of\_Cele-UNSB01\_5:19404337-19404490 Satlength=154 Nr of Repeats=5  
RepeatLength=33 seed=TTAGCAGCGC   Num.seqs=4 Similarity=0.979798  
30   CTACAAACTACA-AGATTTTGGGCGCTGCTAAGA

Rev.of\_Cele-UNSB01\_5:19408877-19410842 Satlength=1966 Nr of Repeats=65  
RepeatLength=33 seed=AGCAGCGCCC   Num.seqs=49 Similarity=0.900143  
61   CTACAAACTACA-AGATTTTGGGCGCTGCTAAGA

Rev.of\_Cele-UNSB01\_6:179889-180069 Satlength=181 Nr of Repeats=5  
RepeatLength=32 seed=TTAGCAGCGC   Num.seqs=3 Similarity=0.944444  
30   CTACAAACTACA-AG-TTTTGGGCGCTGCTAACA

Cele-UNSB01\_6:207322-209932 Satlength=2611 Nr of Repeats=80  
RepeatLength=32 seed=TTTGGGCGCT   Num.seqs=62 Similarity=0.938886  
47   CTACAAACTACA-AG-TTTTGGGCGCTGCTAAGA

Rev.of\_Cele-UNSB01\_5:19172684-19173158 Satlength=475 Nr of Repeats=14  
RepeatLength=32 seed=TTGTAGTTTG   Num.seqs=9 Similarity=0.939815  
13   CTACAAACTACA-AA-TTTTGGGCGCTGCTTAGA

Cele-UNSB01\_5:20243571-20245480 Satlength=1910 Nr of Repeats=58  
RepeatLength=32 seed=ACTACAAACT   Num.seqs=46 Similarity=0.942073  
31   CTACAAACTACA-AG-TTTTGGGCGCTGCTTAGA

Cele-UNSB01\_5:20413138-20414402 Satlength=1265 Nr of Repeats=44  
RepeatLength=32 seed=TTTTGGGCGC   Num.seqs=27 Similarity=0.907170  
14   CTACAAACTACA-AT-TTTTGGGCGCTGCTTAGA

Rev.of\_Cele-UNSB01\_5:19275863-19276354 Satlength=492 Nr of Repeats=14  
RepeatLength=32 seed=TGTAGTTTGT   Num.seqs=9 Similarity=0.905443  
12   CTACAAACTACACAA-TTTTGGGCGCTGCTAA-A

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Consensus:

CTACAAACTACAAGTTTTGGGCGCTGCTaAgA

>Cele-UNSB01\_Fam\_25\_12\_11   Nr. of seq. 11 Alignment length(with gaps) =  
12 Alignment score = 0.746970

Cele-UNSB01\_2:2168167-2168227 Satlength=61 Nr of Repeats=4  
RepeatLength=11 seed=ACCGCAACGC   Num.seqs=3 Similarity=1.000000  
0   AC-CGCAACGCA

Rev.of\_Cele-UNSB01\_5:20920761-20921207 Satlength=447 Nr of Repeats=40  
RepeatLength=11 seed=GTTGCGGTTG Num.seqs=39 Similarity=0.965976  
8 AC-CGCAACGCA  
Rev.of\_Cele-UNSB01\_3:2058475-2058618 Satlength=144 Nr of Repeats=11  
RepeatLength=11 seed=GTCGCGTTGC Num.seqs=9 Similarity=0.885522  
2 AC-CGCAACGCG  
Rev.of\_Cele-UNSB01\_1:567454-567526 Satlength=73 Nr of Repeats=6  
RepeatLength=12 seed=GCGTTGCGTG Num.seqs=6 Similarity=0.896296  
4 ACGCGGCACGCA  
Cele-UNSB01\_1:2284293-2285881 Satlength=1589 Nr of Repeats=82  
RepeatLength=12 seed=CACGCAACGC Num.seqs=74 Similarity=0.933811  
6 ACGCAGCACGCA  
Rev.of\_Cele-UNSB01\_1:11460977-11461721 Satlength=745 Nr of Repeats=60  
RepeatLength=12 seed=CGTTGCGTGT Num.seqs=58 Similarity=0.901727  
15 ACGCGACACGCA  
Cele-UNSB01\_3:13290888-13291020 Satlength=133 Nr of Repeats=7  
RepeatLength=12 seed=CGCGACACGC Num.seqs=5 Similarity=0.822222  
25 ACGCGACACGCA  
Rev.of\_Cele-UNSB01\_4:4229494-4229583 Satlength=90 Nr of Repeats=7  
RepeatLength=12 seed=GTTGCGTGTC Num.seqs=6 Similarity=0.962963  
26 ACGCGACACGCA  
Rev.of\_Cele-UNSB01\_4:4229497-4230359 Satlength=863 Nr of Repeats=71  
RepeatLength=12 seed=GCGTGTCGCG Num.seqs=69 Similarity=0.901298  
23 ACGCGACACGCA  
Cele-UNSB01\_5:17801402-17801541 Satlength=140 Nr of Repeats=10  
RepeatLength=12 seed=ACGCGACACG Num.seqs=8 Similarity=0.972222  
24 ACGCGACACGCA  
Cele-UNSB01\_5:17569173-17569281 Satlength=109 Nr of Repeats=9  
RepeatLength=12 seed=CGCAACGCGA Num.seqs=9 Similarity=0.907407  
8 ACGCGATACGCA

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Consensus:

ACgCGacACGCA

>Cele-UNSB01\_Fam\_26\_163\_10 Nr. of seq. 10 Alignment length(with gaps) =  
172 Alignment score = 0.762446  
Cele-UNSB01\_1:995161-995964 Satlength=804 Nr of Repeats=5  
RepeatLength=162 seed=ATCATATGAA Num.seqs=4 Similarity=0.781893  
0 ATCATATGAAGCGATTCTTTTTCTTTTATAAACCTGTTTCAGAATTGGCAAACTACCAGAAAATAC-  
TAAACAAATTAGGCTAGCATGAACGGAAGT-A-T--TTTTTAAAAATTGAT-AAAAATA-ATG-  
AAAAGCTGA--TATTTTCAAAATTCCAGAATGACGGAAAA  
Rev.of\_Cele-UNSB01\_2:2065528-2066342 Satlength=815 Nr of Repeats=5  
RepeatLength=162 seed=AGTTTTATGA Num.seqs=3 Similarity=0.983539  
36  
ATCATATAGAGTCATTCTTTTTTATTTTCATAAACTCTTCAGCATAGTCAAAAATACCAGAAAATGC-  
TAAACAAAGTATAATAGTTTGTACGGAAGT-A-T--TTTTTAAAAATGGAT-AAAAATATAT--  
AAAAGCTGA--TTTTTTCAAAAATTCAAAAGTATGGGAAA  
Rev.of\_Cele-UNSB01\_2:15429658-15431122 Satlength=1465 Nr of Repeats=9  
RepeatLength=163 seed=AAATAAAAAA Num.seqs=8 Similarity=0.966696  
190  
ATCATATGGAGTCATTCTTTTTTATTTTCATAAACTGTTTCAGCATAGTTAAAATTACCAGAATATGC-

CAATCAAAGTATATTAGCTTGTACGGAAGT-ATT--TTTTTAAAAATTGAT-AAAAATATAT--  
 AAAAGCTGA--TTTTTTCAAAAATTCAAAGTATGGGAAA  
 Cele-UNSB01\_3:10519570-10525291 Satlength=5722 Nr of Repeats=35  
 RepeatLength=164 seed=ATGCCAATCA Num.seqs=23 Similarity=0.972621  
 226  
 ATCATATGGAGTCATTCTTTTTTATTGCATAAACTGTTTCAGTATAGTCAAAAATACCAGAATATGC-  
 CAATCAAAGTATAATAGCTTGTACGGAAGT-ATT--TTTTTAAAAATTGATAAAAAATATAT--  
 AAAAGCTGA--TTTTTTCAAAAATTCAAAGTATGGGAAA  
 Cele-UNSB01\_4:13731432-13732897 Satlength=1466 Nr of Repeats=8  
 RepeatLength=164 seed=AAAATTCAAA Num.seqs=5 Similarity=1.000000  
 306  
 ATCATATGGAGTCATTCTTTTTTATTTCATAAACTCTTCAGCATAGTCAAAAATACCAGAAAATGC-  
 CAATCAAAGTATAATAGCTTGTACGGAAGT-ATT--TTTTTAAAAATTGAT-AAAAATATAT--  
 AAAAGCTGAT-TTTTTTCAAAAATTCAAAGTATGGGAAA  
 Cele-UNSB01\_1:11925845-11930260 Satlength=4416 Nr of Repeats=27  
 RepeatLength=164 seed=ATACCAGAAA Num.seqs=20 Similarity=0.942191  
 216  
 ATCAAATGGAGTCATTCTTTTTTATTCCATAAACTGTTTCAGCATAGTCAAAAATACCAGAAAATGC-  
 CAATCAAAGTATATTAGCTTGTACGGAAGTAATT--TTTTTTTAAATTGAT-AAAAATATAT--  
 AAAAGCTGA--TTTTTTCAAAAATTCAAAGTATGGGAAA  
 Cele-UNSB01\_1:11042845-11046757 Satlength=3913 Nr of Repeats=24  
 RepeatLength=163 seed=GCATAGTCAA Num.seqs=24 Similarity=0.936516  
 41  
 ATCATATGGAGTCATTCTTTTTTATCTCAAAAACTGTTTCAGCATAGTCAAAAATACCAGCAAATAC-  
 CAAACAGAGTATATTAGCTTGTACGGAAGT-ATT--TTTTAGAAAATTGAT-AAAAATATAT--  
 AAAAGCTGA--TTTTTTCAAAAATTCAAAGTATGGGAAA  
 Rev.of\_Cele-UNSB01\_5:16471613-16475389 Satlength=3777 Nr of Repeats=23  
 RepeatLength=164 seed=CGTACAAGCT Num.seqs=17 Similarity=0.961741  
 92  
 ATCATATGGAGTCATTCTTTTTTATTTCATAAAAAATGTTTCAGCATAGTCAAAAACACCAGAATATGC-  
 CAATCAAAGTATAATAGCTTGTACGGAAGT-ATT--CTTTAAAAAATTGAT-AAAAATATAT--  
 AAAATCTGA-TTTTTTTCAAAAATTCAAAGTCCTAGAAA  
 Rev.of\_Cele-UNSB01\_2:2379059-2380853 Satlength=1795 Nr of Repeats=9  
 RepeatLength=163 seed=TGAATTTTGT Num.seqs=7 Similarity=0.906387  
 150  
 ATCATATGAAGTCATTCTTTTTTATTTTATAAACTGTTTCAGCATAGTCAAATGTACCAGAAAATACTTAAAA  
 AAAG-GTGCTAGCTCGTACGGAAGT--TTATTTTTTAAAAATGCAG--AATTTAAC-CAAAGCTG--  
 TTATTTTTCAAAAATTCAAAGTACCTCAAA  
 Cele-UNSB01\_4:2599504-2602273 Satlength=2770 Nr of Repeats=17  
 RepeatLength=164 seed=CTTTTTTCTT Num.seqs=16 Similarity=0.982520  
 179  
 ATCATAAAAAGTGCTTCTTTTTTCTTTTATAACACTGTTTAGCATAGTCAAATATACCAGAAAATAC-  
 CAAACAAAGTATGCTATCTTGTACGAAAGA--TTA-TTTTAAAAAATTCAG--AAAATGCAT-  
 CTAAAGCGGT-TTTTTTTCAAAAATTCAAAGTACCGGAAA

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Consensus:

ATCATATggAGTcATTCTTTTTTaTtTcATAAACTgTTCAGcATAGTCAAAaATACCAGAAaATgCcAAaCA  
 AAGTATanTAGCTTGTACGGAAGTatTTTTTtAAAAAtgAtaAAAATatATAAAAGCTGaTtTTTTCAAAAA  
 TTCAAAAGTAtgggAAA

>Cele-UNSB01\_Fam\_27\_31\_10 Nr. of seq. 10 Alignment length(with gaps) =  
 37 Alignment score = 0.720120  
 Cele-UNSB01\_3:2212231-2213000 Satlength=770 Nr of Repeats=22  
 RepeatLength=31 seed=ATTTCCCGCC Num.seqs=14 Similarity=0.922486  
 0 ATTTCCCGCCAAAAATA--TTT--GAAAATTTGA  
 Rev.of\_Cele-UNSB01\_5:18406789-18410349 Satlength=3561 Nr of Repeats=114  
 RepeatLength=31 seed=GTCAATTTTT Num.seqs=88 Similarity=0.885902  
 20 ATTTCCCGCCAAAAATTG---ACT--GAAAATTTGA  
 Cele-UNSB01\_5:19832755-19833004 Satlength=250 Nr of Repeats=6  
 RepeatLength=31 seed=AATTTCCCGC Num.seqs=5 Similarity=0.756250  
 30 ATTTCCCGCCAAAAATTG---ACT--GAAAATTTGA  
 Rev.of\_Cele-UNSB01\_5:19928437-19928836 Satlength=400 Nr of Repeats=12  
 RepeatLength=31 seed=GGCGGGAAAT Num.seqs=8 Similarity=0.930876  
 41 ATTTCCCGCCAAAAATTG---ACT--GAAAATTTGA  
 Rev.of\_Cele-UNSB01\_5:19938977-19939376 Satlength=400 Nr of Repeats=12  
 RepeatLength=31 seed=GGCGGGAAAT Num.seqs=8 Similarity=0.930876  
 41 ATTTCCCGCCAAAAATTG---ACT--GAAAATTTGA  
 Cele-UNSB01\_5:19998052-19998541 Satlength=490 Nr of Repeats=10  
 RepeatLength=31 seed=AAAATTTGAA Num.seqs=9 Similarity=0.942652  
 22 ATTTCCCGCCAAAAATTG---ACT--GAAAATTTGA  
 Rev.of\_Cele-UNSB01\_5:19670399-19670678 Satlength=280 Nr of Repeats=9  
 RepeatLength=31 seed=CGGGAAATTC Num.seqs=7 Similarity=0.774706  
 39 ATTTCCCGCCAAAAATTA---ACT--GAAAATTTGA  
 Rev.of\_Cele-UNSB01\_5:19913255-19913615 Satlength=361 Nr of Repeats=8  
 RepeatLength=31 seed=TTCAAATTTT Num.seqs=7 Similarity=0.819764  
 32 AATTCCCGCCAAAAATTG---ACT--GAAAATTTGA  
 Cele-UNSB01\_5:20173699-20174897 Satlength=1199 Nr of Repeats=28  
 RepeatLength=31 seed=TTCCCGCCTA Num.seqs=17 Similarity=0.854243  
 2 ATTTCCCGCCTAAACT---ACTC--GAAAATTTCAA  
 Rev.of\_Cele-UNSB01\_5:18924789-18925018 Satlength=230 Nr of Repeats=6  
 RepeatLength=35 seed=GGAAATTCAA Num.seqs=4 Similarity=0.776235  
 6 ATTTTCCCGCCAAAAATATTTTCT-CCGAAAATTTGA

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Consensus:

ATTTCCCGCCAAAAATgACTGAAAATTTGA

>Cele-UNSB01\_Fam\_28\_26\_10 Nr. of seq. 10 Alignment length(with gaps) =  
 27 Alignment score = 0.716324  
 Cele-UNSB01\_2:5166221-5171016 Satlength=4796 Nr of Repeats=184  
 RepeatLength=26 seed=TAGACCATTA Num.seqs=155 Similarity=0.871050  
 0 TAGACCATTAGATGAATTTTCAAAGT  
 Rev.of\_Cele-UNSB01\_4:4479166-4488089 Satlength=8924 Nr of Repeats=327  
 RepeatLength=26 seed=GTCTAACTTT Num.seqs=305 Similarity=0.965297  
 5 TAGACCATTAGATGAATTTTCAAAGT  
 Cele-UNSB01\_4:13295662-13296286 Satlength=625 Nr of Repeats=24  
 RepeatLength=26 seed=ATTAGATGAA Num.seqs=24 Similarity=0.974173  
 6 TAGACCATTAGATGAATTTTCAAAGT  
 Cele-UNSB01\_3:7826007-7841897 Satlength=15891 Nr of Repeats=610  
 RepeatLength=26 seed=CATTAGATGA Num.seqs=417 Similarity=0.923292  
 5 TAGACCATTAGATGAATTCC-CAAAGT

Rev.of\_Cele-UNSB01\_6:16057246-16058243 Satlength=998 Nr of Repeats=38  
RepeatLength=26 seed=AATTCATCTA Num.seqs=36 Similarity=0.954009  
18 TAGACCAGTAGATGAATTCC-CAAAGT  
Cele-UNSB01\_6:12080509-12089472 Satlength=8964 Nr of Repeats=344  
RepeatLength=26 seed=AAGTTAGACC Num.seqs=291 Similarity=0.954261  
22 TAGACCATTAGATGAATTTA-TAAAGT  
Rev.of\_Cele-UNSB01\_6:6135861-6144415 Satlength=8555 Nr of Repeats=329  
RepeatLength=26 seed=TTCTAAATTT Num.seqs=329 Similarity=0.936466  
5 TAGAACGGTAGATGAATTTT-CAAATT  
Rev.of\_Cele-UNSB01\_4:13647739-13648797 Satlength=1059 Nr of Repeats=13  
RepeatLength=27 seed=TTTTTAAAT Num.seqs=11 Similarity=0.892256  
25 TAGAACGGTATATGAATTTTAAAAAGT  
Rev.of\_Cele-UNSB01\_6:11535780-11535884 Satlength=105 Nr of Repeats=4  
RepeatLength=26 seed=AAATTAATCT Num.seqs=4 Similarity=0.803419  
19 TAGAGTGACAGATTAATTTA-AAAAGT  
Rev.of\_Cele-UNSB01\_6:15966442-15966650 Satlength=209 Nr of Repeats=8  
RepeatLength=26 seed=GGTCTAACTT Num.seqs=8 Similarity=0.899267  
32 TAGACCGTCAGATCCATTTA-TAAAGT

\*\*\*\* \* \*\* \*\*\* \*\*\* \*

Consensus:

TAGAcCattAGATgAATTtccAAAGT

>Cele-UNSB01\_Fam\_29\_21\_10 Nr. of seq. 10 Alignment length(with gaps) =  
23 Alignment score = 0.611433  
Cele-UNSB01\_6:960884-960987 Satlength=104 Nr of Repeats=5 RepeatLength=20  
seed=ATGCACTGAC Num.seqs=3 Similarity=0.866667  
0 AT-GCACTGACCAAAAATATG--  
Rev.of\_Cele-UNSB01\_6:998781-998865 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=CAGTGCATTC Num.seqs=4 Similarity=0.830688  
8 AT-GCACTGACCAAGTTCTGA-  
Rev.of\_Cele-UNSB01\_6:998801-998992 Satlength=192 Nr of Repeats=6  
RepeatLength=21 seed=TCAGTGCATT Num.seqs=4 Similarity=0.735450  
9 AT-GCACTGACCAAACTTCTGA-  
Rev.of\_Cele-UNSB01\_6:1060978-1061104 Satlength=127 Nr of Repeats=6  
RepeatLength=21 seed=GTCAGTGCAT Num.seqs=6 Similarity=0.944974  
10 AT-GCACTGACCGAAACTATCA-  
Rev.of\_Cele-UNSB01\_6:1066955-1067057 Satlength=103 Nr of Repeats=5  
RepeatLength=20 seed=TTGGTCAGTG Num.seqs=3 Similarity=0.955556  
13 AT-GCACTGACCAAGACTA-AA-  
Rev.of\_Cele-UNSB01\_6:3814487-3814588 Satlength=102 Nr of Repeats=5  
RepeatLength=20 seed=TTTGGTCAGT Num.seqs=4 Similarity=0.933333  
14 AA-GCACTGACCAAA-ATA-GAA  
Cele-UNSB01\_6:903956-904040 Satlength=85 Nr of Repeats=4 RepeatLength=21  
seed=ACTGACCAAA Num.seqs=4 Similarity=0.936508  
25 AT-GCACTGACCAAAAATA-GAT  
Cele-UNSB01\_6:1342228-1342338 Satlength=111 Nr of Repeats=5  
RepeatLength=22 seed=TCGCACTGAC Num.seqs=5 Similarity=0.915152  
22 ATCGCACTGACCAAACTTA-GAA  
Rev.of\_Cele-UNSB01\_6:743518-743644 Satlength=127 Nr of Repeats=5  
RepeatLength=21 seed=GGTCACTGCA Num.seqs=4 Similarity=0.904762  
32 AT-GCACTGACCAAAATTG-GTA

Rev.of\_Cele-UNSB01\_6:1102792-1102897 Satlength=106 Nr of Repeats=4  
RepeatLength=21 seed=GTCAGTGCAA Num.seqs=3 Similarity=0.661376  
10 TT-GCACTGACCANNACTCTAA-

\*\*\*\*\* \*

Consensus:

ATGCACTGACCAAaanTatga

>Cele-UNSB01\_Fam\_30\_12\_10 Nr. of seq. 10 Alignment length(with gaps) =  
14 Alignment score = 0.713757

Cele-UNSB01\_1:4669638-4670054 Satlength=417 Nr of Repeats=33  
RepeatLength=12 seed=TTTTTATTTT Num.seqs=26 Similarity=0.967179  
0 TTTTTATTTT-TTA-

Cele-UNSB01\_1:4669638-4670196 Satlength=559 Nr of Repeats=41  
RepeatLength=12 seed=TTTTTATTTT Num.seqs=27 Similarity=0.968344  
0 TTTTTATTTT-TTA-

Cele-UNSB01\_1:4669638-4670946 Satlength=1309 Nr of Repeats=43  
RepeatLength=12 seed=TTTTTATTTT Num.seqs=27 Similarity=0.968344  
0 TTTTTATTTT-TTA-

Rev.of\_Cele-UNSB01\_2:11255667-11256407 Satlength=741 Nr of Repeats=61  
RepeatLength=12 seed=AAAAATAAAA Num.seqs=52 Similarity=1.000000  
5 TTTTTATTTT-TTA-

Rev.of\_Cele-UNSB01\_2:11255666-11256503 Satlength=838 Nr of Repeats=64  
RepeatLength=12 seed=TAAAAATAAA Num.seqs=57 Similarity=0.988443  
0 TTTTTATTTT-TTA-

Rev.of\_Cele-UNSB01\_3:3456121-3456336 Satlength=216 Nr of Repeats=18  
RepeatLength=12 seed=AAAATAAAAA Num.seqs=17 Similarity=0.986928  
4 TTTTTATTTT-TTA-

Rev.of\_Cele-UNSB01\_3:10519446-10519548 Satlength=103 Nr of Repeats=8  
RepeatLength=12 seed=AAACTAAAA Num.seqs=5 Similarity=0.815385  
5 GTTTTATTTT-TTA-

Cele-UNSB01\_5:6983222-6984063 Satlength=842 Nr of Repeats=56  
RepeatLength=12 seed=TTTTAATTTT Num.seqs=46 Similarity=1.000000  
0 -TTTTAATT-TTAA

Cele-UNSB01\_4:6359332-6359386 Satlength=55 Nr of Repeats=4  
RepeatLength=13 seed=TTTCATTTGT Num.seqs=3 Similarity=0.931624  
1 TTTTCATTTT-GTAA

Rev.of\_Cele-UNSB01\_6:2109492-2110453 Satlength=962 Nr of Repeats=78  
RepeatLength=12 seed=AATAAATAAT Num.seqs=54 Similarity=1.000000  
0 TATTTATTTTATT--

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Consensus:

tTTTTATTTTTTA

>Cele-UNSB01\_Fam\_31\_42\_9 Nr. of seq. 9 Alignment length(with gaps) = 42  
Alignment score = 0.733686

Cele-UNSB01\_1:980318-980990 Satlength=673 Nr of Repeats=16  
RepeatLength=42 seed=CCGGAAATTT Num.seqs=16 Similarity=0.888889  
0 CCGGAAATTTCGAAAACCGGCAATTGCCGAAATTGCCGATTG

Cele-UNSB01\_2:3617397-3617684 Satlength=288 Nr of Repeats=6  
RepeatLength=42 seed=TTTGAAAACC Num.seqs=4 Similarity=0.851852  
8 CCGGAAATTTTGAAAACCGGCAATAGCCGAAATTGCCGAGTG  
Rev.of\_Cele-UNSB01\_5:20627832-20628586 Satlength=755 Nr of Repeats=12  
RepeatLength=42 seed=ATTGCCGGTT Num.seqs=9 Similarity=0.803351  
24 CCGAAAATTTTAAAAACCGGCAATTGCCGAAATTGCCGATTG  
Cele-UNSB01\_5:3789009-3789261 Satlength=253 Nr of Repeats=6  
RepeatLength=42 seed=ACCGGCAATT Num.seqs=6 Similarity=0.881481  
15 CTGAAAATTTCCAAAACCGGCAATTGCCAAAATTGCCGATTG  
Cele-UNSB01\_2:14381587-14382260 Satlength=674 Nr of Repeats=16  
RepeatLength=42 seed=AAAACCGGCA Num.seqs=10 Similarity=0.749832  
12 CCGGNAATATTAAAAACCGGCAATTGCCGGAATTGCCGATTG  
Rev.of\_Cele-UNSB01\_2:1652802-1653206 Satlength=405 Nr of Repeats=5  
RepeatLength=42 seed=TTGCCGGTTG Num.seqs=3 Similarity=0.809524  
23 CAAAAAATTTTCGGCAACCGGCAATTGCCGAAGTTGCCGAACC  
Cele-UNSB01\_2:1657514-1657909 Satlength=396 Nr of Repeats=5  
RepeatLength=42 seed=CAACCGGCAA Num.seqs=3 Similarity=0.809524  
55 CAAAAAATTTTCGGCAACCGGCAATTGCCGAAGTTGCCGAACC  
Cele-UNSB01\_5:16332671-16332882 Satlength=212 Nr of Repeats=6  
RepeatLength=42 seed=TTTCGGCAAC Num.seqs=4 Similarity=0.899471  
49 CGAAAAATTTTCGGCAACCGGCAATTGCCGATGTTGCCGAACC  
Cele-UNSB01\_2:12718309-12718687 Satlength=379 Nr of Repeats=8  
RepeatLength=42 seed=TTGCCGAACC Num.seqs=7 Similarity=0.797619  
32 GTAAAAATTTTCGGCAACNGGAATTGCCAAAGTTGCCGAACC

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Consensus:

CngaAAAATTTcgaaAACCGGCAATTGCCgAAaTTGCCGAntg

>Cele-UNSB01\_Fam\_32\_26\_9 Nr. of seq. 9 Alignment length(with gaps) = 26  
Alignment score = 0.800214  
Cele-UNSB01\_4:11734646-11742696 Satlength=8051 Nr of Repeats=322  
RepeatLength=25 seed=ATTACGGCAG Num.seqs=322 Similarity=0.947627  
0 ATTACGGCAGATTCTA-TAAATTGGC  
Rev.of\_Cele-UNSB01\_4:14408867-14409192 Satlength=326 Nr of Repeats=13  
RepeatLength=25 seed=TAATGCCAAT Num.seqs=13 Similarity=0.948034  
4 ATTACGGCAGATTCTA-TAAATTGGC  
Rev.of\_Cele-UNSB01\_6:11722486-11725761 Satlength=3276 Nr of Repeats=130  
RepeatLength=25 seed=CTGCCGTAAT Num.seqs=129 Similarity=0.942132  
10 ATTACGGCAGATTCTA-TAAATTGGC  
Rev.of\_Cele-UNSB01\_1:4605678-4635032 Satlength=29355 Nr of Repeats=1129  
RepeatLength=26 seed=TTTTCTAAAA Num.seqs=1129 Similarity=0.999909  
21 ATTGCGGCGGATTTTAGAAAAATGGC  
Rev.of\_Cele-UNSB01\_6:1706298-1706662 Satlength=365 Nr of Repeats=14  
RepeatLength=26 seed=GCCGCAATGC Num.seqs=14 Similarity=0.970132  
34 ATTGCGGCGGATTTTAGAAAAATGGC  
Cele-UNSB01\_6:11725790-11730325 Satlength=4536 Nr of Repeats=175  
RepeatLength=26 seed=CGGCGGATTT Num.seqs=160 Similarity=0.928249  
30 ATTGCGGCGGATTTTAGAAAAATGGC  
Cele-UNSB01\_4:12895275-12902336 Satlength=7062 Nr of Repeats=272  
RepeatLength=26 seed=CATTGCGGCG Num.seqs=261 Similarity=0.919236  
25 ATTGCGGCGGATTTTNGAAAAATGGC



Cele-UNSB01\_1:11159617-11160082 Satlength=466 Nr of Repeats=4  
RepeatLength=26 seed=TTTTTGAAAA Num.seqs=3 Similarity=0.931624  
37 ATTGCGGCGGATTTTGGAAAAATGGC  
Cele-UNSB01\_6:12933662-12933969 Satlength=308 Nr of Repeats=5  
RepeatLength=26 seed=AAAAATGGCA Num.seqs=4 Similarity=0.897436  
43 ATTGCGGCGGATTTTCAGAAAAATGGC

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Consensus:

ATTgCGGcGgATTtTagaAAAaTGGC

>Cele-UNSB01\_Fam\_33\_18\_9 Nr. of seq. 9 Alignment length(with gaps) = 23  
Alignment score = 0.628019

Cele-UNSB01\_1:11696998-11697105 Satlength=108 Nr of Repeats=5  
RepeatLength=19 seed=TCAAAAATCA Num.seqs=4 Similarity=0.873611  
21 CA--TC-AAAAATCAATAA-TTT  
Cele-UNSB01\_1:11591612-11591946 Satlength=335 Nr of Repeats=14  
RepeatLength=20 seed=AAAAATCAAT Num.seqs=11 Similarity=0.883636  
24 CA--TCGAAAAATCAATAA-TTT  
Cele-UNSB01\_1:11696961-11698223 Satlength=1263 Nr of Repeats=20  
RepeatLength=19 seed=AAAAATCGAT Num.seqs=12 Similarity=0.725830  
23 CN--TC-AAAAATCGATAA-TTT  
Cele-UNSB01\_2:2648748-2648862 Satlength=115 Nr of Repeats=6  
RepeatLength=19 seed=AAAATCGATA Num.seqs=6 Similarity=0.601058  
24 CA--TC-GAAAATCGATAA-TTT  
Cele-UNSB01\_1:11744458-11744933 Satlength=476 Nr of Repeats=17  
RepeatLength=19 seed=TTTCACAAAA Num.seqs=12 Similarity=0.943647  
35 CA---C-AAAAATCAATAATTTT  
Cele-UNSB01\_1:11743735-11745857 Satlength=2123 Nr of Repeats=45  
RepeatLength=19 seed=AAAATCGATA Num.seqs=29 Similarity=0.730706  
42 CA---N-AAAAATCGATAATTTT  
Cele-UNSB01\_4:984710-985413 Satlength=704 Nr of Repeats=35  
RepeatLength=19 seed=CAATAATTTT Num.seqs=27 Similarity=0.905233  
28 CC-C-A-AAAAATCAATAA-TTT  
Rev.of\_Cele-UNSB01\_1:11592271-11597890 Satlength=5620 Nr of Repeats=277  
RepeatLength=20 seed=ATTGATTTTT Num.seqs=273 Similarity=0.884518  
32 CCTC-A-AAAAATCAATAA-TTT  
Rev.of\_Cele-UNSB01\_1:2396315-2396849 Satlength=535 Nr of Repeats=20  
RepeatLength=20 seed=TTATTGATTT Num.seqs=12 Similarity=0.816162  
34 CCTA-G-AAAAATCAATAA-TGT

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Consensus:

cAAAAATCaATAATTTCa

>Cele-UNSB01\_Fam\_34\_12\_9 Nr. of seq. 9 Alignment length(with gaps) = 15  
Alignment score = 0.680247

Cele-UNSB01\_6:2369427-2369729 Satlength=303 Nr of Repeats=24  
RepeatLength=11 seed=CCATACCTAT Num.seqs=20 Similarity=1.000000  
0 -CC-ATACCT-ATA-

Cele-UNSB01\_1:12842011-12842077 Satlength=67 Nr of Repeats=5  
RepeatLength=12 seed=TACCTATACC Num.seqs=4 Similarity=0.944444  
3 -CT-ATACCT-ATAC  
Cele-UNSB01\_1:13927551-13927713 Satlength=163 Nr of Repeats=13  
RepeatLength=12 seed=TATACCTATA Num.seqs=10 Similarity=0.955556  
7 -CT-ATACCT-ATAC  
Rev.of\_Cele-UNSB01\_1:13927986-13928124 Satlength=139 Nr of Repeats=11  
RepeatLength=12 seed=ATAGGTATAG Num.seqs=10 Similarity=0.955556  
4 -CT-ATACCT-ATAC  
Rev.of\_Cele-UNSB01\_2:3535061-3535729 Satlength=669 Nr of Repeats=54  
RepeatLength=12 seed=TAGGTATAGG Num.seqs=46 Similarity=0.876973  
3 -CT-ATACCT-ATAC  
Cele-UNSB01\_2:12494810-12494978 Satlength=169 Nr of Repeats=14  
RepeatLength=12 seed=CCTATACCTA Num.seqs=14 Similarity=0.968254  
5 -CT-ATACCT-ATAC  
Cele-UNSB01\_4:13402475-13402619 Satlength=145 Nr of Repeats=12  
RepeatLength=12 seed=TATACCTATA Num.seqs=12 Similarity=0.944444  
7 -CT-ATACCT-ATAC  
Cele-UNSB01\_2:3077809-3078033 Satlength=225 Nr of Repeats=15  
RepeatLength=14 seed=CTTATACCTT Num.seqs=14 Similarity=0.947671  
1 CCTTATACCTTATA-  
Cele-UNSB01\_3:1413910-1414798 Satlength=889 Nr of Repeats=40  
RepeatLength=14 seed=ATACCTAATA Num.seqs=28 Similarity=0.877047  
4 CCTAATACCTAATA-

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Consensus:

CTATACCTATAC

>Cele-UNSB01\_Fam\_35\_12\_9 Nr. of seq. 9 Alignment length(with gaps) = 12  
Alignment score = 0.876543  
Cele-UNSB01\_1:774871-775189 Satlength=319 Nr of Repeats=26  
RepeatLength=12 seed=TCTAGGTCTA Num.seqs=25 Similarity=0.948148  
0 TCTAGGTCTAGG  
Cele-UNSB01\_1:1009660-1009762 Satlength=103 Nr of Repeats=8  
RepeatLength=12 seed=GGTCTAGGTC Num.seqs=7 Similarity=0.936508  
4 TCTAGGTCTAGG  
Cele-UNSB01\_1:11696177-11696255 Satlength=79 Nr of Repeats=6  
RepeatLength=12 seed=TAGGTCTAGG Num.seqs=5 Similarity=1.000000  
2 TCTAGGTCTAGG  
Rev.of\_Cele-UNSB01\_2:885470-885668 Satlength=199 Nr of Repeats=15  
RepeatLength=12 seed=ACCTAGACCT Num.seqs=12 Similarity=0.858586  
1 TCTAGGTCTAGG  
Cele-UNSB01\_1:961195-961471 Satlength=277 Nr of Repeats=23  
RepeatLength=12 seed=CTAAGTCTAA Num.seqs=23 Similarity=1.000000  
1 TCTAAGTCTAAG  
Cele-UNSB01\_1:961002-961808 Satlength=807 Nr of Repeats=44  
RepeatLength=12 seed=TAAGCCTAAG Num.seqs=39 Similarity=0.765770  
2 TCTAAGTCTAAG  
Cele-UNSB01\_1:3303901-3304753 Satlength=853 Nr of Repeats=71  
RepeatLength=12 seed=CTAAGTCTAA Num.seqs=69 Similarity=0.908497  
1 TCTAAGTCTAAG

Rev.of\_Cele-UNSB01\_3:12499748-12499928 Satlength=181 Nr of Repeats=14  
RepeatLength=12 seed=CTTAGACTTA Num.seqs=12 Similarity=0.929293  
6 TCTAAGTCTAAG  
Cele-UNSB01\_5:15130293-15130341 Satlength=49 Nr of Repeats=4  
RepeatLength=12 seed=TCTAAGTCTA Num.seqs=4 Similarity=0.944444  
6 TCTAAGTCTAAG

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Consensus:

TCTAaGTCTAaG

>Cele-UNSB01\_Fam\_36\_10\_9 Nr. of seq. 9 Alignment length(with gaps) = 11  
Alignment score = 0.771465  
Cele-UNSB01\_2:4272676-4272936 Satlength=261 Nr of Repeats=25  
RepeatLength=10 seed=GCGTTAGCAG Num.seqs=24 Similarity=0.977778  
0 GCGTTAGCAG-  
Cele-UNSB01\_5:853469-853759 Satlength=291 Nr of Repeats=23  
RepeatLength=10 seed=GGCGTCAGCG Num.seqs=17 Similarity=0.888235  
9 GCGTCAGCGG-  
Cele-UNSB01\_5:1897354-1897674 Satlength=321 Nr of Repeats=23  
RepeatLength=10 seed=GGGCGTCAGC Num.seqs=15 Similarity=0.949206  
18 GCGTCAGCGG-  
Rev.of\_Cele-UNSB01\_2:13962674-13962948 Satlength=275 Nr of Repeats=23  
RepeatLength=10 seed=CCGCTACCGC Num.seqs=19 Similarity=1.000000  
0 GCGGTAGCGG-  
Rev.of\_Cele-UNSB01\_3:13335994-13337798 Satlength=1805 Nr of Repeats=147  
RepeatLength=10 seed=GCTACCGCCC Num.seqs=101 Similarity=0.923248  
8 GCGGTAGCGG-  
Rev.of\_Cele-UNSB01\_5:2726947-2727107 Satlength=161 Nr of Repeats=12  
RepeatLength=10 seed=GCTACCGCCC Num.seqs=9 Similarity=1.000000  
8 GCGGTAGCGG-  
Rev.of\_Cele-UNSB01\_5:2726947-2728543 Satlength=1597 Nr of Repeats=110  
RepeatLength=10 seed=GCTACCGCCC Num.seqs=99 Similarity=0.951240  
8 GCGGTAGCGG-  
Cele-UNSB01\_5:3102518-3102978 Satlength=461 Nr of Repeats=41  
RepeatLength=10 seed=GGTAGCGGGC Num.seqs=37 Similarity=0.925125  
2 GCGGTAGCGG-  
Rev.of\_Cele-UNSB01\_2:13967191-13967257 Satlength=67 Nr of Repeats=5  
RepeatLength=11 seed=CCGCTACCGC Num.seqs=4 Similarity=0.919192  
0 GCGGTAGCGGT

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Consensus:

GCGgtAGCGG

>Cele-UNSB01\_Fam\_37\_18\_8 Nr. of seq. 8 Alignment length(with gaps) = 19  
Alignment score = 0.681391  
Cele-UNSB01\_4:646705-646786 Satlength=82 Nr of Repeats=4 RepeatLength=15  
seed=TAAGCCTAAG Num.seqs=3 Similarity=1.000000  
0 TAAGCCTA-AGCC-CA-C-

Cele-UNSB01\_5:1895975-1896260 Satlength=286 Nr of Repeats=14  
RepeatLength=17 seed=TAAGCCTAAG Num.seqs=9 Similarity=0.930283  
0 TAAGCCTA-AG-CTTAGCT  
Rev.of\_Cele-UNSB01\_3:662174-662284 Satlength=111 Nr of Repeats=6  
RepeatLength=18 seed=TAGGCTTAGG Num.seqs=4 Similarity=0.527778  
8 TAAGCCTACAG-CTAAGCC  
Cele-UNSB01\_2:371286-371494 Satlength=209 Nr of Repeats=10  
RepeatLength=18 seed=TAAGCCTAAG Num.seqs=6 Similarity=0.619753  
12 TAAGCCTA-AGTCTAAGCC  
Cele-UNSB01\_2:13097657-13097799 Satlength=143 Nr of Repeats=5  
RepeatLength=18 seed=CCTAAGCCTA Num.seqs=3 Similarity=0.660819  
16 TAAGCCTA-AGNCTAAACC  
Cele-UNSB01\_5:1057921-1058017 Satlength=97 Nr of Repeats=6  
RepeatLength=18 seed=AAGCCTAAGC Num.seqs=4 Similarity=0.691358  
19 TAAGCCTA-AGCCTAAACC  
Cele-UNSB01\_5:1707873-1707951 Satlength=79 Nr of Repeats=5  
RepeatLength=18 seed=GCCTAAGCCT Num.seqs=3 Similarity=0.614035  
21 TANGCCTA-AGCCTAAGCA  
Rev.of\_Cele-UNSB01\_2:3500187-3500295 Satlength=109 Nr of Repeats=5  
RepeatLength=18 seed=GGCTTAGGCT Num.seqs=3 Similarity=0.901235  
12 TAAGCCTA-AGCCTGAGCT

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Consensus:

TAAGCCTAAGcCTaAgCc

>Cele-UNSB01\_Fam\_38\_18\_8 Nr. of seq. 8 Alignment length(with gaps) = 19  
Alignment score = 0.829261  
Cele-UNSB01\_5:19164473-19167625 Satlength=3153 Nr of Repeats=148  
RepeatLength=17 seed=ATTAGCAGCG Num.seqs=97 Similarity=0.880902  
0 -ATTAGCAGCGCCCCAAAA-  
Cele-UNSB01\_5:19251983-19252110 Satlength=128 Nr of Repeats=5  
RepeatLength=18 seed=GCAGCGCCCA Num.seqs=3 Similarity=0.950617  
4 -ATTAGCAGCGCCCCAAAA  
Rev.of\_Cele-UNSB01\_5:19255197-19255501 Satlength=305 Nr of Repeats=17  
RepeatLength=18 seed=TGCTAATTTT Num.seqs=15 Similarity=0.936508  
7 -ATTAGCAGCGCCCCAAAA  
Cele-UNSB01\_5:19273514-19273585 Satlength=72 Nr of Repeats=4  
RepeatLength=18 seed=TAGCAGCGCC Num.seqs=3 Similarity=0.901235  
2 -ATTAGCAGCGCCCCAAGAA  
Cele-UNSB01\_5:19170107-19171106 Satlength=1000 Nr of Repeats=12  
RepeatLength=18 seed=AATTAGCAGC Num.seqs=10 Similarity=0.960494  
0 AATTAGCAGCGACCAAAA-  
Cele-UNSB01\_5:19392335-19392460 Satlength=126 Nr of Repeats=6  
RepeatLength=18 seed=ATTAGCAGCG Num.seqs=4 Similarity=1.000000  
1 AATTAGCAGCGACCAAAA-  
Rev.of\_Cele-UNSB01\_5:19480245-19483641 Satlength=3397 Nr of Repeats=189  
RepeatLength=18 seed=GCTGCTAATT Num.seqs=161 Similarity=0.900696  
10 AATTAGCAGCGACCAAAA-  
Cele-UNSB01\_5:19249579-19249688 Satlength=110 Nr of Repeats=6  
RepeatLength=18 seed=AGCAGCGCCC Num.seqs=5 Similarity=0.896296  
3 -AATAGCAGCGCCCCAAAA

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Consensus:

ATTAGCAGCGcCCAAAAa

>Cele-UNSB01\_Fam\_39\_14\_8 Nr. of seq. 8 Alignment length(with gaps) = 14  
Alignment score = 0.894558

Cele-UNSB01\_1:10475895-10475986 Satlength=92 Nr of Repeats=6  
RepeatLength=14 seed=GCTATACGCT Num.seqs=5 Similarity=1.000000  
0 GCTATACGCTATAC

Cele-UNSB01\_2:6280573-6282049 Satlength=1477 Nr of Repeats=96  
RepeatLength=14 seed=CTATACGCTA Num.seqs=79 Similarity=1.000000  
1 GCTATACGCTATAC

Rev.of\_Cele-UNSB01\_4:14409220-14409304 Satlength=85 Nr of Repeats=6  
RepeatLength=14 seed=AGCGTATAGC Num.seqs=6 Similarity=1.000000  
3 GCTATACGCTATAC

Rev.of\_Cele-UNSB01\_6:356210-356329 Satlength=120 Nr of Repeats=8  
RepeatLength=14 seed=ATAGCGTATA Num.seqs=7 Similarity=0.891156  
5 GCTATACGCTATAC

Cele-UNSB01\_6:11722389-11722452 Satlength=64 Nr of Repeats=4  
RepeatLength=14 seed=CTATACGCTA Num.seqs=3 Similarity=0.936508  
1 GCTATACGCTATAC

Cele-UNSB01\_5:12601066-12601185 Satlength=120 Nr of Repeats=8  
RepeatLength=14 seed=CTATACGCTA Num.seqs=7 Similarity=0.891156  
1 GCTATACGCTATGC

Rev.of\_Cele-UNSB01\_6:17259878-17260337 Satlength=460 Nr of Repeats=20  
RepeatLength=14 seed=ATAGCGCATA Num.seqs=18 Similarity=0.808279  
5 GCTATGCGCTATGC

Cele-UNSB01\_4:14407623-14408822 Satlength=1200 Nr of Repeats=70  
RepeatLength=14 seed=GCTATGCGCT Num.seqs=52 Similarity=0.786869  
0 GCTATGCGCTGTAC

\* \* \* \* \*

Consensus:

GCTATaCGCTATaC

>Cele-UNSB01\_Fam\_40\_166\_7 Nr. of seq. 7 Alignment length(with gaps) = 173  
Alignment score = 0.740343

Cele-UNSB01\_6:16300389-16301032 Satlength=644 Nr of Repeats=4  
RepeatLength=158 seed=TATCAATTTT Num.seqs=3 Similarity=0.924051  
0 TATCAATTTTCAGACGCGCTACGGGGGTTTTGTCTTGAATTCCAATTTCAAC-----  
AGGCGCAAAAAACAAAAATAAAATTTTTGGATT-TTTGGAAAAGT-TTTT-

ATAGATTTCTATTCTAGATTGTTTAA-AAATATTATTGGTACGTTTTTGTACCAANA

Cele-UNSB01\_6:16300466-16301134 Satlength=669 Nr of Repeats=4  
RepeatLength=158 seed=CAAAAATAAA Num.seqs=3 Similarity=0.935302  
66 TATCAATTTTCAGACGCGCTACGGGGGTTTTGTCTTGAATTCCAATTTCAAC-----  
AGGCGCAAAAAACAAAAATAAAATTTTTGGATT-TTTGGAAAAGT-TTTT-

ATAGATTTGTATTCTAGATTGTTTAA-AAATATTATTGGTACGTTTTTGTACCAANA

Rev.of\_Cele-UNSB01\_3:2160246-2184061 Satlength=23816 Nr of Repeats=142  
RepeatLength=168 seed=TTTATTTTTG Num.seqs=110 Similarity=0.984798  
86 TATCCATTTTCAGACGCGCTACAGGGGTTTTTGTCTTGAATTCCAATTTCAACAGGTA-

TATGTAGGCACAAAAAACAAAAATAAACATTATGGAAT-TCCGGA-AA-  
 TGTTTTGATAGATTTGGATTCTAGATTGTTTTA-AAATATTATTGGTAAGTTTTGTACCTAGA  
 Cele-UNSB01\_4:15460070-15462017 Satlength=1948 Nr of Repeats=10  
 RepeatLength=168 seed=AAAAACAAAA Num.seqs=7 Similarity=0.956160  
 239 TATCAATTTTCAGATGCGCTAGAGGGGTTTTGTCTTGAATTCCAATTTCAACAGATA-  
 TATACAGGCACAAAAAACAAAAATAAAAAATTTTGGAAATGTTGGGAGAA-T-TTTT-  
 ATAGATTGATTCTAGATT-TTTAACAAATATTTTGGTAAGTTTCTGGACCTAGA  
 Cele-UNSB01\_4:15460844-15462434 Satlength=1591 Nr of Repeats=9  
 RepeatLength=168 seed=AACAAAAATA Num.seqs=7 Similarity=0.956160  
 242 TATCAATTTTCAGATGCGCTAGAGGGGTTTTGTCTTGAATTCCAATTTCAACAGATA-  
 TATACAGGCACAAAAAACAAAAATAAAAAATTTTGGAAATGTTGGGAGAA-T-TTTT-  
 ATAGATTGATTCTAGATT-TTTAACAAATATTTTGGTAAGTTTCTGGACCTAGA  
 Rev.of\_Cele-UNSB01\_4:13110533-13113073 Satlength=2541 Nr of Repeats=14  
 RepeatLength=168 seed=TTTTTAAAAA Num.seqs=12 Similarity=0.993146  
 141 AAGTAAATTTAAGCCGCGCTAGAGAGGTTTTGTGTCGAGTTCCAATTTTACAGGTACTA-  
 GTAGGCTCAAAAAAACAAAAATAAAAAATTATCGAAT-TCCGGA-AA-  
 TGTTTTGATAGATTTGGATTCTAGATTTTTTTAA-AAATATTATTGGTAAGTTTGTGGGCCAGGA  
 Cele-UNSB01\_4:15744856-15746870 Satlength=2015 Nr of Repeats=12  
 RepeatLength=168 seed=GAATTCGGA Num.seqs=10 Similarity=0.953439  
 261 AAGTAACTTAAAGCCGCGCTAGAAAGGTTTTGTGTCGAGTTACAATTTTACAGGTACTA-  
 GTAGGCGCAAAAAAACAAAAATAAAAAATTATGGAAT-TCCGGA-AA-  
 TGTTTTGATAGATTTGGATTCTAGATTTTTTTAA-AAATATTATAGGTGAGTTTTTGGGACAGGA

\* \* \* \* \*  
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 \* \* \* \* \*

Consensus:

tAtcAAtTTTcAGacGCGCTAgaGgGGTTTTTGTcTtGAaTTCCAATTTcaACagntatannAGGCnCAAAAA  
 AACAAAAATAAAAAATtTGGAaTTtnGGAnAATTTTTATAGATTTGgATTCTAGATTnTTTAAAAATATTaTT  
 GGTAAgTTTtTGgaCCaagA

>Cele-UNSB01\_Fam\_41\_95\_7 Nr. of seq. 7 Alignment length(with gaps) = 96  
 Alignment score = 0.868386  
 Cele-UNSB01\_4:13917663-13921092 Satlength=3430 Nr of Repeats=37  
 RepeatLength=93 seed=AGGGCCGCGAG Num.seqs=33 Similarity=0.954220  
 0 AGGGCCGCGAGGCCCGAATAGTCTTGGAAGT--GGGCTGGCTATAATCCTATTCCAAGCAGGT-  
 TGTTATTTCACTCAAGCCTATCAACCAAGTTTG  
 Rev.of\_Cele-UNSB01\_2:2738496-2739194 Satlength=699 Nr of Repeats=7  
 RepeatLength=95 seed=TTGCGGCCTG Num.seqs=6 Similarity=0.981287  
 17 AGGGCCGCGAGGCCCGAATACTCATGGAACTGTGGGCCAGCTTTAATCCTATTCCAAGCAGAT-  
 TGTTATTCGCTCAAGCCTACAAACCAGGTTTG  
 Cele-UNSB01\_3:3518362-3520167 Satlength=1806 Nr of Repeats=19  
 RepeatLength=95 seed=TAATCCTATT Num.seqs=19 Similarity=0.948948  
 43 AGGGCCGCGAGGCCCGAATACTCATGGAACTGTGGGCCAGCTTTAATCCTATTCCAAGCAGAT-  
 TGTTATTCGCTCAAGCCTACAAACCAGGTTTG  
 Rev.of\_Cele-UNSB01\_2:13541965-13542724 Satlength=760 Nr of Repeats=8  
 RepeatLength=95 seed=GGCCTGCGGC Num.seqs=5 Similarity=0.859649  
 108 AGGGCCGCGAGGCCCGAATACTCATGGAACTAAGGGCCAGCTTTAATCCTATTCCAAGCAGAT-  
 TGTTATTCGCTCAAGCCTACCAACCAGGTTTG  
 Rev.of\_Cele-UNSB01\_2:1585165-1585860 Satlength=696 Nr of Repeats=7  
 RepeatLength=96 seed=GGCCTGCGGC Num.seqs=6 Similarity=0.968518  
 109

AGGGCCGCAGGCCCCGAACACTCTTGAAACTATGGGCTGGCTTTGATCCTATTCTAAGCAGATATGTTATTCA  
CTCAAGCCTAACAACCAGGTTCG

Cele-UNSB01\_3:1175770-1176177 Satlength=408 Nr of Repeats=4  
RepeatLength=96 seed=GAGGGCCGCA Num.seqs=3 Similarity=0.949074  
191

AGGGCCGCAGGCCCCGAACACTCTTGAAACTATGGGCTGGCTTTGATCCTATTCTAAGCAGATATGTTATTCA  
CTCAAGCCTAATAACCAGGTTCG

Rev.of\_Cele-UNSB01\_5:5413359-5414150 Satlength=792 Nr of Repeats=8  
RepeatLength=96 seed=TCTGCTTAGA Num.seqs=7 Similarity=0.949735  
254

AGGGCCGCAGGCCCCGAACACTCTTGAAACTATGGGCTGGCTTTGATCCTATTCTAAGCAGATATGTTATTCA  
CTCAAGCCTAATAACCAGGTTTG

\*\*\*\*\* \* \* \* \*  
\*\*\*\*\* \* \* \* \*

Consensus:

AGGGCCGCAGGCCCCGAAtACTCtTGAAACTatGGGctgGCTTTaATCCTATTCCaAGCAGATTGTTATTCaC  
TCAAGCCTAnnAACAGGTTtG

>Cele-UNSB01\_Fam\_42\_19\_7 Nr. of seq. 7 Alignment length(with gaps) = 23  
Alignment score = 0.619048

Cele-UNSB01\_6:2093985-2094613 Satlength=629 Nr of Repeats=30  
RepeatLength=19 seed=TAATATTTAT Num.seqs=22 Similarity=0.883952  
0 ----TAATATTTATTTATTTAAT

Cele-UNSB01\_6:12589530-12590986 Satlength=1457 Nr of Repeats=71  
RepeatLength=19 seed=TTAATTAATA Num.seqs=50 Similarity=0.869728  
14 ----TAATATTTATTTATTTAAT

Cele-UNSB01\_6:2097795-2102366 Satlength=4572 Nr of Repeats=207  
RepeatLength=19 seed=AATTAATATT Num.seqs=127 Similarity=0.940253  
1 ----TAATTAATATTTATTTATT

Cele-UNSB01\_6:2097795-2102461 Satlength=4667 Nr of Repeats=212  
RepeatLength=19 seed=AATTAATATT Num.seqs=132 Similarity=0.937235  
1 ----TAATTAATATTTATTTATT

Cele-UNSB01\_4:1654144-1654247 Satlength=104 Nr of Repeats=5  
RepeatLength=23 seed=ATTTAATTAA Num.seqs=3 Similarity=0.729469  
1 TATTTATTTAATTAATATTTATT

Rev.of\_Cele-UNSB01\_6:5456252-5456359 Satlength=108 Nr of Repeats=5  
RepeatLength=23 seed=AATAAATATT Num.seqs=3 Similarity=0.922705  
23 TATTTAATTAATTAATATTTATT

Cele-UNSB01\_4:13646609-13646697 Satlength=89 Nr of Repeats=4  
RepeatLength=23 seed=AATATTTATT Num.seqs=3 Similarity=0.961353  
9 TATTTAATAAATATTTATTTATT

\*\* \* \* \*\*\*\*\* \*

Consensus:

TAATtaaTattTATTTAtT

>Cele-UNSB01\_Fam\_43\_19\_7 Nr. of seq. 7 Alignment length(with gaps) = 21  
Alignment score = 0.666667

Cele-UNSB01\_4:236013-237239 Satlength=1227 Nr of Repeats=63  
RepeatLength=18 seed=CTCAACCAA Num.seqs=43 Similarity=0.898938  
0 CTCAACCAA--AC-TCTTAGC

Cele-UNSB01\_4:244645-245490 Satlength=846 Nr of Repeats=8 RepeatLength=18  
seed=AGCCTCAACC Num.seqs=5 Similarity=0.925926  
15 CTCAACCAA--AC-TCTTAGC  
Rev.of\_Cele-UNSB01\_4:128195-129066 Satlength=872 Nr of Repeats=28  
RepeatLength=19 seed=TTGGTTGAGG Num.seqs=19 Similarity=0.809582  
9 CTCAACCAA-AAT-TGTTAGC  
Cele-UNSB01\_4:221202-221862 Satlength=661 Nr of Repeats=32  
RepeatLength=20 seed=CTCAGCCTCA Num.seqs=30 Similarity=0.934713  
14 CTCAACCAAAAAT-TCTCAGC  
Rev.of\_Cele-UNSB01\_3:10146078-10146173 Satlength=96 Nr of Repeats=5  
RepeatLength=19 seed=ATTTTGGTTG Num.seqs=5 Similarity=0.818333  
12 CTCAACCAA-AAT-CCTGAGC  
Cele-UNSB01\_4:201016-202120 Satlength=1105 Nr of Repeats=53  
RepeatLength=20 seed=CTCAACCAAA Num.seqs=32 Similarity=0.882930  
20 CTCAACCAA-AAATCCTGAGC  
Cele-UNSB01\_4:3243719-3271867 Satlength=28149 Nr of Repeats=1487  
RepeatLength=19 seed=CCTCACTCAA Num.seqs=1365 Similarity=0.827742  
18 CTCACTCAA-AAT-CCTGAGC

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Consensus:

CTCAACCAaAttCTnAGC

>Cele-UNSB01\_Fam\_44\_21\_7 Nr. of seq. 7 Alignment length(with gaps) = 21  
Alignment score = 0.628118  
Cele-UNSB01\_2:466682-467257 Satlength=576 Nr of Repeats=9 RepeatLength=20  
seed=CAATTTTGA Num.seqs=7 Similarity=0.942857  
0 CAATTTTGGAGTTAAAAATT-  
Rev.of\_Cele-UNSB01\_2:13474627-13476516 Satlength=1890 Nr of Repeats=78  
RepeatLength=20 seed=AAAATTTGAA Num.seqs=57 Similarity=0.826829  
8 CAAATTTTGACTTAAAAATT-  
Rev.of\_Cele-UNSB01\_3:2017089-2018496 Satlength=1408 Nr of Repeats=57  
RepeatLength=21 seed=TGGAAATTTT Num.seqs=45 Similarity=0.855059  
2 CAATTTTGGGTTAAATTTT  
Cele-UNSB01\_3:1642030-1642586 Satlength=557 Nr of Repeats=7  
RepeatLength=21 seed=CCTAAAAATT Num.seqs=5 Similarity=0.695238  
10 CAATTTTNNACCTAAAAATTN  
Rev.of\_Cele-UNSB01\_2:2923591-2929183 Satlength=5593 Nr of Repeats=231  
RepeatLength=21 seed=CCAAAAATTG Num.seqs=201 Similarity=0.731595  
10 CAATTTTGGACTAAAAACCT  
Cele-UNSB01\_3:2204608-2205196 Satlength=589 Nr of Repeats=25  
RepeatLength=21 seed=GCCTAAAAAC Num.seqs=16 Similarity=0.805291  
30 AAATTTTAAGCCTAAAAACGT  
Rev.of\_Cele-UNSB01\_4:2728247-2729274 Satlength=1028 Nr of Repeats=42  
RepeatLength=21 seed=TTTGGATTTT Num.seqs=35 Similarity=0.859037  
45 AAATTTTAAGCCTAAAAATCC

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Consensus:

cAATTTTtggccTAAAAAttn



>Cele-UNSB01\_Fam\_45\_16\_7 Nr. of seq. 7 Alignment length(with gaps) = 16  
Alignment score = 0.732143  
Cele-UNSB01\_2:882806-882988 Satlength=183 Nr of Repeats=12  
RepeatLength=14 seed=TAGGATCTAG Num.seqs=10 Similarity=0.807407  
2 TC-TAGGATCT-AGGA  
Rev.of\_Cele-UNSB01\_2:1625642-1627656 Satlength=2015 Nr of Repeats=131  
RepeatLength=14 seed=GATCCTAGAT Num.seqs=112 Similarity=0.963106  
2 TC-TAGGATCT-AGGA  
Cele-UNSB01\_1:14240945-14242222 Satlength=1278 Nr of Repeats=80  
RepeatLength=16 seed=ATCTAAGGAT Num.seqs=79 Similarity=0.956183  
6 TCTAAGGATCTAAGGA  
Cele-UNSB01\_1:14240945-14243302 Satlength=2358 Nr of Repeats=147  
RepeatLength=16 seed=ATCTAAGGAT Num.seqs=145 Similarity=0.924178  
6 TCTAAGGATCTAAGGA  
Rev.of\_Cele-UNSB01\_1:14245984-14247232 Satlength=1249 Nr of Repeats=59  
RepeatLength=16 seed=AGATCCTTAG Num.seqs=48 Similarity=0.862780  
10 TCTAAGGATCTAAGGA  
Cele-UNSB01\_1:14248002-14248098 Satlength=97 Nr of Repeats=6  
RepeatLength=16 seed=AGGATCTAAG Num.seqs=6 Similarity=0.972222  
11 TCTAAGGATCTAAGGA  
Cele-UNSB01\_4:15869737-15871646 Satlength=1910 Nr of Repeats=128  
RepeatLength=14 seed=GGACTAGGGA Num.seqs=112 Similarity=0.896439  
3 TAGGGACTAGGGA-C-

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Consensus:

TCtaAGGATCTaAGGA

>Cele-UNSB01\_Fam\_46\_226\_6 Nr. of seq. 6 Alignment length(with gaps) = 228  
Alignment score = 0.781092  
Cele-UNSB01\_5:9471886-9475930 Satlength=4045 Nr of Repeats=19  
RepeatLength=214 seed=GTAAGTCTGCTC Num.seqs=12 Similarity=0.965543  
0  
GTAAGTCTGCTCAAAGCTTCTGGCACCTATTGGGATGTTGTTGGTAAATTTCTGAAAAAGCTTGAATTTGCAACA  
AAGTTTCTGAAAGAAATTTT--  
CGAAAAAAGTTGATTTGAAGTGATTTGGGAATTTTCAAAGTTTCATAAATTTACCTA-  
TTTTGCCTATAAATGGTCGTTTTTCATTTAATAATAAAATACGCAC--AAAGGTA---CTG--TAGGT----  
TTTCT  
Rev.of\_Cele-UNSB01\_6:11021354-11026794 Satlength=5441 Nr of Repeats=27  
RepeatLength=214 seed=AAAACCTACA Num.seqs=21 Similarity=0.959472  
212  
GTAAGTCTGCTCAAAGCTTCTGGCACCTACTGGGATGTTGTTGGTAAATTTCTGAAAAAGCTTGAATTTGCAACA  
AAGTTTCTGAAAGAAATTTT--  
CAAAAAAAGTTGGTTTGAAGTGATTTGGGAATTTTCAAAGTTTCATAAATTTACCTA-  
TTTTGCCTATAAATGGTCGTTTTTCATTTAATAATAAAATACGCAC--AAAGGTA---CTG--TAGGT----  
TTTCT  
Rev.of\_Cele-UNSB01\_2:10468271-10470517 Satlength=2247 Nr of Repeats=10  
RepeatLength=225 seed=TTTTCGAAAT Num.seqs=6 Similarity=1.000000  
98  
GTAAGTCTGCTCAAAGCTTCTGTACCTACTGGAATATTGTTAATATAATCTGAAAGAGCTTAAATTTACTACA  
AAGTTTCTGAAAGACATTTTCGAAAA--  
CAGTTACTTTGAAGAGGTTTATGAATTTTCAAAGTTTGTAATAATCCATCTATTTTTGCCTATACATAGTAGTT  
TTCATT-AATAATAAAATACGCCTAAAAGGTAGGGCTGAAAAATGTACTATTTCT

Rev.of\_Cele-UNSB01\_1:4344690-4345849 Satlength=1160 Nr of Repeats=6  
RepeatLength=226 seed=ACAAGAAGCT Num.seqs=5 Similarity=0.915789  
248  
GTAAC TACGTGAAGCTTCTTGTACCTACTGGAATATTGTTAATATATTCTAAAAGAGCTTAAAATTTACTACA  
AAGTTTCTGAAAGACATTTTCGCAAAAAA-  
TTACTTTGAAGAGATTTATGAATTTTCAAATTACGAAAATCCCTCTA-  
TTTTGCCTATAAGTGGTAGTTTTTCATTAAATAATAAAATACGCACTAAAAGGTAGGGCTGAAAATGTACTATT  
TCT

Rev.of\_Cele-UNSB01\_6:6133294-6134199 Satlength=906 Nr of Repeats=4  
RepeatLength=226 seed=CAAGAAGCTT Num.seqs=3 Similarity=0.929204  
473  
GTAAC TACGTGAAGCTTCTTGCACCTACTGGAGTATTGTTGGTATATTCTAAAAGAGCTTAAAATTTACTACA  
AAGTTTCTGAAAGACATTT-  
CAAAAAAAGTTACATTGAAGAGATTTATGAATTTTCAAAGTTTCGAAAATTTATCTATTTTTGCCTATAAAATG  
GTAGTTTTTCATTAAATAATAAAATACGCGCTAAAAGGTAGCTCTGAAAATGTACTATTTCT

Cele-UNSB01\_6:12201539-12202895 Satlength=1357 Nr of Repeats=6  
RepeatLength=226 seed=TGTACTATTT Num.seqs=6 Similarity=0.964602  
666  
GTAAC TACGTGAAGCTTCTTGTACCTACTGAAATATTGTTGGTATATTCTAAAAGAGCTTAAAATTTACTACA  
AAGTTTCTAAAAGACATTT-  
CAAAAAAAGTTACTTTGAAGAGATTTATGAATTTTCAAAGTTACGAAAATTCGTCTATTTTTGCCTATAAAATG  
GTAGTTTTTCATTAAATAATAAAATACGCATTATAAGGTAGGGCTGAAAATGTACTATTTCT

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****      *** ***** * ** ***** ***** ***** ***** ***** ***
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Consensus:

GTAAC TaCgtGAAGCTTCTtGcACCTACTGGaATaTTGTTggTAtATTCTaAAAgAGCTTaaAATTTaCtACA  
AAGTTTCTGAAAGAcATTTCAAAAAAAGTTacTTTGAAGaGATTTatGAATTTTCAAAGTTtCgaAAATtcat  
CTatTTTGCCTATAAAATGGTaGTTTTTCATTaATAATAAAATACGCACtaAAAGGTAgggCTGaaaAtGTac  
taTTTCT

>Cele-UNSB01\_Fam\_47\_94\_6 Nr. of seq. 6 Alignment length(with gaps) = 94  
Alignment score = 0.946099  
Cele-UNSB01\_1:4346155-4359862 Satlength=13708 Nr of Repeats=146  
RepeatLength=94 seed=TCAAAATCTT Num.seqs=130 Similarity=0.962485  
0

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAATCAATGGGAAAATCATC  
AATTTCTGAAGGCAGTAATTC

Rev.of\_Cele-UNSB01\_3:7632425-7683091 Satlength=50667 Nr of Repeats=426  
RepeatLength=94 seed=AAAGCACCCA Num.seqs=425 Similarity=1.000000  
35

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAATCAATGGGAAAATCATC  
AATTTCTGGAGGCAGTAATTC

Cele-UNSB01\_1:11104747-11105884 Satlength=1138 Nr of Repeats=5  
RepeatLength=94 seed=TGTAGACAAA Num.seqs=4 Similarity=0.971631  
46

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGTCCTTTGTAGACAAATCAATGGGAGAATCATC  
AATTTCTGAAGGCAGTAATTC

Rev.of\_Cele-UNSB01\_4:1558589-1558964 Satlength=376 Nr of Repeats=4  
RepeatLength=94 seed=TCCCATTGAT Num.seqs=3 Similarity=0.924350  
65

TCAAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTTTGTAGACAAATCAATGGGAAAATTGTC  
CATTTCTGAAGGCAGTAATTC

Cele-UNSB01\_6:350789-351447 Satlength=659 Nr of Repeats=7 RepeatLength=94  
seed=GCAGTAATTC Num.seqs=7 Similarity=0.944613

84

TCAAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTTTGTAGACAAATCAATGAGAAAATTGTC  
AATTTCTGAAGGCAGTAATTC

Rev.of\_Cele-UNSB01\_6:7055357-7058647 Satlength=3291 Nr of Repeats=35  
RepeatLength=94 seed=TGCCCTTCAGA Num.seqs=35 Similarity=0.978211

87

TCAAAAATCTTCTGTTCTCTAAATATTGAGTGCTTTTCGATGCCCTATGTAGACAAATCAATGGGAAAATTGTC  
AATTTCTGAAGGCAGTAATTC

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Consensus:

TCAAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTaGTAGACAAATCAATGGGAAAATcaTC  
AATTTCTGAAGGCAGTAATTC

>Cele-UNSB01\_Fam\_48\_33\_6 Nr. of seq. 6 Alignment length(with gaps) = 33  
Alignment score = 0.649832

Cele-UNSB01\_1:12834373-12834766 Satlength=394 Nr of Repeats=5  
RepeatLength=32 seed=GCTGATTGGT Num.seqs=3 Similarity=0.861111

0 GCTGATTGGTTCA-AAAGTGGGCGTGGCTAATC

Rev.of\_Cele-UNSB01\_3:13044209-13044762 Satlength=554 Nr of Repeats=5  
RepeatLength=32 seed=ACCAATCAGC Num.seqs=3 Similarity=0.916667

10 GCTGATTGGTTCA-AAAGTGGGCGGAGCAAAATC

Rev.of\_Cele-UNSB01\_3:13000875-13002076 Satlength=1202 Nr of Repeats=5  
RepeatLength=32 seed=GACCAATCAG Num.seqs=3 Similarity=0.861111

11 GCTGATTGG-TCAGAGAGTGGGCGGGGCGAATC

Rev.of\_Cele-UNSB01\_2:14464146-14465077 Satlength=932 Nr of Repeats=26  
RepeatLength=32 seed=AACCAATCAG Num.seqs=19 Similarity=0.803296

11 GCTGATTGGTTCC-AAAATGGGTGGAGCTGAGC

Cele-UNSB01\_5:16730521-16730649 Satlength=129 Nr of Repeats=4  
RepeatLength=32 seed=GCTGATTGGT Num.seqs=4 Similarity=0.508488

0 GCTGATTGG-TAAGAACTGGGCGTGGCTGAAA

Rev.of\_Cele-UNSB01\_3:2325106-2325938 Satlength=833 Nr of Repeats=23  
RepeatLength=32 seed=CTCAGCCAAT Num.seqs=17 Similarity=0.871936

14 GTTGATTGGCTGAGAAA-TAGGCGGAGCTAAAC

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Consensus:

GCTGATTGGtTcAgAAAgTGGGCGgaGCTaAtC

>Cele-UNSB01\_Fam\_49\_21\_6 Nr. of seq. 6 Alignment length(with gaps) = 25  
Alignment score = 0.624889

Cele-UNSB01\_3:2342333-2342437 Satlength=105 Nr of Repeats=5  
RepeatLength=21 seed=CTGACCAAAT Num.seqs=4 Similarity=0.841270

0 CTGACC---AAATTTGT-TTCAGCA

Rev.of\_Cele-UNSB01\_3:2351961-2352192 Satlength=232 Nr of Repeats=9  
RepeatLength=21 seed=GTGAGTGTG Num.seqs=6 Similarity=0.856085

5 CTGACA---AAATTTGT-TCCAGCA

Cele-UNSB01\_3:3394846-3394930 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=TCCAGCACTG Num.seqs=4 Similarity=0.936508  
14 CTGACA---AAATTGT-TCCAGCA  
Rev.of\_Cele-UNSB01\_6:763886-764130 Satlength=245 Nr of Repeats=5  
RepeatLength=22 seed=TGGTCAGTGC Num.seqs=4 Similarity=0.777778  
7 CTGACC---AAATTGGTCGCCAGCA  
Rev.of\_Cele-UNSB01\_6:1033071-1033155 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=TGGTCAGTGC Num.seqs=4 Similarity=0.968254  
7 CTGACC---AAATTGTT-TCTTGCA  
Cele-UNSB01\_6:1569817-1569931 Satlength=115 Nr of Repeats=5  
RepeatLength=23 seed=AAAAAATTTG Num.seqs=4 Similarity=0.971014  
6 CTGACCAAAAAATTTGT-TTC-GCA

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Consensus:

CTGACcAAATTTGTTcCaGCA

>Cele-UNSB01\_Fam\_50\_21\_6 Nr. of seq. 6 Alignment length(with gaps) = 22  
Alignment score = 0.621212  
Cele-UNSB01\_6:1052300-1052972 Satlength=673 Nr of Repeats=4  
RepeatLength=21 seed=TGACAAAACA Num.seqs=3 Similarity=1.000000  
0 TGACAAAA-CATAACTTTGCAC  
Rev.of\_Cele-UNSB01\_6:12031687-12031907 Satlength=221 Nr of Repeats=10  
RepeatLength=22 seed=TCAGTGCAAA Num.seqs=8 Similarity=0.818182  
3 TGACAAAAGTGTCACCTTGCAC  
Rev.of\_Cele-UNSB01\_6:1106813-1106897 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=GTCAGTGCAA Num.seqs=4 Similarity=0.841270  
4 TGACAATA-TTTGAATTTGCAC  
Cele-UNSB01\_6:1365926-1366333 Satlength=408 Nr of Repeats=5  
RepeatLength=21 seed=TTGCACTGAC Num.seqs=3 Similarity=0.747475  
15 TGACAAAA-TTTCGTNTTGCAC  
Rev.of\_Cele-UNSB01\_6:1259650-1260300 Satlength=651 Nr of Repeats=6  
RepeatLength=21 seed=GTCAGTGCAA Num.seqs=4 Similarity=0.809524  
4 TGACCAAA-AATGCATTTGCAC  
Cele-UNSB01\_6:1371051-1371242 Satlength=192 Nr of Repeats=7  
RepeatLength=21 seed=TTGCACTGAC Num.seqs=6 Similarity=0.630303  
15 TGACCAAC-TCTTCATTTGCAC

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Consensus:

TGACaAAAtnTnaaTTTGCAC

>Cele-UNSB01\_Fam\_51\_19\_6 Nr. of seq. 6 Alignment length(with gaps) = 21  
Alignment score = 0.706878  
Cele-UNSB01\_1:11697315-11697448 Satlength=134 Nr of Repeats=7  
RepeatLength=19 seed=TTATCGATTT Num.seqs=5 Similarity=0.873684  
46 TCNA--GAAATTATCGATTTT  
Rev.of\_Cele-UNSB01\_3:2955858-2957390 Satlength=1533 Nr of Repeats=44  
RepeatLength=19 seed=AAAATCGATA Num.seqs=31 Similarity=0.912620  
57 TCCG--GAAATTATCGATTTT

Rev.of\_Cele-UNSB01\_3:1887376-1889731 Satlength=2356 Nr of Repeats=56  
RepeatLength=19 seed=AAAATCGATA Num.seqs=36 Similarity=0.647665  
57 CCGA--TAAATTATCGATTTT  
Rev.of\_Cele-UNSB01\_3:1974698-1975558 Satlength=861 Nr of Repeats=44  
RepeatLength=19 seed=AAAATCGATA Num.seqs=39 Similarity=0.805668  
57 CCGA--GNAATTATCGATTTT  
Cele-UNSB01\_3:2095462-2096950 Satlength=1489 Nr of Repeats=36  
RepeatLength=19 seed=TATCGATTTT Num.seqs=22 Similarity=0.729931  
47 TCGT--AAAATTATCGATTTT  
Cele-UNSB01\_5:19225003-19225171 Satlength=169 Nr of Repeats=8  
RepeatLength=21 seed=ATTATTGATT Num.seqs=8 Similarity=0.778409  
23 GAAAAATTATTGATTTTTCAA

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Consensus:

gaAATTATCGATTTTtCga

>Cele-UNSB01\_Fam\_52\_18\_6 Nr. of seq. 6 Alignment length(with gaps) = 19  
Alignment score = 0.691228  
Cele-UNSB01\_1:6226496-6226583 Satlength=88 Nr of Repeats=5  
RepeatLength=17 seed=AGGTAGTCAA Num.seqs=3 Similarity=1.000000  
0 AGGTAGTCAATGAGCA-A-  
Rev.of\_Cele-UNSB01\_5:8373901-8376688 Satlength=2788 Nr of Repeats=161  
RepeatLength=17 seed=TCATTGACTA Num.seqs=112 Similarity=0.914313  
13 AGGTAGTCAATGAGCA-A-  
Rev.of\_Cele-UNSB01\_4:7715733-7715854 Satlength=122 Nr of Repeats=6  
RepeatLength=17 seed=CTCATTGCCT Num.seqs=4 Similarity=0.764706  
14 GGTAGTCAATGAGCA-C-  
Cele-UNSB01\_4:9041393-9041548 Satlength=156 Nr of Repeats=8  
RepeatLength=17 seed=AGGCAATGAG Num.seqs=5 Similarity=0.781482  
3 -AGTAGGCAATGAGAA-AG  
Rev.of\_Cele-UNSB01\_5:6928533-6928671 Satlength=139 Nr of Repeats=7  
RepeatLength=17 seed=CTCATTGCCT Num.seqs=5 Similarity=0.703704  
13 -NGTAGGCAATGAGCA-AG  
Rev.of\_Cele-UNSB01\_5:7745857-7745978 Satlength=122 Nr of Repeats=6  
RepeatLength=17 seed=CTCATTGCCT Num.seqs=4 Similarity=0.697531  
13 -NGTAGGCAATGAGCACAG

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Consensus:

ngGTAGgCAATGAGCAAg

>Cele-UNSB01\_Fam\_53\_17\_6 Nr. of seq. 6 Alignment length(with gaps) = 18  
Alignment score = 0.858025  
Cele-UNSB01\_2:1681965-1682083 Satlength=119 Nr of Repeats=7  
RepeatLength=17 seed=GATGCCCCCT Num.seqs=5 Similarity=0.729630  
0 GATGCCCCCTTTGAACG-  
Rev.of\_Cele-UNSB01\_3:4389614-4389732 Satlength=119 Nr of Repeats=7  
RepeatLength=17 seed=AGGGGGCATC Num.seqs=5 Similarity=0.749020  
10 GATGCCCCCTCTGAACG-

Cele-UNSB01\_3:4392502-4392620 Satlength=119 Nr of Repeats=7  
RepeatLength=17 seed=GATGCCCCCT Num.seqs=5 Similarity=0.729630  
17 GATGCCCCCTCTGAACG-  
Cele-UNSB01\_4:4261575-4261676 Satlength=102 Nr of Repeats=6  
RepeatLength=17 seed=GATGCCCCCT Num.seqs=4 Similarity=0.722222  
0 GATGCCCCCTCTGAACGN  
Cele-UNSB01\_6:8886112-8886213 Satlength=102 Nr of Repeats=6  
RepeatLength=17 seed=GATGCCCCCT Num.seqs=4 Similarity=0.722222  
0 GATGCCCCCTCTGAACGN  
Rev.of\_Cele-UNSB01\_6:8885720-8885804 Satlength=85 Nr of Repeats=5  
RepeatLength=17 seed=AGGGGGCATC Num.seqs=3 Similarity=0.686275  
10 AATGCCCCCTNTGAACN-

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Consensus:

GATGCCCCCTcTGAACG

>Cele-UNSB01\_Fam\_54\_16\_6 Nr. of seq. 6 Alignment length(with gaps) = 16  
Alignment score = 0.865278  
Cele-UNSB01\_1:7925712-7926382 Satlength=671 Nr of Repeats=39  
RepeatLength=16 seed=AATTTTCCG Num.seqs=31 Similarity=0.813978  
0 AATTTTCCGCNGCGA  
Rev.of\_Cele-UNSB01\_2:7566750-7567567 Satlength=818 Nr of Repeats=42  
RepeatLength=16 seed=CGGAAAAATT Num.seqs=27 Similarity=0.719401  
10 AATTTTCCGCNGCNA  
Rev.of\_Cele-UNSB01\_5:13735981-13739186 Satlength=3206 Nr of Repeats=193  
RepeatLength=16 seed=GAAAAATTTT Num.seqs=167 Similarity=0.786698  
8 AATTTTTCAGCAGCAA  
Rev.of\_Cele-UNSB01\_5:13735981-13740432 Satlength=4452 Nr of Repeats=256  
RepeatLength=16 seed=GAAAAATTTT Num.seqs=212 Similarity=0.783548  
8 AATTTTTCAGCAGCAA  
Rev.of\_Cele-UNSB01\_5:13735981-13741243 Satlength=5263 Nr of Repeats=280  
RepeatLength=16 seed=GAAAAATTTT Num.seqs=227 Similarity=0.784063  
8 AATTTTTCNGCAGCAA  
Rev.of\_Cele-UNSB01\_5:13735981-13743674 Satlength=7694 Nr of Repeats=334  
RepeatLength=16 seed=GAAAAATTTT Num.seqs=260 Similarity=0.786925  
8 AATTTTCCGCAGCAA

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Consensus:

AATTTTTCcGCaGCaA

>Cele-UNSB01\_Fam\_55\_15\_6 Nr. of seq. 6 Alignment length(with gaps) = 15  
Alignment score = 0.952593  
Cele-UNSB01\_1:14535288-14535435 Satlength=148 Nr of Repeats=8  
RepeatLength=15 seed=GGGGGCAACA Num.seqs=5 Similarity=0.822222  
0 GGGGGCAACAAAATA  
Rev.of\_Cele-UNSB01\_1:14537614-14537761 Satlength=148 Nr of Repeats=8  
RepeatLength=15 seed=TGTTGCCCCC Num.seqs=5 Similarity=0.822222  
10 GGGGGCAACAAAATA

Rev.of\_Cele-UNSB01\_3:731921-732069 Satlength=149 Nr of Repeats=8  
RepeatLength=15 seed=TGTTGCCCCC Num.seqs=5 Similarity=0.795556  
10 GGGGGCAACAAAATA  
Cele-UNSB01\_6:17722232-17722379 Satlength=148 Nr of Repeats=8  
RepeatLength=15 seed=GGGGGCAACA Num.seqs=5 Similarity=0.822222  
0 GGGGGCAACAAAATA  
Cele-UNSB01\_2:1507976-1508324 Satlength=349 Nr of Repeats=19  
RepeatLength=15 seed=GGGGGCAACA Num.seqs=12 Similarity=0.807407  
0 GGGGGCAACAAAAA  
Cele-UNSB01\_3:727287-727380 Satlength=94 Nr of Repeats=5 RepeatLength=15  
seed=GGGGGCAACA Num.seqs=3 Similarity=0.822222  
0 GGGGGCAACAAAAA

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Consensus:

GGGGGCAACAAAAtA

>Cele-UNSB01\_Fam\_56\_11\_6 Nr. of seq. 6 Alignment length(with gaps) = 11  
Alignment score = 0.838384  
Cele-UNSB01\_2:4377229-4377482 Satlength=254 Nr of Repeats=23  
RepeatLength=11 seed=CAGTTGTCAC Num.seqs=19 Similarity=0.897927  
0 CAGTTGTCAC  
Cele-UNSB01\_6:3747622-3752392 Satlength=4771 Nr of Repeats=406  
RepeatLength=11 seed=CAGTTGTCAC Num.seqs=340 Similarity=0.892175  
0 CAGTTGTCACC  
Rev.of\_Cele-UNSB01\_4:4665165-4665209 Satlength=45 Nr of Repeats=4  
RepeatLength=11 seed=TGACAACCTT Num.seqs=4 Similarity=1.000000  
9 AAGTTGTCACA  
Rev.of\_Cele-UNSB01\_4:7151737-7153750 Satlength=2014 Nr of Repeats=178  
RepeatLength=11 seed=TGACAACCTC Num.seqs=131 Similarity=0.801993  
9 AAGTTGTCACG  
Cele-UNSB01\_5:4751883-4752158 Satlength=276 Nr of Repeats=22  
RepeatLength=11 seed=CACGAAGTTG Num.seqs=19 Similarity=0.914939  
18 AAGTTGTCACG  
Cele-UNSB01\_6:12089493-12089669 Satlength=177 Nr of Repeats=16  
RepeatLength=11 seed=CGAAGTTGTC Num.seqs=16 Similarity=0.870707  
9 AAGTTGTCACG

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Consensus:

aAGTTGTCACg

>Cele-UNSB01\_Fam\_57\_200\_5 Nr. of seq. 5 Alignment length(with gaps) =  
228 Alignment score = 0.666228  
Cele-UNSB01\_1:9974009-9976809 Satlength=2801 Nr of Repeats=15  
RepeatLength=200 seed=AACAGAATTT Num.seqs=13 Similarity=0.975385  
0 AACAGAATTTTAAAAAATTCGAAACCGCCAA-----  
GTTCAAGCAGAAAAAGT-GA---ATTTTCAGTCATACCTTG---  
TAGACCACAAATTTATATACAAAATTAATAGATTTTCCAAACTTTGAAAATTAATTTCTGGCTTCAAACCTAACT  
TTTTTAGAAATTCCCGTTGCCATTTTGTAGCAAATTTTATGTTCTTTCAGAAATTTGAA  
Cele-UNSB01\_4:14618655-14620445 Satlength=1791 Nr of Repeats=7  
RepeatLength=200 seed=GAAAAAGTGA Num.seqs=6 Similarity=0.937778

41 AACAGAATTTCAAAAAATTTTGAAACCACCAA-----  
 GTTCAAGCAGAAAAAGT-GA---ATTTTCAGTCATACCTTG---  
 TAGACCACAATTTATATGCAAAATTAATAGATTTTCCAAACTTTGAAAATTAATTTCTGGCTTCAAACCTAACT  
 TTTTAAAAAATTCCTAGCCATTTTGTAGCAAATTTTATGTTCTATCAGAATTTAAA  
 Rev.of\_Cele-UNSB01\_5:4216093-4219558 Satlength=3466 Nr of Repeats=18  
 RepeatLength=200 seed=GTGCGTCCAG Num.seqs=13 Similarity=0.916410  
 78 AACGGCATTTCAAAAAATTTAAAATCTGCCAA-----  
 GTTCAAGCAGAAAAAGT-GA---ATTTTCAGTCATACCTTC---  
 TGGACCACAATTTATATGCAAAATTAATAGATTTTCCAAACTTTGAAAATTAATTTCTGGCTTGAAACCTAACT  
 TTTTAAAAAATTCCTAGCCATTTTGTAGCAAATTTTAAAGTTCTTTTCTAGAAATTTGAA  
 Cele-UNSB01\_2:5970897-5971730 Satlength=834 Nr of Repeats=4  
 RepeatLength=203 seed=GTTCAAGCAG Num.seqs=3 Similarity=0.935730  
 32 AACGGCATTCCAAACATTTCCATATTCGCCGA-----  
 GTTCAAGCAGAACAGTAGATCAGATTTTGTAG--ATTGAATGGAATAAACG---  
 AGTTATATGCAAAATTAGTAGACTTTCCAAACTTTGAAAATTAATATCTGGCTTCAAACCTAACTTTTCTGAAA  
 ATCCCCGTAGCCATTTTGTGTGCAATTTTGTGCTCTTTTCTAGAAATTTAAA  
 Cele-UNSB01\_1:4183555-4184714 Satlength=1160 Nr of Repeats=5  
 RepeatLength=223 seed=TTTCAGAATT Num.seqs=4 Similarity=0.971101  
 189  
 AACGGCATTCCAAAACTTTTCAACCGCCAAGTTCAAGCAAAAAAAGTAACTTCAGTCATACCTTTTCTAGAG  
 CAACTTTGAA--ATTGAATGAAATAGACC---  
 ATTTATTTGCAAAATTAGTAGATTTTCCAATTTTAAAAATTAATATCTGGCTTCAAATAACTTTTTTTGAAA  
 ATCCCCGTAGCCATTTTGTGTGCAATTTTGTGCTCTTTTCTAGAAATTTAAA

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Consensus:

AACgGcATTtCAAAaAaTTtcaaAaccgCCaAgTTCAagCagAaaaagtGAAtTTTcAgtcATacctTgTagA  
 CcacaAtTTATaTgCAAAATTAaTAGAtTTTCCAAacTTTgAAAAATTAATtTCTGGCTTcAAAcTAACTTTTTt  
 TaaAAATtCCCGTaGCCATTTTGTaGCAAATTTTatGtTCTtTCAGAATTTaAA

>Cele-UNSB01\_Fam\_58\_48\_5 Nr. of seq. 5 Alignment length(with gaps) = 48  
 Alignment score = 0.900000  
 Cele-UNSB01\_4:5529418-5534698 Satlength=5281 Nr of Repeats=110  
 RepeatLength=48 seed=TTGCCCCGTAA Num.seqs=110 Similarity=0.963752  
 0 TTGCCCCGTAAATTTATATTTTCTGAAGATGAGCAATTCATTTTGTAT  
 Rev.of\_Cele-UNSB01\_4:13061036-13070540 Satlength=9505 Nr of Repeats=198  
 RepeatLength=48 seed=ACGGGCAAAT Num.seqs=198 Similarity=0.966024  
 8 TTGCCCCGTAAATTTATAATTTTCTGAAGATGAGCAATTTAATTTTGTAT  
 Cele-UNSB01\_6:3098438-3098774 Satlength=337 Nr of Repeats=7  
 RepeatLength=48 seed=AAGATGAGGA Num.seqs=7 Similarity=0.933862  
 24 TTGCCCCGTAAATTTATATTTTCTGAAGATGAGGAATTTATTTTGTAT  
 Rev.of\_Cele-UNSB01\_6:14711854-14734555 Satlength=22702 Nr of Repeats=477  
 RepeatLength=48 seed=GGCAAATCAA Num.seqs=293 Similarity=0.961435  
 53 TTGCCCCGTAAATTTATATTTTCTGAAGATGAGGAATTTAATTGTTGTAT  
 Cele-UNSB01\_5:1676007-1687585 Satlength=11579 Nr of Repeats=242  
 RepeatLength=48 seed=AATTTCTGAA Num.seqs=199 Similarity=0.901202  
 16 TTGCCCCGTAAATTTATAAATTTCTGAAGATGAGCAATTTAATTTTGTAG

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 Consensus:



TTGCCCCGTAATTTATAttTTTCTGAAGATGAGcAATTTAatTtTTGAt

>Cele-UNSB01\_Fam\_59\_31\_5 Nr. of seq. 5 Alignment length(with gaps) = 32  
Alignment score = 0.826042  
Cele-UNSB01\_2:858289-858649 Satlength=361 Nr of Repeats=5 RepeatLength=31  
seed=TGTCTAGCGA Num.seqs=3 Similarity=0.799283  
0 TGTCTAGCGAGACCTCAGAAG-AGAGCTGAGT  
Cele-UNSB01\_2:2619434-2619682 Satlength=249 Nr of Repeats=8  
RepeatLength=31 seed=AGAGCTGAGT Num.seqs=8 Similarity=0.806548  
22 TGTCTAGCGAGACAGCAGAAGAAGAGCTGAGT  
Cele-UNSB01\_2:1984417-1985378 Satlength=962 Nr of Repeats=31  
RepeatLength=31 seed=AGAGCTGAGT Num.seqs=31 Similarity=0.809341  
21 TGTCTAGCGAGATAGCAGANA-AGAGCTGAGT  
Cele-UNSB01\_2:1992839-1994265 Satlength=1427 Nr of Repeats=46  
RepeatLength=31 seed=AGAGCTGAGT Num.seqs=46 Similarity=0.811262  
21 TGTCTAGCGAGATAGCAGANA-AGAGCTGAGT  
Rev.of\_Cele-UNSB01\_2:2023342-2024644 Satlength=1303 Nr of Repeats=42  
RepeatLength=31 seed=GACAACTCAG Num.seqs=42 Similarity=0.826558  
35 TGTCTAGCGAGATAGCAGAAA-AGAGCTGAGT

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Consensus:

TGTCTAGCGAGAtagCAGAAaAGAGCTGAGT

>Cele-UNSB01\_Fam\_60\_25\_5 Nr. of seq. 5 Alignment length(with gaps) = 25  
Alignment score = 0.904000  
Cele-UNSB01\_1:10295164-10303189 Satlength=8026 Nr of Repeats=319  
RepeatLength=25 seed=TTACTCTAAT Num.seqs=293 Similarity=0.953127  
0 TTACTCTAATGTTCTGCCAATATAT  
Rev.of\_Cele-UNSB01\_6:10621309-10621525 Satlength=217 Nr of Repeats=4  
RepeatLength=25 seed=ATTGGCAGAA Num.seqs=3 Similarity=0.837607  
21 TTACTCTAATGTTCTGCCAATATAT  
Cele-UNSB01\_6:4149433-4175058 Satlength=25626 Nr of Repeats=1025  
RepeatLength=25 seed=AATGTTCTGTC Num.seqs=1025 Similarity=0.999688  
7 TTACTCTAATGTTCTGCCAATTTAT  
Rev.of\_Cele-UNSB01\_4:6425603-6430447 Satlength=4845 Nr of Repeats=192  
RepeatLength=25 seed=TTAGAGTAAA Num.seqs=177 Similarity=0.908867  
9 TTACTCTAATGTTCTGCTAATTTAT  
Rev.of\_Cele-UNSB01\_6:2091376-2093692 Satlength=2317 Nr of Repeats=86  
RepeatLength=25 seed=TTAGAGTAAA Num.seqs=71 Similarity=0.941451  
9 TTACTCTAATGTTCTGCCAATAAT

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Consensus:

TTACTCTAATGTTCTGCCAAtttAT

>Cele-UNSB01\_Fam\_61\_19\_5 Nr. of seq. 5 Alignment length(with gaps) = 22  
Alignment score = 0.775758  
Cele-UNSB01\_3:10140093-10140163 Satlength=71 Nr of Repeats=4  
RepeatLength=19 seed=TGGTTGAGGC Num.seqs=3 Similarity=0.906433  
0 -TGGTTGAGGCTCTA--GATT

Rev.of\_Cele-UNSB01\_4:186112-186245 Satlength=134 Nr of Repeats=7  
RepeatLength=19 seed=CCTCAACCAA Num.seqs=7 Similarity=0.826232  
9 -TGGTTGAGGCTCTN--GATTT  
Cele-UNSB01\_4:125359-125607 Satlength=249 Nr of Repeats=13  
RepeatLength=19 seed=TGGTTGAGGC Num.seqs=12 Similarity=0.880914  
0 -TGGTTGAGGCTCTC--TATTT  
Cele-UNSB01\_4:129890-130903 Satlength=1014 Nr of Repeats=21  
RepeatLength=22 seed=TTGGTTGAGG Num.seqs=16 Similarity=0.915152  
0 TTGGTTGAGGCTCTCTGGATTT  
Cele-UNSB01\_4:242271-242555 Satlength=285 Nr of Repeats=12  
RepeatLength=22 seed=TGAGGCTCTC Num.seqs=11 Similarity=0.886501  
5 TTGGTTGAGGCTCTCTGGATTT

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Consensus:

TGGTTGAGGCTCTcgATTT

>Cele-UNSB01\_Fam\_62\_21\_5 Nr. of seq. 5 Alignment length(with gaps) = 22  
Alignment score = 0.863636  
Cele-UNSB01\_1:13132164-13132288 Satlength=125 Nr of Repeats=6  
RepeatLength=21 seed=AATCCAATAT Num.seqs=5 Similarity=0.790476  
0 AATCCAATATGG-ANGAAATCT  
Rev.of\_Cele-UNSB01\_2:15030456-15030601 Satlength=146 Nr of Repeats=7  
RepeatLength=21 seed=ATTGGATTAG Num.seqs=6 Similarity=0.792593  
8 AATCCAATATGG-AAGAAATCT  
Cele-UNSB01\_3:6807960-6808176 Satlength=217 Nr of Repeats=6  
RepeatLength=21 seed=AAATCTAATC Num.seqs=5 Similarity=0.822727  
15 AATCCAATATGG-NCGAAATCT  
Rev.of\_Cele-UNSB01\_5:2584213-2584387 Satlength=175 Nr of Repeats=6  
RepeatLength=21 seed=GATTAGATTT Num.seqs=5 Similarity=0.841270  
25 AATCCAATATGG-ACNAAATCT  
Cele-UNSB01\_4:11101964-11102048 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=AAATCTAATC Num.seqs=4 Similarity=0.777778  
16 AATCCAATATGGAACGAAATCT

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Consensus:

AATCCAATATGGacgAAATCT

>Cele-UNSB01\_Fam\_63\_19\_5 Nr. of seq. 5 Alignment length(with gaps) = 21  
Alignment score = 0.695238  
Cele-UNSB01\_2:13971711-13972389 Satlength=679 Nr of Repeats=37  
RepeatLength=18 seed=AATTTACCAA Num.seqs=29 Similarity=0.745813  
0 AATTTACC-AA-TTTACCAA-  
Cele-UNSB01\_3:12492090-12492261 Satlength=172 Nr of Repeats=7  
RepeatLength=19 seed=CAATTTACCA Num.seqs=5 Similarity=0.791667  
7 AATTTGNC-AA-TTTACCAA  
Cele-UNSB01\_3:13143562-13144065 Satlength=504 Nr of Repeats=16  
RepeatLength=19 seed=TTGGCAATTT Num.seqs=10 Similarity=0.809747  
22 AATTTGGC-AA-TTTACCAA

Rev.of\_Cele-UNSB01\_3:1391886-1392275 Satlength=390 Nr of Repeats=16  
RepeatLength=21 seed=TTTTTGGTAA Num.seqs=13 Similarity=0.873016  
2 AAGTTACCAAATTTTACCAA  
Cele-UNSB01\_3:1394199-1394513 Satlength=315 Nr of Repeats=12  
RepeatLength=21 seed=CAAAAAGTTA Num.seqs=10 Similarity=0.923810  
17 AAGTTACCAAATTTTAACAA

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Consensus:

AAAtTTacCAATTTAcCAAa

>Cele-UNSB01\_Fam\_64\_17\_5 Nr. of seq. 5 Alignment length(with gaps) = 18  
Alignment score = 0.848148  
Cele-UNSB01\_2:1617453-1617521 Satlength=69 Nr of Repeats=4  
RepeatLength=17 seed=TCATTCCGTG Num.seqs=4 Similarity=1.000000  
0 TCATTCC-GTGATTATTT  
Cele-UNSB01\_3:4778835-4779093 Satlength=259 Nr of Repeats=5  
RepeatLength=17 seed=ATTATTTTCA Num.seqs=4 Similarity=1.000000  
10 TCATTCC-GTGATTATTT  
Rev.of\_Cele-UNSB01\_3:12626974-12627042 Satlength=69 Nr of Repeats=4  
RepeatLength=17 seed=TGAAAATAAT Num.seqs=4 Similarity=1.000000  
3 TCATTCC-GTGATTATTT  
Cele-UNSB01\_4:8831351-8831453 Satlength=103 Nr of Repeats=6  
RepeatLength=17 seed=TTCATTCCGT Num.seqs=6 Similarity=1.000000  
16 TCATTCC-GTGATTATTT  
Rev.of\_Cele-UNSB01\_6:6343035-6343121 Satlength=87 Nr of Repeats=5  
RepeatLength=17 seed=TAATTACTGG Num.seqs=4 Similarity=0.921569  
14 T-ATTCCAGTAATTATTT

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Consensus:

TcATTCCGTgATTATTT

>Cele-UNSB01\_Fam\_65\_11\_5 Nr. of seq. 5 Alignment length(with gaps) = 14  
Alignment score = 0.697619  
Cele-UNSB01\_2:4203805-4204480 Satlength=676 Nr of Repeats=4  
RepeatLength=11 seed=TGCCTGCCTA Num.seqs=3 Similarity=0.919192  
0 TGCCT--GCCTAC-  
Rev.of\_Cele-UNSB01\_2:4205915-4205959 Satlength=45 Nr of Repeats=4  
RepeatLength=11 seed=GGCAGGCAGT Num.seqs=4 Similarity=0.898990  
8 TGCCT--GCCTAC-  
Rev.of\_Cele-UNSB01\_4:4598852-4599551 Satlength=700 Nr of Repeats=6  
RepeatLength=11 seed=GCAGTAGGCA Num.seqs=5 Similarity=0.878788  
3 TGCCT--GCCTAC-  
Rev.of\_Cele-UNSB01\_1:742856-743285 Satlength=430 Nr of Repeats=11  
RepeatLength=12 seed=GCAGGTAGGT Num.seqs=7 Similarity=0.841270  
3 TGCCTA--CCTACC  
Cele-UNSB01\_2:2995760-2997536 Satlength=1777 Nr of Repeats=53  
RepeatLength=14 seed=CTACCTGCCT Num.seqs=34 Similarity=0.798659  
9 TGCCTATGCCTACC

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Consensus:

TGCCTgCCTAC

>Cele-UNSB01\_Fam\_66\_11\_5 Nr. of seq. 5 Alignment length(with gaps) = 11  
Alignment score = 0.951515  
Cele-UNSB01\_1:12905958-12906024 Satlength=67 Nr of Repeats=5  
RepeatLength=11 seed=TTTGGAGCGG Num.seqs=4 Similarity=0.777778  
0 TTTGGAGCGGA  
Cele-UNSB01\_3:7683133-7684661 Satlength=1529 Nr of Repeats=131  
RepeatLength=11 seed=TGGAGCGGTT Num.seqs=122 Similarity=0.884864  
2 TTTGGAGCGGT  
Cele-UNSB01\_6:1700308-1706287 Satlength=5980 Nr of Repeats=323  
RepeatLength=11 seed=GGAGCGGTTT Num.seqs=251 Similarity=0.936599  
3 TTTGGAGCGGT  
Cele-UNSB01\_6:8414337-8415392 Satlength=1056 Nr of Repeats=85  
RepeatLength=11 seed=GAGCGGTTTT Num.seqs=64 Similarity=0.790068  
4 TTTGGAGCGGT  
Cele-UNSB01\_6:10641130-10642329 Satlength=1200 Nr of Repeats=107  
RepeatLength=11 seed=TGGAGCGGTT Num.seqs=105 Similarity=0.866467  
2 TTTGGAGCGGT

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Consensus:

TTTGGAGCGGt

>Cele-UNSB01\_Fam\_67\_184\_4 Nr. of seq. 4 Alignment length(with gaps) = 189  
Alignment score = 0.862140  
Cele-UNSB01\_1:340649-342857 Satlength=2209 Nr of Repeats=12  
RepeatLength=184 seed=GAATACAGAA Num.seqs=12 Similarity=0.974089  
0 GAATACAGAACACCAATTATGCCCCGAG-AAAAAG-  
ATCCTACTCAGAATATAAACATAGTCGAATTTATCGGATGTATAAAGATTCCCGAAGACACTTTCCAATTACC  
CAAATTGTTTCATATTCTA--AATGAAAT-  
TCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGT  
Rev.of\_Cele-UNSB01\_2:14513028-14524678 Satlength=11651 Nr of Repeats=63  
RepeatLength=185 seed=CTCGGACATA Num.seqs=58 Similarity=0.981369  
27 GAATACAGAACACCAATTATGTCCGAG-  
AAAAAGAATCCAATTCAGAATATTAACATACTCGAATTTGTTCGGATGTATAAAGATTCCCGAAGACACTTTCC  
AATTACCCAAATTGTTTCATATTCTA--AATGAAAT-  
TCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGT  
Cele-UNSB01\_5:1233778-1237846 Satlength=4069 Nr of Repeats=22  
RepeatLength=185 seed=AATATAAACA Num.seqs=15 Similarity=0.974054  
45 GAATACAGAACACCAAGTTATGTCCGAGCAAAAAG-  
ATCCGATTCAGAATATAAACATATTTGAATTTGACGGATGTATAAAGATTCCCGAAGACACTTTCCAATTACC  
CAAATTGTTTCATATTCTA--AATGAGAT-  
TCTCTTACTAGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGT  
Cele-UNSB01\_3:11898352-11906615 Satlength=8264 Nr of Repeats=45  
RepeatLength=184 seed=TACGCAGCCG Num.seqs=41 Similarity=0.970891  
160 GAATACAGAACACCAATTATGTCCGAG-AAAAAG-  
ATCCTACTCAGAATATGAACATATTCGAATACATCGGAGGTATATAGATTCCCGAAGAGCCTTTCCAATTAAC  
CAAACGGTTCAAATTCCTAGCAA--ACATCTC-  
CTTACTTGAACACTCTTGGCCAATGTACGCAGCCGAACGTATCATAAGT

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Consensus:

GAATACAGAACACCAaTTATGtCCGAGAAAAAGATCctAcTCAGAATATaAACATATtCgAATttatCGGAtG  
TATAaAGATTCCCGAAGAcACTTTCCAATTAcCCAAAttGTTCAtATTCTAAAtgAaATTctCTTACTaGAAC  
ACTCTTGCCAATGTACGCAGCCGAACGTATCATAAGT

>Cele-UNSB01\_Fam\_68\_64\_4 Nr. of seq. 4 Alignment length(with gaps) = 67  
Alignment score = 0.721393  
Cele-UNSB01\_2:1316328-1316758 Satlength=431 Nr of Repeats=7  
RepeatLength=63 seed=GGTCTGCTAA Num.seqs=6 Similarity=0.855035  
0 GGTCTGCTAAATCGAACTTGTAGTTTGTAGCCTAGCAGACCAAATTTCTTCAAACT-AC---TTG  
Cele-UNSB01\_2:1412228-1413706 Satlength=1479 Nr of Repeats=12  
RepeatLength=63 seed=TAGTTTGTAG Num.seqs=8 Similarity=0.873016  
20 -GTCTGCTAAATCGAACTTGTAGTTTGTAGTCTAGCAGACCAAATTTCTTCAAAACC-CC--ATTG  
Rev.of\_Cele-UNSB01\_2:1422798-1423926 Satlength=1129 Nr of Repeats=9  
RepeatLength=63 seed=TTGGTCTGCT Num.seqs=6 Similarity=0.976014  
43 -GTCTGCTAAATCAAAAGTTGTAGTTTGTAGTCTAGCAGACCAAATTTCTTCAAAACC-CC--ATGG  
Cele-UNSB01\_2:590141-590909 Satlength=769 Nr of Repeats=12  
RepeatLength=64 seed=AAATTTTGTA Num.seqs=12 Similarity=0.921402  
13 GGTCTGCCAGATCAAATTTGTAGTTTGTAGTCTAGCAGACCCA--TT-TAGAATACCAACAAATTG

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Consensus:

gGTCTGctAaATCaAAacTTGTAGTTTGTAGtCTAGCAGACCaAatTTcTtcAAaACCaCaTtG

>Cele-UNSB01\_Fam\_69\_39\_4 Nr. of seq. 4 Alignment length(with gaps) = 40  
Alignment score = 0.856944  
Cele-UNSB01\_1:4232491-4233003 Satlength=513 Nr of Repeats=13  
RepeatLength=39 seed=TATTTTAAAT Num.seqs=8 Similarity=0.954823  
0 TA-TTTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACC  
Cele-UNSB01\_1:13379937-13380822 Satlength=886 Nr of Repeats=18  
RepeatLength=39 seed=TTAAAAAGTA Num.seqs=13 Similarity=0.822863  
19 TA-ATTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACC  
Cele-UNSB01\_1:13114799-13114994 Satlength=196 Nr of Repeats=5  
RepeatLength=39 seed=TATTTTAAAT Num.seqs=5 Similarity=0.965812  
0 TA-TTTTAAATTTAACCTACTTAAAAAGTAGGTCATGACC  
Cele-UNSB01\_3:10614332-10615157 Satlength=826 Nr of Repeats=20  
RepeatLength=40 seed=AAAAGTAGGT Num.seqs=16 Similarity=0.951944  
23 TAGTTTTTAACTGACCTCCTTAAAAAGTAGGTCATGACC

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Consensus:

TAtTTTAAAttGacCTaCTTAAAAAGTAGGTCATGACC

>Cele-UNSB01\_Fam\_70\_36\_4 Nr. of seq. 4 Alignment length(with gaps) = 36  
Alignment score = 0.754630

Cele-UNSB01\_1:3489580-3490945 Satlength=1366 Nr of Repeats=56  
RepeatLength=35 seed=TTTCGGCAAT Num.seqs=35 Similarity=0.808371  
0 TTTCGGCAATTTTCGGCAATTGCCGGTTTCNTGAAT-  
Rev.of\_Cele-UNSB01\_4:12842983-12843155 Satlength=173 Nr of Repeats=5  
RepeatLength=35 seed=AAACCGGCAA Num.seqs=3 Similarity=0.759259  
28 TTTCGGCAATTTTCGGCAATTGCCGGTTTGGAGAAT-  
Cele-UNSB01\_1:15073460-15073709 Satlength=250 Nr of Repeats=7  
RepeatLength=35 seed=CGGTTTGGGA Num.seqs=5 Similarity=0.885714  
21 -TTTCGGCAATTTTCGATAATTGCCGGTTTGGAAAAT  
Cele-UNSB01\_5:18345564-18345809 Satlength=246 Nr of Repeats=7  
RepeatLength=35 seed=AAATTTTCGG Num.seqs=7 Similarity=0.945578  
30 -TTTCGGCAAATTTGATAATTGCCGGTTTGGAAAATT

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Consensus:

tTTTCGGCAAtTTcGacAATTGCCGGTTTtggAAAtt

>Cele-UNSB01\_Fam\_71\_30\_4 Nr. of seq. 4 Alignment length(with gaps) = 30  
Alignment score = 0.777778  
Cele-UNSB01\_2:14178691-14179588 Satlength=898 Nr of Repeats=30  
RepeatLength=30 seed=TTTCTAGAAA Num.seqs=24 Similarity=0.857649  
0 TTTCTAGAAAAATCTGGAACTTCTAGAAC  
Rev.of\_Cele-UNSB01\_3:3351031-3351269 Satlength=239 Nr of Repeats=7  
RepeatLength=30 seed=TAGAACTTTC Num.seqs=5 Similarity=0.786667  
26 TTTCTAGAAAAATTGGAAAGTTCTAGAAAT  
Rev.of\_Cele-UNSB01\_3:3352849-3353088 Satlength=240 Nr of Repeats=8  
RepeatLength=30 seed=TAGAACTTTC Num.seqs=6 Similarity=0.925926  
26 TTTCTAGAGAAATTGGAAAGTTCTAGAAAT  
Rev.of\_Cele-UNSB01\_2:15064033-15064173 Satlength=141 Nr of Repeats=5  
RepeatLength=30 seed=TTCTGGAAAA Num.seqs=3 Similarity=0.762963  
9 TTTCCAGAAGGTTCTGGAACATTCTAGAAAT

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Consensus:

TTTCTAGAAAAATcTGGAAGTTCTAGAAAT

>Cele-UNSB01\_Fam\_72\_30\_4 Nr. of seq. 4 Alignment length(with gaps) = 30  
Alignment score = 0.983333  
Cele-UNSB01\_2:15106314-15106454 Satlength=141 Nr of Repeats=5  
RepeatLength=30 seed=AATTTTCCAG Num.seqs=3 Similarity=0.792593  
0 AATTTTCCAGAAGGTTCTGGAACATTCCAG  
Cele-UNSB01\_4:9470711-9470851 Satlength=141 Nr of Repeats=5  
RepeatLength=30 seed=AATTTTCCAG Num.seqs=3 Similarity=0.822222  
0 AATTTTCCAGAAGGTTCTGGAACATTCCAG  
Cele-UNSB01\_6:1421957-1422097 Satlength=141 Nr of Repeats=5  
RepeatLength=30 seed=AATTTTCCAG Num.seqs=3 Similarity=0.792593  
0 AATTTTCCAGAAGGTTCTGGAACATTCCAG  
Cele-UNSB01\_6:556993-557132 Satlength=140 Nr of Repeats=5 RepeatLength=30  
seed=AATTTTCCAG Num.seqs=3 Similarity=0.807407  
0 AATTTTCCAGAAGGTTCTGGAACNTTCCAG

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Consensus:

AATTTTCCAGAAGGTTCTGGAACaTTCCAG

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>Cele-UNSB01_Fam_73_20_4  Nr. of seq. 4 Alignment length(with gaps) = 23
Alignment score = 0.677536
Cele-UNSB01_3:1617648-1618407 Satlength=760 Nr of Repeats=37
RepeatLength=20 seed=TTTCACTAAA  Num.seqs=36 Similarity=0.904019
0   TTTCACTAAAAAT--C-TCAAAA
Rev.of_Cele-UNSB01_4:16675153-16675373 Satlength=221 Nr of Repeats=8
RepeatLength=20 seed=TTTTAGTGAA  Num.seqs=5 Similarity=1.000000
11  TTTCACTAAAAAT--C-TCAAAAT
Cele-UNSB01_4:1429332-1429629 Satlength=298 Nr of Repeats=15
RepeatLength=21 seed=AAAATTGACT  Num.seqs=10 Similarity=0.908289
18  ATTGACTAAAAAT--CGTCAAAA
Cele-UNSB01_4:2205280-2205605 Satlength=326 Nr of Repeats=13
RepeatLength=21 seed=AAAATAGCTT  Num.seqs=9 Similarity=0.765993
7   -TTGACTAAAAATAGC-TTAAAA
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Consensus:

tTTcACTAAAAATCTcAAaA

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>Cele-UNSB01_Fam_74_21_4  Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.651515
Cele-UNSB01_6:6516089-6517558 Satlength=1470 Nr of Repeats=50
RepeatLength=19 seed=GTCAGTGCAA  Num.seqs=37 Similarity=0.811390
0   GTCAGTGCAAC---TGCAANTG
Rev.of_Cele-UNSB01_5:18442188-18442272 Satlength=85 Nr of Repeats=4
RepeatLength=21 seed=GCACTGACCA  Num.seqs=4 Similarity=1.000000
8   GTCAGTGCAACAT-TGCATTTG
Cele-UNSB01_6:1138488-1138593 Satlength=106 Nr of Repeats=5
RepeatLength=21 seed=TTGGTCAGTG  Num.seqs=5 Similarity=0.746032
18  GTCAGTGCAATTT-TNNAATTG
Cele-UNSB01_6:1324054-1324372 Satlength=319 Nr of Repeats=7
RepeatLength=22 seed=GTCAGTGCAA  Num.seqs=5 Similarity=0.692754
0   GTCAGTGCAAATTGTGCACATG
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Consensus:

GTCAGTGCAActtTgcAatTG

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>Cele-UNSB01_Fam_75_20_4  Nr. of seq. 4 Alignment length(with gaps) = 20
Alignment score = 0.744444
Cele-UNSB01_1:14726982-14727102 Satlength=121 Nr of Repeats=6
RepeatLength=20 seed=GTGAAATTTT  Num.seqs=6 Similarity=0.705820
0   GTGAAATTTTAAATTTTAA
Cele-UNSB01_2:15212191-15212515 Satlength=325 Nr of Repeats=14
RepeatLength=20 seed=TTCACTCAAA  Num.seqs=10 Similarity=0.802963
16  GTCAAAATTTAAATTTTCA
```

Cele-UNSB01\_5:20247169-20247404 Satlength=236 Nr of Repeats=11  
RepeatLength=20 seed=TTTGAATTTT Num.seqs=7 Similarity=0.936508  
7 GTGAAAATTTGAATTTTGA  
Cele-UNSB01\_5:20719213-20719394 Satlength=182 Nr of Repeats=9  
RepeatLength=20 seed=AAAATTCAAA Num.seqs=6 Similarity=0.778836  
3 CTGAAAATTCAAATTTCTGA

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Consensus:

gTgAAAaTTtaAATTTtTgA

>Cele-UNSB01\_Fam\_76\_14\_4 Nr. of seq. 4 Alignment length(with gaps) = 15  
Alignment score = 0.727778  
Cele-UNSB01\_2:3063296-3063566 Satlength=271 Nr of Repeats=18  
RepeatLength=14 seed=TTAGGGCCTT Num.seqs=17 Similarity=0.949580  
0 TTAGGGCCTTGGGC-  
Rev.of\_Cele-UNSB01\_4:160082-160208 Satlength=127 Nr of Repeats=8  
RepeatLength=14 seed=CCTAAGCCTA Num.seqs=7 Similarity=0.918367  
5 TTAGGGCCTTAGGC-  
Cele-UNSB01\_6:16570815-16570983 Satlength=169 Nr of Repeats=12  
RepeatLength=14 seed=CTTAGGGCTT Num.seqs=12 Similarity=0.894661  
6 TTAGGGCTTAGGGC-  
Rev.of\_Cele-UNSB01\_2:3184073-3184138 Satlength=66 Nr of Repeats=4  
RepeatLength=14 seed=CCAAGGCCCA Num.seqs=3 Similarity=0.746032  
4 TT-GGGCCTTGGGCC

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Consensus:

TTaGGGCcTtgGGC

>Cele-UNSB01\_Fam\_77\_15\_4 Nr. of seq. 4 Alignment length(with gaps) = 15  
Alignment score = 0.955556  
Cele-UNSB01\_1:4250268-4250328 Satlength=61 Nr of Repeats=4  
RepeatLength=15 seed=TTTCCGGATC Num.seqs=4 Similarity=0.911111  
0 TTTCCGGATCTACGT  
Rev.of\_Cele-UNSB01\_1:4250510-4250645 Satlength=136 Nr of Repeats=9  
RepeatLength=15 seed=AGATCCGGAA Num.seqs=9 Similarity=1.000000  
11 TTTCCGGATCTACGT  
Rev.of\_Cele-UNSB01\_1:7000180-7000255 Satlength=76 Nr of Repeats=5  
RepeatLength=15 seed=AGATCCGGAA Num.seqs=5 Similarity=0.928889  
11 TTTCCGGATCTACGT  
Cele-UNSB01\_2:12906532-12906652 Satlength=121 Nr of Repeats=7  
RepeatLength=15 seed=ATTTCCGGAT Num.seqs=6 Similarity=0.922963  
14 TTTCCGGATCTACGA

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Consensus:

TTTCCGGATCTACGt

>Cele-UNSB01\_Fam\_78\_13\_4 Nr. of seq. 4 Alignment length(with gaps) = 13  
Alignment score = 0.897436



Cele-UNSB01\_5:1038307-1038528 Satlength=222 Nr of Repeats=11  
RepeatLength=13 seed=GCCTATGGCC Num.seqs=7 Similarity=0.912088  
0 GCCTATGGCCTAC  
Rev.of\_Cele-UNSB01\_5:1039029-1039263 Satlength=235 Nr of Repeats=18  
RepeatLength=13 seed=CGTAGGCCAT Num.seqs=18 Similarity=0.894754  
1 GCCTATGGCCTAC  
Cele-UNSB01\_5:2151047-2151352 Satlength=306 Nr of Repeats=21  
RepeatLength=13 seed=GCCTAAGCCT Num.seqs=17 Similarity=0.930618  
7 GCCTATGGCCTAA  
Rev.of\_Cele-UNSB01\_6:5352204-5352282 Satlength=79 Nr of Repeats=6  
RepeatLength=13 seed=GCCATAGGCG Num.seqs=6 Similarity=0.931624  
9 GCCTATGGCTTAC

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Consensus:

GCCTATGGCcTAc

>Cele-UNSB01\_Fam\_79\_12\_4 Nr. of seq. 4 Alignment length(with gaps) = 12  
Alignment score = 0.840278  
Cele-UNSB01\_1:2044939-2045157 Satlength=219 Nr of Repeats=13  
RepeatLength=11 seed=TTTTGCCGAA Num.seqs=10 Similarity=0.811448  
0 TTTTGCCGAAC-  
Cele-UNSB01\_1:5700313-5700505 Satlength=193 Nr of Repeats=16  
RepeatLength=12 seed=GAAATTTTTT Num.seqs=16 Similarity=0.949074  
7 TTTTTCGAAAT  
Cele-UNSB01\_1:12700590-12700802 Satlength=213 Nr of Repeats=16  
RepeatLength=12 seed=GAAATTTTTT Num.seqs=12 Similarity=0.915825  
7 TTTTTCGAAAT  
Rev.of\_Cele-UNSB01\_1:12700867-12701490 Satlength=624 Nr of Repeats=50  
RepeatLength=12 seed=AAAAAATTTTC Num.seqs=37 Similarity=0.905572  
17 TTTTTCGAAAT

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Consensus:

TTTTtCCGAAAt

>Cele-UNSB01\_Fam\_80\_12\_4 Nr. of seq. 4 Alignment length(with gaps) = 12  
Alignment score = 0.662037  
Cele-UNSB01\_4:5337721-5338093 Satlength=373 Nr of Repeats=18  
RepeatLength=12 seed=AGAAGGAGGA Num.seqs=11 Similarity=0.864646  
0 AGAAGGAGGAAA  
Rev.of\_Cele-UNSB01\_4:5366596-5366788 Satlength=193 Nr of Repeats=10  
RepeatLength=12 seed=TCCTCTTTCT Num.seqs=8 Similarity=0.896825  
10 AGAAAGAGGAGA  
Rev.of\_Cele-UNSB01\_6:7918402-7918617 Satlength=216 Nr of Repeats=6  
RepeatLength=12 seed=TCTTCCTCCT Num.seqs=4 Similarity=0.870370  
1 AGGAGGAGGAAG  
Rev.of\_Cele-UNSB01\_5:14055771-14055849 Satlength=79 Nr of Repeats=6  
RepeatLength=12 seed=TCTTTCTCCT Num.seqs=5 Similarity=0.866667  
1 ANAAGGAGAAAAG

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Consensus:

AgaAgGAGgAaa

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>Cele-UNSB01_Fam_81_10_4  Nr. of seq. 4 Alignment length(with gaps) = 10
Alignment score = 0.800000
Cele-UNSB01_2:6282823-6283646 Satlength=824 Nr of Repeats=34
RepeatLength=10 seed=TCCCGATCCA Num.seqs=22 Similarity=0.952670
0   TCCCGATCCA
Cele-UNSB01_2:7569779-7570282 Satlength=504 Nr of Repeats=27
RepeatLength=10 seed=TCCATCCCGA Num.seqs=19 Similarity=0.831650
6   TCCCGATCCA
Rev.of_Cele-UNSB01_6:17257914-17259280 Satlength=1367 Nr of Repeats=37
RepeatLength=10 seed=TGGATCGGGA Num.seqs=23 Similarity=0.908300
0   TCCCGATCCA
Cele-UNSB01_6:15839450-15840189 Satlength=740 Nr of Repeats=22
RepeatLength=10 seed=TATCTAGATC Num.seqs=15 Similarity=0.964444
8   TCTAGATCTA
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Consensus:

TCccGATCcA

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>Cele-UNSB01_Fam_82_167_3  Nr. of seq. 3 Alignment length(with gaps) =
172 Alignment score = 0.651809
Cele-UNSB01_3:464201-477164 Satlength=12964 Nr of Repeats=79
RepeatLength=164 seed=ATATAATGCT Num.seqs=68 Similarity=0.967912
0
ATATAATGCTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAGCCACGTCTGAAAATACAGATTTTTTCTCGA
AAATTT---CAAAACCTTTGTA-GAAATTCGATTTTTTGAC--
ATAAATGATCGCTCTTTTTTCTGACATGTATTTTCAGTGACAAA-TGGANT-AGAAA
Cele-UNSB01_2:14526196-14534994 Satlength=8799 Nr of Repeats=53
RepeatLength=166 seed=TCGTAATTAT Num.seqs=53 Similarity=0.999091
8   -
TATAATGTTTCGTAATTATTCATAAGTTTGTGTTGTCTCAGAGCCATGTCTGAAAAACAGATTTTTTTTCGAA
AATTT---TAAAAAGTTCGTA-
AAAATTGGATTTTTGACAAATCTATGCTCTCTTTTTTTGTTTGAAATTTAGTTCAGTGACATA-
CAATTTCAAAAA
Cele-UNSB01_2:13398823-13400207 Satlength=1385 Nr of Repeats=8
RepeatLength=165 seed=AAAATTCAAT Num.seqs=7 Similarity=0.943050
94   TTATAATGCTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAATCAATTCT-
AAAAAACAGATTTTTTTT-GAAAGTTTAAAGTAATATCCGCGGAGAAAATTCAATTTTGACATTTCTAT--
TATCT-TTTTTTTAAACATGTATTTTCAGTGA-ATAGAAGACTCAAAA-
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Consensus:

nTATAATGcTCGTAATTATTTATAAGTgTGTGTTGTCTCAGAgcCAngTCTgAAAAaACAGATTTTTTTtTcGA  
AAaTTTTtAAaAacttcGtAaAAATTCgATTTTTtGACanaTctATgnTctCTnTTTTTTtTntgAcATgTAtTTC  
AGTGAcAtAnagAnTcAaAAa

>Cele-UNSB01\_Fam\_83\_90\_3 Nr. of seq. 3 Alignment length(with gaps) = 95  
Alignment score = 0.673684  
Cele-UNSB01\_5:19764010-19764338 Satlength=329 Nr of Repeats=4  
RepeatLength=82 seed=CCCCGAACGT Num.seqs=4 Similarity=0.948510  
0 CCCCCAACGTGTCGGCCGCTTCC--AAATAACCACCTCCTTGCACTACGTTGCGCACACA-----  
CTCATTTACGCCAAGCTGCGGAA--  
Cele-UNSB01\_5:1577782-1578190 Satlength=409 Nr of Repeats=5  
RepeatLength=89 seed=GCACTACGTT Num.seqs=3 Similarity=0.740741  
38 CCCTGAACGTGTCGGCCGC-TCC--  
AAATAACTACCTTCTNGCACTACGTTGCGCACACACTAAGCTACTCGTTTCACGCCAAGCTACGGAA---  
Cele-UNSB01\_3:1724995-1725361 Satlength=367 Nr of Repeats=4  
RepeatLength=92 seed=CTGCGGAACC Num.seqs=3 Similarity=1.000000  
81 ---  
CGAACGTGTCGGCCGCTTCCAAAAACAACCACCTCTTCACACTTCATTGCGCACACACCAAATACTAGTTTC  
ACGTCAAATACTGCGGAACCC

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Consensus:

ccccGAACGTGTCGGCCGCTTCCAAAtAACcACCTccTngCACTaCgTTGCGCACACAcnaantcACTcgTTT  
CACGcCAAgCTgCGGAA

>Cele-UNSB01\_Fam\_84\_79\_3 Nr. of seq. 3 Alignment length(with gaps) = 79  
Alignment score = 0.909986  
Cele-UNSB01\_2:3993365-3994945 Satlength=1581 Nr of Repeats=20  
RepeatLength=79 seed=GTGAATCTCC Num.seqs=20 Similarity=0.984544  
0  
GTGAATCTCCTCTCCACCTAATGATTCTTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTT  
TCTTCT  
Rev.of\_Cele-UNSB01\_4:11132963-11135728 Satlength=2766 Nr of Repeats=35  
RepeatLength=79 seed=GAAACTAAAA Num.seqs=35 Similarity=0.918347  
75  
GTGAATCTCCTCTCTACCTAATGAGTCCTTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTT  
TCTTCT  
Cele-UNSB01\_2:8406477-8418390 Satlength=11914 Nr of Repeats=144  
RepeatLength=79 seed=TGACAGAATA Num.seqs=143 Similarity=0.910204  
28  
CTGAATCTCCACTCTTCCTAATGAGTCCTTGACAGAATACCGGCAGTATTTTGGGGTCTCATTAGGTTTTCGTT  
TCTTTT

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Consensus:

gTGAATCTCCTCTCtaCCTAATGAgTCCTTGACAGAATACCGGCAGTATTcTGGGGTCTCATTAGGTTTTaGTT  
TCTTcT

>Cele-UNSB01\_Fam\_85\_76\_3 Nr. of seq. 3 Alignment length(with gaps) = 76  
Alignment score = 0.906433  
Cele-UNSB01\_4:14405343-14406331 Satlength=989 Nr of Repeats=13  
RepeatLength=76 seed=AATGCTAGAG Num.seqs=13 Similarity=0.967611  
0

AATGCTAGAGGACACTCCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTTCGGTGTCTTTGTGCATGC  
TCG

Rev.of\_Cele-UNSB01\_4:14410457-14414735 Satlength=4279 Nr of Repeats=57  
RepeatLength=76 seed=TCGTGCAAAG Num.seqs=56 Similarity=0.948849  
27

AATGCTAGAGGACATTTCCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTTCGGTGTCTTTGTGCATGC  
TCG

Rev.of\_Cele-UNSB01\_6:17130007-17135013 Satlength=5007 Nr of Repeats=66  
RepeatLength=76 seed=AGCATTAGAG Num.seqs=56 Similarity=0.950911  
6

AATGCTAGAAGACACTCCTTTGCACGAAGGAAAGTGGGAGAGACTGTGGTGTTCGGTGTCTGTGTACATGC  
TCT

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Consensus:

AATGCTAGAgGACAcTCCTTTGCACGAAGgAAGTGGGAGAGACTGTGGaGTTGTTCGGTGTCTtTGTgCATGC  
TCg

>Cele-UNSB01\_Fam\_86\_64\_3 Nr. of seq. 3 Alignment length(with gaps) = 64  
Alignment score = 0.954861

Cele-UNSB01\_1:14168111-14168331 Satlength=221 Nr of Repeats=5  
RepeatLength=63 seed=TTTTTGACTA Num.seqs=3 Similarity=0.876736

0 TTTTTGACTACGGAATGTCTTTTTTCGCTACTGACTG-AAAAATAGCTACATTCGCACTTTTGNC

Rev.of\_Cele-UNSB01\_1:14174364-14175224 Satlength=861 Nr of Repeats=15  
RepeatLength=64 seed=GTAGTCAAAA Num.seqs=10 Similarity=0.982870

11 TTTTTGACTACTGAATGTCTTTTTTCGCTACTGACTGAAAAAATAGCTACATTCGCACTTTTGTC

Rev.of\_Cele-UNSB01\_5:14309212-14310008 Satlength=797 Nr of Repeats=14  
RepeatLength=64 seed=GTAGTCAAAA Num.seqs=9 Similarity=0.983796

11 TTTTTGACTACTGAATGTCTTTTTTCGCTACTGACTGAAAAAATAGCTACATTCGCACTTTTGTC

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Consensus:

TTTTTGACTACTGAATGTCTTTTTTCGCTACTGACTGaAAAAATAGCTACATTCGCACTTTTGtC

>Cele-UNSB01\_Fam\_87\_34\_3 Nr. of seq. 3 Alignment length(with gaps) = 34  
Alignment score = 0.980392

Cele-UNSB01\_1:11643779-11644036 Satlength=258 Nr of Repeats=6  
RepeatLength=34 seed=ATGCACCATG Num.seqs=4 Similarity=0.679739

0 ATGCACCATGTCAAAAAATATATCCAAAAGTACG

Cele-UNSB01\_1:11667166-11667423 Satlength=258 Nr of Repeats=6  
RepeatLength=34 seed=ATGCACCATG Num.seqs=4 Similarity=0.679739

0 ATGCACCATGTCAAAAAATATATCCAAAAGTACG

Cele-UNSB01\_1:12478910-12479068 Satlength=159 Nr of Repeats=5  
RepeatLength=34 seed=ATGCACCATG Num.seqs=4 Similarity=0.712418

0 ATGCACCATGTCAAAAAATATATCCAAAANTACG

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Consensus:

ATGCACCATGTCAAAAAATATATCCAAAAGTACG

>Cele-UNSB01\_Fam\_88\_32\_3 Nr. of seq. 3 Alignment length(with gaps) = 32  
Alignment score = 0.972222  
Cele-UNSB01\_1:11137320-11159590 Satlength=22271 Nr of Repeats=783  
RepeatLength=32 seed=GCACCAAATA Num.seqs=516 Similarity=0.905773  
0 GCACCAAATAGCACCAATTTAGCACCGATGGA  
Rev.of\_Cele-UNSB01\_6:12591006-12601690 Satlength=10685 Nr of Repeats=320  
RepeatLength=32 seed=GCTATTTGGT Num.seqs=268 Similarity=0.880720  
12 GCACCAAATAGCACCAATGTAGCACCGATGGA  
Rev.of\_Cele-UNSB01\_6:12591003-12604866 Satlength=13864 Nr of Repeats=415  
RepeatLength=32 seed=GGTGCTATTT Num.seqs=356 Similarity=0.868768  
15 GCACCAAATAGCACCAATGTAGCACCGATGGA

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Consensus:

GCACCAAATAGCACCAATgTAGCACCGATGGA

>Cele-UNSB01\_Fam\_89\_32\_3 Nr. of seq. 3 Alignment length(with gaps) = 32  
Alignment score = 0.972222  
Cele-UNSB01\_4:14093954-14094851 Satlength=898 Nr of Repeats=32  
RepeatLength=32 seed=CGACCTGCGA Num.seqs=24 Similarity=0.987923  
0 CGACCTGCGACCTAGCGACCTGGGTCGCTTTG  
Cele-UNSB01\_6:2413161-2413272 Satlength=112 Nr of Repeats=4  
RepeatLength=32 seed=CGACCTGCGA Num.seqs=3 Similarity=0.805556  
0 CGACCTGCGACCTAGCGACCTAGGTCGCTTTG  
Cele-UNSB01\_6:12904034-12904836 Satlength=803 Nr of Repeats=12  
RepeatLength=32 seed=CGACCTAGGT Num.seqs=8 Similarity=0.956845  
15 CGACCTGCGACCTAGCGACCTAGGTCGCTTTG

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Consensus:

CGACCTGCGACCTAGCGACCTaGGTCGCTTTG

>Cele-UNSB01\_Fam\_90\_27\_3 Nr. of seq. 3 Alignment length(with gaps) = 27  
Alignment score = 0.658436  
Cele-UNSB01\_4:3004201-3004345 Satlength=145 Nr of Repeats=6  
RepeatLength=24 seed=GCGGCCGACA Num.seqs=6 Similarity=0.855556  
0 -GCGGCCGACACCTTACGGGTTG--TA  
Cele-UNSB01\_2:13658533-13659809 Satlength=1277 Nr of Repeats=26  
RepeatLength=27 seed=AGCAGCCGAC Num.seqs=20 Similarity=0.791813  
0 AGCAGCCGACACCTTGcNGGTTGCTTA  
Cele-UNSB01\_5:19852888-19853192 Satlength=305 Nr of Repeats=8  
RepeatLength=27 seed=GCAGCCGACA Num.seqs=6 Similarity=0.584291  
1 AGCAGCCGACACCTCACTGGTCCCTNA

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Consensus:

aGCaGCCGACACCTtaCnGGTtgcttA

>Cele-UNSB01\_Fam\_91\_21\_3 Nr. of seq. 3 Alignment length(with gaps) = 23  
Alignment score = 0.801932

Cele-UNSB01\_2:13499104-13499209 Satlength=106 Nr of Repeats=5  
RepeatLength=21 seed=CTAGAAAAAC Num.seqs=5 Similarity=0.898413  
0 CTA-GAAAAACTCGGCCATCAA-  
Rev.of\_Cele-UNSB01\_2:13500094-13501231 Satlength=1138 Nr of Repeats=46  
RepeatLength=21 seed=TTTTCTAGTT Num.seqs=34 Similarity=0.794245  
8 CTA-GAAAAACTCGGCCATCAA-  
Cele-UNSB01\_2:646191-646835 Satlength=645 Nr of Repeats=25  
RepeatLength=23 seed=GGCCACCAAT Num.seqs=20 Similarity=0.753776  
13 CTATAAAAAACTCGGCCACCAAT

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Consensus:

CTAgAAAAACTCGGCCAtCAA

>Cele-UNSB01\_Fam\_92\_21\_3 Nr. of seq. 3 Alignment length(with gaps) = 23  
Alignment score = 0.748792  
Cele-UNSB01\_4:3817232-3817391 Satlength=160 Nr of Repeats=5  
RepeatLength=21 seed=TAGTTTGTAG Num.seqs=3 Similarity=0.661376  
0 TAG-TTT-ATAGTTTGCAGTTTG  
Cele-UNSB01\_5:3623960-3624037 Satlength=78 Nr of Repeats=4  
RepeatLength=21 seed=AGTTTGTAGT Num.seqs=3 Similarity=0.640212  
1 TAG-TTT-GTAGTTTGTNGTTTG  
Rev.of\_Cele-UNSB01\_1:13115312-13116088 Satlength=777 Nr of Repeats=11  
RepeatLength=23 seed=ACTACAAACT Num.seqs=10 Similarity=1.000000  
4 TAGTTTTCATAGTTTGTAGTTTG

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Consensus:

TAGTTTaTAGTTTGtaGTTTG

>Cele-UNSB01\_Fam\_93\_20\_3 Nr. of seq. 3 Alignment length(with gaps) = 22  
Alignment score = 0.656566  
Cele-UNSB01\_3:3164980-3165718 Satlength=739 Nr of Repeats=38  
RepeatLength=18 seed=GTCGATTAC Num.seqs=33 Similarity=0.778900  
0 GTCGATTACG-AGA-TTN--T  
Rev.of\_Cele-UNSB01\_2:13900624-13901003 Satlength=380 Nr of Repeats=15  
RepeatLength=21 seed=CTCGTAAATC Num.seqs=9 Similarity=0.754630  
13 GTCGATTACGAGGAGTTC-TT  
Cele-UNSB01\_4:1866819-1867315 Satlength=497 Nr of Repeats=18  
RepeatLength=21 seed=TGTCGATTTA Num.seqs=15 Similarity=0.738095  
21 GTCGATTACG-GGAGTTCAGT

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Consensus:

GTCGATTACGgGAgTTcnT

>Cele-UNSB01\_Fam\_94\_21\_3 Nr. of seq. 3 Alignment length(with gaps) = 22  
Alignment score = 0.843434  
Cele-UNSB01\_3:86662-86935 Satlength=274 Nr of Repeats=13 RepeatLength=21  
seed=CCATTTTAAG Num.seqs=13 Similarity=0.947904  
0 CCATTTTAAGCC-AATTTTGGA

Cele-UNSB01\_3:86662-87180 Satlength=519 Nr of Repeats=25 RepeatLength=21  
seed=CCATTTTAAG Num.seqs=16 Similarity=0.877588  
0 CCATTTTAAGCC-AATTTTGGA  
Rev.of\_Cele-UNSB01\_3:83964-84341 Satlength=378 Nr of Repeats=14  
RepeatLength=21 seed=AAATTTGGCT Num.seqs=11 Similarity=0.774105  
18 CCATTTTAAGCCAAATTTTCAA

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Consensus:

CCATTTTAAGCCAATTTTggA

>Cele-UNSB01\_Fam\_95\_22\_3 Nr. of seq. 3 Alignment length(with gaps) = 22  
Alignment score = 0.777778  
Cele-UNSB01\_2:2758878-2759540 Satlength=663 Nr of Repeats=24  
RepeatLength=22 seed=ACTACAGTAA Num.seqs=18 Similarity=0.729847  
0 ACTACAGTAACCCTACANTACC  
Cele-UNSB01\_5:1035824-1036308 Satlength=485 Nr of Repeats=20  
RepeatLength=22 seed=ACAGTACTCC Num.seqs=16 Similarity=0.776630  
3 ANTACAGTACTCCTACAGTACC  
Rev.of\_Cele-UNSB01\_5:16682435-16683237 Satlength=803 Nr of Repeats=14  
RepeatLength=22 seed=GGGTACTGTA Num.seqs=9 Similarity=0.840067  
12 ACTACAGTACCCATACAGTACT

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Consensus:

AcTACAGTAccCcTACAgTACc

>Cele-UNSB01\_Fam\_96\_19\_3 Nr. of seq. 3 Alignment length(with gaps) = 21  
Alignment score = 0.608466  
Cele-UNSB01\_1:2556234-2556523 Satlength=290 Nr of Repeats=10  
RepeatLength=18 seed=GCCTAGGAAT Num.seqs=8 Similarity=0.772487  
0 GCCTAGGAAT-CCAAT--ATG  
Rev.of\_Cele-UNSB01\_1:1302534-1303556 Satlength=1023 Nr of Repeats=33  
RepeatLength=19 seed=TTCTAGGCCA Num.seqs=21 Similarity=0.753383  
8 GCCTAGAAATCCTCA--GATG  
Rev.of\_Cele-UNSB01\_1:1127917-1128577 Satlength=661 Nr of Repeats=21  
RepeatLength=20 seed=ATTTCTAGGC Num.seqs=13 Similarity=0.625153  
10 GCCTAGAAAT-CTNATNGATG

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Consensus:

GCCTAGaAATCtnAtgATG

>Cele-UNSB01\_Fam\_97\_18\_3 Nr. of seq. 3 Alignment length(with gaps) = 21  
Alignment score = 0.761905  
Cele-UNSB01\_6:3455223-3455778 Satlength=556 Nr of Repeats=27  
RepeatLength=18 seed=TTTTGTCAGT Num.seqs=20 Similarity=0.766579  
0 TTTTGTCAGTGCT--ATAGT  
Cele-UNSB01\_6:3508288-3508508 Satlength=221 Nr of Repeats=10  
RepeatLength=18 seed=TTGTCAGTGC Num.seqs=7 Similarity=0.848325  
2 TTTTGTCAGTGCT--ATAGT

Rev.of\_Cele-UNSB01\_6:1590254-1590338 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=TCTGAGCACT Num.seqs=4 Similarity=0.925926  
17 TTTTGTCACTGCTCAGATAAT

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Consensus:

TTTTGTCACTGCTATAgT

>Cele-UNSB01\_Fam\_98\_20\_3 Nr. of seq. 3 Alignment length(with gaps) = 21  
Alignment score = 0.719577

Cele-UNSB01\_2:3287465-3288008 Satlength=544 Nr of Repeats=19  
RepeatLength=20 seed=GTAAATCTAC Num.seqs=12 Similarity=0.565197  
0 GTAAATCTACACTA-GCTTCC

Rev.of\_Cele-UNSB01\_4:3714325-3715225 Satlength=901 Nr of Repeats=15  
RepeatLength=21 seed=TGTAGATTTA Num.seqs=10 Similarity=0.670875

11 GTAAATCTACANTAGGCTCCC  
Cele-UNSB01\_2:12047204-12047947 Satlength=744 Nr of Repeats=32  
RepeatLength=20 seed=TAAATCTACA Num.seqs=25 Similarity=0.700222  
1 GTAAATCTACACNG-GCTNGC

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Consensus:

GTAAATCTACActaGCTncC

>Cele-UNSB01\_Fam\_99\_21\_3 Nr. of seq. 3 Alignment length(with gaps) = 21  
Alignment score = 0.767196

Cele-UNSB01\_3:1210986-1211328 Satlength=343 Nr of Repeats=4  
RepeatLength=21 seed=ACTACAGTAC Num.seqs=3 Similarity=0.788360  
0 ACTACAGTACCCCNACNACT

Cele-UNSB01\_4:14628221-14628977 Satlength=757 Nr of Repeats=36  
RepeatLength=21 seed=CAACTACCAC Num.seqs=36 Similarity=0.943361  
10 ACTACCGTACCAACTACCACA

Cele-UNSB01\_4:14648431-14648725 Satlength=295 Nr of Repeats=13  
RepeatLength=21 seed=ACTACCGTAC Num.seqs=12 Similarity=0.895142  
21 ACTACCGTACCAACTACCACA

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Consensus:

ACTACcGTACCaaCtACcACa

>Cele-UNSB01\_Fam\_100\_21\_3 Nr. of seq. 3 Alignment length(with gaps) = 21  
Alignment score = 0.957672

Cele-UNSB01\_5:3330728-3331463 Satlength=736 Nr of Repeats=20  
RepeatLength=21 seed=CTAACATTTT Num.seqs=12 Similarity=0.927850  
0 CTAACATTTTTCATTTTCGT

Cele-UNSB01\_5:16772051-16772198 Satlength=148 Nr of Repeats=7  
RepeatLength=21 seed=ATTTTTCAT Num.seqs=7 Similarity=0.848828  
5 CTAACATTTTTCATTTTCGT

Cele-UNSB01\_5:3604514-3604619 Satlength=106 Nr of Repeats=5  
RepeatLength=21 seed=TTTCAGTTTT Num.seqs=5 Similarity=0.911111  
8 CTAACATTTTTCAGTTTTTCGT



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Consensus:

CTAACATTTTTCaTTTTTCGT

>Cele-UNSB01\_Fam\_101\_21\_3 Nr. of seq. 3 Alignment length(with gaps) = 21  
Alignment score = 0.682540

Cele-UNSB01\_6:1259650-1260300 Satlength=651 Nr of Repeats=6  
RepeatLength=21 seed=GTCAGTGCAA Num.seqs=4 Similarity=0.809524

34 AAATGCATTTTGGTCAGTGC

Rev.of\_Cele-UNSB01\_6:1371051-1371242 Satlength=192 Nr of Repeats=7

RepeatLength=21 seed=TTGCACTGAC Num.seqs=6 Similarity=0.630303

44 AAATGAAGAGTTGGTCAGTGC

Cele-UNSB01\_6:15665052-15665283 Satlength=232 Nr of Repeats=11

RepeatLength=21 seed=TGAAAGATTG Num.seqs=9 Similarity=0.957672

28 GTGCCTATGAAAGATTGGTCA

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Consensus:

GTgcaaatgnAtnnnttGgTca

>Cele-UNSB01\_Fam\_102\_20\_3 Nr. of seq. 3 Alignment length(with gaps) = 20  
Alignment score = 0.688889

Cele-UNSB01\_2:13684820-13685366 Satlength=547 Nr of Repeats=24

RepeatLength=20 seed=GTAAATCGAC Num.seqs=16 Similarity=0.655886

10 ACACNACGTCGTAAATCGAC

Rev.of\_Cele-UNSB01\_3:2118949-2119137 Satlength=189 Nr of Repeats=9

RepeatLength=20 seed=TGTAGATTTA Num.seqs=6 Similarity=0.697778

21 ATAGAACCCCGTAAATCTAC

Rev.of\_Cele-UNSB01\_3:13139705-13140905 Satlength=1201 Nr of Repeats=30

RepeatLength=20 seed=TGTAGATTTA Num.seqs=22 Similarity=0.674981

21 ATAGANCTTCGTAAATCTAC

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Consensus:

GTAAATCtACAtAgaaCntC

>Cele-UNSB01\_Fam\_103\_20\_3 Nr. of seq. 3 Alignment length(with gaps) = 20  
Alignment score = 0.822222

Cele-UNSB01\_4:8607400-8623699 Satlength=16300 Nr of Repeats=831

RepeatLength=20 seed=ATACGATATA Num.seqs=721 Similarity=0.881205

0 ATACGATATAGCTATTTACG

Rev.of\_Cele-UNSB01\_6:4175079-4227144 Satlength=52066 Nr of Repeats=2000

RepeatLength=20 seed=CTATATCGTA Num.seqs=1999 Similarity=1.000000

11 ATACGATATAGCTATTTACG

Rev.of\_Cele-UNSB01\_6:7306204-7313772 Satlength=7569 Nr of Repeats=373

RepeatLength=20 seed=ATAGCTATGT Num.seqs=332 Similarity=0.894033

15 ACACGACATAGCTATAAACG

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Consensus:

AtACGAtATAGCTATttACG

>Cele-UNSB01\_Fam\_104\_16\_3 Nr. of seq. 3 Alignment length(with gaps) = 16  
Alignment score = 0.777778  
Cele-UNSB01\_1:758474-759042 Satlength=569 Nr of Repeats=35  
RepeatLength=16 seed=TTTCAGGCTT Num.seqs=34 Similarity=0.947564  
0 TTTCAGGCTTTTCAGGC  
Cele-UNSB01\_5:17844176-17844688 Satlength=513 Nr of Repeats=32  
RepeatLength=16 seed=CCAGGGTTCC Num.seqs=32 Similarity=1.000000  
2 TTCCAGGGTTCCAGGG  
Cele-UNSB01\_5:17844176-17845043 Satlength=868 Nr of Repeats=35  
RepeatLength=16 seed=CCAGGGTTCC Num.seqs=33 Similarity=0.989899  
2 TTCCAGGGTTCCAGGG

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Consensus:

TTcCAGGgTTcCAGGg

>Cele-UNSB01\_Fam\_105\_11\_3 Nr. of seq. 3 Alignment length(with gaps) = 12  
Alignment score = 0.787037  
Cele-UNSB01\_3:9173467-9173588 Satlength=122 Nr of Repeats=11  
RepeatLength=11 seed=ATTTGGAATA Num.seqs=11 Similarity=0.903030  
0 ATT-TGGAATAT  
Cele-UNSB01\_4:11083607-11084360 Satlength=754 Nr of Repeats=4  
RepeatLength=11 seed=TTTGAAATAT Num.seqs=3 Similarity=1.000000  
1 ATT-TGAAATAT  
Rev.of\_Cele-UNSB01\_4:6539759-6539908 Satlength=150 Nr of Repeats=10  
RepeatLength=12 seed=CAGAAATATAT Num.seqs=7 Similarity=0.915344  
6 ATTCTGGAATAT

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Consensus:

ATTTGgAATAT

>Cele-UNSB01\_Fam\_106\_11\_3 Nr. of seq. 3 Alignment length(with gaps) = 12  
Alignment score = 0.722222  
Cele-UNSB01\_4:5758139-5758194 Satlength=56 Nr of Repeats=5  
RepeatLength=11 seed=TCCACTGACC Num.seqs=5 Similarity=0.951515  
0 TCCACTGACCA-  
Cele-UNSB01\_2:6392491-6392539 Satlength=49 Nr of Repeats=4  
RepeatLength=12 seed=CCACTGACCA Num.seqs=4 Similarity=0.944444  
1 CCCACTGACCAT  
Rev.of\_Cele-UNSB01\_6:14101701-14101756 Satlength=56 Nr of Repeats=5  
RepeatLength=11 seed=GTGCTTGGTC Num.seqs=5 Similarity=0.951515  
5 AGCACTGACCA-

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Consensus:

ncCACTGACCA

>Cele-UNSB01\_Fam\_107\_151\_2 Nr. of seq. 2 Alignment length(with gaps) =  
 151 Alignment score = 0.924945  
 Cele-UNSB01\_3:3200630-3201398 Satlength=769 Nr of Repeats=4  
 RepeatLength=151 seed=TTTAAAGGCG Num.seqs=3 Similarity=0.500000  
 0  
 TTTAAAGGCGCATAGGTAGNTCAAANTTCAAANTTGACGGATTCTAGTCAATATGGGGCTTATTTTAAAGCTC  
 TCAGTAAGCTNAATNTANTTNAGCTACTNAAAATTGAANATTTTNAATTTTTTGGGTCTCGCAGCGAAAATT  
 TCGAA  
 Cele-UNSB01\_3:3207516-3208428 Satlength=913 Nr of Repeats=5  
 RepeatLength=151 seed=TTTAAAGGCG Num.seqs=3 Similarity=0.500000  
 0  
 TTTAAAGGCGCATAGGTAGTTCAAANTTCAAANTTGACGGATTCTAGTCAATATGGGGCTTATTTTAAAGCTC  
 TCAGTAAGCTNAATNTANTTNAGCTACTAACAATTGAANATTTTNAATTTTTTGGGTCTCGCAGCGAAAATT  
 TCGAA

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 Consensus:

TTTAAAGGCGCATAGGTAGTCAAANTTCAAANTTGACGGATTCTAGTCAATATGGGGCTTATTTTAAAGCTC  
 TCAGTAAGCTNAATNTANTTNAGCTACTAaAATTGAANATTTTNAATTTTTTGGGTCTCGCAGCGAAAATT  
 TCGAA

>Cele-UNSB01\_Fam\_108\_119\_2 Nr. of seq. 2 Alignment length(with gaps) =  
 119 Alignment score = 0.607843  
 Cele-UNSB01\_1:5777645-5778359 Satlength=715 Nr of Repeats=6  
 RepeatLength=119 seed=GCCACCTTTA Num.seqs=6 Similarity=0.967880  
 0  
 GCCACCTTTAACCCTAATCCAAGCAGAGCAGGCCGTAGGCCTGCTATGCGGTAGCGACACGCTCAGGCCCAAT  
 AGTCCGGGATGAGGGCCGCAGGCCCTCTTACTCTTAGAACTTTAG  
 Cele-UNSB01\_5:17249920-17250872 Satlength=953 Nr of Repeats=8  
 RepeatLength=119 seed=AACTGTGGGC Num.seqs=8 Similarity=0.947979  
 111  
 GCTGGCCTTAATCCTAACCCACGCAGAGCAGGATGTAGGCCTGAAACGTGGTTGTTATTCAATCAAGCCTAAC  
 AACCAGGTTTGAGGGCCGCAGGCCCGAAAACCTCTTGAAACTGTGG

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 Consensus:

GCcacCcTTAAcCCTAAcCCAaGCAGAGCAGGacGTAGGCCTGaaAcGcGGTaGcgAcaCaaTCAaGCCcAAc  
 AacCaGGgaTGAGGGCCGCAGGCCCGaaaaACTCTTaGAAACTgTaG

>Cele-UNSB01\_Fam\_109\_110\_2 Nr. of seq. 2 Alignment length(with gaps) =  
 110 Alignment score = 0.745455  
 Cele-UNSB01\_6:11975065-11975494 Satlength=430 Nr of Repeats=4  
 RepeatLength=108 seed=TTTCACGTTT Num.seqs=3 Similarity=0.860082  
 0 TTTCACGTTTTTCAGGTGATTATCTAGGTCACGAACTAATTTATTTTGAAAATTGACCT--  
 GTGGACCTATACTTTGGAGATATGGGAAATTGAGTATGGGCTTTCAGAT  
 Cele-UNSB01\_6:13568461-13570473 Satlength=2013 Nr of Repeats=18  
 RepeatLength=108 seed=TTTCAGATTT Num.seqs=17 Similarity=0.875000  
 100 TTTCACATTTTCACTTGATTATATAGGTCACGACCCAAATTATTTTGAAAATTGAGCTACACGG--  
 CTGTAACCTTTGGAGCTATGGGTAATCAAGTATGAGCTTTTCAGAT

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Consensus:

TTTCACaTTTTCacgTGATTATaTAGGTCACGAaCcAAaTTATTTTGAAAATTGAcCTacacGGacCTaTAAC  
TTTGGAGaTATGGGaAATcaAGTATGaGCTTTCAGAT

>Cele-UNSB01\_Fam\_110\_86\_2 Nr. of seq. 2 Alignment length(with gaps) = 86  
Alignment score = 0.689922  
Cele-UNSB01\_2:5140446-5146375 Satlength=5930 Nr of Repeats=77  
RepeatLength=76 seed=CAATAGAAAA Num.seqs=56 Similarity=0.988380  
0 CAATA--GAAAAGATGGAAGACTAC--AG--AA--A-AA-  
CTATTGAGAGACCCCGAAATACTGGCTGTATTTTGAAAGGTCATCT  
Rev.of\_Cele-UNSB01\_2:9101090-9103530 Satlength=2441 Nr of Repeats=29  
RepeatLength=86 seed=AGCCAGTATT Num.seqs=28 Similarity=0.980066  
67  
CAATAGGGAAAAGATGGAAGAGTTTGAAGTTAACGAGAAGCTATTGCCAGACCCCGAAATACTGGCTGTATTT  
TGAAAGGTCGTGG

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Consensus:

CAATAggGAAAAGATGGAAGAcTaCgaAGttAAcgAgAAgCTATTGacAGACCCCGAAATACTGGCTGTATTT  
TGAAAGGTCaTcg

>Cele-UNSB01\_Fam\_111\_73\_2 Nr. of seq. 2 Alignment length(with gaps) = 73  
Alignment score = 0.945205  
Cele-UNSB01\_1:12413207-12413533 Satlength=327 Nr of Repeats=4  
RepeatLength=73 seed=AATAAAATAT Num.seqs=3 Similarity=0.963470  
0  
AATAAAATATTGGAAATCCCTATGACACACTTAAGCCTAAAGGCCCGAAAAACATACTAGGATGCCCAACTGG  
Rev.of\_Cele-UNSB01\_5:15668468-15668848 Satlength=381 Nr of Repeats=5  
RepeatLength=73 seed=TTAGGCTTAA Num.seqs=3 Similarity=0.939117  
40  
AATAAAATATTGGAAATCCTTATGACACACTTAAGCCTAAAGGCCCGAAAAAAACTAGGATGCCCAACTGG

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Consensus:

AATAAAATATTGGAAATCCcTATGACACACTTAAGCCTAAAGGCCCGAAAAaAaACTAGGATGCCCAACTGG

>Cele-UNSB01\_Fam\_112\_71\_2 Nr. of seq. 2 Alignment length(with gaps) = 71  
Alignment score = 0.626761  
Cele-UNSB01\_3:3799869-3800537 Satlength=669 Nr of Repeats=5  
RepeatLength=65 seed=AAGACACTAA Num.seqs=3 Similarity=0.945299  
0 AAGACACTAATAAAAATATT--ATTTTATTCGTCTTTAATTTTAGAA-A-ATTTTC--  
AATAAAATTT  
Rev.of\_Cele-UNSB01\_2:6392670-6395650 Satlength=2981 Nr of Repeats=44  
RepeatLength=68 seed=AATAAAATT Num.seqs=38 Similarity=0.936325  
30 -AGACACTAATAAAAATTTTAAATTTTATTCGTC-TCTATTTTGAAAATATATTTTCTTGAT-  
AAAATAG

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Consensus:

aAGACACTAATAAAAAATaTTaaATTTTTATTCGTCTcTcTaaTTgAaAAtAtATTTTCttaATaAAAAATag

>Cele-UNSB01\_Fam\_113\_68\_2 Nr. of seq. 2 Alignment length(with gaps) = 68  
Alignment score = 0.838235

Cele-UNSB01\_4:17319515-17323871 Satlength=4357 Nr of Repeats=66  
RepeatLength=66 seed=CAAATCAACC Num.seqs=66 Similarity=0.958428  
0 CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTTATCAAATTTTTTNAATTT--TAAAGAAAACA  
Rev.of\_Cele-UNSB01\_1:10374816-10387323 Satlength=12508 Nr of Repeats=186  
RepeatLength=68 seed=AAAACCATTG Num.seqs=123 Similarity=0.979909  
31

CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTTACCAAAATCTTAGAATTTTCAGAAAGAAAACA

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Consensus:

CAAATCAACCTATTCAGTTGACAATGGTTTTCTTTTAcCAAAaTTcTTaaAATTTcagAAAGAAAACA

>Cele-UNSB01\_Fam\_114\_44\_2 Nr. of seq. 2 Alignment length(with gaps) = 44  
Alignment score = 0.681818

Cele-UNSB01\_2:9825153-9825520 Satlength=368 Nr of Repeats=4  
RepeatLength=42 seed=CAGCCGACAG Num.seqs=3 Similarity=0.533769  
0 -CAGCCGACAGCCGAAAAATT--GGAATTTTCGGCTGGTAGCAC  
Cele-UNSB01\_5:4001570-4002151 Satlength=582 Nr of Repeats=5  
RepeatLength=42 seed=CCAGCCGACA Num.seqs=3 Similarity=0.684755  
0 CCAGCCGACAGCCGAAATTTTCACG-ATTTTCGGCTGGTNGCG-

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Consensus:

cCAGCCGACAGCCGAAaATTcacGaATTTTCGGCTGGTaGCac

>Cele-UNSB01\_Fam\_115\_44\_2 Nr. of seq. 2 Alignment length(with gaps) = 44  
Alignment score = 0.704545

Cele-UNSB01\_1:12045808-12046235 Satlength=428 Nr of Repeats=5  
RepeatLength=42 seed=TCGGCAAATC Num.seqs=3 Similarity=0.723514  
0 TCGGCAAA-TCGGCAATTNCTGGTTTTTTNAA-ATTTGCCGAGC  
Rev.of\_Cele-UNSB01\_4:16010822-16011211 Satlength=390 Nr of Repeats=5  
RepeatLength=42 seed=GCTCGGCAAA Num.seqs=3 Similarity=0.957672  
0 ACGGCAAATTCGGCAAAT-CT-CTTTTTTCAATATTGCCGAGC

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Consensus:

aCGGCAAAATTCGGCAAAtnCTgcTTTTTTcAAtATTTGCCGAGC

>Cele-UNSB01\_Fam\_116\_44\_2 Nr. of seq. 2 Alignment length(with gaps) = 44  
Alignment score = 0.969697

Cele-UNSB01\_1:9793063-9794825 Satlength=1763 Nr of Repeats=41  
RepeatLength=44 seed=CTGTTTTCTG Num.seqs=35 Similarity=0.988999  
0 CTGTTTTCTGAGCATTTTAGATTTTCGGATTGATGGCCGAAAGG

Cele-UNSB01\_4:17389165-17390089 Satlength=925 Nr of Repeats=21  
RepeatLength=44 seed=GATTGATGGC Num.seqs=21 Similarity=0.961328  
27 CTGTTTTCTGAGCATTGTAGATTTTCGGATTGATGGCCGAAAGG

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Consensus:

CTGTTTTCTGAGCATTgTAGATTTTCGGATTGATGGCCGAAAGG

>Cele-UNSB01\_Fam\_117\_41\_2 Nr. of seq. 2 Alignment length(with gaps) = 41  
Alignment score = 0.711382

Cele-UNSB01\_6:17501177-17501366 Satlength=190 Nr of Repeats=5  
RepeatLength=38 seed=CCGTTTCGCC Num.seqs=4 Similarity=0.982456

0 CCGTTTCGCCTTGAGCGATT-C--ACCCTTAAATGGGCCTC

Cele-UNSB01\_6:7586233-7592821 Satlength=6589 Nr of Repeats=165  
RepeatLength=40 seed=TTACCCTTAA Num.seqs=156 Similarity=0.968630

21 -GGTTTCGCTTTGAGCGATTcCTTACCCTTAAATGGGCGCC

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Consensus:

ccGTTTCGCcTTGAGCGATTcCttACCCTTAAATGGGCccC

>Cele-UNSB01\_Fam\_118\_41\_2 Nr. of seq. 2 Alignment length(with gaps) = 41  
Alignment score = 1.000000

Cele-UNSB01\_2:7497139-7497311 Satlength=173 Nr of Repeats=4  
RepeatLength=41 seed=AAAACGGGAA Num.seqs=3 Similarity=0.978320

0 AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTTA

Cele-UNSB01\_2:7497138-7497671 Satlength=534 Nr of Repeats=10  
RepeatLength=41 seed=AAAACGGGA Num.seqs=6 Similarity=0.956640

40 AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTTA

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Consensus:

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTTA

>Cele-UNSB01\_Fam\_119\_40\_2 Nr. of seq. 2 Alignment length(with gaps) = 40  
Alignment score = 0.975000

Cele-UNSB01\_3:1112086-1112814 Satlength=729 Nr of Repeats=14  
RepeatLength=40 seed=AAAATCCACG Num.seqs=12 Similarity=0.883838

0 AAAATCCACGTAGATTATTGATTTTTCATNGAATTTTGCA

Cele-UNSB01\_3:1112079-1113479 Satlength=1401 Nr of Repeats=16  
RepeatLength=40 seed=TTTTGCAAAA Num.seqs=11 Similarity=0.759596

33 AAAATCCACGTAGATTATTGATTTTTCATGGAATTTTGCA

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Consensus:

AAAATCCACGTAGATTATTGATTTTTCATgGAATTTTGCA

>Cele-UNSB01\_Fam\_120\_39\_2 Nr. of seq. 2 Alignment length(with gaps) = 39  
Alignment score = 0.897436

Cele-UNSB01\_4:11180885-11199179 Satlength=18295 Nr of Repeats=470  
RepeatLength=39 seed=TTTATGGAAA Num.seqs=408 Similarity=0.953106  
0 TTTATGGAAAAGTGGCTCTAGAGCCACAAGAAATACCAG  
Cele-UNSB01\_5:10655040-10675549 Satlength=20510 Nr of Repeats=527  
RepeatLength=39 seed=CCACCAGAAA Num.seqs=467 Similarity=0.955996  
23 TTTATGAAAAAGTGGCTCTAGGGCCACCAGAAATACCAG

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Consensus:

TTTATGaAAAAGTGGCTCTAGaGCCACaAGAAATACCAG

>Cele-UNSB01\_Fam\_121\_36\_2 Nr. of seq. 2 Alignment length(with gaps) = 36  
Alignment score = 0.601852

Cele-UNSB01\_4:3353341-3353481 Satlength=141 Nr of Repeats=5  
RepeatLength=33 seed=CGGCATATGC Num.seqs=3 Similarity=0.946128  
0 CGGCATA-TGCCGTGAATTTTAAAT-CGGCATAA-  
Rev.of\_Cele-UNSB01\_4:15750800-15751080 Satlength=281 Nr of Repeats=8  
RepeatLength=35 seed=TTGCCGATT Num.seqs=8 Similarity=0.983673  
32 -GGCAAATTACCATAAATTTTCAAATCCGGCAAAAC

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Consensus:

cGGCAaAtTaCCaTaAATTTTaAAATcCGGCAaAAc

>Cele-UNSB01\_Fam\_122\_35\_2 Nr. of seq. 2 Alignment length(with gaps) = 35  
Alignment score = 0.666667

Cele-UNSB01\_1:8640900-8641029 Satlength=130 Nr of Repeats=4  
RepeatLength=32 seed=AAAATCGAAA Num.seqs=3 Similarity=1.000000  
0 AAAATCGAAAATTCTCG-TTTTTCAATTTTAA--  
Cele-UNSB01\_3:11834269-11834616 Satlength=348 Nr of Repeats=10  
RepeatLength=34 seed=TTTTTCGATTT Num.seqs=8 Similarity=0.935574  
11 AAAATCG-GGAATTTTCGATTTTCAATTTTGA

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Consensus:

AAAATCGaaaAATTcTCGaTTTTTCAATTTTTaga

>Cele-UNSB01\_Fam\_123\_34\_2 Nr. of seq. 2 Alignment length(with gaps) = 34  
Alignment score = 0.612745

Cele-UNSB01\_4:1530750-1530982 Satlength=233 Nr of Repeats=8  
RepeatLength=29 seed=CCACCCGGGA Num.seqs=8 Similarity=0.850575  
0 CCACCCGGGAGGTGTCGGCTGCT---CTA-AAC  
Cele-UNSB01\_5:18836263-18836629 Satlength=367 Nr of Repeats=11  
RepeatLength=33 seed=TGTCGGCTGC Num.seqs=10 Similarity=0.876094  
11 -CTCCCGCAGGTGTCGGCTGCTAAACTATAGC

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Consensus:

cCaCCCGGcAGGTGTCGGCTGCTaaaaCTAtAaC

>Cele-UNSB01\_Fam\_124\_32\_2 Nr. of seq. 2 Alignment length(with gaps) = 32  
Alignment score = 0.671875  
Cele-UNSB01\_3:260141-260567 Satlength=427 Nr of Repeats=12  
RepeatLength=30 seed=TTTTTTGAGC Num.seqs=9 Similarity=0.761574  
0 TTTTTTGAGCCAAAAATTC-AAAAAAT-CTCG  
Cele-UNSB01\_3:249570-249725 Satlength=156 Nr of Repeats=4 RepeatLength=31  
seed=AGCTCAAAAT Num.seqs=3 Similarity=0.711806  
6 -TTTTTGAGCTCAAAATTCTGAAAAATGCTCA

\*\*\*\*\*  
Consensus:

tTTTTTGAGCcAAAAATTCTaAAAAATgCTCa

>Cele-UNSB01\_Fam\_125\_31\_2 Nr. of seq. 2 Alignment length(with gaps) = 31  
Alignment score = 0.752688  
Cele-UNSB01\_1:1530606-1531290 Satlength=685 Nr of Repeats=18  
RepeatLength=31 seed=GGTTACTGTA Num.seqs=11 Similarity=0.738025  
0 GGTTACTGTA ACTCAATTATAGGATACTTNG  
Cele-UNSB01\_2:3540761-3541492 Satlength=732 Nr of Repeats=18  
RepeatLength=31 seed=GGTTACTGTA Num.seqs=11 Similarity=0.669318  
0 GGTTACTGTAGATCGATCCTAGGATACTTTG

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Consensus:

GGTTACTGTAAaTCaATcaTAGGATACTTtG

>Cele-UNSB01\_Fam\_126\_31\_2 Nr. of seq. 2 Alignment length(with gaps) = 31  
Alignment score = 0.784946  
Cele-UNSB01\_2:2602717-2603767 Satlength=1051 Nr of Repeats=24  
RepeatLength=31 seed=CTGAAATTCC Num.seqs=16 Similarity=0.855556  
0 CTGAAATTCCAATTTTCCAGTGTA AAAATGT  
Cele-UNSB01\_5:19020255-19020473 Satlength=219 Nr of Repeats=6  
RepeatLength=31 seed=TGTAAAAATG Num.seqs=5 Similarity=0.651613  
20 CTGAAATTATGAATTTCCAATGTAAAAATGT

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Consensus:

CTGAAATTacaAaTTTCCAaTGTA AAAATGT

>Cele-UNSB01\_Fam\_127\_31\_2 Nr. of seq. 2 Alignment length(with gaps) = 31  
Alignment score = 0.956989  
Cele-UNSB01\_4:16019565-16019814 Satlength=250 Nr of Repeats=6  
RepeatLength=31 seed=TCGACAGAAG Num.seqs=4 Similarity=0.665825  
0 TCGACAGAAGCTGTCTGGAAATCACA CTTTCC  
Cele-UNSB01\_6:12932636-12932914 Satlength=279 Nr of Repeats=9  
RepeatLength=31 seed=TCGACAGAAG Num.seqs=8 Similarity=0.729437  
0 TCGACAGAAGCTGTCTGGACATCACA CTTTCC

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Consensus:



TCGACAGAAGCTGTCTGGAAATCACACTTTCC

>Cele-UNSB01\_Fam\_128\_27\_2 Nr. of seq. 2 Alignment length(with gaps) = 27  
Alignment score = 0.901235  
Cele-UNSB01\_2:3132033-3132195 Satlength=163 Nr of Repeats=6  
RepeatLength=27 seed=GCTGCTGGAG Num.seqs=6 Similarity=0.881481  
0 GCTGCTGGAGGATCCACTGCATCAACT  
Cele-UNSB01\_2:3135702-3137322 Satlength=1621 Nr of Repeats=60  
RepeatLength=27 seed=TGCTGGAGGA Num.seqs=60 Similarity=0.923806  
2 GCTGCTGGAGGATCAACTGCATCAACC

\*\*\*\*\*  
Consensus:

GCTGCTGGAGGATCaACTGCATCAACc

>Cele-UNSB01\_Fam\_129\_26\_2 Nr. of seq. 2 Alignment length(with gaps) = 26  
Alignment score = 1.000000  
Cele-UNSB01\_1:1685357-1686631 Satlength=1275 Nr of Repeats=49  
RepeatLength=26 seed=CAAAACCGGC Num.seqs=49 Similarity=0.924036  
0 CAAAACCGGCAATTGCCGAAAATTCC  
Rev.of\_Cele-UNSB01\_1:1833668-1834030 Satlength=363 Nr of Repeats=11  
RepeatLength=26 seed=TTGCCGTTT Num.seqs=8 Similarity=0.798535  
12 CAAAACCGGCAATTGCCGAAAATTCC

\*\*\*\*\*  
Consensus:

CAAAACCGGCAATTGCCGAAAATTCC

>Cele-UNSB01\_Fam\_130\_26\_2 Nr. of seq. 2 Alignment length(with gaps) = 26  
Alignment score = 0.948718  
Cele-UNSB01\_2:2174137-2174267 Satlength=131 Nr of Repeats=5  
RepeatLength=26 seed=TCAAGGCGGAA Num.seqs=5 Similarity=0.979487  
0 TCAAGGCGAAACGGGAGGTGAATCGC  
Rev.of\_Cele-UNSB01\_5:8921030-8921237 Satlength=208 Nr of Repeats=8  
RepeatLength=26 seed=TTGCCCTGA Num.seqs=7 Similarity=0.907204  
10 TCAGGGCGAAACGGGAGGTGAATCGC

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Consensus:

TCAaGGCGAAACGGGAGGTGAATCGC

>Cele-UNSB01\_Fam\_131\_24\_2 Nr. of seq. 2 Alignment length(with gaps) = 24  
Alignment score = 0.722222  
Cele-UNSB01\_2:3799242-3799338 Satlength=97 Nr of Repeats=4  
RepeatLength=24 seed=TGCTCTGCC Num.seqs=4 Similarity=0.750000  
0 TGCTCTGCCGCTGGAGCTGGCGC  
Rev.of\_Cele-UNSB01\_5:14425209-14425464 Satlength=256 Nr of Repeats=5  
RepeatLength=24 seed=GCCGCTCCAG Num.seqs=3 Similarity=0.814815  
3 GGCATCTGGTGCCGAGCTGGAGC

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Consensus:

gGCATCTGccGCcGGAGCTGGaGC

>Cele-UNSB01\_Fam\_132\_24\_2 Nr. of seq. 2 Alignment length(with gaps) = 24  
Alignment score = 0.680556

Cele-UNSB01\_2:11502184-11502280 Satlength=97 Nr of Repeats=5  
RepeatLength=24 seed=GCTTAGGCTT Num.seqs=3 Similarity=0.648148  
0 GCTTAGGCTTGGGCTTAGGCTNAA

Rev.of\_Cele-UNSB01\_5:19079815-19080004 Satlength=190 Nr of Repeats=5  
RepeatLength=24 seed=GCCTAAGCCT Num.seqs=3 Similarity=0.666667  
2 GCCTAGACTCAGGCTTAGGCTTAG

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Consensus:

GCcTAGaCTcaGGCTTAGGCTtAa

>Cele-UNSB01\_Fam\_133\_23\_2 Nr. of seq. 2 Alignment length(with gaps) = 23  
Alignment score = 0.630435

Cele-UNSB01\_1:932742-934750 Satlength=2009 Nr of Repeats=89  
RepeatLength=21 seed=AATTTCTAGG Num.seqs=60 Similarity=0.911757  
0 AATTTCTAGGCCACGA-TTTGA-

Rev.of\_Cele-UNSB01\_1:1117625-1118154 Satlength=530 Nr of Repeats=23  
RepeatLength=23 seed=GGCCTAGAAA Num.seqs=23 Similarity=0.818525  
12 TATTTCTAGGCCACCACGTTTCAG

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Consensus:

aATTTCTAGGCCACcAcgTTcAg

>Cele-UNSB01\_Fam\_134\_23\_2 Nr. of seq. 2 Alignment length(with gaps) = 23  
Alignment score = 0.673913

Cele-UNSB01\_5:19643678-19643940 Satlength=263 Nr of Repeats=11  
RepeatLength=21 seed=TCTAATTAGA Num.seqs=10 Similarity=0.939330  
0 TCTAATTAGAT-CACCTT-TTTT

Cele-UNSB01\_5:19645516-19645794 Satlength=279 Nr of Repeats=13  
RepeatLength=21 seed=TTCTAATTAG Num.seqs=10 Similarity=0.650000  
20 -CTAATTAGATNCGCCNTCTTTT

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Consensus:

tCTAATTAGATnCaCCTtCtTTTT

>Cele-UNSB01\_Fam\_135\_23\_2 Nr. of seq. 2 Alignment length(with gaps) = 23  
Alignment score = 0.659420

Cele-UNSB01\_5:19987417-19987506 Satlength=90 Nr of Repeats=4  
RepeatLength=22 seed=ATTGGATTTT Num.seqs=3 Similarity=0.959596  
0 ATTGGATTTTTTACCCCAAAA-

Cele-UNSB01\_1:625093-626033 Satlength=941 Nr of Repeats=22  
RepeatLength=23 seed=AAAAAAAAATT Num.seqs=14 Similarity=0.950948  
16 ATTAAATTTTCAACAAAAA

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Consensus:

ATTaaATTTTTCaAcaAAAAAa

>Cele-UNSB01\_Fam\_136\_22\_2 Nr. of seq. 2 Alignment length(with gaps) = 22  
Alignment score = 0.643939

Cele-UNSB01\_3:1616576-1616906 Satlength=331 Nr of Repeats=16  
RepeatLength=20 seed=CATAAAAATT Num.seqs=13 Similarity=0.947009  
0 CATAAAAAT-TCAGAAAA-ATG

Rev.of\_Cele-UNSB01\_1:14199204-14199288 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=ATATTTTGTG Num.seqs=4 Similarity=0.936508  
0 AATAAAAATGTCACAAAATAT-

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Consensus:

aATAAAAATgTCaCAAAAtATg

>Cele-UNSB01\_Fam\_137\_22\_2 Nr. of seq. 2 Alignment length(with gaps) = 22  
Alignment score = 0.681818

Cele-UNSB01\_4:1966969-1971964 Satlength=4996 Nr of Repeats=213  
RepeatLength=21 seed=GTAAATCTAC Num.seqs=158 Similarity=0.856783  
0 GTAAATCTACAGTAAT-NCCCC

Cele-UNSB01\_3:1041359-1041618 Satlength=260 Nr of Repeats=12  
RepeatLength=22 seed=TAAATCTACA Num.seqs=10 Similarity=0.692929  
1 GTAAATCTACACACATAGCCCC

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Consensus:

GTAAATCTACaAAATagCCCC

>Cele-UNSB01\_Fam\_138\_22\_2 Nr. of seq. 2 Alignment length(with gaps) = 22  
Alignment score = 0.621212

Cele-UNSB01\_4:16741502-16741626 Satlength=125 Nr of Repeats=5  
RepeatLength=21 seed=TTCAAGCCTT Num.seqs=3 Similarity=0.915344  
0 TTCAAGCC-TTTCAGACCAAT

Rev.of\_Cele-UNSB01\_1:14006347-14006515 Satlength=169 Nr of Repeats=7  
RepeatLength=21 seed=CAAAATTTCGT Num.seqs=6 Similarity=0.814646  
4 TTTGAGCNATTTTCGGACGAAT

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Consensus:

TTcaAGCcaTTTTCaGACcAAT

>Cele-UNSB01\_Fam\_139\_22\_2 Nr. of seq. 2 Alignment length(with gaps) = 22  
Alignment score = 0.765152

Cele-UNSB01\_6:1338339-1338633 Satlength=295 Nr of Repeats=14  
RepeatLength=21 seed=TTTGCACTGA Num.seqs=14 Similarity=0.853480  
0 TTTGCACTGACCAACACGAAT-  
Rev.of\_Cele-UNSB01\_2:2125481-2125594 Satlength=114 Nr of Repeats=5  
RepeatLength=22 seed=TGGTCAGTGC Num.seqs=3 Similarity=0.959596  
13 TTTGCACTGACCAATAAAAATG

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Consensus:

TTTGCACTGACCAAcAaaAATg

>Cele-UNSB01\_Fam\_140\_22\_2 Nr. of seq. 2 Alignment length(with gaps) = 22  
Alignment score = 1.000000  
Cele-UNSB01\_1:13307625-13307715 Satlength=91 Nr of Repeats=4  
RepeatLength=22 seed=TCGAGAAAAA Num.seqs=3 Similarity=1.000000  
0 TCGAGAAAAAATCTGAAAAAAT  
Rev.of\_Cele-UNSB01\_1:13324034-13324147 Satlength=114 Nr of Repeats=5  
RepeatLength=22 seed=TTTTTCTCG Num.seqs=4 Similarity=1.000000  
11 TCGAGAAAAAATCTGAAAAAAT

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Consensus:

TCGAGAAAAAATCTGAAAAAAT

>Cele-UNSB01\_Fam\_141\_22\_2 Nr. of seq. 2 Alignment length(with gaps) = 22  
Alignment score = 0.954545  
Cele-UNSB01\_2:3341963-3342088 Satlength=126 Nr of Repeats=4  
RepeatLength=22 seed=ATTCTGCGCA Num.seqs=3 Similarity=0.656566  
0 ATTCTGCGCACCCCCTGCGCNG  
Rev.of\_Cele-UNSB01\_5:19604230-19604355 Satlength=126 Nr of Repeats=4  
RepeatLength=22 seed=GTGCGCAGAA Num.seqs=3 Similarity=0.676768  
11 ATTCTGCGCACCCCCTGCGCAG

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Consensus:

ATTCTGCGCACCCCCTGCGCaG

>Cele-UNSB01\_Fam\_142\_20\_2 Nr. of seq. 2 Alignment length(with gaps) = 20  
Alignment score = 0.933333  
Cele-UNSB01\_1:1781850-1784996 Satlength=3147 Nr of Repeats=154  
RepeatLength=20 seed=CCACCAAAAA Num.seqs=145 Similarity=0.874815  
0 CCACCAAAAAGGTTTCTAGG  
Cele-UNSB01\_1:1787086-1788479 Satlength=1394 Nr of Repeats=64  
RepeatLength=20 seed=TTCTAGGCCA Num.seqs=51 Similarity=0.812235  
13 CCACCAAAAATGTTTCTAGG

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Consensus:

CCACCAAAAAGGTTTCTAGG

>Cele-UNSB01\_Fam\_143\_20\_2 Nr. of seq. 2 Alignment length(with gaps) = 20  
Alignment score = 0.950000  
Cele-UNSB01\_1:2365340-2366051 Satlength=712 Nr of Repeats=8  
RepeatLength=20 seed=GGACTAGTTT Num.seqs=6 Similarity=0.880000  
0 GGACTAGTTTTTCGAGTAGAG  
Cele-UNSB01\_1:2365340-2366212 Satlength=873 Nr of Repeats=11  
RepeatLength=20 seed=GGACTAGTTT Num.seqs=7 Similarity=0.745276  
0 GGACTAGTTTTNGAGTAGAG

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Consensus:

GGACTAGTTTTcGAGTAGAG

>Cele-UNSB01\_Fam\_144\_20\_2 Nr. of seq. 2 Alignment length(with gaps) = 20  
Alignment score = 0.750000  
Cele-UNSB01\_2:15437952-15438032 Satlength=81 Nr of Repeats=4  
RepeatLength=20 seed=TGTAGATTTA Num.seqs=4 Similarity=0.688889  
0 TGTAGATTTACAAAGGACAA  
Rev.of\_Cele-UNSB01\_5:18842565-18843912 Satlength=1348 Nr of Repeats=50  
RepeatLength=20 seed=GTAAATCTAC Num.seqs=35 Similarity=0.635294  
11 TGTAGATTTACGGAGGTCNA

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Consensus:

TGTAGATTTACaaAGGaCaA

>Cele-UNSB01\_Fam\_145\_20\_2 Nr. of seq. 2 Alignment length(with gaps) = 20  
Alignment score = 0.866667  
Cele-UNSB01\_5:2582229-2582433 Satlength=205 Nr of Repeats=7  
RepeatLength=20 seed=CCCCGACGCT Num.seqs=5 Similarity=0.920000  
0 CCCCgACGCTCGAGCTCAAA  
Cele-UNSB01\_5:2582360-2582560 Satlength=201 Nr of Repeats=10  
RepeatLength=20 seed=GCTCGAGCTC Num.seqs=10 Similarity=0.928889  
7 CCCCgAAGCTCGAGCTCAAG

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Consensus:

CCCCGAaGCTCGAGCTCAAA

>Cele-UNSB01\_Fam\_146\_20\_2 Nr. of seq. 2 Alignment length(with gaps) = 20  
Alignment score = 0.800000  
Cele-UNSB01\_6:16421783-16421902 Satlength=120 Nr of Repeats=6  
RepeatLength=20 seed=CCACCCTGTA Num.seqs=5 Similarity=0.706349  
0 CCACCCTGTAATATCATGGA  
Rev.of\_Cele-UNSB01\_6:16657827-16657967 Satlength=141 Nr of Repeats=7  
RepeatLength=20 seed=TACAGGGTGG Num.seqs=5 Similarity=0.920000  
10 CCACCCTGTATAATTATGGA

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Consensus:

CCACCCTGTAAaATcATGGA

>Cele-UNSB01\_Fam\_147\_19\_2 Nr. of seq. 2 Alignment length(with gaps) = 19  
Alignment score = 0.684211  
Cele-UNSB01\_2:14294397-14294650 Satlength=254 Nr of Repeats=11  
RepeatLength=18 seed=CTAGGTGCCT Num.seqs=8 Similarity=0.804233  
0 CTAGGTGCCTA-TCCATTC  
Rev.of\_Cele-UNSB01\_4:2898426-2898868 Satlength=443 Nr of Repeats=12  
RepeatLength=19 seed=ACCTAGGCAT Num.seqs=8 Similarity=0.751880  
6 CTAGGTGCCTACTTTATGC

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Consensus:

CTAGGTGCCTAcTccATgC

>Cele-UNSB01\_Fam\_148\_19\_2 Nr. of seq. 2 Alignment length(with gaps) = 19  
Alignment score = 0.929825  
Cele-UNSB01\_4:2676914-2677180 Satlength=267 Nr of Repeats=11  
RepeatLength=19 seed=CGCCAAGTAT Num.seqs=8 Similarity=0.694345  
0 CGCCAAGTATCGAGAAAAG  
Rev.of\_Cele-UNSB01\_5:19666114-19666380 Satlength=267 Nr of Repeats=11  
RepeatLength=19 seed=GATCCTTGCC Num.seqs=9 Similarity=0.898636  
11 CGCCAAGGATCGAGAAAAG

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Consensus:

CGCCAAGgATCGAGAAAAG

>Cele-UNSB01\_Fam\_149\_17\_2 Nr. of seq. 2 Alignment length(with gaps) = 17  
Alignment score = 0.656863  
Cele-UNSB01\_2:14966230-14966326 Satlength=97 Nr of Repeats=6  
RepeatLength=16 seed=GCAGTTTGCC Num.seqs=6 Similarity=0.794444  
0 GCAGTTTGCC-GAATTG  
Rev.of\_Cele-UNSB01\_6:16744464-16744698 Satlength=235 Nr of Repeats=10  
RepeatLength=16 seed=TTCCGGCAAT Num.seqs=6 Similarity=0.972222  
13 -CCGATTGCCGGAATTG

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Consensus:

gCaGaTTGCCgGAATTG

>Cele-UNSB01\_Fam\_150\_17\_2 Nr. of seq. 2 Alignment length(with gaps) = 17  
Alignment score = 0.803922  
Cele-UNSB01\_6:6441827-6441956 Satlength=130 Nr of Repeats=8  
RepeatLength=16 seed=GCACTGACAA Num.seqs=7 Similarity=0.876984  
0 GCACTGA-CAATTTTTT  
Rev.of\_Cele-UNSB01\_6:1379546-1379614 Satlength=69 Nr of Repeats=4  
RepeatLength=17 seed=TGGTCAGTGC Num.seqs=4 Similarity=0.882353  
10 GCACTGACCAACTTTTT

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Consensus:

GCACTGAcCAAcTTTTT

>Cele-UNSB01\_Fam\_151\_16\_2 Nr. of seq. 2 Alignment length(with gaps) = 16  
Alignment score = 0.750000

Cele-UNSB01\_5:18664756-18664882 Satlength=127 Nr of Repeats=9  
RepeatLength=14 seed=GTCTGGGGTC Num.seqs=9 Similarity=0.978836  
1 GGT-CTGGGGT-CTGG

Cele-UNSB01\_5:20839531-20839647 Satlength=117 Nr of Repeats=5  
RepeatLength=16 seed=GTACTAGGGT Num.seqs=3 Similarity=0.888889  
1 GGTACTGGGGTACTGG

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Consensus:

GTaCTGGGGTaCTGGG

>Cele-UNSB01\_Fam\_152\_15\_2 Nr. of seq. 2 Alignment length(with gaps) = 15  
Alignment score = 0.622222

Cele-UNSB01\_1:11276130-11276202 Satlength=73 Nr of Repeats=6  
RepeatLength=12 seed=CGATCTCCAC Num.seqs=6 Similarity=0.933333  
0 CGAT-CTCCACCA--

Cele-UNSB01\_1:11267568-11267793 Satlength=226 Nr of Repeats=15  
RepeatLength=15 seed=CGATGCTCCA Num.seqs=15 Similarity=0.900106  
0 CGATGCTCCACCCGA

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Consensus:

CGATgCTCCACCaga

>Cele-UNSB01\_Fam\_153\_14\_2 Nr. of seq. 2 Alignment length(with gaps) = 14  
Alignment score = 0.761905

Cele-UNSB01\_2:14379544-14380198 Satlength=655 Nr of Repeats=13  
RepeatLength=13 seed=TATACAAAAA Num.seqs=9 Similarity=0.837607  
0 TATACAAAAA-GTA

Rev.of\_Cele-UNSB01\_1:3764869-3765030 Satlength=162 Nr of Repeats=5  
RepeatLength=14 seed=TTTTTGTAGA Num.seqs=3 Similarity=0.588235  
10 TCTACAAAAANGTA

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Consensus:

TaTACAAAAAnGTA

>Cele-UNSB01\_Fam\_154\_14\_2 Nr. of seq. 2 Alignment length(with gaps) = 14  
Alignment score = 0.666667

Cele-UNSB01\_5:1765405-1765535 Satlength=131 Nr of Repeats=9  
RepeatLength=13 seed=GCTCAAGCTA Num.seqs=6 Similarity=0.815385  
0 GCTCAAGC-TAGGA

Cele-UNSB01\_6:1926117-1926284 Satlength=168 Nr of Repeats=11  
RepeatLength=14 seed=TAGGCCCTCA Num.seqs=8 Similarity=0.823129  
9 CCTCAAGCGTAGGC

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Consensus:

cCTCAAGCgTAGGa

>Cele-UNSB01\_Fam\_155\_14\_2 Nr. of seq. 2 Alignment length(with gaps) = 14  
Alignment score = 1.000000

Cele-UNSB01\_2:7564245-7565607 Satlength=1363 Nr of Repeats=34  
RepeatLength=14 seed=GAAGGATCGG Num.seqs=26 Similarity=0.910916  
0 GAAGGATCGGGCCG

Rev.of\_Cele-UNSB01\_2:7568262-7569624 Satlength=1363 Nr of Repeats=34  
RepeatLength=14 seed=CCGATCCTTC Num.seqs=26 Similarity=0.898608  
10 GAAGGATCGGGCCG

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Consensus:

GAAGGATCGGGCCG

>Cele-UNSB01\_Fam\_156\_14\_2 Nr. of seq. 2 Alignment length(with gaps) = 14  
Alignment score = 0.619048

Cele-UNSB01\_3:11522131-11522299 Satlength=169 Nr of Repeats=11  
RepeatLength=14 seed=GATAATTGAA Num.seqs=10 Similarity=0.980952  
0 GATAATTGAAAATC

Rev.of\_Cele-UNSB01\_3:11700261-11701084 Satlength=824 Nr of Repeats=59  
RepeatLength=14 seed=AATTATAAAT Num.seqs=56 Similarity=0.980334  
0 TATAATTTATAATT

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Consensus:

gATAATTgAaAATc

>Cele-UNSB01\_Fam\_157\_12\_2 Nr. of seq. 2 Alignment length(with gaps) = 12  
Alignment score = 0.680556

Cele-UNSB01\_5:3042873-3042939 Satlength=67 Nr of Repeats=5  
RepeatLength=11 seed=TTTGGCAAGA Num.seqs=4 Similarity=0.818182  
0 TTGGGCAAGAA-

Rev.of\_Cele-UNSB01\_2:146899-146982 Satlength=84 Nr of Repeats=6  
RepeatLength=12 seed=ATTTCTTGCA Num.seqs=5 Similarity=0.844444  
1 TTTTGCAAGAAA

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Consensus:

TTggGCAAGAAa

>Cele-UNSB01\_Fam\_158\_11\_2 Nr. of seq. 2 Alignment length(with gaps) = 11  
Alignment score = 0.878788



Cele-UNSB01\_1:2691842-2691886 Satlength=45 Nr of Repeats=4  
RepeatLength=11 seed=AAACTTGGGC Num.seqs=4 Similarity=0.770833  
0     AAACTTGGGCT  
Cele-UNSB01\_3:11327560-11327604 Satlength=45 Nr of Repeats=4  
RepeatLength=11 seed=AAACTTGGGC Num.seqs=4 Similarity=0.858586  
0     AAACTTGGGCA

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Consensus:

AAACTTGGGCa

>Cele-UNSB01\_Fam\_159\_11\_2 Nr. of seq. 2 Alignment length(with gaps) = 11  
Alignment score = 0.636364  
Cele-UNSB01\_2:13528433-13528477 Satlength=45 Nr of Repeats=4  
RepeatLength=11 seed=TGGAAAATTG Num.seqs=4 Similarity=1.000000  
0     TGGAAAATTGA  
Cele-UNSB01\_3:7825014-7825135 Satlength=122 Nr of Repeats=11  
RepeatLength=11 seed=CGGATAATTA Num.seqs=11 Similarity=1.000000  
0     CGGATAATTAA

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Consensus:

cGGAAaAATTaA

>Cele-UNSB01\_Fam\_160\_11\_2 Nr. of seq. 2 Alignment length(with gaps) = 11  
Alignment score = 0.636364  
Cele-UNSB01\_6:444285-444373 Satlength=89 Nr of Repeats=7 RepeatLength=11  
seed=CATAACTGAG Num.seqs=6 Similarity=1.000000  
0     CATAACTGAGA  
Rev.of\_Cele-UNSB01\_6:3482169-3482345 Satlength=177 Nr of Repeats=12  
RepeatLength=11 seed=TAGCTCAGCT Num.seqs=8 Similarity=0.883117  
2     TATAGCTGAGC

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Consensus:

cATAaCTGAGa

>Cele-UNSB01\_Fam\_161\_255\_1 Nr. of seq. 1 Alignment length(with gaps) =  
255 Alignment score = 0.000000  
Cele-UNSB01\_5:17737089-17738916 Satlength=1828 Nr of Repeats=7  
RepeatLength=255 seed=AACAAGTCGG Num.seqs=5 Similarity=0.720930  
0  
AACAAGTCGGGAACGTTTCGGAAAGCTCTGAGGAAAACCTCCGACAATATCATGCTTAAGTACGCAATTGAGCTA  
TCTTTATTAGATTTCGAAAAGGACTCTTCAAAAATTGAAGCAATAACGAAGAAGCTTAAGTTGGAAGTGGCGA  
AGCTTAAATTTGGGANTTATGCAGTCTTTATCAGATTCAAAAGACGATTCTTCGACCAATGAAGCAAGTCCGGA  
GNACGATCTACCTTCGACTTCTGATGGCAGAACTCC

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Consensus :

AACAAGTCGGGAACGTTTCGGAAAGCTCTGAGGAAAACCTCCGACAATATCATGCTTAAGTACGCAATTGAGCTA  
TCTTTATTAGATTCGAAAAAGGACTCTTCAAAAATTGAAGCAATAACGAAGAAGCTTAAGTTGGAAGTGGCGA  
AGCTTAAATTGGGANTTATGCAGTCTTTATCAGATTCAAAAGACGATTCTTCGACCAATGAAGCAAGTCCGGA  
GNACGATCTACCTTCGACTTCTGATGGCAGAACTCC

>Cele-UNSB01\_Fam\_162\_249\_1 Nr. of seq. 1 Alignment length(with gaps) =  
249 Alignment score = 0.000000

Cele-UNSB01\_6:1598138-1600934 Satlength=2797 Nr of Repeats=10  
RepeatLength=249 seed=CTGGAAGCAC Num.seqs=7 Similarity=0.929623

0

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTTCCACATCTTCAGCATCCAGTACTCAGCC  
TCAGATGAGCACTTCACAAGGAAGTTTCAGCAGGATCCACAGTTGCTTCATCAACCGCTGGCCTTGTTTCAACT  
TCCACAGTTCCATCCTCGACAGGAACAATGGGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAAT  
CATCGACAACAGCATCTGCAAGTTCTCAGA

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Consensus :

CTGGAAGCACTGTAACCATGGGATCATCAAGCACTTCCGGTGTTTCCACATCTTCAGCATCCAGTACTCAGCC  
TCAGATGAGCACTTCACAAGGAAGTTTCAGCAGGATCCACAGTTGCTTCATCAACCGCTGGCCTTGTTTCAACT  
TCCACAGTTCCATCCTCGACAGGAACAATGGGCTCCACTTCTAGTGGAACAGTTGGATCTACAATTTCTGAAT  
CATCGACAACAGCATCTGCAAGTTCTCAGA

>Cele-UNSB01\_Fam\_163\_231\_1 Nr. of seq. 1 Alignment length(with gaps) =  
231 Alignment score = 0.000000

Cele-UNSB01\_1:10434433-10461186 Satlength=26754 Nr of Repeats=116  
RepeatLength=231 seed=GCTGAATTCA Num.seqs=92 Similarity=0.829532

0

GCTGAATTCAAGTTGGATATGAATGCACTTCCGTTGTGAGTGGAATATCATGAATGTTNGATGCTCGTGAAGTA  
GANTCNAGTGGTCCATCATAAGATTCAGACACTGGATAATCAAGATGAGATGGTGATTTCTTGAACAATCCAG  
TGATCTTAGATTTTCAGTGATGGCTCGTCCTTCTTCTGTCTCCTCGATCACAACCTGGAATGACATGCTCTGG  
CAGCTTCTCATA

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Consensus :

GCTGAATTCAAGTTGGATATGAATGCACTTCCGTTGTGAGTGGAATATCATGAATGTTNGATGCTCGTGAAGTA  
GANTCNAGTGGTCCATCATAAGATTCAGACACTGGATAATCAAGATGAGATGGTGATTTCTTGAACAATCCAG  
TGATCTTAGATTTTCAGTGATGGCTCGTCCTTCTTCTGTCTCCTCGATCACAACCTGGAATGACATGCTCTGG  
CAGCTTCTCATA

>Cele-UNSB01\_Fam\_164\_228\_1 Nr. of seq. 1 Alignment length(with gaps) =  
228 Alignment score = 0.000000

Cele-UNSB01\_3:6120416-6122897 Satlength=2482 Nr of Repeats=10  
RepeatLength=228 seed=CCACCAGATC Num.seqs=6 Similarity=0.843765

0

CCACCAGATCAGCAACGTCTCATCTTCGCCGAAAGCAACTCGAGGACGGCCGCACCCTTTCGGACTACAACA  
TCCAGAAGGAATCAACTCTTCATTTGGTTCTCCGTCTGAGAGGAGGTATGCAGATCTTCGTCAAGACATTGAC  
CGGAAAAGACCATCACCTCGAAGTCGAAGCCTCCGACACCATCGAAAATGTCAAGGCCAAGATCCAAGACAAG  
GAAGGAATC

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Consensus:

CCACCAGATCAGCAACGTCTCATCTTCGCCGAAAGCAACTCGAGGACGGCCGCACCCTTTCGGACTACAACA  
TCCAGAAGGAATCAACTCTTCATTTGGTTCTCCGTCTGAGAGGAGGTATGCAGATCTTCGTCAAGACATTGAC  
CGGAAAAGACCATCACCTCGAAGTCGAAGCCTCCGACACCATCGAAAATGTCAAGGCCAAGATCCAAGACAAG  
GAAGGAATC

>Cele-UNSB01\_Fam\_165\_189\_1 Nr. of seq. 1 Alignment length(with gaps) =  
189 Alignment score = 0.000000

Cele-UNSB01\_1:1620106-1621181 Satlength=1076 Nr of Repeats=5  
RepeatLength=189 seed=TTTTTTTGA Num.seqs=3 Similarity=1.000000

0  
TTTTTTTGGACTATGGAATTATAAAGAAAATCGAATTTCAAAAAAGCATGTATTAGCCAATGTAAACGCGCTC  
CAATGATGATGTAGCCACGTGGTATCAGAGTGTCTCTTTACGGCTTGATTAAATACGTAGATCTACAAATT  
CACTTATCTGTTTTCTCACGGGTTTAGGATATTTTTTCTGTTA

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Consensus:

TTTTTTTGGACTATGGAATTATAAAGAAAATCGAATTTCAAAAAAGCATGTATTAGCCAATGTAAACGCGCTC  
CAATGATGATGTAGCCACGTGGTATCAGAGTGTCTCTTTACGGCTTGATTAAATACGTAGATCTACAAATT  
CACTTATCTGTTTTCTCACGGGTTTAGGATATTTTTTCTGTTA

>Cele-UNSB01\_Fam\_166\_184\_1 Nr. of seq. 1 Alignment length(with gaps) =  
184 Alignment score = 0.000000

Cele-UNSB01\_2:891851-892689 Satlength=839 Nr of Repeats=4  
RepeatLength=184 seed=GTTCAAAAGA Num.seqs=3 Similarity=1.000000

0  
GTTCAAAAGATACAAAATTTATCTACACATCTACAAGTTAAACTTGCAACTTAGTTAACCAAATTCAAAAGTT  
ATGAGCCGGGGAACATAATAACCAACGTTTCACACTAAAAAGCCCAAAAAATTCGAAAATCATTTTTATC  
TCATGACGCGGACAAGCTACAAATGTCTAGTTAGGCTT

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Consensus:

GTTCAAAAGATACAAAATTTATCTACACATCTACAAGTTAAACTTGCAACTTAGTTAACCAAATTCAAAAGTT  
ATGAGCCGGGGAACATAATAACCAACGTTTCACACTAAAAAGCCCAAAAAATTCGAAAATCATTTTTATC  
TCATGACGCGGACAAGCTACAAATGTCTAGTTAGGCTT

>Cele-UNSB01\_Fam\_167\_183\_1 Nr. of seq. 1 Alignment length(with gaps) =  
183 Alignment score = 0.000000

Cele-UNSB01\_5:19795988-19796719 Satlength=732 Nr of Repeats=4  
RepeatLength=183 seed=TTTCTCTGCG Num.seqs=3 Similarity=0.615789  
0

TTTCTCTGCGTCTCGCCTCGCCTCACACTATTTTNCACACCAAACTTTGAGNCTATGTATCTCTGTAACGGGT  
TGCGCTTTCTGAAAAATTCCAAGTACGGGATATATAAAATTTNGAATTCTTTCTCACCGTTAAAAAACTAAA  
CACCTAGGCAAGACGCAGACAGCGAGANACCCCAAT

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Consensus:

TTTCTCTGCGTCTCGCCTCGCCTCACACTATTTTNCACACCAAACTTTGAGNCTATGTATCTCTGTAACGGGT  
TGCGCTTTCTGAAAAATTCCAAGTACGGGATATATAAAATTTNGAATTCTTTCTCACCGTTAAAAAACTAAA  
CACCTAGGCAAGACGCAGACAGCGAGANACCCCAAT

>Cele-UNSB01\_Fam\_168\_181\_1 Nr. of seq. 1 Alignment length(with gaps) =  
181 Alignment score = 0.000000  
Cele-UNSB01\_2:6168224-6172025 Satlength=3802 Nr of Repeats=21  
RepeatLength=181 seed=TTTTTAACTT Num.seqs=21 Similarity=0.964746  
0

TTTTTAACTTTTAAATCCACTAAAACCTCGGAATGGTACAGAACATGCAAATTGTAATTTCAAGAACTGAATGT  
GGTTTCGAATATTTATGGATTGCTTTATTCTAAAACCTGACTCTGAAATATTTTGCATCCATTTGACTACTAAT  
TGTCATATTATACCGAACACTACTAACTTTAGTGG

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Consensus:

TTTTTAACTTTTAAATCCACTAAAACCTCGGAATGGTACAGAACATGCAAATTGTAATTTCAAGAACTGAATGT  
GGTTTCGAATATTTATGGATTGCTTTATTCTAAAACCTGACTCTGAAATATTTTGCATCCATTTGACTACTAAT  
TGTCATATTATACCGAACACTACTAACTTTAGTGG

>Cele-UNSB01\_Fam\_169\_180\_1 Nr. of seq. 1 Alignment length(with gaps) =  
180 Alignment score = 0.000000  
Cele-UNSB01\_3:3099001-3099720 Satlength=720 Nr of Repeats=4  
RepeatLength=180 seed=TGTCGGCCGC Num.seqs=3 Similarity=0.750153  
0

TGTCGGCCGCTGTATCTTTTGCCTCAATTTTTTTTNAATTTTNAACATNCATATTCCAGTAGATAACATTAT  
GAGCTACAGTTTGTTAGTTAAAATTTTATTTCTAAAATTACTAGTTTCTGAGTTATACTCATTCCAACCCACC  
CCAAGAGAAATTTCTTAAAATGAACTCGCGAGG

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Consensus:

TGTCGGCCGCTGTATCTTTTGCCTCAATTTTTTTTNAATTTTNAACATNCATATTCCAGTAGATAACATTAT  
GAGCTACAGTTTGTTAGTTAAAATTTTATTTCTAAAATTACTAGTTTCTGAGTTATACTCATTCCAACCCACC  
CCAAGAGAAATTTCTTAAAATGAACTCGCGAGG

>Cele-UNSB01\_Fam\_170\_179\_1 Nr. of seq. 1 Alignment length(with gaps) =  
179 Alignment score = 0.000000

Cele-UNSB01\_1:14266018-14266935 Satlength=918 Nr of Repeats=5  
RepeatLength=179 seed=CTACCCAAAT Num.seqs=3 Similarity=0.995034  
0

CTACCCAAATTTTTGAAATTTGGAAATTTTTCAAAAATTCTCAAATTTTCAAATCCCATAATTCAGCCAATT  
TTTGAGATTTTCAGATATTTTTTAATTGAAAATTCTGTTTGTCTTATCCATTAACTATATCGCTGCATCTAC  
ATTTTTCACAGTACCCCATGACTTTTCCCGATT

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Consensus:

CTACCCAAATTTTTGAAATTTGGAAATTTTTCAAAAATTCTCAAATTTTCAAATCCCATAATTCAGCCAATT  
TTTGAGATTTTCAGATATTTTTTAATTGAAAATTCTGTTTGTCTTATCCATTAACTATATCGCTGCATCTAC  
ATTTTTCACAGTACCCCATGACTTTTCCCGATT

>Cele-UNSB01\_Fam\_171\_177\_1 Nr. of seq. 1 Alignment length(with gaps) =  
177 Alignment score = 0.000000

Cele-UNSB01\_1:14392151-14393037 Satlength=887 Nr of Repeats=5  
RepeatLength=177 seed=CTAACAAAAT Num.seqs=4 Similarity=0.721286  
0

CTAACAAAATAATCAGCGTAAATTTCTACATTTTACTAGTTAACAATATTTTGATAACATCAGTGGTTTTT  
GAGATACGCAAGTTTTAAGGTGGACGCCCAAAAATAGTTGTGAGCAGCTTTAATCAAAAACCGACATAACTTT  
TTACTACTAACGGTATCAAAAATGTTTTAA

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Consensus:

CTAACAAAATAATCAGCGTAAATTTCTACATTTTACTAGTTAACAATATTTTGATAACATCAGTGGTTTTT  
GAGATACGCAAGTTTTAAGGTGGACGCCCAAAAATAGTTGTGAGCAGCTTTAATCAAAAACCGACATAACTTT  
TTACTACTAACGGTATCAAAAATGTTTTAA

>Cele-UNSB01\_Fam\_172\_177\_1 Nr. of seq. 1 Alignment length(with gaps) =  
177 Alignment score = 0.000000

Cele-UNSB01\_5:2439353-2440062 Satlength=710 Nr of Repeats=4  
RepeatLength=177 seed=GAGTCTCACG Num.seqs=3 Similarity=0.943196  
0

GAGTCTCACGATGTGTCAACGTGTCTCAGTCGGCTTGATCTACGTAGATCTACAAAAAATGCGGGAGAAGAGA  
CGCAGACTTATTCTCTGATTTTGCATGAGTAAGAGCGTGCTGGCGTCACATTTTTGTCTGGCAAAAAATTCCCG  
CATTTTTTTGTAGATCAAACCGTAATGGGACG

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Consensus:

GAGTCTCACGATGTGTCAACGTGTCTCAGTCGGCTTGATCTACGTAGATCTACAAAAAATGCGGGAGAAGAGA  
CGCAGACTTATTCTCTGATTTTGCATGAGTAAGAGCGTGCTGGCGTCACATTTTTGTCTGGCAAAAAATTCCCG  
CATTTTTTTGTAGATCAAACCGTAATGGGACG

>Cele-UNSB01\_Fam\_173\_175\_1 Nr. of seq. 1 Alignment length(with gaps) =  
175 Alignment score = 0.000000

Cele-UNSB01\_1:2461739-2462720 Satlength=982 Nr of Repeats=5  
RepeatLength=175 seed=GATGCACCAT Num.seqs=3 Similarity=0.840552  
0

GATGCACCATGTCTTTGACAGTCAATATCTCGGTTTATTTTGTAGCTATCAAAAAATTTTCAACTACAAATCT  
ATAGAAAAATTAAATGTTCAACATTTTCTCAGTTGACAGTTTTTTGATAACTGCAATGACATCCGAGATATGAG  
CTTTCAAAAGTTGAGAGACCTCACTCGGTT

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Consensus:

GATGCACCATGTCTTTGACAGTCAATATCTCGGTTTATTTTGTAGCTATCAAAAAATTTTCAACTACAAATCT  
ATAGAAAAATTAAATGTTCAACATTTTCTCAGTTGACAGTTTTTTGATAACTGCAATGACATCCGAGATATGAG  
CTTTCAAAAGTTGAGAGACCTCACTCGGTT

>Cele-UNSB01\_Fam\_174\_175\_1 Nr. of seq. 1 Alignment length(with gaps) =  
175 Alignment score = 0.000000

Cele-UNSB01\_4:2701520-2702341 Satlength=822 Nr of Repeats=4  
RepeatLength=175 seed=AACTTGTGAC Num.seqs=3 Similarity=0.715980  
0

AACTTGTGACGGTGGGTATGGATTTTATGCACATAATTTGTTTCGAAATAGTCTACCNAGTAAACTGGTGAAGT  
TTCAAAAACTTTGTGGATCTAGTTTTTGA AAAAAGTTCAAAATTGTGCCAATTTTGACCAATTTTGGTGGTTT  
TCTGAGCTAAAATTGAAAAGTTGGGAATG

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Consensus:

AACTTGTGACGGTGGGTATGGATTTTATGCACATAATTTGTTTCGAAATAGTCTACCNAGTAAACTGGTGAAGT  
TTCAAAAACTTTGTGGATCTAGTTTTTGA AAAAAGTTCAAAATTGTGCCAATTTTGACCAATTTTGGTGGTTT  
TCTGAGCTAAAATTGAAAAGTTGGGAATG

>Cele-UNSB01\_Fam\_175\_175\_1 Nr. of seq. 1 Alignment length(with gaps) =  
175 Alignment score = 0.000000

Cele-UNSB01\_5:328030-329092 Satlength=1063 Nr of Repeats=6  
RepeatLength=175 seed=AAATTTTGGG Num.seqs=4 Similarity=0.911111  
0

AAATTTTGGGTTCACTCTTTTTACTAGACAGTGATTGTTGCATTGTAGGATTCGGTGGACTTGTCCAACAAC  
TACTTTGGCATGAGTTTAATAAAAAGGTTTTACCATGAACTGAATCAATTCAAAATAAAAACCTCGAGAATGA  
AAACATCCTCAGTAATTTCAATCCTGTTC

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Consensus:

AAATTTTGGGTTCACTCTTTTTACTAGACAGTGATTGTTGCATTGTAGGATTCGGTGGACTTGTCCAACAAC  
TACTTTGGCATGAGTTTAATAAAAAGGTTTTACCATGAACTGAATCAATTCAAAATAAAAACCTCGAGAATGA  
AAACATCCTCAGTAATTTCAATCCTGTTC

>Cele-UNSB01\_Fam\_176\_174\_1 Nr. of seq. 1 Alignment length(with gaps) =  
174 Alignment score = 0.000000

Cele-UNSB01\_1:4404167-4404863 Satlength=697 Nr of Repeats=4  
RepeatLength=174 seed=CTTCAAGAGC Num.seqs=4 Similarity=0.868455  
0

CTTCAAGAGCTCAGTGTTATTTATGACATGCCAACCTCGACAATTGACCTGAACATGCTCCAAGGAATCGAAG  
ACAACTTGAACAGCCTTCCAGCTGAAGAATCTGATAAGATCCGAGAGAAGATTAACGATCTGAGAAGAAGGAA  
ACAAGAAAGCGATCAAGCTGAAGCTCTT

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Consensus:

CTTCAAGAGCTCAGTGTTATTTATGACATGCCAACCTCGACAATTGACCTGAACATGCTCCAAGGAATCGAAG  
ACAACTTGAACAGCCTTCCAGCTGAAGAATCTGATAAGATCCGAGAGAAGATTAACGATCTGAGAAGAAGGAA  
ACAAGAAAGCGATCAAGCTGAAGCTCTT

>Cele-UNSB01\_Fam\_177\_165\_1 Nr. of seq. 1 Alignment length(with gaps) =  
165 Alignment score = 0.000000

Cele-UNSB01\_6:1780465-1781641 Satlength=1177 Nr of Repeats=4  
RepeatLength=165 seed=CTTTTCCAAA Num.seqs=3 Similarity=1.000000  
0

CTTTTCCAAAATGGCAATTTTTGATGAAAAAATCCGAATTTTCACAAATTTCAAAAAATTTTTAACTTTA  
TAATTTTAGCTTTGAATATTCCAAATGGAAGTGCATAACCTATCAATTTGATATATAAACTCGTGCCTACCT  
TCAGGCATTCAGTTTTTCAC

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Consensus:

CTTTTCCAAAATGGCAATTTTTGATGAAAAAATCCGAATTTTCACAAATTTCAAAAAATTTTTAACTTTA  
TAATTTTAGCTTTGAATATTCCAAATGGAAGTGCATAACCTATCAATTTGATATATAAACTCGTGCCTACCT  
TCAGGCATTCAGTTTTTCAC

>Cele-UNSB01\_Fam\_178\_155\_1 Nr. of seq. 1 Alignment length(with gaps) =  
155 Alignment score = 0.000000

Cele-UNSB01\_2:2979318-2980713 Satlength=1396 Nr of Repeats=9  
RepeatLength=155 seed=TCCCGCTGTG Num.seqs=6 Similarity=0.781691  
0

TCCCGCTGTGGTTAAAAGTTTTTTCGTGCTCAGTTCTGTACGGTAAATGTGTTAAAACTTCTGGAACTTG  
AAATTCCAAGTTATTCAGAAAATTGTTCAAATGGCGCAGTGGGAAATTCGATTTCTCAGACCCAAGAGGCCAC  
GGGTTCAAT

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Consensus:

TCCCGCTGTGGTTAAAAGTTTTTTCGTGCTCAGTTCTGTACGGTAAATGTGTTAAAACTTCTGGAACTTG  
AAATTCCAAGTTATTCAGAAAATTGTTCAAATGGCGCAGTGGGAAATTCGATTTCTCAGACCCAAGAGGCCAC  
GGGTTCAAT

>Cele-UNSB01\_Fam\_179\_153\_1 Nr. of seq. 1 Alignment length(with gaps) =  
153 Alignment score = 0.000000

Cele-UNSB01\_6:14250466-14251066 Satlength=601 Nr of Repeats=4  
RepeatLength=153 seed=TGAGGTGCAG Num.seqs=3 Similarity=0.872186  
0  
TGAGGTGCAGGGCGTGATGAGCTTTGTTGAACTGGGAACTGTTGATTCCCGGAGCCGTGATTCATAGATGAGT  
TGGAGGGACCTGCTGTGGAACCTGTTTCAACTTGAGCAATTCCATGAGCCATCAAGAAGCTTCCGGCAGATT  
GGGCAAC

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Consensus:

TGAGGTGCAGGGCGTGATGAGCTTTGTTGAACTGGGAACTGTTGATTCCCGGAGCCGTGATTCATAGATGAGT  
TGGAGGGACCTGCTGTGGAACCTGTTTCAACTTGAGCAATTCCATGAGCCATCAAGAAGCTTCCGGCAGATT  
GGGCAAC

>Cele-UNSB01\_Fam\_180\_151\_1 Nr. of seq. 1 Alignment length(with gaps) =  
151 Alignment score = 0.000000  
Cele-UNSB01\_5:14155473-14156076 Satlength=604 Nr of Repeats=4  
RepeatLength=151 seed=CATTTTCAGAT Num.seqs=3 Similarity=0.988227  
0  
CATTTTCAGATATTCATCACCACCAACACCTTCATCCACTTCTTCGCCTGGAACGACGGGATTTTCTACAAAA  
ATCGGATTTTTTCTCTATGTCAGTTTAATTGATGTATAATTCCGAAAAGTCAGTCTTTCCTAGGTTTTTAAAT  
TGAAA

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Consensus:

CATTTTCAGATATTCATCACCACCAACACCTTCATCCACTTCTTCGCCTGGAACGACGGGATTTTCTACAAAA  
ATCGGATTTTTTCTCTATGTCAGTTTAATTGATGTATAATTCCGAAAAGTCAGTCTTTCCTAGGTTTTTAAAT  
TGAAA

>Cele-UNSB01\_Fam\_181\_150\_1 Nr. of seq. 1 Alignment length(with gaps) =  
150 Alignment score = 0.000000  
Cele-UNSB01\_2:1517382-1518287 Satlength=906 Nr of Repeats=6  
RepeatLength=150 seed=TTGCAACATG Num.seqs=4 Similarity=0.817145  
0  
TTGCAACATGCGGTCGGCGGAAAATTTCGAATTTTTTCAGTCCAAAACAGGTTTTTCGACCAATTTTTTCATATTT  
TCAAGCGAAAATTATGATAGAAAATTCAAATTTTCACTAAAAATCGCCAATTTTCCACATTTTCTCATTGGAGC  
GCAC

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Consensus:

TTGCAACATGCGGTCGGCGGAAAATTTCGAATTTTTTCAGTCCAAAACAGGTTTTTCGACCAATTTTTTCATATTT  
TCAAGCGAAAATTATGATAGAAAATTCAAATTTTCACTAAAAATCGCCAATTTTCCACATTTTCTCATTGGAGC  
GCAC

>Cele-UNSB01\_Fam\_182\_150\_1 Nr. of seq. 1 Alignment length(with gaps) =  
150 Alignment score = 0.000000



Cele-UNSB01\_4:16931676-16932199 Satlength=524 Nr of Repeats=4  
RepeatLength=150 seed=TTGAGGGCCG Num.seqs=3 Similarity=0.940741  
0  
TTGAGGGCCGCAGTCCCGAATACACGAAGAAGTGTGGAGATCCGTCAAGCCTATTCTAAGCATAATAATTCA  
GTTTCGAGTGTTCGCAAGCCCAAATAGACGCAGAAGCGTTGGACAACCTTTTAGGCCTATTCTGAGCCCAATAATT  
CATG

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Consensus:

TTGAGGGCCGCAGTCCCGAATACACGAAGAAGTGTGGAGATCCGTCAAGCCTATTCTAAGCATAATAATTCA  
GTTTCGAGTGTTCGCAAGCCCAAATAGACGCAGAAGCGTTGGACAACCTTTTAGGCCTATTCTGAGCCCAATAATT  
CATG

>Cele-UNSB01\_Fam\_183\_146\_1 Nr. of seq. 1 Alignment length(with gaps) =  
146 Alignment score = 0.000000  
Cele-UNSB01\_2:2836927-2837967 Satlength=1041 Nr of Repeats=6  
RepeatLength=144 seed=TGGCCTAGAA Num.seqs=4 Similarity=0.634815  
0  
TGGCCTAGAAATCNCAAGTTTGCAAAAGTTAGGCCACCAACTTCAAATGCCTATAACTCAGCGGAAAATCAAT  
ATTTTCCATTGATTTTAACTGCTAAGATGTAGCCAATTACGTAGCGCAACTTTTTTGGCCTACTTAACAATTGG

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Consensus:

TGGCCTAGAAATCNCAAGTTTGCAAAAGTTAGGCCACCAACTTCAAATGCCTATAACTCAGCGGAAAATCAAT  
ATTTTCCATTGATTTTAACTGCTAAGATGTAGCCAATTACGTAGCGCAACTTTTTTGGCCTACTTAACAATTGG

>Cele-UNSB01\_Fam\_184\_144\_1 Nr. of seq. 1 Alignment length(with gaps) =  
144 Alignment score = 0.000000  
Cele-UNSB01\_4:2456640-2457356 Satlength=717 Nr of Repeats=5  
RepeatLength=144 seed=TTCTAGGCCA Num.seqs=4 Similarity=0.915326  
0  
TTCTAGGCCACCAATTGGAAATCATCATAACTTGGCTTAAAATCCAGATTTTTTGGAGTCTGGTAACTGCAACA  
TGTTGCCCTGTAGTTTTTCTACAAGTTAGGATATATTAATTTTTTGGTGGCCTAAAAGTCCAAATTATGGAT

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Consensus:

TTCTAGGCCACCAATTGGAAATCATCATAACTTGGCTTAAAATCCAGATTTTTTGGAGTCTGGTAACTGCAACA  
TGTTGCCCTGTAGTTTTTCTACAAGTTAGGATATATTAATTTTTTGGTGGCCTAAAAGTCCAAATTATGGAT

>Cele-UNSB01\_Fam\_185\_143\_1 Nr. of seq. 1 Alignment length(with gaps) =  
143 Alignment score = 0.000000  
Cele-UNSB01\_5:17962175-17963525 Satlength=1351 Nr of Repeats=6  
RepeatLength=143 seed=CAGTGGGATT Num.seqs=4 Similarity=0.759132  
0  
CAGTGGGATTTTCAATGTCTTCCAATCAAACGTCCGGGGTTCGAGTCCGCACAGGGGTATTTATTTTTTGCAA  
GCTGTGATTAACAAGTTTATAGCTGCAAAAGTCATTTTAATCGAACTTTCAGGAAAATGTCCGAATGGCG

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Consensus:

CAGTGGGATTTTCAATGTCTTCCAATCAAACGTCCGGGGTTCGAGTCCGCACAGGGGTATTTATTTTTTGCAA  
GCTGTGATTAACAAGTTTATAGCTGCAAAAGTCATTTTAATCGAACTTTCAGGAAAATGTCCGAATGGCG

>Cele-UNSB01\_Fam\_186\_124\_1 Nr. of seq. 1 Alignment length(with gaps) =  
124 Alignment score = 0.000000

Cele-UNSB01\_2:11256637-11258512 Satlength=1876 Nr of Repeats=15  
RepeatLength=124 seed=AATTTTCAAA Num.seqs=9 Similarity=0.708025

0

AATTTTCAAAGTTTGGAAAATCTATTAATTTTGCATATAATTTTATAAATTCTGAAAGAACATAAAATTTGC  
TACAAAATGGCTACGGGAATTTCTAAAAAATTTAGTTTGAAGNCAGAAATT

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Consensus:

AATTTTCAAAGTTTGGAAAATCTATTAATTTTGCATATAATTTTATAAATTCTGAAAGAACATAAAATTTGC  
TACAAAATGGCTACGGGAATTTCTAAAAAATTTAGTTTGAAGNCAGAAATT

>Cele-UNSB01\_Fam\_187\_122\_1 Nr. of seq. 1 Alignment length(with gaps) =  
122 Alignment score = 0.000000

Cele-UNSB01\_2:13490523-13491161 Satlength=639 Nr of Repeats=5  
RepeatLength=122 seed=GATCTACAAA Num.seqs=3 Similarity=0.927140

0

GATCTACAAAAATGCGGGAAAAGTGACACAGAGTTCTCAACTGATTTTGCATAAAAATTCCTCGCATTTTTTGG  
AGATCAAACCGTGATGGGACAGCCTGGCACCACTTGCTTGATCTACGTA

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Consensus:

GATCTACAAAAATGCGGGAAAAGTGACACAGAGTTCTCAACTGATTTTGCATAAAAATTCCTCGCATTTTTTGG  
AGATCAAACCGTGATGGGACAGCCTGGCACCACTTGCTTGATCTACGTA

>Cele-UNSB01\_Fam\_188\_121\_1 Nr. of seq. 1 Alignment length(with gaps) =  
121 Alignment score = 0.000000

Cele-UNSB01\_5:16591935-16597985 Satlength=6051 Nr of Repeats=50  
RepeatLength=121 seed=GTTGCAAACC Num.seqs=50 Similarity=0.958478

0

GTTGCAAACCGCAAGAGCAAACCTGCCAAATGAAAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGC  
TCGTAGACTATAATTTCTCTGAAAAGATAGTTGCCCTAATAGCAGAAG

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Consensus:

GTTGCAAACCGCAAGAGCAAACCTGCCAAATGAAAAGCCACCCAAGTACTCGTTGCACCTACCTATCATAAGC  
TCGTAGACTATAATTTCTCTGAAAAGATAGTTGCCCTAATAGCAGAAG

>Cele-UNSB01\_Fam\_189\_119\_1 Nr. of seq. 1 Alignment length(with gaps) =  
119 Alignment score = 0.000000  
Cele-UNSB01\_6:309569-317496 Satlength=7928 Nr of Repeats=66  
RepeatLength=119 seed=GGCCACCGTT Num.seqs=63 Similarity=0.981664  
0  
GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTAC  
CCACACGGCAAGGTTTAATTTTTGAAATTTGGTCGCGGATTTTCTC

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Consensus:

GGCCACCGTTGCATATTTTCGCAATAATTTTTACGGGAACGTAATCTCCACGTCACCAGCTTTCATTTAAGTAC  
CCACACGGCAAGGTTTAATTTTTGAAATTTGGTCGCGGATTTTCTC

>Cele-UNSB01\_Fam\_190\_117\_1 Nr. of seq. 1 Alignment length(with gaps) =  
117 Alignment score = 0.000000  
Cele-UNSB01\_5:6179564-6194498 Satlength=14935 Nr of Repeats=110  
RepeatLength=117 seed=TACTTCAGAT Num.seqs=94 Similarity=0.905974  
0  
TACTTCAGATGTTTCCTTTGATTCCACAGGTGCAAGTTTCTCAACTGTTGGTTCGACAGTAGGTGCACTAGTC  
TCTGGCACTGGAACATCCTTTTGCTCAACAATTTTCAGCTGGTTG

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Consensus:

TACTTCAGATGTTTCCTTTGATTCCACAGGTGCAAGTTTCTCAACTGTTGGTTCGACAGTAGGTGCACTAGTC  
TCTGGCACTGGAACATCCTTTTGCTCAACAATTTTCAGCTGGTTG

>Cele-UNSB01\_Fam\_191\_114\_1 Nr. of seq. 1 Alignment length(with gaps) =  
114 Alignment score = 0.000000  
Cele-UNSB01\_5:8785418-8789720 Satlength=4303 Nr of Repeats=37  
RepeatLength=114 seed=GTGTTTCAGA Num.seqs=35 Similarity=0.970986  
0  
GTGTTTCAGAATTACATGGAGTCTCACTACTTGCAGAATTTGTGGCTGTAGACGATGGGCCTGCTGTAGTTGA  
ATCGTTTGGAACGTGCATAGTGGATGTTCCATCAGACGTTT

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Consensus:

GTGTTTCAGAATTACATGGAGTCTCACTACTTGCAGAATTTGTGGCTGTAGACGATGGGCCTGCTGTAGTTGA  
ATCGTTTGGAACGTGCATAGTGGATGTTCCATCAGACGTTT

>Cele-UNSB01\_Fam\_192\_108\_1 Nr. of seq. 1 Alignment length(with gaps) =  
108 Alignment score = 0.000000  
Cele-UNSB01\_6:1595379-1595859 Satlength=481 Nr of Repeats=5  
RepeatLength=108 seed=ATCCTCAACA Num.seqs=3 Similarity=0.732510  
0  
ATCCTCAACACCATCNGCGTCATCTAGTTCCTCCGGAACATATGTCGACAATTTTCAGGATCAACTGGTTCNACA  
GTTACAGTTGTACCAGGATCNTCTAGCACATTTGG

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Consensus:

ATCCTCAACACCATCNGCGTCATCTAGTTCTCCGGAAGTATGTCGACAATTTTCAGGATCAACTGGTTCNACA  
GTTACAGTTGTACCAGGATCNTCTAGCACATTTGG

>Cele-UNSB01\_Fam\_193\_108\_1 Nr. of seq. 1 Alignment length(with gaps) =  
108 Alignment score = 0.000000

Cele-UNSB01\_6:14010915-14011665 Satlength=751 Nr of Repeats=7

RepeatLength=108 seed=TGGGTAATCA Num.seqs=6 Similarity=0.845267

0

TGGGTAATCAGGTACGGGCTTTTCAGATTTTCAAGTTTTCACGTGAATATCTAGGTCACGAGCCAATTTTCAGCC  
AGGAGTGGGACTAGAGATATGAAACTCTTGGGTTA

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Consensus:

TGGGTAATCAGGTACGGGCTTTTCAGATTTTCAAGTTTTCACGTGAATATCTAGGTCACGAGCCAATTTTCAGCC  
AGGAGTGGGACTAGAGATATGAAACTCTTGGGTTA

>Cele-UNSB01\_Fam\_194\_108\_1 Nr. of seq. 1 Alignment length(with gaps) =  
108 Alignment score = 0.000000

Cele-UNSB01\_6:15588433-15598390 Satlength=9958 Nr of Repeats=92

RepeatLength=108 seed=AAGTCTTCTT Num.seqs=90 Similarity=0.968330

0

AAGTCTTCTTGATTCTGAGTTCTTGCTTCGAACTGTTGACCATCTCCTTGCAGGATCTTATTGTCAGATGGAA  
CCTTCTTGGCATAACGTTCTCCACTGATGTGAGTG

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Consensus:

AAGTCTTCTTGATTCTGAGTTCTTGCTTCGAACTGTTGACCATCTCCTTGCAGGATCTTATTGTCAGATGGAA  
CCTTCTTGGCATAACGTTCTCCACTGATGTGAGTG

>Cele-UNSB01\_Fam\_195\_104\_1 Nr. of seq. 1 Alignment length(with gaps) =  
104 Alignment score = 0.000000

Cele-UNSB01\_4:2422782-2423615 Satlength=834 Nr of Repeats=8

RepeatLength=104 seed=CCTGCGAAAG Num.seqs=7 Similarity=0.985348

0

CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGG  
GTTATCGGTGAATTTTTGGGTCTGTCAGGGT

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Consensus:

CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGG  
GTTATCGGTGAATTTTTGGGTCTGTCAGGGT

>Cele-UNSB01\_Fam\_196\_102\_1 Nr. of seq. 1 Alignment length(with gaps) =  
102 Alignment score = 0.000000  
Cele-UNSB01\_4:695215-705007 Satlength=9793 Nr of Repeats=96  
RepeatLength=102 seed=TGATATGTCG Num.seqs=96 Similarity=0.972641  
0  
TGATATGTCGAACGATTGATAGTTTGAGAATCAAGAGAATCTGTTGGACGATCAATTCCATCTTTGGGTCTTG  
CTGCAGCATATCTTTCTCCAGTACCACCT

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Consensus:

TGATATGTCGAACGATTGATAGTTTGAGAATCAAGAGAATCTGTTGGACGATCAATTCCATCTTTGGGTCTTG  
CTGCAGCATATCTTTCTCCAGTACCACCT

>Cele-UNSB01\_Fam\_197\_102\_1 Nr. of seq. 1 Alignment length(with gaps) =  
102 Alignment score = 0.000000  
Cele-UNSB01\_6:1180467-1185764 Satlength=5298 Nr of Repeats=52  
RepeatLength=102 seed=TGTACACTTC Num.seqs=37 Similarity=0.984062  
0  
TGTACACTTCTCCCAAATTGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAAA  
CTTCTCTCAAAAAGAAAATAGACTTCACA

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Consensus:

TGTACACTTCTCCCAAATTGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAAA  
CTTCTCTCAAAAAGAAAATAGACTTCACA

>Cele-UNSB01\_Fam\_198\_101\_1 Nr. of seq. 1 Alignment length(with gaps) =  
101 Alignment score = 0.000000  
Cele-UNSB01\_1:14574460-14574865 Satlength=406 Nr of Repeats=4  
RepeatLength=101 seed=GCATTTGCAT Num.seqs=3 Similarity=0.826797  
0  
GCATTTGCATATNGAGATCAGATAAAAGTTAGAATTTTCCAGCCGTTGCAAGTGCGCTCTATTGAGAACATTT  
TGAAAAATTGAATGTTTTACATTAGAGC

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Consensus:

GCATTTGCATATNGAGATCAGATAAAAGTTAGAATTTTCCAGCCGTTGCAAGTGCGCTCTATTGAGAACATTT  
TGAAAAATTGAATGTTTTACATTAGAGC

>Cele-UNSB01\_Fam\_199\_101\_1 Nr. of seq. 1 Alignment length(with gaps) =  
101 Alignment score = 0.000000  
Cele-UNSB01\_3:272176-273482 Satlength=1307 Nr of Repeats=13  
RepeatLength=101 seed=GGTTACTGTA Num.seqs=11 Similarity=0.942394  
0  
GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGC  
AGAAAAATCGCTAAAAATGACTTTACTGG

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Consensus:

GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGC  
AGAAAATCGCTAAAAATGACTTTACTGG

>Cele-UNSB01\_Fam\_200\_101\_1 Nr. of seq. 1 Alignment length(with gaps) =  
101 Alignment score = 0.000000

Cele-UNSB01\_4:1584655-1585480 Satlength=826 Nr of Repeats=7  
RepeatLength=101 seed=TTGATTTTTC Num.seqs=5 Similarity=0.952475

0

TTGATTTTTCGTCTTATGAAGGAATATTGGTTTCGGGGTAGTGGGCGGATATGGTCGGGGTACTGTAGGTATA  
CGGTAGGGTTACTGTAGTTTGGAAATT

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Consensus:

TTGATTTTTCGTCTTATGAAGGAATATTGGTTTCGGGGTAGTGGGCGGATATGGTCGGGGTACTGTAGGTATA  
CGGTAGGGTTACTGTAGTTTGGAAATT

>Cele-UNSB01\_Fam\_201\_96\_1 Nr. of seq. 1 Alignment length(with gaps) = 96  
Alignment score = 0.000000

Cele-UNSB01\_4:12453898-12454471 Satlength=574 Nr of Repeats=6  
RepeatLength=96 seed=GGTTGATTTG Num.seqs=5 Similarity=0.991667

0

GGTTGATTTGCGGCACTCTACAGATAGTGGATCTGCTTCTTACCAATCTTCCCGTTACCGCCACGCACTTAAG  
CTCCAAACTATTTTATTTTTTTTG

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Consensus:

GGTTGATTTGCGGCACTCTACAGATAGTGGATCTGCTTCTTACCAATCTTCCCGTTACCGCCACGCACTTAAG  
CTCCAAACTATTTTATTTTTTTTG

>Cele-UNSB01\_Fam\_202\_96\_1 Nr. of seq. 1 Alignment length(with gaps) = 96  
Alignment score = 0.000000

Cele-UNSB01\_4:12787287-12803219 Satlength=15933 Nr of Repeats=166  
RepeatLength=96 seed=GTTCGCATAA Num.seqs=162 Similarity=0.969395

0

GTTCGCATAAATTGGGTAAATACCACTCATAAGTAACTAGTATGGGACTGAAAAGATACTAAATGAGCTTATT  
CTAAGGGTGAAGCTTCTGGTAAT

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Consensus:

GTTCGCATAAATTGGGTAAATACCACTCATAAGTAACTAGTATGGGACTGAAAAGATACTAAATGAGCTTATT  
CTAAGGGTGAAGCTTCTGGTAAT

>Cele-UNSB01\_Fam\_203\_93\_1 Nr. of seq. 1 Alignment length(with gaps) = 93  
Alignment score = 0.000000  
Cele-UNSB01\_4:6945378-6946401 Satlength=1024 Nr of Repeats=11  
RepeatLength=93 seed=TGCTTCTCGT Num.seqs=11 Similarity=0.961942  
0  
TGCTTCTCGTTCGTCACCAACCACCAAGGGAAGTGAAGCCCACCACCACCAACTGGAGAACCACAG  
GATCTTTCTGGAGAAGGTAA

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Consensus:

TGCTTCTCGTTCGTCACCAACCACCAAGGGAAGTGAAGCCCACCACCACCAACTGGAGAACCACAG  
GATCTTTCTGGAGAAGGTAA

>Cele-UNSB01\_Fam\_204\_93\_1 Nr. of seq. 1 Alignment length(with gaps) = 93  
Alignment score = 0.000000  
Cele-UNSB01\_5:1955153-1955723 Satlength=571 Nr of Repeats=7  
RepeatLength=93 seed=CAGTACCCTC Num.seqs=5 Similarity=0.954122  
0  
CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCCGGTAACATAATGCCTTTGCCAGCACTTCCGATGCTC  
CACAGTATCCAGGATCCTCC

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Consensus:

CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCCGGTAACATAATGCCTTTGCCAGCACTTCCGATGCTC  
CACAGTATCCAGGATCCTCC

>Cele-UNSB01\_Fam\_205\_87\_1 Nr. of seq. 1 Alignment length(with gaps) = 87  
Alignment score = 0.000000  
Cele-UNSB01\_4:2843789-2844131 Satlength=343 Nr of Repeats=4  
RepeatLength=87 seed=TGAAGTCGTA Num.seqs=3 Similarity=0.685393  
0  
TGAAGTCGTAGGATTCTGTGTGGTGAAGTGGTGTGCGTTGTANTCTGTGAAGGGGACGTGGCTTCTTCCGTTGTG  
TCATGCTTCTNNGG

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Consensus:

TGAAGTCGTAGGATTCTGTGTGGTGAAGTGGTGTGCGTTGTANTCTGTGAAGGGGACGTGGCTTCTTCCGTTGTG  
TCATGCTTCTNNGG

>Cele-UNSB01\_Fam\_206\_81\_1 Nr. of seq. 1 Alignment length(with gaps) = 81  
Alignment score = 0.000000  
Cele-UNSB01\_1:14687699-14688279 Satlength=581 Nr of Repeats=8  
RepeatLength=73 seed=TGTCGGCCGC Num.seqs=6 Similarity=0.624829  
0  
TGTCGGCCGCTACCAAACTATTTAGCANACACACCAAGCACTACGTTGCGCACACACCAAACTGCGGAACC  
CCGAACAG

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Consensus:

TGTCGGCCGCTACCAAACCTATTTAGCANACACACCAAGCACTACGTTGCGCACACACACCAAACCTGCGGAACC  
CCGAACAG

>Cele-UNSB01\_Fam\_207\_80\_1 Nr. of seq. 1 Alignment length(with gaps) = 80  
Alignment score = 0.000000

Cele-UNSB01\_4:1985632-1987358 Satlength=1727 Nr of Repeats=15

RepeatLength=80 seed=AATTTCTCAA Num.seqs=14 Similarity=0.854212

0

AATTTCTCAATAGGGCGCGCTTGCAACATCTGAACGGCGCGAAATTTGAATTTTGGCCATAAAATAACGAAA  
ACTAACT

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Consensus:

AATTTCTCAATAGGGCGCGCTTGCAACATCTGAACGGCGCGAAATTTGAATTTTGGCCATAAAATAACGAAA  
ACTAACT

>Cele-UNSB01\_Fam\_208\_78\_1 Nr. of seq. 1 Alignment length(with gaps) = 78  
Alignment score = 0.000000

Cele-UNSB01\_3:13289132-13289912 Satlength=781 Nr of Repeats=10

RepeatLength=78 seed=CGAAGTTGCT Num.seqs=10 Similarity=0.831974

0

CGAAGTTGCTGGACCAAAGATCACAACAGGCGGATTTGGCGGCATAACCGGAGCAACAGTAGTGTCATTTGGT  
TCTTC

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Consensus:

CGAAGTTGCTGGACCAAAGATCACAACAGGCGGATTTGGCGGCATAACCGGAGCAACAGTAGTGTCATTTGGT  
TCTTC

>Cele-UNSB01\_Fam\_209\_78\_1 Nr. of seq. 1 Alignment length(with gaps) = 78  
Alignment score = 0.000000

Cele-UNSB01\_5:8793961-8799031 Satlength=5071 Nr of Repeats=65

RepeatLength=78 seed=TGCAAGGCTC Num.seqs=65 Similarity=0.932885

0

TGCAAGGCTCCGATGATGATACCACTTCTAAAGTCGAGGTGTCACAATTTTCGGGTGTCGTAGAACTTGAATC  
AGTGA

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\*\*\*\*\*

Consensus:

TGCAAGGCTCCGATGATGATACCACTTCTAAAGTCGAGGTGTCACAATTTTCGGGTGTCGTAGAACTTGAATC  
AGTGA



>Cele-UNSB01\_Fam\_210\_78\_1 Nr. of seq. 1 Alignment length(with gaps) = 78  
Alignment score = 0.000000  
Cele-UNSB01\_5:18412081-18412792 Satlength=712 Nr of Repeats=10  
RepeatLength=78 seed=GAGCTTTGGG Num.seqs=7 Similarity=0.947904  
0  
GAGCTTTGGGGCTTTTGGCTTGATCTCAGTCGACTTGATGGATTCTGGCTTGGGTCTGCAGGCTTTTCGGGC  
TCCTT

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\*\*\*\*\*  
Consensus:

GAGCTTTGGGGCTTTTGGCTTGATCTCAGTCGACTTGATGGATTCTGGCTTGGGTCTGCAGGCTTTTCGGGC  
TCCTT

>Cele-UNSB01\_Fam\_211\_77\_1 Nr. of seq. 1 Alignment length(with gaps) = 77  
Alignment score = 0.000000  
Cele-UNSB01\_4:10610325-10610863 Satlength=539 Nr of Repeats=7  
RepeatLength=77 seed=GGAAGCTTCA Num.seqs=6 Similarity=0.984993  
0  
GGAAGCTTCATCTTTTGAATTATAAAAAATAAATTTCAATTCAAAATCAGTGTGTGCACTATCAAAAGTGTC  
CACT

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\*\*\*\*  
Consensus:

GGAAGCTTCATCTTTTGAATTATAAAAAATAAATTTCAATTCAAAATCAGTGTGTGCACTATCAAAAGTGTC  
CACT

>Cele-UNSB01\_Fam\_212\_73\_1 Nr. of seq. 1 Alignment length(with gaps) = 73  
Alignment score = 0.000000  
Cele-UNSB01\_2:1327419-1327790 Satlength=372 Nr of Repeats=5  
RepeatLength=73 seed=AGTTTGTAGT Num.seqs=3 Similarity=0.920852  
0  
ANTTTGTAGTTTGTAGTCTAGCAGACCAAATTTATTAAAACTGCAGAAAATTGATGGGTCTGCTAATTAAG

\*\*\*\*\*  
Consensus:

ANTTTGTAGTTTGTAGTCTAGCAGACCAAATTTATTAAAACTGCAGAAAATTGATGGGTCTGCTAATTAAG

>Cele-UNSB01\_Fam\_213\_72\_1 Nr. of seq. 1 Alignment length(with gaps) = 72  
Alignment score = 0.000000  
Cele-UNSB01\_2:870904-873513 Satlength=2610 Nr of Repeats=35  
RepeatLength=72 seed=TCCATCCAGC Num.seqs=29 Similarity=0.928845  
0  
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACTAGTAGTACCATTGGCTCCGTTCCG

\*\*\*\*\*  
Consensus:

TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACTAGTAGTACCATTGGCTCCGTTCCG

>Cele-UNSB01\_Fam\_214\_72\_1 Nr. of seq. 1 Alignment length(with gaps) = 72  
Alignment score = 0.000000  
Cele-UNSB01\_3:1690415-1691093 Satlength=679 Nr of Repeats=5  
RepeatLength=72 seed=ATGAATTTTA Num.seqs=3 Similarity=0.975309  
0  
ATGAATTTTAATACAATTTTCCTGACGATGAAGTCATAAAAAATTCATTTTTTGACCTTTCACCTTTAGTTTT

\*\*\*\*\*  
Consensus:

ATGAATTTTAATACAATTTTCCTGACGATGAAGTCATAAAAAATTCATTTTTTGACCTTTCACCTTTAGTTTT

>Cele-UNSB01\_Fam\_215\_72\_1 Nr. of seq. 1 Alignment length(with gaps) = 72  
Alignment score = 0.000000  
Cele-UNSB01\_6:15412985-15413295 Satlength=311 Nr of Repeats=5  
RepeatLength=72 seed=TGGTTGTGTT Num.seqs=4 Similarity=0.990741  
0  
TGGTTGTGTTCCCAAAGTGAGAAAAGAGGGTACAGACCTCTGTACGAATATGTCTTATCAGCTTCAAAGA

\*\*\*\*\*  
Consensus:

TGGTTGTGTTCCCAAAGTGAGAAAAGAGGGTACAGACCTCTGTACGAATATGTCTTATCAGCTTCAAAGA

>Cele-UNSB01\_Fam\_216\_71\_1 Nr. of seq. 1 Alignment length(with gaps) = 71  
Alignment score = 0.000000  
Cele-UNSB01\_1:1435639-1436319 Satlength=681 Nr of Repeats=8  
RepeatLength=71 seed=ATTTATGTGA Num.seqs=6 Similarity=0.847840  
0  
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAGGGAAATCTGAATTTTTCCGATTTTTCTGACGA

\*\*\*\*\*  
Consensus:

ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAGGGAAATCTGAATTTTTCCGATTTTTCTGACGA

>Cele-UNSB01\_Fam\_217\_70\_1 Nr. of seq. 1 Alignment length(with gaps) = 70  
Alignment score = 0.000000  
Cele-UNSB01\_4:2419217-2421562 Satlength=2346 Nr of Repeats=23  
RepeatLength=70 seed=AAAAATCGAT Num.seqs=14 Similarity=0.884668  
0  
AAAAATCGATTTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTCAACAGCGAAAAAATTGAATTTTCCGCC

\*\*\*\*\*  
Consensus:

AAAAATCGATTTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTCAACAGCGAAAAAATTGAATTTTCCGCC

>Cele-UNSB01\_Fam\_218\_69\_1 Nr. of seq. 1 Alignment length(with gaps) = 69  
Alignment score = 0.000000  
Cele-UNSB01\_2:12477614-12477893 Satlength=280 Nr of Repeats=4  
RepeatLength=69 seed=AGGTAGGCCT Num.seqs=3 Similarity=0.747619  
0  
AGGTAGGCCTGTAGGCATTGACTGNCAGAAAAGCGTAGACAGGCAAGCAGGTAAAAAGATACATGAGGC

\*\*\*\*\*

Consensus:

AGGTAGGCCTGTAGGCATTGACTGNCAGAAAAGCGTAGACAGGCAAGCAGGTAAAAAGATACATGAGGC

>Cele-UNSB01\_Fam\_219\_69\_1 Nr. of seq. 1 Alignment length(with gaps) = 69  
Alignment score = 0.000000

Cele-UNSB01\_5:8388026-8392649 Satlength=4624 Nr of Repeats=67  
RepeatLength=69 seed=GTCTGGACTG Num.seqs=67 Similarity=0.948872

0  
GTCTGGACTGGTGTAGTAGAACTGCTTGGAGGTTCTGTACTGGTTGTCTCTGGAGCCGTGGTAGTAGTA

\*\*\*\*\*

Consensus:

GTCTGGACTGGTGTAGTAGAACTGCTTGGAGGTTCTGTACTGGTTGTCTCTGGAGCCGTGGTAGTAGTA

>Cele-UNSB01\_Fam\_220\_68\_1 Nr. of seq. 1 Alignment length(with gaps) = 68  
Alignment score = 0.000000

Cele-UNSB01\_1:14122632-14123925 Satlength=1294 Nr of Repeats=19  
RepeatLength=68 seed=TTGGTTGAGG Num.seqs=14 Similarity=0.987503

0 TTGGTTGAGGCTAGAAAATGTTGTAGTTTGTAGTGTGTTAGCCTCAACCAAATTAATTTTTTTTTTAA

\*\*\*\*\*

Consensus:

TTGGTTGAGGCTAGAAAATGTTGTAGTTTGTAGTGTGTTAGCCTCAACCAAATTAATTTTTTTTTTAA

>Cele-UNSB01\_Fam\_221\_65\_1 Nr. of seq. 1 Alignment length(with gaps) = 65  
Alignment score = 0.000000

Cele-UNSB01\_2:1881035-1881350 Satlength=316 Nr of Repeats=5  
RepeatLength=65 seed=TATCGAGAGA Num.seqs=3 Similarity=0.658497

0 TATCGAGAGAATNTTCCACATTCACCTTTGAATTCCNTTCCAATTTCAATAAGACTCTCAGTAAG

\*\*\*\*\*

Consensus:

TATCGAGAGAATNTTCCACATTCACCTTTGAATTCCNTTCCAATTTCAATAAGACTCTCAGTAAG

>Cele-UNSB01\_Fam\_222\_62\_1 Nr. of seq. 1 Alignment length(with gaps) = 62  
Alignment score = 0.000000

Cele-UNSB01\_1:14343732-14344621 Satlength=890 Nr of Repeats=4  
RepeatLength=62 seed=GTAGTTTGTA Num.seqs=3 Similarity=0.928315

0 GTAGTTTGTAAGCTTTAGCCTCAACCAAATTAGCTAAAGCTTGAGTGAGGCTATGGTGATTTT

\*\*\*\*\*

Consensus:

GTAGTTTGTAAGCTTTAGCCTCAACCAAATTAGCTAAAGCTTGAGTGAGGCTATGGTGATTTT

>Cele-UNSB01\_Fam\_223\_62\_1 Nr. of seq. 1 Alignment length(with gaps) = 62  
Alignment score = 0.000000

Cele-UNSB01\_2:14141898-14142455 Satlength=558 Nr of Repeats=7  
RepeatLength=62 seed=TGCTAACTAG Num.seqs=6 Similarity=0.822222  
0 TGCTAACTAGCTACGGCCAGCTTAGGTGCCGGCTGCACGAGCAGTCCTGGTTTAATGTCGGC

\*\*\*\*\*

Consensus:

TGCTAACTAGCTACGGCCAGCTTAGGTGCCGGCTGCACGAGCAGTCCTGGTTTAATGTCGGC

>Cele-UNSB01\_Fam\_224\_60\_1 Nr. of seq. 1 Alignment length(with gaps) = 60  
Alignment score = 0.000000

Cele-UNSB01\_5:7301688-7302048 Satlength=361 Nr of Repeats=6  
RepeatLength=60 seed=CTAGCTAGAT Num.seqs=6 Similarity=0.943704  
0 CTAGCTAGATTAAACGCTCTCAAGAGACAGCATGTTGTTGTTGCCCAAGAAGAAGGCT

\*\*\*\*\*

Consensus:

CTAGCTAGATTAAACGCTCTCAAGAGACAGCATGTTGTTGTTGCCCAAGAAGAAGGCT

>Cele-UNSB01\_Fam\_225\_60\_1 Nr. of seq. 1 Alignment length(with gaps) = 60  
Alignment score = 0.000000

Cele-UNSB01\_5:8761530-8782970 Satlength=21441 Nr of Repeats=357  
RepeatLength=60 seed=ACACAATTGG Num.seqs=349 Similarity=0.921038  
0 ACACAATTGGAGTGGTGCTTGAGGAGCTGGATTGAGCTCGTTATGTCGGTTGAAG

\*\*\*\*\*

Consensus:

ACACAATTGGAGTGGTGCTTGAGGAGCTGGATTGAGCTCGTTATGTCGGTTGAAG

>Cele-UNSB01\_Fam\_226\_60\_1 Nr. of seq. 1 Alignment length(with gaps) = 60  
Alignment score = 0.000000

Cele-UNSB01\_5:14209723-14211643 Satlength=1921 Nr of Repeats=32  
RepeatLength=60 seed=CTGCTGATTC Num.seqs=32 Similarity=0.925493  
0 CTGCTGATTCGAGAAGAAGGCCCCAGCCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

\*\*\*\*\*

Consensus:

CTGCTGATTCGAGAAGAAGGCCCCAGCCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

>Cele-UNSB01\_Fam\_227\_59\_1 Nr. of seq. 1 Alignment length(with gaps) = 59  
Alignment score = 0.000000

Cele-UNSB01\_2:1416594-1416934 Satlength=341 Nr of Repeats=5  
RepeatLength=59 seed=CTACAAACTA Num.seqs=3 Similarity=0.969868  
0 CTACAAACTACAAAAGCCTATTTAGCAGACCCACGCCAACTTCTGATGGGTCTGCTAGA

\*\*\*\*\*

Consensus:

CTACAAACTACAAAAGCCTATTTAGCAGACCCACGCCAACTTCTGATGGGTCTGCTAGA

>Cele-UNSB01\_Fam\_228\_57\_1 Nr. of seq. 1 Alignment length(with gaps) = 57  
Alignment score = 0.000000  
Cele-UNSB01\_5:14206302-14207970 Satlength=1669 Nr of Repeats=22  
RepeatLength=57 seed=GAAGTCAACA Num.seqs=15 Similarity=0.952771  
0 GAAGTCAACAAGCTGATCAAGAGCAACACCGTGGATCCCGAGCTGCCGGACAGAAGG

\*\*\*\*\*  
Consensus:

GAAGTCAACAAGCTGATCAAGAGCAACACCGTGGATCCCGAGCTGCCGGACAGAAGG

>Cele-UNSB01\_Fam\_229\_55\_1 Nr. of seq. 1 Alignment length(with gaps) = 55  
Alignment score = 0.000000  
Cele-UNSB01\_2:1212949-1213169 Satlength=221 Nr of Repeats=4  
RepeatLength=55 seed=GGGATTATTG Num.seqs=4 Similarity=0.903030  
0 GGGATTATTGGAGTTTCTTTTCTAGAATTTTTTGAAAATTTTGGACAGTTTTTT

\*\*\*\*\*  
Consensus:

GGGATTATTGGAGTTTCTTTTCTAGAATTTTTTGAAAATTTTGGACAGTTTTTT

>Cele-UNSB01\_Fam\_230\_55\_1 Nr. of seq. 1 Alignment length(with gaps) = 55  
Alignment score = 0.000000  
Cele-UNSB01\_4:6076861-6077186 Satlength=326 Nr of Repeats=6  
RepeatLength=55 seed=AAGAGTCCCC Num.seqs=4 Similarity=1.000000  
0 AAGAGTCCCCACACACTGAAAGGTTTTTAAGGAATTTTTTGAGGATTCCTAGGGTT

\*\*\*\*\*  
Consensus:

AAGAGTCCCCACACACTGAAAGGTTTTTAAGGAATTTTTTGAGGATTCCTAGGGTT

>Cele-UNSB01\_Fam\_231\_52\_1 Nr. of seq. 1 Alignment length(with gaps) = 52  
Alignment score = 0.000000  
Cele-UNSB01\_6:17211035-17211529 Satlength=495 Nr of Repeats=4  
RepeatLength=52 seed=GCATGTCTTC Num.seqs=3 Similarity=0.626263  
0 GCATGTCTTCCAAGCGTTTTGAGCCACGCNTGGGATTCCTATACACGGCTG

\*\*\*\*\*  
Consensus:

GCATGTCTTCCAAGCGTTTTGAGCCACGCNTGGGATTCCTATACACGGCTG

>Cele-UNSB01\_Fam\_232\_50\_1 Nr. of seq. 1 Alignment length(with gaps) = 50  
Alignment score = 0.000000  
Cele-UNSB01\_1:12702448-12702698 Satlength=251 Nr of Repeats=5  
RepeatLength=50 seed=ACACATGCTA Num.seqs=5 Similarity=0.952000  
0 ACACATGCTATAACATTGTCTCCTTCCCCTAGTGCACGAGAGCGGCCGTT

\*\*\*\*\*  
Consensus:

ACACATGCTATAACATTGTCTCCTTCCCCTAGTGCACGAGAGCGGCCGTT

>Cele-UNSB01\_Fam\_233\_50\_1 Nr. of seq. 1 Alignment length(with gaps) = 50  
Alignment score = 0.000000  
Cele-UNSB01\_4:16678025-16678676 Satlength=652 Nr of Repeats=13  
RepeatLength=50 seed=GGGCGTGTTT Num.seqs=10 Similarity=0.897482  
0 GGGCGTGTTTTACATGCCCCGCCACAAAATTGATGTTTCCACCAAAAT

\*\*\*\*\*  
Consensus:

GGGCGTGTTTTACATGCCCCGCCACAAAATTGATGTTTCCACCAAAAT

>Cele-UNSB01\_Fam\_234\_49\_1 Nr. of seq. 1 Alignment length(with gaps) = 49  
Alignment score = 0.000000  
Cele-UNSB01\_1:1647038-1647577 Satlength=540 Nr of Repeats=9  
RepeatLength=49 seed=CAATAATTTT Num.seqs=7 Similarity=0.909297  
0 CAATAATTTTAAATTAAATTATCGATTTTTCTAAATTTTCCGAAAAAT

\*\*\*\*\*  
Consensus:

CAATAATTTTAAATTAAATTATCGATTTTTCTAAATTTTCCGAAAAAT

>Cele-UNSB01\_Fam\_235\_48\_1 Nr. of seq. 1 Alignment length(with gaps) = 48  
Alignment score = 0.000000  
Cele-UNSB01\_2:13440285-13440859 Satlength=575 Nr of Repeats=12  
RepeatLength=48 seed=TGCCTACGTG Num.seqs=10 Similarity=0.812346  
0 TGCCTACGTGCCTACAAAACAGGCGTAGGCAGCTTTAAAGGTGATGCA

\*\*\*\*\*  
Consensus:

TGCCTACGTGCCTACAAAACAGGCGTAGGCAGCTTTAAAGGTGATGCA

>Cele-UNSB01\_Fam\_236\_48\_1 Nr. of seq. 1 Alignment length(with gaps) = 48  
Alignment score = 0.000000  
Cele-UNSB01\_6:14589132-14589372 Satlength=241 Nr of Repeats=5  
RepeatLength=48 seed=GGAGGTGGAG Num.seqs=5 Similarity=0.841667  
0 GGAGGTGGAGAAAGTGTAGTTCCCGGTGGTCGNGGCTCTTCNGAGGGT

\*\*\*\*\*  
Consensus:

GGAGGTGGAGAAAGTGTAGTTCCCGGTGGTCGNGGCTCTTCNGAGGGT

>Cele-UNSB01\_Fam\_237\_46\_1 Nr. of seq. 1 Alignment length(with gaps) = 46  
Alignment score = 0.000000  
Cele-UNSB01\_6:2065387-2065569 Satlength=183 Nr of Repeats=4  
RepeatLength=46 seed=TGGTAAATTG Num.seqs=3 Similarity=0.835749  
0 TGGTAAATTGCCTCCCGANCACTTTTCTTATTTCCCAACTA

\*\*\*\*\*  
Consensus:

TGGTAAATTGCCTCCCGGANCACTTTTCTTATTTCCCAACTA

>Cele-UNSB01\_Fam\_238\_45\_1 Nr. of seq. 1 Alignment length(with gaps) = 45  
Alignment score = 0.000000  
Cele-UNSB01\_4:7767635-7768760 Satlength=1126 Nr of Repeats=25  
RepeatLength=45 seed=AGCACCACCA Num.seqs=25 Similarity=0.965432  
0 AGCACCACCATCAGGCGGACCACCAGGACCATTTGATCCATCAGG

\*\*\*\*\*  
Consensus:

AGCACCACCATCAGGCGGACCACCAGGACCATTTGATCCATCAGG

>Cele-UNSB01\_Fam\_239\_45\_1 Nr. of seq. 1 Alignment length(with gaps) = 45  
Alignment score = 0.000000  
Cele-UNSB01\_5:11342057-11345882 Satlength=3826 Nr of Repeats=85  
RepeatLength=45 seed=CCAAGCACAT Num.seqs=85 Similarity=0.985127  
0 CCAAGCACATCTACAGAGACACCTACAACCTGAATCAACTGCAGCA

\*\*\*\*\*  
Consensus:

CCAAGCACATCTACAGAGACACCTACAACCTGAATCAACTGCAGCA

>Cele-UNSB01\_Fam\_240\_45\_1 Nr. of seq. 1 Alignment length(with gaps) = 45  
Alignment score = 0.000000  
Cele-UNSB01\_6:17820421-17836619 Satlength=16199 Nr of Repeats=357  
RepeatLength=45 seed=CTCCATCCAC Num.seqs=275 Similarity=0.944464  
0 CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

\*\*\*\*\*  
Consensus:

CTCCATCCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGA

>Cele-UNSB01\_Fam\_241\_43\_1 Nr. of seq. 1 Alignment length(with gaps) = 43  
Alignment score = 0.000000  
Cele-UNSB01\_2:2187430-2189107 Satlength=1678 Nr of Repeats=38  
RepeatLength=43 seed=CGAGTTTGGC Num.seqs=37 Similarity=0.823312  
0 CGAGTTTGGCCTACANCAAATTTGGCAAATTCGGCAAATTTGC

\*\*\*\*\*  
Consensus:

CGAGTTTGGCCTACANCAAATTTGGCAAATTCGGCAAATTTGC

>Cele-UNSB01\_Fam\_242\_43\_1 Nr. of seq. 1 Alignment length(with gaps) = 43  
Alignment score = 0.000000  
Cele-UNSB01\_2:14320079-14320251 Satlength=173 Nr of Repeats=4  
RepeatLength=43 seed=GAAAACTAGG Num.seqs=4 Similarity=0.715762  
0 GAAAACTAGGCCACAGAGTTCAAATTGATGGCCTAGAAATCTA

\*\*\*\*\*

Consensus:

GAAAACTAGGCCACAGAGTTCAAATTGATGGCCTAGAAATCTA

>Cele-UNSB01\_Fam\_243\_43\_1 Nr. of seq. 1 Alignment length(with gaps) = 43  
Alignment score = 0.000000  
Cele-UNSB01\_3:1466668-1467327 Satlength=660 Nr of Repeats=5  
RepeatLength=43 seed=GGCTCTCGGC Num.seqs=3 Similarity=0.627907  
0 GGCTCTCGGCTCGCGCCGAGAGCCGAGNTCTACTNAAAGTTTC

\*\*\*\*\*

Consensus:

GGCTCTCGGCTCGCGCCGAGAGCCGAGNTCTACTNAAAGTTTC

>Cele-UNSB01\_Fam\_244\_43\_1 Nr. of seq. 1 Alignment length(with gaps) = 43  
Alignment score = 0.000000  
Cele-UNSB01\_3:12608882-12609486 Satlength=605 Nr of Repeats=14  
RepeatLength=43 seed=AGCAGCCGAC Num.seqs=11 Similarity=0.800423  
0 AGCAGCCGACAGTTGCCGTTGCCGAAAAATTGCAGTAATTTTC

\*\*\*\*\*

Consensus:

AGCAGCCGACAGTTGCCGTTGCCGAAAAATTGCAGTAATTTTC

>Cele-UNSB01\_Fam\_245\_42\_1 Nr. of seq. 1 Alignment length(with gaps) = 42  
Alignment score = 0.000000  
Cele-UNSB01\_1:733992-734160 Satlength=169 Nr of Repeats=4 RepeatLength=42  
seed=TTTGATCTAC Num.seqs=4 Similarity=0.968254  
0 TTTGATCTACAAAAAATGCGGGAATTTTCCCAGCATTGCTCA

\*\*\*\*\*

Consensus:

TTTGATCTACAAAAAATGCGGGAATTTTCCCAGCATTGCTCA

>Cele-UNSB01\_Fam\_246\_42\_1 Nr. of seq. 1 Alignment length(with gaps) = 42  
Alignment score = 0.000000  
Cele-UNSB01\_5:6199698-6200391 Satlength=694 Nr of Repeats=15  
RepeatLength=42 seed=AGGTGCTGCT Num.seqs=9 Similarity=0.859788  
0 AGGTGCTGCTTCCTTTGGAACATCTGCTTGGGTTGGCTCCGA

\*\*\*\*\*

Consensus:

AGGTGCTGCTTCCTTTGGAACATCTGCTTGGGTTGGCTCCGA

>Cele-UNSB01\_Fam\_247\_41\_1 Nr. of seq. 1 Alignment length(with gaps) = 41  
Alignment score = 0.000000  
Cele-UNSB01\_4:3758727-3758973 Satlength=247 Nr of Repeats=6  
RepeatLength=41 seed=AAATTTTAA Num.seqs=6 Similarity=0.945799  
0 AAATTTTAAACGAGAAGTGGCGAAAAATCATTCAAAAATTC



\*\*\*\*\*

Consensus:

AAATTTTAAACGAGAAGTGGGCGAAAATCATTCAAAAATTC

>Cele-UNSB01\_Fam\_248\_41\_1 Nr. of seq. 1 Alignment length(with gaps) = 41  
Alignment score = 0.000000  
Cele-UNSB01\_5:20548445-20548748 Satlength=304 Nr of Repeats=5  
RepeatLength=41 seed=GCATTTTTCG Num.seqs=3 Similarity=0.772358  
0 GCATTTTTCGCCGATTTTNNATTAATTTTCAGTGAAAATTC

\*\*\*\*\*

Consensus:

GCATTTTTCGCCGATTTTNNATTAATTTTCAGTGAAAATTC

>Cele-UNSB01\_Fam\_249\_40\_1 Nr. of seq. 1 Alignment length(with gaps) = 40  
Alignment score = 0.000000  
Cele-UNSB01\_3:415402-416126 Satlength=725 Nr of Repeats=7 RepeatLength=40  
seed=TCCACGTGGA Num.seqs=5 Similarity=0.650794  
0 TCCACGTGGAATTTTCAGAATTTTCNCAGAAAATTTGAAA

\*\*\*\*\*

Consensus:

TCCACGTGGAATTTTCAGAATTTTCNCAGAAAATTTGAAA

>Cele-UNSB01\_Fam\_250\_40\_1 Nr. of seq. 1 Alignment length(with gaps) = 40  
Alignment score = 0.000000  
Cele-UNSB01\_5:19147729-19148084 Satlength=356 Nr of Repeats=7  
RepeatLength=40 seed=GAATTTTTCG Num.seqs=6 Similarity=0.926667  
0 GAATTTTTCGCAATTCTACTGAATTTTCCAAATTTTCAGC

\*\*\*\*\*

Consensus:

GAATTTTTCGCAATTCTACTGAATTTTCCAAATTTTCAGC

>Cele-UNSB01\_Fam\_251\_40\_1 Nr. of seq. 1 Alignment length(with gaps) = 40  
Alignment score = 0.000000  
Cele-UNSB01\_5:19162213-19162392 Satlength=180 Nr of Repeats=5  
RepeatLength=40 seed=TTTTGCCGAA Num.seqs=3 Similarity=0.629630  
0 TTTTGCCAAAAATNTGTCAATTTTGTGGAATTTCTNTCAT

\*\*\*\*\*

Consensus:

TTTTTGCCAAAAATNTGTCAATTTTGTGGAATTTCTNTCAT

>Cele-UNSB01\_Fam\_252\_39\_1 Nr. of seq. 1 Alignment length(with gaps) = 39  
Alignment score = 0.000000

Cele-UNSB01\_2:3539245-3539476 Satlength=232 Nr of Repeats=5  
RepeatLength=39 seed=AATTTCCCGC Num.seqs=3 Similarity=0.769444  
0 AATTTCCCGCCAAAATTGAATTTTTTTTAAAGAAAATTTA

\*\*\*\*\*

Consensus:

AATTTCCCGCCAAAATTGAATTTTTTTTAAAGAAAATTTA

>Cele-UNSB01\_Fam\_253\_39\_1 Nr. of seq. 1 Alignment length(with gaps) = 39  
Alignment score = 0.000000

Cele-UNSB01\_4:5061085-5061475 Satlength=391 Nr of Repeats=8  
RepeatLength=39 seed=CCAACTGGAG Num.seqs=7 Similarity=0.784921  
0 CCAACTGGAGCCAGCACNATGACCGCTGTTGGAGGAGCA

\*\*\*\*\*

Consensus:

CCAACTGGAGCCAGCACNATGACCGCTGTTGGAGGAGCA

>Cele-UNSB01\_Fam\_254\_39\_1 Nr. of seq. 1 Alignment length(with gaps) = 39  
Alignment score = 0.000000

Cele-UNSB01\_5:3666468-3666780 Satlength=313 Nr of Repeats=8  
RepeatLength=39 seed=GATTTACGGG Num.seqs=6 Similarity=0.849573  
0 GATTTACGGGCTTTAATCAGTTTCGAAAAAGCTTGTGTC

\*\*\*\*\*

Consensus:

GATTTACGGGCTTTAATCAGTTTCGAAAAAGCTTGTGTC

>Cele-UNSB01\_Fam\_255\_39\_1 Nr. of seq. 1 Alignment length(with gaps) = 39  
Alignment score = 0.000000

Cele-UNSB01\_5:12723614-12724001 Satlength=388 Nr of Repeats=10  
RepeatLength=39 seed=TGGTACGGTA Num.seqs=9 Similarity=0.880342  
0 TGGTACGGTAGTTGTAGTGGTAGTGGAGGTTGTTGTTGG

\*\*\*\*\*

Consensus:

TGGTACGGTAGTTGTAGTGGTAGTGGAGGTTGTTGTTGG

>Cele-UNSB01\_Fam\_256\_39\_1 Nr. of seq. 1 Alignment length(with gaps) = 39  
Alignment score = 0.000000

Cele-UNSB01\_5:18895119-18895676 Satlength=558 Nr of Repeats=15  
RepeatLength=39 seed=GTAATTTATA Num.seqs=13 Similarity=0.917598  
0 GTAATTTATAATTTTTTAAAGATGAGTAATATATTGCC

\*\*\*\*\*

Consensus:

GTAATTTATAATTTTTTAAAGATGAGTAATATATTGCC

>Cele-UNSB01\_Fam\_257\_39\_1 Nr. of seq. 1 Alignment length(with gaps) = 39  
Alignment score = 0.000000  
Cele-UNSB01\_6:17555071-17555695 Satlength=625 Nr of Repeats=16  
RepeatLength=39 seed=ATTGATACTT Num.seqs=16 Similarity=0.929345  
0 ATTGATACTTTGTCGGGTTTAGACCATCGGCCGAGCTTC

\*\*\*\*\*  
Consensus:

ATTGATACTTTGTCGGGTTTAGACCATCGGCCGAGCTTC

>Cele-UNSB01\_Fam\_258\_38\_1 Nr. of seq. 1 Alignment length(with gaps) = 38  
Alignment score = 0.000000  
Cele-UNSB01\_1:2017348-2017684 Satlength=337 Nr of Repeats=5  
RepeatLength=38 seed=AAAATCGATA Num.seqs=3 Similarity=1.000000  
0 AAAATCGATAATTTTCAGTATGCAGTGAAATTCTTGGA

\*\*\*\*\*  
Consensus:

AAAATCGATAATTTTCAGTATGCAGTGAAATTCTTGGA

>Cele-UNSB01\_Fam\_259\_37\_1 Nr. of seq. 1 Alignment length(with gaps) = 37  
Alignment score = 0.000000  
Cele-UNSB01\_1:10089590-10089728 Satlength=139 Nr of Repeats=5  
RepeatLength=37 seed=ATAATTTTTTC Num.seqs=3 Similarity=1.000000  
0 ATAATTTTTCTTGAGTAATGAGAGACTTTTTTCATAAT

\*\*\*\*\*  
Consensus:

ATAATTTTTCTTGAGTAATGAGAGACTTTTTTCATAAT

>Cele-UNSB01\_Fam\_260\_36\_1 Nr. of seq. 1 Alignment length(with gaps) = 36  
Alignment score = 0.000000  
Cele-UNSB01\_3:12817254-12818910 Satlength=1657 Nr of Repeats=46  
RepeatLength=36 seed=GATATTTTCA Num.seqs=46 Similarity=0.952800  
0 GATATTTTCATGTTTCGGCAAAGTACCGATTGCA

\*\*\*\*\*  
Consensus:

GATATTTTCATGTTTCGGCAAAGTACCGATTGCA

>Cele-UNSB01\_Fam\_261\_36\_1 Nr. of seq. 1 Alignment length(with gaps) = 36  
Alignment score = 0.000000  
Cele-UNSB01\_6:18063681-18064057 Satlength=377 Nr of Repeats=7  
RepeatLength=36 seed=CCACCAACTC Num.seqs=6 Similarity=0.728395  
0 CCACCAACTCCAAAATCAGCTGCTCCATCAGAAGTC

\*\*\*\*\*  
Consensus:

CCACCAACTCCAAAATCAGCTGCTCCATCAGAAGTC

>Cele-UNSB01\_Fam\_262\_35\_1 Nr. of seq. 1 Alignment length(with gaps) = 35  
Alignment score = 0.000000  
Cele-UNSB01\_1:11408393-11409029 Satlength=637 Nr of Repeats=9  
RepeatLength=35 seed=AATTGCCGAA Num.seqs=7 Similarity=0.793210  
0 AATTGCCGAATTTCTCGTTTTTGGCAATTTACCAA

\*\*\*\*\*  
Consensus:

AATTGCCGAATTTCTCGTTTTTGGCAATTTACCAA

>Cele-UNSB01\_Fam\_263\_35\_1 Nr. of seq. 1 Alignment length(with gaps) = 35  
Alignment score = 0.000000  
Cele-UNSB01\_2:12938825-12939101 Satlength=277 Nr of Repeats=8  
RepeatLength=35 seed=TGTGTAATAA Num.seqs=5 Similarity=0.794286  
0 TGTGTAATAAGAAAATTTCAAATTTTTTTTACGAA

\*\*\*\*\*  
Consensus:

TGTGTAATAAGAAAATTTCAAATTTTTTTTACGAA

>Cele-UNSB01\_Fam\_264\_35\_1 Nr. of seq. 1 Alignment length(with gaps) = 35  
Alignment score = 0.000000  
Cele-UNSB01\_5:1026357-1026873 Satlength=517 Nr of Repeats=9  
RepeatLength=35 seed=GCATTTGCCG Num.seqs=6 Similarity=0.817143  
0 GCATTTGCCGATTTTTTAAATTTCTGGCAATTCCA

\*\*\*\*\*  
Consensus:

GCATTTGCCGATTTTTTAAATTTCTGGCAATTCCA

>Cele-UNSB01\_Fam\_265\_34\_1 Nr. of seq. 1 Alignment length(with gaps) = 34  
Alignment score = 0.000000  
Cele-UNSB01\_2:14289556-14289862 Satlength=307 Nr of Repeats=8  
RepeatLength=34 seed=CCGTGCCTAC Num.seqs=7 Similarity=0.828198  
0 CCGTGCCTACTAACCTACCGACCTTGCCTGCCTT

\*\*\*\*\*  
Consensus:

CCGTGCCTACTAACCTACCGACCTTGCCTGCCTT

>Cele-UNSB01\_Fam\_266\_34\_1 Nr. of seq. 1 Alignment length(with gaps) = 34  
Alignment score = 0.000000  
Cele-UNSB01\_3:12102276-12102493 Satlength=218 Nr of Repeats=6  
RepeatLength=34 seed=TTGCCGAATT Num.seqs=5 Similarity=0.811765  
0 TTGCCGAATTTGCCGTTTGCCGAGCTCGTCAAAT

\*\*\*\*\*  
Consensus:

TTGCCGAATTTGCCGTTTGCCGAGCTCGTCAAAT

>Cele-UNSB01\_Fam\_267\_34\_1 Nr. of seq. 1 Alignment length(with gaps) = 34  
Alignment score = 0.000000  
Cele-UNSB01\_3:12168292-12168722 Satlength=431 Nr of Repeats=13  
RepeatLength=34 seed=AAGTATTTTT Num.seqs=12 Similarity=0.954843  
0 AAGTATTTTTGCCGTTTTTTTTGCCGAAATTTC

\*\*\*\*\*  
Consensus:

AAGTATTTTTGCCGTTTTTTTTGCCGAAATTTC

>Cele-UNSB01\_Fam\_268\_33\_1 Nr. of seq. 1 Alignment length(with gaps) = 33  
Alignment score = 0.000000  
Cele-UNSB01\_1:2281114-2281247 Satlength=134 Nr of Repeats=4  
RepeatLength=33 seed=TAAGAAAAGT Num.seqs=3 Similarity=0.892256  
0 TAAGAAAAGTTAGGCCACCAAACCTTGGTGAAC

\*\*\*\*\*  
Consensus:

TAAGAAAAGTTAGGCCACCAAACCTTGGTGAAC

>Cele-UNSB01\_Fam\_269\_32\_1 Nr. of seq. 1 Alignment length(with gaps) = 32  
Alignment score = 0.000000  
Cele-UNSB01\_1:11521003-11522550 Satlength=1548 Nr of Repeats=48  
RepeatLength=32 seed=GCAATTTTTTA Num.seqs=37 Similarity=0.890140  
0 GCAATTTTTTAGGCTAAAAATCACTAAAAAACT

\*\*\*\*\*  
Consensus:

GCAATTTTTTAGGCTAAAAATCACTAAAAAACT

>Cele-UNSB01\_Fam\_270\_32\_1 Nr. of seq. 1 Alignment length(with gaps) = 32  
Alignment score = 0.000000  
Cele-UNSB01\_3:12376126-12377123 Satlength=998 Nr of Repeats=30  
RepeatLength=32 seed=AAATTTGTGA Num.seqs=18 Similarity=0.874992  
0 AAATTTGTGAAAATTTAGGCCCATTTTGCTCA

\*\*\*\*\*  
Consensus:

AAATTTGTGAAAATTTAGGCCCATTTTGCTCA

>Cele-UNSB01\_Fam\_271\_32\_1 Nr. of seq. 1 Alignment length(with gaps) = 32  
Alignment score = 0.000000  
Cele-UNSB01\_5:21020210-21020336 Satlength=127 Nr of Repeats=4  
RepeatLength=32 seed=GTGCGTCCGG Num.seqs=3 Similarity=0.888889  
0 GTGCGTCCGGCGTCCGGAAAAAGCGGACGCGT

\*\*\*\*\*

Consensus:

GTGCGTCCGGCGTCCGGAAAAAGCGGACGCGT

>Cele-UNSB01\_Fam\_272\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_2:3099938-3100072 Satlength=135 Nr of Repeats=4  
RepeatLength=31 seed=ATCGATTTTT Num.seqs=3 Similarity=0.700337  
0 ATCGATTTTTTCGTTAAAAAATCAATAAAAT

\*\*\*\*\*

Consensus:

ATCGATTTTTTCGTTAAAAAATCAATAAAAT

>Cele-UNSB01\_Fam\_273\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_2:3736361-3736609 Satlength=249 Nr of Repeats=8  
RepeatLength=31 seed=GCTGATTGGT Num.seqs=8 Similarity=0.553571  
0 GCTGATTGGTCGGCGNGGTTGCCCCATCNTT

\*\*\*\*\*

Consensus:

GCTGATTGGTCGGCGNGGTTGCCCCATCNTT

>Cele-UNSB01\_Fam\_274\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_2:12597085-12597273 Satlength=189 Nr of Repeats=6  
RepeatLength=31 seed=GACATCTCGC Num.seqs=4 Similarity=0.584229  
0 GACATCTCGCAGGACATTATAAGAAGCGACC

\*\*\*\*\*

Consensus:

GACATCTCGCAGGACATTATAAGAAGCGACC

>Cele-UNSB01\_Fam\_275\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_2:13437444-13437847 Satlength=404 Nr of Repeats=10  
RepeatLength=31 seed=CACGCCTATT Num.seqs=7 Similarity=0.811572  
0 CACGCCTATTTTATGGGCGGAGTCTACAAGC

\*\*\*\*\*

Consensus:

CACGCCTATTTTATGGGCGGAGTCTACAAGC

>Cele-UNSB01\_Fam\_276\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_3:2092267-2093197 Satlength=931 Nr of Repeats=27  
RepeatLength=31 seed=TGCGTCGGAA Num.seqs=23 Similarity=0.733775  
0 TGCGTCGGAAATTNATTCGATCATCGCCGG

\*\*\*\*\*

Consensus:

TGCGTCGGAAATTNATTCGGATCATCGCCGG

>Cele-UNSB01\_Fam\_277\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_3:2094174-2094918 Satlength=745 Nr of Repeats=17  
RepeatLength=31 seed=TCCGATGCAT Num.seqs=13 Similarity=0.625486  
0 TCCGATGCATTGCCGATAATCGGAACCTGGT

\*\*\*\*\*

Consensus:

TCCGATGCATTGCCGATAATCGGAACCTGGT

>Cele-UNSB01\_Fam\_278\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_3:11300832-11300986 Satlength=155 Nr of Repeats=5  
RepeatLength=31 seed=GCAGCCGACG Num.seqs=4 Similarity=0.524411  
0 GCAGCCGACGCTATACGGGTCTGATGGAGTA

\*\*\*\*\*

Consensus:

GCAGCCGACGCTATACGGGTCTGATGGAGTA

>Cele-UNSB01\_Fam\_279\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_3:11489719-11490125 Satlength=407 Nr of Repeats=12  
RepeatLength=31 seed=TCTGAGCTAC Num.seqs=11 Similarity=0.755258  
0 TCTGAGCTACAGTACTCCTGTCAAGAACAAAT

\*\*\*\*\*

Consensus:

TCTGAGCTACAGTACTCCTGTCAAGAACAAAT

>Cele-UNSB01\_Fam\_280\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_3:13121321-13121505 Satlength=185 Nr of Repeats=5  
RepeatLength=31 seed=GATTTTTTCA Num.seqs=3 Similarity=0.659722  
0 GATTTTTTCAGNGAAAANCNAAAAATTTTCG

\*\*\*\*\*

Consensus:

GATTTTTTCAGNGAAAANCNAAAAATTTTCG

>Cele-UNSB01\_Fam\_281\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000

Cele-UNSB01\_3:13483516-13483661 Satlength=146 Nr of Repeats=5  
RepeatLength=31 seed=CCAAAAATGA Num.seqs=4 Similarity=0.863799  
0 CCAAAAATGACTGAAAATAGTCAAAAATTAG

\*\*\*\*\*

Consensus:

CCAAAAATGACTGAAAATAGTCAAAAATTAG

>Cele-UNSB01\_Fam\_282\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000

Cele-UNSB01\_4:782171-782295 Satlength=125 Nr of Repeats=4 RepeatLength=31  
seed=CAAAAATCGG Num.seqs=4 Similarity=0.949821  
0 CAAAAATCGGAAATTTTCACAAAAAAATGC

\*\*\*\*\*

Consensus:

CAAAAATCGGAAATTTTCACAAAAAAATGC

>Cele-UNSB01\_Fam\_283\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000

Cele-UNSB01\_5:18669912-18670449 Satlength=538 Nr of Repeats=16  
RepeatLength=31 seed=TTGGCCCGAGA Num.seqs=11 Similarity=0.885826  
0 TTGGCCCGAGCTCTCTTGACCCAAGCCCC

\*\*\*\*\*

Consensus:

TTGGCCCGAGCTCTCTTGACCCAAGCCCC

>Cele-UNSB01\_Fam\_284\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000

Cele-UNSB01\_5:18793643-18794338 Satlength=696 Nr of Repeats=5  
RepeatLength=31 seed=AAAATTTTGA Num.seqs=3 Similarity=0.971326  
0 AAAATTTTGACCCAGAAATCGAAAAATTCGC

\*\*\*\*\*

Consensus:

AAAATTTTGACCCAGAAATCGAAAAATTCGC

>Cele-UNSB01\_Fam\_285\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000

Cele-UNSB01\_5:19138115-19138319 Satlength=205 Nr of Repeats=6  
RepeatLength=31 seed=TCGTTTTTTC Num.seqs=5 Similarity=0.819355  
0 TCGTTTTTTCATGAAAAAATCAATTTTCGG

\*\*\*\*\*

Consensus:

TCGTTTTTTCATGAAAAAATCAATTTTCGG



>Cele-UNSB01\_Fam\_286\_31\_1 Nr. of seq. 1 Alignment length(with gaps) = 31  
Alignment score = 0.000000  
Cele-UNSB01\_5:20720350-20720568 Satlength=219 Nr of Repeats=4  
RepeatLength=31 seed=GAAAAAGTGC Num.seqs=3 Similarity=0.784722  
0 GAAAAAGTGCTGAAAATCACATTTTGAAC

\*\*\*\*\*  
Consensus:

GAAAAAGTGCTGAAAATCACATTTTGAAC

>Cele-UNSB01\_Fam\_287\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_1:1730783-1731662 Satlength=880 Nr of Repeats=24  
RepeatLength=30 seed=AATTTGAATT Num.seqs=15 Similarity=0.732487  
0 AATTTGAATTTTCCCGAATTTTNAACGAA

\*\*\*\*\*  
Consensus:

AATTTGAATTTTCCCGAATTTTNAACGAA

>Cele-UNSB01\_Fam\_288\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_1:6651710-6652545 Satlength=836 Nr of Repeats=13  
RepeatLength=30 seed=TGGTGGAAC Num.seqs=11 Similarity=0.953131  
0 TGGTGGAACGGATTCGGCAGTGGAATGC

\*\*\*\*\*  
Consensus:

TGGTGGAACGGATTCGGCAGTGGAATGC

>Cele-UNSB01\_Fam\_289\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_1:11615647-11616001 Satlength=355 Nr of Repeats=10  
RepeatLength=30 seed=CCTTGGGCTC Num.seqs=7 Similarity=0.875132  
0 CCTTGGGCTCCCTGAGCTCCAAATTGTGCT

\*\*\*\*\*  
Consensus:

CCTTGGGCTCCCTGAGCTCCAAATTGTGCT

>Cele-UNSB01\_Fam\_290\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_1:12330775-12330985 Satlength=211 Nr of Repeats=7  
RepeatLength=30 seed=GTCATTATCA Num.seqs=7 Similarity=0.974603  
0 GTCATTATCAGCTTCTGGTGTCTTAGAAGA

\*\*\*\*\*  
Consensus:

GTCATTATCAGCTTCTGGTGTCTTAGAAGA

>Cele-UNSB01\_Fam\_291\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_2:12311843-12313532 Satlength=1690 Nr of Repeats=56  
RepeatLength=30 seed=CAAACCTACAG Num.seqs=47 Similarity=0.880029  
0 CAAACCTACAGTAGTACTGTAGTACCATAAC

\*\*\*\*\*  
Consensus:

CAAACCTACAGTAGTACTGTAGTACCATAAC

>Cele-UNSB01\_Fam\_292\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_2:13134300-13134450 Satlength=151 Nr of Repeats=4  
RepeatLength=30 seed=TTCCAGGCAGG Num.seqs=3 Similarity=0.644444  
0 TTCCAGGCAGGCATAGGTTACTTTGAAAATT

\*\*\*\*\*  
Consensus:

TTCCAGGCAGGCATAGGTTACTTTGAAAATT

>Cele-UNSB01\_Fam\_293\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_3:3873879-3874448 Satlength=570 Nr of Repeats=9  
RepeatLength=30 seed=CCTTGTTAGGC Num.seqs=6 Similarity=0.842963  
0 CCTTGTTAGGCAAGGAGGTAGGCGTAGGTCA

\*\*\*\*\*  
Consensus:

CCTTGTTAGGCAAGGAGGTAGGCGTAGGTCA

>Cele-UNSB01\_Fam\_294\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_3:13583922-13584205 Satlength=284 Nr of Repeats=8  
RepeatLength=30 seed=TTTCAGGCCA Num.seqs=5 Similarity=0.822222  
0 TTTCAGGCCAATTTTCNGTCATTTTTGGACA

\*\*\*\*\*  
Consensus:

TTTCAGGCCAATTTTCNGTCATTTTTGGACA

>Cele-UNSB01\_Fam\_295\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_4:16899632-16900079 Satlength=448 Nr of Repeats=15  
RepeatLength=30 seed=AAAATCAAAA Num.seqs=12 Similarity=0.938721  
0 AAAATCAAAAATTAGATGAATTTTCGATTA

\*\*\*\*\*  
Consensus:

AAAATCAAAAATTAGATGAATTTTCGATTA

>Cele-UNSB01\_Fam\_296\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_5:20558603-20558932 Satlength=330 Nr of Repeats=11  
RepeatLength=30 seed=CTCAAATTTG Num.seqs=10 Similarity=0.911111  
0 CTCAAATTTGCACTAAAAATTCCAATTTTT

\*\*\*\*\*  
Consensus:

CTCAAATTTGCACTAAAAATTCCAATTTTT

>Cele-UNSB01\_Fam\_297\_30\_1 Nr. of seq. 1 Alignment length(with gaps) = 30  
Alignment score = 0.000000  
Cele-UNSB01\_6:1594210-1594900 Satlength=691 Nr of Repeats=19  
RepeatLength=30 seed=ACTACCCAAC Num.seqs=18 Similarity=0.920407  
0 ACTACCCAACCGGCTCCGGCAACCAGTCCA

\*\*\*\*\*  
Consensus:

ACTACCCAACCGGCTCCGGCAACCAGTCCA

>Cele-UNSB01\_Fam\_298\_29\_1 Nr. of seq. 1 Alignment length(with gaps) = 29  
Alignment score = 0.000000  
Cele-UNSB01\_1:5273525-5290948 Satlength=17424 Nr of Repeats=599  
RepeatLength=29 seed=TTGTAAGGAT Num.seqs=565 Similarity=0.955515  
0 TTGTAAGGATTTCCCACTATGTCAATACA

\*\*\*\*\*  
Consensus:

TTGTAAGGATTTCCCACTATGTCAATACA

>Cele-UNSB01\_Fam\_299\_29\_1 Nr. of seq. 1 Alignment length(with gaps) = 29  
Alignment score = 0.000000  
Cele-UNSB01\_3:10934450-10934819 Satlength=370 Nr of Repeats=11  
RepeatLength=29 seed=GGCCTAGAAA Num.seqs=7 Similarity=0.700055  
0 GGCCTAGAAANTTCTATTTGAAAGTTGAT

\*\*\*\*\*  
Consensus:

GGCCTAGAAANTTCTATTTGAAAGTTGAT

>Cele-UNSB01\_Fam\_300\_29\_1 Nr. of seq. 1 Alignment length(with gaps) = 29  
Alignment score = 0.000000  
Cele-UNSB01\_4:14154469-14154585 Satlength=117 Nr of Repeats=4  
RepeatLength=29 seed=TACATTGCAA Num.seqs=4 Similarity=0.946360  
25 TTGCAAGATCTTCTTACTATGTAGGTACA

\*\*\*\*\*

Consensus:

TACATTGCAAGATCTTCTTACTATGTAGG

>Cele-UNSB01\_Fam\_301\_29\_1 Nr. of seq. 1 Alignment length(with gaps) = 29  
Alignment score = 0.000000  
Cele-UNSB01\_5:19567297-19567464 Satlength=168 Nr of Repeats=5  
RepeatLength=29 seed=CTCGTCAGTG Num.seqs=4 Similarity=0.954023  
0 CTCGTCAGTGGGTGGACGAGGAATGAGCG

\*\*\*\*\*

Consensus:

CTCGTCAGTGGGTGGACGAGGAATGAGCG

>Cele-UNSB01\_Fam\_302\_28\_1 Nr. of seq. 1 Alignment length(with gaps) = 28  
Alignment score = 0.000000  
Cele-UNSB01\_2:3009682-3009822 Satlength=141 Nr of Repeats=5  
RepeatLength=28 seed=AATGTCGGCT Num.seqs=5 Similarity=0.847619  
0 AATGTCGGCTGCTTCTAGAAACCAGGCA

\*\*\*\*\*

Consensus:

AATGTCGGCTGCTTCTAGAAACCAGGCA

>Cele-UNSB01\_Fam\_303\_28\_1 Nr. of seq. 1 Alignment length(with gaps) = 28  
Alignment score = 0.000000  
Cele-UNSB01\_2:3456136-3456276 Satlength=141 Nr of Repeats=4  
RepeatLength=28 seed=TGCCTCGCCT Num.seqs=3 Similarity=0.968254  
0 TGCCTCGCCTACGTGCTTATTTTCAGGCA

\*\*\*\*\*

Consensus:

TGCCTCGCCTACGTGCTTATTTTCAGGCA

>Cele-UNSB01\_Fam\_304\_28\_1 Nr. of seq. 1 Alignment length(with gaps) = 28  
Alignment score = 0.000000  
Cele-UNSB01\_5:18701783-18702035 Satlength=253 Nr of Repeats=9  
RepeatLength=28 seed=CCAAGAGAAT Num.seqs=9 Similarity=0.915344  
0 CCAAGAGAATTTCAACCACCTGGAAATT

\*\*\*\*\*

Consensus:

CCAAGAGAATTTCAACCACCTGGAAATT

>Cele-UNSB01\_Fam\_305\_27\_1 Nr. of seq. 1 Alignment length(with gaps) = 27  
Alignment score = 0.000000  
Cele-UNSB01\_2:13831609-13831953 Satlength=345 Nr of Repeats=12  
RepeatLength=27 seed=TTCCGGCAAA Num.seqs=8 Similarity=0.904762  
0 TTCCGGCAAATCGGCAAATTGCAAAAT

\*\*\*\*\*

Consensus:

TTCCGGCAAATCGGCAAATTGCAAAAT

>Cele-UNSB01\_Fam\_306\_27\_1 Nr. of seq. 1 Alignment length(with gaps) = 27  
Alignment score = 0.000000  
Cele-UNSB01\_4:12649750-12649885 Satlength=136 Nr of Repeats=5  
RepeatLength=27 seed=ACAATAAAGT Num.seqs=5 Similarity=1.000000  
0 ACAATAAAGTACTATGTATTACCGTAT

\*\*\*\*\*

Consensus:

ACAATAAAGTACTATGTATTACCGTAT

>Cele-UNSB01\_Fam\_307\_27\_1 Nr. of seq. 1 Alignment length(with gaps) = 27  
Alignment score = 0.000000  
Cele-UNSB01\_5:5757785-5758298 Satlength=514 Nr of Repeats=19  
RepeatLength=27 seed=TGGAGGCGGC Num.seqs=19 Similarity=0.948018  
0 TGGAGGCGGCTTCTGGCCTGGTGGTGG

\*\*\*\*\*

Consensus:

TGGAGGCGGCTTCTGGCCTGGTGGTGG

>Cele-UNSB01\_Fam\_308\_27\_1 Nr. of seq. 1 Alignment length(with gaps) = 27  
Alignment score = 0.000000  
Cele-UNSB01\_6:11249167-11249852 Satlength=686 Nr of Repeats=21  
RepeatLength=27 seed=CACTGACCAA Num.seqs=15 Similarity=0.793063  
0 CACTGACCAAAGAAAATATTANACGTG

\*\*\*\*\*

Consensus:

CACTGACCAAAGAAAATATTANACGTG

>Cele-UNSB01\_Fam\_309\_26\_1 Nr. of seq. 1 Alignment length(with gaps) = 26  
Alignment score = 0.000000  
Cele-UNSB01\_1:3159205-3159335 Satlength=131 Nr of Repeats=4  
RepeatLength=26 seed=GGCAGGCGTC Num.seqs=3 Similarity=0.931624  
0 GGCAGGCGTCAAGCAGGCAGGTTTCA

\*\*\*\*\*

Consensus:

GGCAGGCGTCAAGCAGGCAGGTTTCA

>Cele-UNSB01\_Fam\_310\_26\_1 Nr. of seq. 1 Alignment length(with gaps) = 26  
Alignment score = 0.000000

Cele-UNSB01\_1:11519985-11520529 Satlength=545 Nr of Repeats=18  
RepeatLength=26 seed=ACCTACAGTA Num.seqs=12 Similarity=0.881896  
0 ACCTACAGTACCCCTGTCCTAGAATG

\*\*\*\*\*

Consensus:

ACCTACAGTACCCCTGTCCTAGAATG

>Cele-UNSB01\_Fam\_311\_26\_1 Nr. of seq. 1 Alignment length(with gaps) = 26  
Alignment score = 0.000000

Cele-UNSB01\_2:1186731-1187015 Satlength=285 Nr of Repeats=8  
RepeatLength=26 seed=TACTGTAGTT Num.seqs=5 Similarity=0.621429  
0 TACTGTAGTTTGACCTACTTANGGAT

\*\*\*\*\*

Consensus:

TACTGTAGTTTGACCTACTTANGGAT

>Cele-UNSB01\_Fam\_312\_26\_1 Nr. of seq. 1 Alignment length(with gaps) = 26  
Alignment score = 0.000000

Cele-UNSB01\_2:1915179-1915855 Satlength=677 Nr of Repeats=26  
RepeatLength=26 seed=ATTTACGGAG Num.seqs=22 Similarity=0.829282  
0 ATTTACGGAGCTTCAAGCTTGTGTCG

\*\*\*\*\*

Consensus:

ATTTACGGAGCTTCAAGCTTGTGTCG

>Cele-UNSB01\_Fam\_313\_26\_1 Nr. of seq. 1 Alignment length(with gaps) = 26  
Alignment score = 0.000000

Cele-UNSB01\_5:19352170-19352944 Satlength=775 Nr of Repeats=29  
RepeatLength=26 seed=TGAAATTTCA Num.seqs=20 Similarity=0.904453  
0 TGAAATTTCACAAAATATCGATTTTC

\*\*\*\*\*

Consensus:

TGAAATTTCACAAAATATCGATTTTC

>Cele-UNSB01\_Fam\_314\_25\_1 Nr. of seq. 1 Alignment length(with gaps) = 25  
Alignment score = 0.000000

Cele-UNSB01\_2:1097712-1098091 Satlength=380 Nr of Repeats=5  
RepeatLength=26 seed=GTCGGCTGCT Num.seqs=3 Similarity=0.339869  
0 GTCGGCTGCTTNCAAACCCTGAGTT

\*\*\*\*\*

Consensus:

GTCGGCTGCTTNCAAACCCTGAGTT

>Cele-UNSB01\_Fam\_315\_25\_1 Nr. of seq. 1 Alignment length(with gaps) = 25  
Alignment score = 0.000000  
Cele-UNSB01\_5:19714208-19714335 Satlength=128 Nr of Repeats=5  
RepeatLength=25 seed=AAAAATCTGT Num.seqs=3 Similarity=0.822222  
0 AAAAAATCTGTTCTNNGAGGTCCCTG

\*\*\*\*\*  
Consensus:

AAAAATCTGTTCTNNGAGGTCCCTG

>Cele-UNSB01\_Fam\_316\_24\_1 Nr. of seq. 1 Alignment length(with gaps) = 24  
Alignment score = 0.000000  
Cele-UNSB01\_2:4270872-4271040 Satlength=169 Nr of Repeats=5  
RepeatLength=24 seed=GTGAGGTACG Num.seqs=3 Similarity=0.611111  
0 GTGAGGTACGAGGTGAGGTANGAG

\*\*\*\*\*  
Consensus:

GTGAGGTACGAGGTGAGGTANGAG

>Cele-UNSB01\_Fam\_317\_24\_1 Nr. of seq. 1 Alignment length(with gaps) = 24  
Alignment score = 0.000000  
Cele-UNSB01\_3:12700775-12700871 Satlength=97 Nr of Repeats=4  
RepeatLength=24 seed=AAGCACCACC Num.seqs=4 Similarity=0.972222  
0 AAGCACCACCTCCTCCAACTACAA

\*\*\*\*\*  
Consensus:

AAGCACCACCTCCTCCAACTACAA

>Cele-UNSB01\_Fam\_318\_24\_1 Nr. of seq. 1 Alignment length(with gaps) = 24  
Alignment score = 0.000000  
Cele-UNSB01\_3:13900788-13900959 Satlength=172 Nr of Repeats=7  
RepeatLength=24 seed=AAGAAGGATG Num.seqs=6 Similarity=0.825926  
0 AAGAAGGATGCTGAAGAGAAGAAG

\*\*\*\*\*  
Consensus:

AAGAAGGATGCTGAAGAGAAGAAG

>Cele-UNSB01\_Fam\_319\_24\_1 Nr. of seq. 1 Alignment length(with gaps) = 24  
Alignment score = 0.000000  
Cele-UNSB01\_4:2892401-2892617 Satlength=217 Nr of Repeats=5  
RepeatLength=24 seed=GCTTCTGGAG Num.seqs=3 Similarity=0.777778  
0 GCTTCTGGAGCTACAGGTTATCCA

\*\*\*\*\*  
Consensus:

GCTTCTGGAGCTACAGGTTATCCA

>Cele-UNSB01\_Fam\_320\_24\_1 Nr. of seq. 1 Alignment length(with gaps) = 24  
Alignment score = 0.000000  
Cele-UNSB01\_4:17584126-17584294 Satlength=169 Nr of Repeats=7  
RepeatLength=24 seed=TCAACAACAA Num.seqs=7 Similarity=1.000000  
0 TCAACAACAACAGGAGAAGCTTCT

\*\*\*\*\*  
Consensus:

TCAACAACAACAGGAGAAGCTTCT

>Cele-UNSB01\_Fam\_321\_24\_1 Nr. of seq. 1 Alignment length(with gaps) = 24  
Alignment score = 0.000000  
Cele-UNSB01\_6:8111999-8112167 Satlength=169 Nr of Repeats=7  
RepeatLength=24 seed=GGTGGCTGGT Num.seqs=7 Similarity=1.000000  
0 GGTGGCTGGTCACAAAAGTAAGTT

\*\*\*\*\*  
Consensus:

GGTGGCTGGTCACAAAAGTAAGTT

>Cele-UNSB01\_Fam\_322\_23\_1 Nr. of seq. 1 Alignment length(with gaps) = 23  
Alignment score = 0.000000  
Cele-UNSB01\_1:14577219-14577388 Satlength=170 Nr of Repeats=5  
RepeatLength=23 seed=GCACCATAAG Num.seqs=3 Similarity=0.726852  
0 GCATCATAAGGATCATAGTTGAT

\*\*\*\*\*  
Consensus:

GCATCATAAGGATCATAGTTGAT

>Cele-UNSB01\_Fam\_323\_23\_1 Nr. of seq. 1 Alignment length(with gaps) = 23  
Alignment score = 0.000000  
Cele-UNSB01\_2:1599041-1599824 Satlength=784 Nr of Repeats=24  
RepeatLength=23 seed=CGCTGTAAGA Num.seqs=16 Similarity=0.806763  
0 CGCTGTAAGACCCTTCGCTGTAC

\*\*\*\*\*  
Consensus:

CGCTGTAAGACCCTTCGCTGTAC

>Cele-UNSB01\_Fam\_324\_23\_1 Nr. of seq. 1 Alignment length(with gaps) = 23  
Alignment score = 0.000000  
Cele-UNSB01\_2:15522229-15522469 Satlength=241 Nr of Repeats=12  
RepeatLength=23 seed=GCTACAGTAC Num.seqs=8 Similarity=0.821946  
0 GCTACAGTACCCAGCTTGACTT

\*\*\*\*\*  
Consensus:



GCTACAGTACCCCAGCTTGACTT

>Cele-UNSB01\_Fam\_325\_23\_1 Nr. of seq. 1 Alignment length(with gaps) = 23  
Alignment score = 0.000000  
Cele-UNSB01\_5:19784949-19785086 Satlength=138 Nr of Repeats=6  
RepeatLength=23 seed=TTTTCAGAAA Num.seqs=5 Similarity=0.631944  
0 TTTTCAGAAATAGGTATTTTCAGA

\*\*\*\*\*  
Consensus:

TTTTCAGAAATAGGTATTTTCAGA

>Cele-UNSB01\_Fam\_326\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_1:817628-817952 Satlength=325 Nr of Repeats=8 RepeatLength=22  
seed=TTAAAATTTT Num.seqs=6 Similarity=0.886869  
0 TTAAAATTTTGTTCAGTTTGACC

\*\*\*\*\*  
Consensus:

TTAAAATTTTGTTCAGTTTGACC

>Cele-UNSB01\_Fam\_327\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_1:907957-908415 Satlength=459 Nr of Repeats=21  
RepeatLength=22 seed=TTTTAGCCAA Num.seqs=17 Similarity=0.862299  
0 TTTTAGCCAAAAATCCGTAA

\*\*\*\*\*  
Consensus:

TTTTAGCCAAAAATCCGTAA

>Cele-UNSB01\_Fam\_328\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_1:14511380-14511819 Satlength=440 Nr of Repeats=17  
RepeatLength=22 seed=GCACGGCCTG Num.seqs=13 Similarity=0.701226  
0 GCACGGCCTGGCGTCCTGAGG

\*\*\*\*\*  
Consensus:

GCACGGCCTGGCGTCCTGAGG

>Cele-UNSB01\_Fam\_329\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_2:14303812-14304194 Satlength=383 Nr of Repeats=12  
RepeatLength=22 seed=CTACAGTAAC Num.seqs=8 Similarity=0.798395  
0 CTACAGTAACCCTAGTATTGAA

\*\*\*\*\*

Consensus:

CTACAGTAACCCTAGTATTGAA

>Cele-UNSB01\_Fam\_330\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_3:4344679-4344767 Satlength=89 Nr of Repeats=4  
RepeatLength=22 seed=CAAACCCAA Num.seqs=4 Similarity=0.939394  
0 CAAACCCCAAGTAGATCCCACT

\*\*\*\*\*

Consensus:

CAAACCCCAAGTAGATCCCACT

>Cele-UNSB01\_Fam\_331\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_4:6669007-6669090 Satlength=84 Nr of Repeats=4  
RepeatLength=22 seed=AAGCGGTAAC Num.seqs=3 Similarity=1.000000  
0 AAGCGGTAACGTCGTCTATATA

\*\*\*\*\*

Consensus:

AAGCGGTAACGTCGTCTATATA

>Cele-UNSB01\_Fam\_332\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_5:17108364-17108469 Satlength=106 Nr of Repeats=5  
RepeatLength=21 seed=TGCTAATTAG Num.seqs=3 Similarity=0.545455  
0 TGCTAATTAGCGCGGNTGCGTN

\*\*\*\*\*

Consensus:

TGCTAATTAGCGCGGNTGCGTN

>Cele-UNSB01\_Fam\_333\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_5:19721189-19721423 Satlength=235 Nr of Repeats=7  
RepeatLength=22 seed=ACGTATACAG Num.seqs=5 Similarity=0.915152  
0 ACGTATACAGGCATATACACAT

\*\*\*\*\*

Consensus:

ACGTATACAGGCATATACACAT

>Cele-UNSB01\_Fam\_334\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_6:1991346-1991764 Satlength=419 Nr of Repeats=14  
RepeatLength=22 seed=CCGGCGTGGT Num.seqs=9 Similarity=0.677134  
0 CCGGCGTGGTNTTGAAGCGGTC

\*\*\*\*\*

Consensus:

CCGGCGTGGTNTTGAAGCGGTC

>Cele-UNSB01\_Fam\_335\_22\_1 Nr. of seq. 1 Alignment length(with gaps) = 22  
Alignment score = 0.000000  
Cele-UNSB01\_6:14983794-14983948 Satlength=155 Nr of Repeats=5  
RepeatLength=22 seed=TTTGTGGGAG Num.seqs=3 Similarity=0.757576  
0 TTTGTGGGAGGCGACATATACC

\*\*\*\*\*

Consensus:

TTTGTGGGAGGCGACATATACC

>Cele-UNSB01\_Fam\_336\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_1:833000-833653 Satlength=654 Nr of Repeats=29  
RepeatLength=21 seed=TGGCCTAGAT Num.seqs=21 Similarity=0.658586  
0 TGGCCTAGATTNTTTACAGGG

\*\*\*\*\*

Consensus:

TGGCCTAGATTNTTTACAGGG

>Cele-UNSB01\_Fam\_337\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_1:1679297-1679633 Satlength=337 Nr of Repeats=16  
RepeatLength=21 seed=TCTCCTGGTA Num.seqs=16 Similarity=0.963492  
0 TCTCCTGGTAAATTTAAAAAT

\*\*\*\*\*

Consensus:

TCTCCTGGTAAATTTAAAAAT

>Cele-UNSB01\_Fam\_338\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_1:12807224-12807329 Satlength=106 Nr of Repeats=5  
RepeatLength=21 seed=ACCACCCCTA Num.seqs=5 Similarity=0.815873  
0 ACCACCCCTACAACNACCACC

\*\*\*\*\*

Consensus:

ACCACCCCTACAACNACCACC

>Cele-UNSB01\_Fam\_339\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000

Cele-UNSB01\_1:15278589-15278861 Satlength=273 Nr of Repeats=10  
RepeatLength=21 seed=AACTTTTTGG Num.seqs=6 Similarity=0.791919  
0 AACTTTTTGGCAATTTTCCAA

\*\*\*\*\*

Consensus:

AACTTTTTGGCAATTTTCCAA

>Cele-UNSB01\_Fam\_340\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000

Cele-UNSB01\_2:2291158-2291371 Satlength=214 Nr of Repeats=8  
RepeatLength=21 seed=TGTGCCCTGG Num.seqs=6 Similarity=0.936508  
0 TGTGCCCTGGAAAGCTGGCAG

\*\*\*\*\*

Consensus:

TGTGCCCTGGAAAGCTGGCAG

>Cele-UNSB01\_Fam\_341\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000

Cele-UNSB01\_2:4119390-4119751 Satlength=362 Nr of Repeats=4  
RepeatLength=21 seed=CTACGTAAGA Num.seqs=3 Similarity=0.830688  
0 CTACGTAAGAGTAGCGCAGGA

\*\*\*\*\*

Consensus:

CTACGTAAGAGTAGCGCAGGA

>Cele-UNSB01\_Fam\_342\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000

Cele-UNSB01\_2:13339084-13339231 Satlength=148 Nr of Repeats=7  
RepeatLength=21 seed=AATCTAGCCA Num.seqs=7 Similarity=0.930461  
0 AATCTAGCCAGACGCACACCT

\*\*\*\*\*

Consensus:

AATCTAGCCAGACGCACACCT

>Cele-UNSB01\_Fam\_343\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000

Cele-UNSB01\_2:14401364-14401594 Satlength=231 Nr of Repeats=10  
RepeatLength=21 seed=CAATTTTCTG Num.seqs=8 Similarity=0.841270  
0 CAATTTTCTGTTNAACTTTGA

\*\*\*\*\*

Consensus:

CAATTTTCTGTTNAACTTTGA

>Cele-UNSB01\_Fam\_344\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_3:8499608-8499713 Satlength=106 Nr of Repeats=5  
RepeatLength=21 seed=AAGTTTTACT Num.seqs=5 Similarity=0.974603  
0 AAGTTTTACTTTGATTTTTTTT

\*\*\*\*\*  
Consensus:

AAGTTTTACTTTGATTTTTTTT

>Cele-UNSB01\_Fam\_345\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_3:11543247-11543687 Satlength=441 Nr of Repeats=21  
RepeatLength=21 seed=GGCAATTTTC Num.seqs=20 Similarity=0.903425  
0 GGCAATTTTCAGTGCAATTC

\*\*\*\*\*  
Consensus:

GGCAATTTTCAGTGCAATTC

>Cele-UNSB01\_Fam\_346\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_4:1580035-1580182 Satlength=148 Nr of Repeats=7  
RepeatLength=21 seed=CCATAGGTGG Num.seqs=7 Similarity=0.794407  
0 CCATAGGTGGAAGATCTNATA

\*\*\*\*\*  
Consensus:

CCATAGGTGGAAGATCTNATA

>Cele-UNSB01\_Fam\_347\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_4:2179058-2179920 Satlength=863 Nr of Repeats=38  
RepeatLength=21 seed=GATTTACGGG Num.seqs=31 Similarity=0.686520  
0 GATTTACGGGGTGAACATGTG

\*\*\*\*\*  
Consensus:

GATTTACGGGGTGAACATGTG

>Cele-UNSB01\_Fam\_348\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_5:6410601-6410727 Satlength=127 Nr of Repeats=6  
RepeatLength=21 seed=TTGGTGACAA Num.seqs=6 Similarity=1.000000  
0 TTGGTGACAATGTGGAAACAA

\*\*\*\*\*  
Consensus:

TTGGTGACAATGTGGAAACAA

>Cele-UNSB01\_Fam\_349\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_5:9975370-9975475 Satlength=106 Nr of Repeats=5  
RepeatLength=21 seed=TTCTAATTTCG Num.seqs=5 Similarity=0.726984  
0 TTCTAATTTCGACGCGCATNGT

\*\*\*\*\*

Consensus:

TTCTAATTTCGACGCGCATNGT

>Cele-UNSB01\_Fam\_350\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_5:17104481-17104658 Satlength=178 Nr of Repeats=5  
RepeatLength=21 seed=CTAATTAGCG Num.seqs=3 Similarity=0.640212  
0 CTAATTAGCGTCGCTTCCNTT

\*\*\*\*\*

Consensus:

CTAATTAGCGTCGCTTCCNTT

>Cele-UNSB01\_Fam\_351\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_5:18902702-18903276 Satlength=575 Nr of Repeats=24  
RepeatLength=21 seed=AAAAATCGAT Num.seqs=18 Similarity=0.739602  
0 AAAAATCGATAAAATTTGGAN

\*\*\*\*\*

Consensus:

AAAAATCGATAAAATTTGGAN

>Cele-UNSB01\_Fam\_352\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_5:19549755-19549902 Satlength=148 Nr of Repeats=7  
RepeatLength=21 seed=CACACGAGCT Num.seqs=7 Similarity=0.727891  
0 CACACGAGCTTGAGAGCCCGG

\*\*\*\*\*

Consensus:

CACACGAGCTTGAGAGCCCGG

>Cele-UNSB01\_Fam\_353\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_5:19721079-19721595 Satlength=517 Nr of Repeats=5  
RepeatLength=21 seed=TATTTTCAAA Num.seqs=3 Similarity=0.957672  
0 TATTTTCAAAAAATTTAAAA

\*\*\*\*\*

Consensus:

TATTTTCAAAAAAATTTAAAA

>Cele-UNSB01\_Fam\_354\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_5:19953202-19953370 Satlength=169 Nr of Repeats=6  
RepeatLength=21 seed=ACCCCGATTT Num.seqs=5 Similarity=0.911111  
0 ACCCCGATTTTCACCCAAAAA

\*\*\*\*\*  
Consensus:

ACCCCGATTTTCACCCAAAAA

>Cele-UNSB01\_Fam\_355\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_5:20275164-20275248 Satlength=85 Nr of Repeats=4  
RepeatLength=21 seed=CTCAATTCAA Num.seqs=4 Similarity=0.883598  
0 CTCAATTCAATCAAGGAAATC

\*\*\*\*\*  
Consensus:

CTCAATTCAATCAAGGAAATC

>Cele-UNSB01\_Fam\_356\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_6:3834410-3834530 Satlength=121 Nr of Repeats=5  
RepeatLength=20 seed=CCATGTAGCT Num.seqs=4 Similarity=0.561869  
0 CCATGTAGCTTCAAATTNCT

\*\*\*\*\*  
Consensus:

CCATGTAGCTTCAAATTNCT

>Cele-UNSB01\_Fam\_357\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_6:15876707-15876856 Satlength=150 Nr of Repeats=4  
RepeatLength=21 seed=TGTCCGTGAT Num.seqs=3 Similarity=0.666667  
0 TGTCCGTGATGATCATGNGCA

\*\*\*\*\*  
Consensus:

TGTCCGTGATGATCATGNGCA

>Cele-UNSB01\_Fam\_358\_21\_1 Nr. of seq. 1 Alignment length(with gaps) = 21  
Alignment score = 0.000000  
Cele-UNSB01\_6:17463543-17463648 Satlength=106 Nr of Repeats=5  
RepeatLength=21 seed=GGTGGACCCA Num.seqs=5 Similarity=0.822222  
0 GGTGGACCCANGGGTTCCTAG

\*\*\*\*\*

Consensus:

GGTGGACCCANGGGTTCCTAG

>Cele-UNSB01\_Fam\_359\_20\_1 Nr. of seq. 1 Alignment length(with gaps) = 20  
Alignment score = 0.000000  
Cele-UNSB01\_2:3687013-3687103 Satlength=91 Nr of Repeats=5  
RepeatLength=20 seed=CTATCGCCTG Num.seqs=4 Similarity=0.833333  
0 CTATCGCCTGCTATCGCCTA

\*\*\*\*\*

Consensus:

CTATCGCCTGCTATCGCCTA

>Cele-UNSB01\_Fam\_360\_20\_1 Nr. of seq. 1 Alignment length(with gaps) = 20  
Alignment score = 0.000000  
Cele-UNSB01\_5:17995705-17996016 Satlength=312 Nr of Repeats=5  
RepeatLength=20 seed=ATTTGACCTA Num.seqs=4 Similarity=0.900000  
0 ATTTGACCTACTTTTTAAAA

\*\*\*\*\*

Consensus:

ATTTGACCTACTTTTTAAAA

>Cele-UNSB01\_Fam\_361\_19\_1 Nr. of seq. 1 Alignment length(with gaps) = 19  
Alignment score = 0.000000  
Cele-UNSB01\_1:360798-360950 Satlength=153 Nr of Repeats=8 RepeatLength=19  
seed=GTACTACCTT Num.seqs=8 Similarity=0.982456  
0 GTACTACCTTTTAATGTAT

\*\*\*\*\*

Consensus:

GTACTACCTTTTAATGTAT

>Cele-UNSB01\_Fam\_362\_19\_1 Nr. of seq. 1 Alignment length(with gaps) = 19  
Alignment score = 0.000000  
Cele-UNSB01\_1:14381938-14382071 Satlength=134 Nr of Repeats=7  
RepeatLength=19 seed=CCCTGATACC Num.seqs=7 Similarity=0.788889  
0 CCCTGATACCCCCTAGTCC

\*\*\*\*\*

Consensus:

CCCTGATACCCCCTAGTCC

>Cele-UNSB01\_Fam\_363\_19\_1 Nr. of seq. 1 Alignment length(with gaps) = 19  
Alignment score = 0.000000  
Cele-UNSB01\_2:13161799-13161943 Satlength=145 Nr of Repeats=6  
RepeatLength=19 seed=TATGGTGCAT Num.seqs=4 Similarity=0.707602  
0 TATGGTGCATCTAACTAGT



\*\*\*\*\*

Consensus:

TATGGTGCATCTAACTAGT

>Cele-UNSB01\_Fam\_364\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000  
Cele-UNSB01\_1:10842122-10842194 Satlength=73 Nr of Repeats=4  
RepeatLength=18 seed=AAAAGTTACA Num.seqs=4 Similarity=1.000000  
0 AAAAGTTACAGTGTCTT

\*\*\*\*\*

Consensus:

AAAAGTTACAGTGTCTT

>Cele-UNSB01\_Fam\_365\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000  
Cele-UNSB01\_1:14582954-14583490 Satlength=537 Nr of Repeats=26  
RepeatLength=18 seed=TTGTAGATCA Num.seqs=22 Similarity=0.869489  
0 TTGTAGATCAACGGGGTC

\*\*\*\*\*

Consensus:

TTGTAGATCAACGGGGTC

>Cele-UNSB01\_Fam\_366\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000  
Cele-UNSB01\_2:1488365-1488455 Satlength=91 Nr of Repeats=5  
RepeatLength=18 seed=GGAGGTCCAG Num.seqs=5 Similarity=0.859259  
0 GGAGGTCCAGGTACCCCG

\*\*\*\*\*

Consensus:

GGAGGTCCAGGTACCCCG

>Cele-UNSB01\_Fam\_367\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000  
Cele-UNSB01\_2:10597740-10597833 Satlength=94 Nr of Repeats=5  
RepeatLength=18 seed=TAAATAAGTG Num.seqs=3 Similarity=0.950617  
0 TAAATAAGTGGCTATAAT

\*\*\*\*\*

Consensus:

TAAATAAGTGGCTATAAT

>Cele-UNSB01\_Fam\_368\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000

Cele-UNSB01\_2:13043920-13044316 Satlength=397 Nr of Repeats=21  
RepeatLength=18 seed=ACTACTGTAT Num.seqs=18 Similarity=0.797628  
0 ACTACTGTATCNCAGGAG

\*\*\*\*\*

Consensus:

ACTACTGTATCNCAGGAG

>Cele-UNSB01\_Fam\_369\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000

Cele-UNSB01\_4:3232737-3232899 Satlength=163 Nr of Repeats=6  
RepeatLength=18 seed=CCTTCGCCTA Num.seqs=4 Similarity=0.765432  
0 CCTTCGCCTACCTACGTG

\*\*\*\*\*

Consensus:

CCTTCGCCTACCTACGTG

>Cele-UNSB01\_Fam\_370\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000

Cele-UNSB01\_4:4398109-4398181 Satlength=73 Nr of Repeats=4  
RepeatLength=18 seed=TTTTTTGATA Num.seqs=4 Similarity=0.962963  
0 TTTTTTGATAATTCTTGA

\*\*\*\*\*

Consensus:

TTTTTTGATAATTCTTGA

>Cele-UNSB01\_Fam\_371\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000

Cele-UNSB01\_5:4240718-4240800 Satlength=83 Nr of Repeats=4  
RepeatLength=18 seed=AAATATTCTT Num.seqs=3 Similarity=0.851852  
0 AAATATTCTTATTTTCAG

\*\*\*\*\*

Consensus:

AAATATTCTTATTTTCAG

>Cele-UNSB01\_Fam\_372\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000

Cele-UNSB01\_5:4631559-4631760 Satlength=202 Nr of Repeats=8  
RepeatLength=18 seed=CCTGGCTGTC Num.seqs=5 Similarity=0.607407  
0 CCTGGTTGTCCNTCTNNT

\*\*\*\*\*

Consensus:

CCTGGTTGTCCNTCTNNT

>Cele-UNSB01\_Fam\_373\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000  
Cele-UNSB01\_5:7379892-7380037 Satlength=146 Nr of Repeats=8  
RepeatLength=18 seed=TTTCATAAGA Num.seqs=7 Similarity=0.943563  
0 TTTCATAAGAAGTAAATN

\*\*\*\*\*

Consensus:

TTTCATAAGAAGTAAATN

>Cele-UNSB01\_Fam\_374\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000  
Cele-UNSB01\_5:20522553-20523111 Satlength=559 Nr of Repeats=29  
RepeatLength=18 seed=CATTGTCACT Num.seqs=27 Similarity=0.884774  
0 CATTGTCACTTTCTTCTC

\*\*\*\*\*

Consensus:

CATTGTCACTTTCTTCTC

>Cele-UNSB01\_Fam\_375\_18\_1 Nr. of seq. 1 Alignment length(with gaps) = 18  
Alignment score = 0.000000  
Cele-UNSB01\_6:1911366-1912554 Satlength=1189 Nr of Repeats=59  
RepeatLength=18 seed=AAGCCTATGC Num.seqs=44 Similarity=0.776212  
0 AAGCCTATGCCTTTCCCA

\*\*\*\*\*

Consensus:

AAGCCTATGCCTTTCCCA

>Cele-UNSB01\_Fam\_376\_17\_1 Nr. of seq. 1 Alignment length(with gaps) = 17  
Alignment score = 0.000000  
Cele-UNSB01\_2:12716681-12716766 Satlength=86 Nr of Repeats=5  
RepeatLength=17 seed=ACTTGGTACA Num.seqs=5 Similarity=0.890196  
0 ACTTGGTACATAGGCCA

\*\*\*\*\*

Consensus:

ACTTGGTACATAGGCCA

>Cele-UNSB01\_Fam\_377\_17\_1 Nr. of seq. 1 Alignment length(with gaps) = 17  
Alignment score = 0.000000  
Cele-UNSB01\_3:12692847-12693292 Satlength=446 Nr of Repeats=15  
RepeatLength=17 seed=ATTTTTCCTCG Num.seqs=10 Similarity=0.687449  
0 ATTTTTCCTCGCAAGTAG

\*\*\*\*\*

Consensus:

ATTTTTCCTCGCAAGTAG

>Cele-UNSB01\_Fam\_378\_17\_1 Nr. of seq. 1 Alignment length(with gaps) = 17  
Alignment score = 0.000000  
Cele-UNSB01\_4:11742877-11743140 Satlength=264 Nr of Repeats=13  
RepeatLength=17 seed=AAAATCAAAC Num.seqs=10 Similarity=0.809259  
0 AAAATCAAACCGGCGGA

\*\*\*\*\*

Consensus:

AAAATCAAACCGGCGGA

>Cele-UNSB01\_Fam\_379\_17\_1 Nr. of seq. 1 Alignment length(with gaps) = 17  
Alignment score = 0.000000  
Cele-UNSB01\_5:4844742-4844913 Satlength=172 Nr of Repeats=5  
RepeatLength=17 seed=AAATGCCAAA Num.seqs=3 Similarity=0.641975  
0 AAATGCCAAAANTGCCA

\*\*\*\*\*

Consensus:

AAATGCCAAAANTGCCA

>Cele-UNSB01\_Fam\_380\_17\_1 Nr. of seq. 1 Alignment length(with gaps) = 17  
Alignment score = 0.000000  
Cele-UNSB01\_5:16819160-16819347 Satlength=188 Nr of Repeats=11  
RepeatLength=17 seed=TAACCTGACT Num.seqs=11 Similarity=0.957219  
0 TAACCTGACTGCTACAG

\*\*\*\*\*

Consensus:

TAACCTGACTGCTACAG

>Cele-UNSB01\_Fam\_381\_17\_1 Nr. of seq. 1 Alignment length(with gaps) = 17  
Alignment score = 0.000000  
Cele-UNSB01\_5:19696042-19696279 Satlength=238 Nr of Repeats=14  
RepeatLength=17 seed=GAATTAGAAA Num.seqs=13 Similarity=0.554584  
0 GAATTAGAAAAATTTGA

\*\*\*\*\*

Consensus:

GAATTAGAAAAATTTGA

>Cele-UNSB01\_Fam\_382\_17\_1 Nr. of seq. 1 Alignment length(with gaps) = 17  
Alignment score = 0.000000  
Cele-UNSB01\_5:19785568-19787058 Satlength=1491 Nr of Repeats=85  
RepeatLength=17 seed=TTGCAAGAAA Num.seqs=83 Similarity=0.953951  
0 TTGCAAGAAAATCTGCA

\*\*\*\*\*

Consensus:

TTGCAAGAAAATCTGCA

>Cele-UNSB01\_Fam\_383\_17\_1 Nr. of seq. 1 Alignment length(with gaps) = 17  
Alignment score = 0.000000  
Cele-UNSB01\_6:3463610-3463814 Satlength=205 Nr of Repeats=10  
RepeatLength=17 seed=TTTTAACGTG Num.seqs=8 Similarity=0.901961  
0 TTTTAACGTGACCTAGT

\*\*\*\*\*  
Consensus:

TTTTAACGTGACCTAGT

>Cele-UNSB01\_Fam\_384\_16\_1 Nr. of seq. 1 Alignment length(with gaps) = 16  
Alignment score = 0.000000  
Cele-UNSB01\_1:12783664-12784000 Satlength=337 Nr of Repeats=20  
RepeatLength=16 seed=TGATCTGATG Num.seqs=18 Similarity=0.831699  
0 TGATCTGATGATCTGA

\*\*\*\*\*  
Consensus:

TGATCTGATGATCTGA

>Cele-UNSB01\_Fam\_385\_16\_1 Nr. of seq. 1 Alignment length(with gaps) = 16  
Alignment score = 0.000000  
Cele-UNSB01\_1:13315136-13315216 Satlength=81 Nr of Repeats=5  
RepeatLength=16 seed=AATACGGGAA Num.seqs=5 Similarity=1.000000  
0 AATACGGGAATACGGG

\*\*\*\*\*  
Consensus:

AATACGGGAATACGGG

>Cele-UNSB01\_Fam\_386\_16\_1 Nr. of seq. 1 Alignment length(with gaps) = 16  
Alignment score = 0.000000  
Cele-UNSB01\_3:1053032-1053110 Satlength=79 Nr of Repeats=5  
RepeatLength=16 seed=TTATAGTGTT Num.seqs=3 Similarity=0.888889  
0 TTATAGTGTTATAGTG

\*\*\*\*\*  
Consensus:

TTATAGTGTTATAGTG

>Cele-UNSB01\_Fam\_387\_16\_1 Nr. of seq. 1 Alignment length(with gaps) = 16  
Alignment score = 0.000000  
Cele-UNSB01\_3:3140206-3140936 Satlength=731 Nr of Repeats=5  
RepeatLength=16 seed=TGTATATATA Num.seqs=3 Similarity=1.000000  
0 TGTATATATATATATA

\*\*\*\*\*

Consensus:

TGTATATATATATATA

>Cele-UNSB01\_Fam\_388\_16\_1 Nr. of seq. 1 Alignment length(with gaps) = 16  
Alignment score = 0.000000  
Cele-UNSB01\_5:12149471-12149551 Satlength=81 Nr of Repeats=5  
RepeatLength=16 seed=AAAAATTATT Num.seqs=5 Similarity=1.000000  
0 AAAAAATTATTGAATAC

\*\*\*\*\*

Consensus:

AAAAATTATTGAATAC

>Cele-UNSB01\_Fam\_389\_16\_1 Nr. of seq. 1 Alignment length(with gaps) = 16  
Alignment score = 0.000000  
Cele-UNSB01\_5:17868232-17868328 Satlength=97 Nr of Repeats=6  
RepeatLength=16 seed=GAATAATATT Num.seqs=6 Similarity=0.972222  
0 GAATAATATTGGAGAA

\*\*\*\*\*

Consensus:

GAATAATATTGGAGAA

>Cele-UNSB01\_Fam\_390\_16\_1 Nr. of seq. 1 Alignment length(with gaps) = 16  
Alignment score = 0.000000  
Cele-UNSB01\_5:20061429-20063397 Satlength=1969 Nr of Repeats=117  
RepeatLength=16 seed=CTTAGATCTC Num.seqs=111 Similarity=0.886787  
0 CTTAGATCTCAATTCC

\*\*\*\*\*

Consensus:

CTTAGATCTCAATTCC

>Cele-UNSB01\_Fam\_391\_16\_1 Nr. of seq. 1 Alignment length(with gaps) = 16  
Alignment score = 0.000000  
Cele-UNSB01\_6:3096507-3096571 Satlength=65 Nr of Repeats=4  
RepeatLength=16 seed=AGAGAGTATA Num.seqs=4 Similarity=1.000000  
0 AGAGAGTATAGATTAG

\*\*\*\*\*

Consensus:

AGAGAGTATAGATTAG

>Cele-UNSB01\_Fam\_392\_15\_1 Nr. of seq. 1 Alignment length(with gaps) = 15  
Alignment score = 0.000000  
Cele-UNSB01\_3:12542724-12542833 Satlength=110 Nr of Repeats=5  
RepeatLength=15 seed=CGACCTGCGA Num.seqs=3 Similarity=0.940741  
0 CGACCTGCGACCTAG

\*\*\*\*\*

Consensus:

CGACCTGCGACCTAG

>Cele-UNSB01\_Fam\_393\_15\_1 Nr. of seq. 1 Alignment length(with gaps) = 15  
Alignment score = 0.000000  
Cele-UNSB01\_4:13614335-13614410 Satlength=76 Nr of Repeats=5  
RepeatLength=15 seed=CACAGGAGGC Num.seqs=5 Similarity=1.000000  
0 CACAGGAGGCTGGGA

\*\*\*\*\*

Consensus:

CACAGGAGGCTGGGA

>Cele-UNSB01\_Fam\_394\_14\_1 Nr. of seq. 1 Alignment length(with gaps) = 14  
Alignment score = 0.000000  
Cele-UNSB01\_1:11291527-11291639 Satlength=113 Nr of Repeats=7  
RepeatLength=14 seed=AGCTTGAAGC Num.seqs=5 Similarity=0.800000  
0 AGCTTGAAGCTTGG

\*\*\*\*\*

Consensus:

AGCTTGAAGCTTGG

>Cele-UNSB01\_Fam\_395\_14\_1 Nr. of seq. 1 Alignment length(with gaps) = 14  
Alignment score = 0.000000  
Cele-UNSB01\_6:8150139-8150195 Satlength=57 Nr of Repeats=4  
RepeatLength=14 seed=TTACCAAAAT Num.seqs=4 Similarity=0.888889  
0 TTACCAAAATCTAA

\*\*\*\*\*

Consensus:

TTACCAAAATCTAA

>Cele-UNSB01\_Fam\_396\_13\_1 Nr. of seq. 1 Alignment length(with gaps) = 13  
Alignment score = 0.000000  
Cele-UNSB01\_2:13903082-13903160 Satlength=79 Nr of Repeats=5  
RepeatLength=13 seed=GGCTTCTAGT Num.seqs=4 Similarity=0.880342  
0 GGCTTCTAGTCCA

\*\*\*\*\*

Consensus:

GGCTTCTAGTCCA

>Cele-UNSB01\_Fam\_397\_13\_1 Nr. of seq. 1 Alignment length(with gaps) = 13  
Alignment score = 0.000000

Cele-UNSB01\_5:19792863-19792928 Satlength=66 Nr of Repeats=5  
RepeatLength=13 seed=TTGGGGTGGG Num.seqs=5 Similarity=1.000000  
0 TTGGGGTGGGCCT

\*\*\*\*\*

Consensus:

TTGGGGTGGGCCT

>Cele-UNSB01\_Fam\_398\_12\_1 Nr. of seq. 1 Alignment length(with gaps) = 12  
Alignment score = 0.000000

Cele-UNSB01\_2:13678541-13678601 Satlength=61 Nr of Repeats=5  
RepeatLength=12 seed=AATACCAACC Num.seqs=5 Similarity=0.933333  
0 AATACCAACCAC

\*\*\*\*\*

Consensus:

AATACCAACCAC

>Cele-UNSB01\_Fam\_399\_12\_1 Nr. of seq. 1 Alignment length(with gaps) = 12  
Alignment score = 0.000000

Cele-UNSB01\_3:13445252-13445836 Satlength=585 Nr of Repeats=45  
RepeatLength=12 seed=AGTTATATAG Num.seqs=41 Similarity=0.931707  
0 AGTTATATAGTA

\*\*\*\*\*

Consensus:

AGTTATATAGTA

>Cele-UNSB01\_Fam\_400\_12\_1 Nr. of seq. 1 Alignment length(with gaps) = 12  
Alignment score = 0.000000

Cele-UNSB01\_5:16677048-16677311 Satlength=264 Nr of Repeats=16  
RepeatLength=12 seed=CATTGACTTG Num.seqs=13 Similarity=0.842209  
0 CATTGACTTGAG

\*\*\*\*\*

Consensus:

CATTGACTTGAG

>Cele-UNSB01\_Fam\_401\_11\_1 Nr. of seq. 1 Alignment length(with gaps) = 11  
Alignment score = 0.000000

Cele-UNSB01\_4:2933784-2933839 Satlength=56 Nr of Repeats=5  
RepeatLength=11 seed=TTGTTTACAA Num.seqs=5 Similarity=1.000000  
0 TTGTTTACAAG

\*\*\*\*\*

Consensus:

TTGTTTACAAG



>Cele-UNSB01\_Fam\_402\_11\_1 Nr. of seq. 1 Alignment length(with gaps) = 11  
Alignment score = 0.000000  
Cele-UNSB01\_5:1284626-1284947 Satlength=322 Nr of Repeats=10  
RepeatLength=11 seed=TACCTACTAG Num.seqs=6 Similarity=0.789899  
0 TACCTACTAGA

\*\*\*\*\*  
Consensus:

TACCTACTAGA

>Cele-UNSB01\_Fam\_403\_11\_1 Nr. of seq. 1 Alignment length(with gaps) = 11  
Alignment score = 0.000000  
Cele-UNSB01\_5:10500053-10500266 Satlength=214 Nr of Repeats=19  
RepeatLength=11 seed=AGATACTT Num.seqs=15 Similarity=0.983838  
0 AGATACTTC

\*\*\*\*\*  
Consensus:

AGATACTTC

>Cele-UNSB01\_Fam\_404\_11\_1 Nr. of seq. 1 Alignment length(with gaps) = 11  
Alignment score = 0.000000  
Cele-UNSB01\_5:18899719-18900018 Satlength=300 Nr of Repeats=5  
RepeatLength=11 seed=TTTCAGGCCT Num.seqs=3 Similarity=0.796296  
0 TTTCAGGCCTA

\*\*\*\*\*  
Consensus:

TTTCAGGCCTA

>Cele-UNSB01\_Fam\_405\_10\_1 Nr. of seq. 1 Alignment length(with gaps) = 10  
Alignment score = 0.000000  
Cele-UNSB01\_1:14207225-14207295 Satlength=71 Nr of Repeats=6  
RepeatLength=10 seed=GATTTTCATA Num.seqs=5 Similarity=1.000000  
0 GATTTTCATA

\*\*\*\*\*  
Consensus:

GATTTTCATA

>Cele-UNSB01\_Fam\_406\_10\_1 Nr. of seq. 1 Alignment length(with gaps) = 10  
Alignment score = 0.000000  
Cele-UNSB01\_2:2296694-2296754 Satlength=61 Nr of Repeats=4  
RepeatLength=10 seed=CAGCAGAGTG Num.seqs=3 Similarity=1.000000  
0 CAGCAGAGTG

\*\*\*\*\*  
Consensus:

CAGCAGAGTG

>Cele-UNSB01\_Fam\_407\_10\_1 Nr. of seq. 1 Alignment length(with gaps) = 10  
Alignment score = 0.000000  
Cele-UNSB01\_2:3175289-3175339 Satlength=51 Nr of Repeats=4  
RepeatLength=10 seed=AACTTTCGAA Num.seqs=3 Similarity=1.000000  
0 AACTTTCGAA

\*\*\*\*\*  
Consensus:

AACTTTCGAA

>Cele-UNSB01\_Fam\_408\_10\_1 Nr. of seq. 1 Alignment length(with gaps) = 10  
Alignment score = 0.000000  
Cele-UNSB01\_5:19792773-19792843 Satlength=71 Nr of Repeats=5  
RepeatLength=10 seed=TGGCGAAAGC Num.seqs=3 Similarity=1.000000  
12 GCTGGCGAAA

\*\*\*\*\*  
Consensus:

TGGCGAAAGC