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*****
The program is running under the following parameters:
Output:
  Prefix of the family name WB235
  Columns for the name: 150
  Cluster with more than 0 sequences are printed
  File with the table:
/home/peypoch/disk1/bioinformatica/sra/nemapodes/WB235/WB235.fa.1-0-0-4-
800-10-1-60-2-0-0-2-0-1-2.sat.fa.0-1-1-1-1-1-0.6-0-1-150-1.fam.t
  File with families in format fasta:
/home/peypoch/disk1/bioinformatica/sra/nemapodes/WB235/WB235.fa.1-0-0-4-
800-10-1-60-2-0-0-2-0-1-2.sat.fa.0-1-1-1-1-1-0.6-0-1-150-1.fam.fa
  Alphabet 0 (size 5) (0:dna bases, 1 aminoacids, 2 codons)
  Length of the mer 1
  Circular permutations are allowed
  Reverse sequencess are considerd.
  Sequences are aligned while similarity : 0.600000
  Alignment score: Normalized respect to the length and number of
sequences.
  Alignment parameters:
    opening gap: -3.000000
    extensio gap: -1.000000
    extreme gaph: -0.500000
  Consensus type: without gap columns
  Similarity matrix file:
/home/peypoch/disk1/bioinformatica/malig/darreraversio/score_matrix.3.-1
  Multifasta file:
/home/peypoch/disk1/bioinformatica/sra/nemapodes/WB235/WB235.fa.1-0-0-4-
800-10-1-60-2-0-0-2-0-1-2.sat.fa

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Number of sequences=3978
There are 402 alignments:

>WB235_Fam_1_35_172 Nr. of seq. 172 Alignment length(with gaps) = 44
Alignment score = 0.653800
WB235_2:11660023-11660287 Satlength=265 Nr of Repeats=8 RepeatLength=33
seed=AATTGAAAAT Num.seqs=8 Similarity=0.834055
0 AATT--G--AA-AA---TCCGGCAAATGGGC-AAATTGCCG-G-
WB235_1:3835938-3837024 Satlength=1087 Nr of Repeats=26 RepeatLength=34
seed=TGCCGGAATT Num.seqs=16 Similarity=0.878105
28 AATT--G--AA--A-TTTCCAGCAAATCGGC-AAATTGCCG-G-
WB235_2:5627848-5628154 Satlength=307 Nr of Repeats=9 RepeatLength=34
seed=GGAATTGAAA Num.seqs=9 Similarity=0.831481
32 AATT--G--AA--A-TTTCCGGCAAATCGGC-AAATTGCCG-G-
Rev.of_WB235_2:15188581-15189224 Satlength=644 Nr of Repeats=18
RepeatLength=34 seed=TTTCAATTCC Num.seqs=12 Similarity=0.906120
42 AATT--G--AA--A-TTTCCGGCAAATCGGC-AAATTGCCG-G-
Rev.of_WB235_3:11495534-11496085 Satlength=552 Nr of Repeats=15
RepeatLength=34 seed=AAATTTCAAT Num.seqs=10 Similarity=0.841394
45 AATT--G--AA--A-TTTCCGGCAAATCGGC-AAATTGCCG-G-

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WB235_3:13095846-13096595 Satlength=750 Nr of Repeats=22 RepeatLength=34
seed=AAATCGGCAA Num.seqs=21 Similarity=0.849300
50 AATT--G--AA--A-TTTCGGCAAATCGGC-AAATTGCCG-G-
WB235_3:13099929-13100574 Satlength=646 Nr of Repeats=18 RepeatLength=34
seed=CGGAATTGAA Num.seqs=15 Similarity=0.854715
65 AATT--G--AA--A-TTTCGGCAAATCGGC-AAATTGCCG-G-
Rev.of_WB235_3:12584489-12584865 Satlength=377 Nr of Repeats=11
RepeatLength=34 seed=TTTCAATTCC Num.seqs=7 Similarity=0.788982
42 AATT--G--AA--A-TTTCGGTAAATCGGC-AAATTGCCG-G-
Rev.of_WB235_1:14772871-14773518 Satlength=648 Nr of Repeats=19
RepeatLength=34 seed=CGGAAATTTTC Num.seqs=18 Similarity=0.965142
48 AATT--G--AA--A-TTTCGGCAAATCGGC-AAATTGCTG-G-
WB235_2:14870141-14870668 Satlength=528 Nr of Repeats=13 RepeatLength=35
seed=TTTCCGGCAA Num.seqs=8 Similarity=0.791837
77 AATT--GA-AA--A-TTTCGGCAAATCGGC-AAATTGCTG-G-
Rev.of_WB235_4:382116-382388 Satlength=273 Nr of Repeats=8
RepeatLength=34 seed=TTGCAGGAAA Num.seqs=8 Similarity=0.823529
52 AATT--G--AA--A-TTTCCTGCAAACCGGC-AAATTGCCG-G-
Rev.of_WB235_5:775516-775721 Satlength=206 Nr of Repeats=6
RepeatLength=34 seed=CAATTTGCCG Num.seqs=5 Similarity=0.788235
64 AATT--G--AA--A-TTTCGGCAAACCGGC-AAATTGCCG-A-
Rev.of_WB235_2:13037761-13037897 Satlength=137 Nr of Repeats=4
RepeatLength=34 seed=TTCAATTCCG Num.seqs=4 Similarity=0.803922
41 AATT--G--AA--A-TTTCGGCAAATCGAC-GAATTGCCG-G-
WB235_1:11061949-11062380 Satlength=432 Nr of Repeats=11 RepeatLength=34
seed=TTCCGGCAAA Num.seqs=9 Similarity=0.844227
43 AATT--T--AA--A-TTTCGGCAAATCGGA-AAATTGCCG-G-
Rev.of_WB235_4:3004801-3005510 Satlength=710 Nr of Repeats=20
RepeatLength=34 seed=CCGATTTGCC Num.seqs=12 Similarity=0.843731
57 AGTT--G--AA--A-TTTCGGCAAATCGGT-AAATTGCCG-G-
WB235_3:12531237-12531912 Satlength=676 Nr of Repeats=18 RepeatLength=35
seed=TTCCGGCAA Num.seqs=13 Similarity=0.878877
77 AATT--G--AAC-A-TTTCGGCAAATCGGT-AAATTGCCG-G-
Rev.of_WB235_1:1012604-1013479 Satlength=876 Nr of Repeats=25
RepeatLength=35 seed=ATTTTCAATT Num.seqs=25 Similarity=0.921397
44 AATT--G--AA-AA-TTTCGGCAAATCGGC-AACTGCCG-G-
WB235_1:1564845-1565136 Satlength=292 Nr of Repeats=7 RepeatLength=35
seed=CGGCAAATCG Num.seqs=6 Similarity=0.895873
47 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
Rev.of_WB235_1:1605584-1606132 Satlength=549 Nr of Repeats=6
RepeatLength=35 seed=AAATTTTCAA Num.seqs=5 Similarity=0.878095
81 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
Rev.of_WB235_1:1946493-1947006 Satlength=514 Nr of Repeats=5
RepeatLength=35 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.759259
54 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
WB235_1:2809445-2809654 Satlength=210 Nr of Repeats=5 RepeatLength=35
seed=GGAATTGAAA Num.seqs=3 Similarity=0.898413
67 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
Rev.of_WB235_1:10977031-10977503 Satlength=473 Nr of Repeats=10
RepeatLength=35 seed=TTGCCGATTT Num.seqs=6 Similarity=0.702469
61 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
Rev.of_WB235_2:12770724-12771186 Satlength=463 Nr of Repeats=10
RepeatLength=35 seed=TCAATTCGG Num.seqs=9 Similarity=0.876190
75 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-

Rev.of_WB235_2:13394857-13395660 Satlength=804 Nr of Repeats=20
 RepeatLength=35 seed=GATTTGCCGG Num.seqs=15 Similarity=0.816490
 56 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_2:14239112-14239812 Satlength=701 Nr of Repeats=18 RepeatLength=35
 seed=GCAAATCGGC Num.seqs=14 Similarity=0.835060
 49 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_2:15111116-15111396 Satlength=281 Nr of Repeats=8
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=8 Similarity=0.858503
 54 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_3:1148439-1149466 Satlength=1028 Nr of Repeats=13 RepeatLength=35
 seed=TTTAAAATTT Num.seqs=8 Similarity=0.863946
 71 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_3:1315590-1315824 Satlength=235 Nr of Repeats=5 RepeatLength=35
 seed=CAAATCGGCA Num.seqs=3 Similarity=0.695238
 50 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_3:2545690-2546082 Satlength=393 Nr of Repeats=11
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=7 Similarity=0.807710
 54 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_3:3661285-3661688 Satlength=404 Nr of Repeats=8 RepeatLength=35
 seed=TTCCGGCAAA Num.seqs=5 Similarity=0.760000
 79 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_3:11817185-11817612 Satlength=428 Nr of Repeats=12 RepeatLength=35
 seed=AATTGCCGGA Num.seqs=10 Similarity=0.840847
 60 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_3:12408999-12409471 Satlength=473 Nr of Repeats=10
 RepeatLength=35 seed=GATTTGCCGG Num.seqs=7 Similarity=0.791446
 56 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_5:4197817-4198139 Satlength=323 Nr of Repeats=8
 RepeatLength=35 seed=TTTCAATTCC Num.seqs=7 Similarity=0.885714
 77 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_5:4718387-4718578 Satlength=192 Nr of Repeats=5 RepeatLength=35
 seed=CGGCAAATCG Num.seqs=3 Similarity=0.479798
 47 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_1:13014176-13014829 Satlength=654 Nr of Repeats=16 RepeatLength=35
 seed=ATTGCCGGAA Num.seqs=10 Similarity=0.780741
 61 AATT--G--AA-AA-TTTCGGCAAATCGGN-AAATTGCCG-G-
 WB235_2:233654-235183 Satlength=1530 Nr of Repeats=40 RepeatLength=35
 seed=TTTCCGGCAA Num.seqs=27 Similarity=0.708272
 78 AATT--G--AA-AA-TTTCGGCAAATCGGC-ANATTGCCG-G-
 Rev.of_WB235_5:2391673-2391869 Satlength=197 Nr of Repeats=4
 RepeatLength=35 seed=AAATTTTCAA Num.seqs=3 Similarity=0.780864
 81 AATT--G--AA-AA-TTTCGGCNAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_5:2499952-2500148 Satlength=197 Nr of Repeats=4
 RepeatLength=35 seed=AAATTTTCAA Num.seqs=3 Similarity=0.780864
 81 AATT--G--AA-AA-TTTCGGCNAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_3:11687193-11687714 Satlength=522 Nr of Repeats=14
 RepeatLength=35 seed=CCGATTGCGC Num.seqs=10 Similarity=0.809053
 58 AATT--G--AA-AA-TTTCNGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_3:11925619-11926677 Satlength=1059 Nr of Repeats=29
 RepeatLength=35 seed=TTCAATTCCG Num.seqs=21 Similarity=0.856834
 76 AATT--G--AA-AA-TTTCNGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_5:1377073-1377773 Satlength=701 Nr of Repeats=21
 RepeatLength=35 seed=ATTTTCAATT Num.seqs=15 Similarity=0.700680
 79 AATT--G--AA-AA-TTTCNGGCAAATCGGC-AAATTGCCG-G-

WB235_2:14264215-14264530 Satlength=316 Nr of Repeats=8 RepeatLength=35
 seed=CGGCAAATCG Num.seqs=7 Similarity=0.780864
 47 AATT--G--NA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_2:14278881-14279293 Satlength=413 Nr of Repeats=12
 RepeatLength=35 seed=GCCGGAAATT Num.seqs=11 Similarity=0.952900
 51 AATT--G--GA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_1:1814405-1814778 Satlength=374 Nr of Repeats=9
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=8 Similarity=0.766700
 54 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_2:15047976-15048537 Satlength=562 Nr of Repeats=16
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=11 Similarity=0.731650
 54 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_1:2139349-2139629 Satlength=281 Nr of Repeats=8
 RepeatLength=35 seed=CGGCAAATTG Num.seqs=5 Similarity=0.885714
 68 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_5:2670563-2670782 Satlength=220 Nr of Repeats=6
 RepeatLength=35 seed=GCCGGAAATT Num.seqs=4 Similarity=0.752381
 51 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_2:15210567-15211143 Satlength=577 Nr of Repeats=12
 RepeatLength=35 seed=CCGATTGCGC Num.seqs=11 Similarity=0.807446
 58 AATT--C--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_3:12244502-12244747 Satlength=246 Nr of Repeats=7 RepeatLength=35
 seed=AATTGCCGGA Num.seqs=7 Similarity=0.912925
 60 AATT--C--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_3:2791812-2792160 Satlength=349 Nr of Repeats=10
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=8 Similarity=0.859864
 89 AATT--A--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_3:12884539-12885107 Satlength=569 Nr of Repeats=13 RepeatLength=35
 seed=TGCCGGAATT Num.seqs=8 Similarity=0.817687
 63 AATT--T--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_5:2660817-2661267 Satlength=451 Nr of Repeats=10 RepeatLength=35
 seed=TTTCGGCAA Num.seqs=7 Similarity=0.807710
 78 AATT--T--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_1:11349013-11350796 Satlength=1784 Nr of Repeats=47 RepeatLength=35
 seed=GGCAAATCAG Num.seqs=42 Similarity=0.911023
 48 AATT--G--AA-AA-TTTCGGCAAATCAGC-AAATTGCCG-G-
 WB235_2:13598247-13598526 Satlength=280 Nr of Repeats=7 RepeatLength=35
 seed=TTGCCGGAAT Num.seqs=6 Similarity=0.784127
 62 AATT--G--AA-TA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_5:3765128-3765284 Satlength=157 Nr of Repeats=4
 RepeatLength=35 seed=TTGCCGATTT Num.seqs=3 Similarity=0.784127
 96 AATT--G--AA-TN-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_1:12977769-12978231 Satlength=463 Nr of Repeats=10
 RepeatLength=35 seed=GCCGGAAATT Num.seqs=7 Similarity=0.776871
 51 AATT--N--AN-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_5:2640455-2641508 Satlength=1054 Nr of Repeats=15
 RepeatLength=35 seed=TCAATTCCGG Num.seqs=10 Similarity=0.832381
 75 AATT--G--AG-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_2:14273310-14273525 Satlength=216 Nr of Repeats=5 RepeatLength=35
 seed=CGGCAAATTG Num.seqs=3 Similarity=0.586563
 55 AATT--G--AA-AA-TTTCGGNAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_4:1928447-1928762 Satlength=316 Nr of Repeats=8
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=7 Similarity=0.927438
 82 AATT--G--AA-AA-TTTCGTCAAATCGGC-AAATTGCCG-G-

Rev.of_WB235_2:15044151-15044326 Satlength=176 Nr of Repeats=5
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.771429
 54 AATT--N--AA-AA-TTTCGGCAAATCGGC-AAATTGCCN-G-
 Rev.of_WB235_1:2165416-2165854 Satlength=439 Nr of Repeats=10
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=6 Similarity=0.735873
 54 AATT--C--AA-AA-TTTCGGCAAATCGGC-AAATTGTCG-G-
 WB235_1:13453071-13453246 Satlength=176 Nr of Repeats=5 RepeatLength=35
 seed=TGAAAATTTTC Num.seqs=5 Similarity=0.878095
 72 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGTCG-G-
 WB235_1:14619236-14619481 Satlength=246 Nr of Repeats=6 RepeatLength=35
 seed=CAAATCGGCA Num.seqs=4 Similarity=0.733333
 85 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGTCG-G-
 Rev.of_WB235_3:2066729-2067447 Satlength=719 Nr of Repeats=12
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=10 Similarity=0.926349
 89 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGTCG-G-
 Rev.of_WB235_5:5125946-5126346 Satlength=401 Nr of Repeats=8
 RepeatLength=35 seed=TTGCCGATTT Num.seqs=5 Similarity=0.767619
 61 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGNCG-G-
 WB235_2:14269513-14269895 Satlength=383 Nr of Repeats=11 RepeatLength=35
 seed=CCGGCAAATC Num.seqs=8 Similarity=0.757275
 81 AATT--G--AA-AC-TTTCGGCAAATCGGC-AAATTGGCG-G-
 WB235_3:12005666-12006008 Satlength=343 Nr of Repeats=8 RepeatLength=35
 seed=GGAATTGAAA Num.seqs=5 Similarity=0.843810
 102 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGGCG-G-
 WB235_5:15168733-15168927 Satlength=195 Nr of Repeats=6 RepeatLength=35
 seed=GGAATTGAAA Num.seqs=4 Similarity=0.904762
 102 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGGCG-G-
 Rev.of_WB235_1:14843491-14843700 Satlength=210 Nr of Repeats=6
 RepeatLength=35 seed=TTTCAATTCC Num.seqs=5 Similarity=0.878095
 77 AATT--G--AA-AG-TTTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_4:2872402-2872909 Satlength=508 Nr of Repeats=14
 RepeatLength=35 seed=ATTCCGGCAA Num.seqs=11 Similarity=0.820606
 107 AATT--G--AA-AA-TTTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_1:2738743-2738953 Satlength=211 Nr of Repeats=6
 RepeatLength=35 seed=AATTTCATT Num.seqs=6 Similarity=0.860317
 44 AATT--G--AA-AT-TTTCGGCAAATCGGC-AAGTTGCCG-G-
 WB235_1:10993314-10993636 Satlength=323 Nr of Repeats=8 RepeatLength=35
 seed=GCCGGAATTG Num.seqs=7 Similarity=0.829478
 64 AATT--G--AA-AT-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_2:13642102-13642382 Satlength=281 Nr of Repeats=7
 RepeatLength=35 seed=CTTGCCGATT Num.seqs=6 Similarity=0.862857
 62 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAGTTGCCG-G-
 WB235_4:3309618-3310597 Satlength=980 Nr of Repeats=27 RepeatLength=35
 seed=AATCGGCAAG Num.seqs=25 Similarity=0.850540
 87 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAGTTACCG-G-
 Rev.of_WB235_3:10661890-10662218 Satlength=329 Nr of Repeats=9
 RepeatLength=35 seed=CAATTGCGG Num.seqs=6 Similarity=0.885714
 65 ATAT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_5:1813009-1813219 Satlength=211 Nr of Repeats=7
 RepeatLength=35 seed=TCCGGCAATT Num.seqs=5 Similarity=0.833333
 70 ATTT--N--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-G-
 WB235_1:1884484-1884939 Satlength=456 Nr of Repeats=11 RepeatLength=35
 seed=AAATCGGCAA Num.seqs=8 Similarity=0.753742
 51 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-A-

Rev.of_WB235_2:13740296-13741317 Satlength=1022 Nr of Repeats=28
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=18 Similarity=0.750016
 54 AATT--C--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-A-
 Rev.of_WB235_1:1949999-1950277 Satlength=279 Nr of Repeats=8
 RepeatLength=35 seed=TTGCCGGAAA Num.seqs=6 Similarity=0.654655
 53 AATT--G--AA-CA-TTTCGGCAAATCGGC-AAATTGCCG-A-
 WB235_5:17880208-17882252 Satlength=2045 Nr of Repeats=55 RepeatLength=35
 seed=TCCGGCAAAT Num.seqs=37 Similarity=0.726298
 80 AATT--G--AA-AA-TTTCGGCAAATCGGC-AAATTGCCG-A-
 WB235_4:3149092-3151000 Satlength=1909 Nr of Repeats=53 RepeatLength=35
 seed=GGCAAATTGC Num.seqs=42 Similarity=0.867264
 56 AATT--G--AA-CA-TTTCGGCAAATAGGC-AAATTGCCG-A-
 WB235_1:1083222-1083538 Satlength=317 Nr of Repeats=8 RepeatLength=35
 seed=CGGCAAATCG Num.seqs=7 Similarity=0.873016
 47 AATT--G--AA-AA-TTTCGGCAAATCGGC-ATTTTGCCG-G-
 Rev.of_WB235_5:1385851-1386349 Satlength=499 Nr of Repeats=9
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=6 Similarity=0.779048
 54 AATT--G--AA-AA-TTTCGGCAAATCCGC-AAATTGCCG-G-
 Rev.of_WB235_5:17991128-17991485 Satlength=358 Nr of Repeats=5
 RepeatLength=35 seed=AATTCCGGCA Num.seqs=3 Similarity=0.822222
 73 AATT--G--AA-AA-TTTCGGCAAACGGC-ATATTGCCG-G-
 WB235_1:14481352-14481947 Satlength=596 Nr of Repeats=17 RepeatLength=35
 seed=CGGCAAATTG Num.seqs=11 Similarity=0.941818
 55 AATC--G--AA-AA-TTTCGGCAAACGGC-AAATTGCCG-G-
 Rev.of_WB235_5:4193678-4193984 Satlength=307 Nr of Repeats=5
 RepeatLength=35 seed=AATTTTCAAT Num.seqs=4 Similarity=0.847619
 80 AATT--G--AA-AA-TTTCGGCAAACGGC-AAATTGCAG-G-
 Rev.of_WB235_3:12629696-12629957 Satlength=262 Nr of Repeats=7
 RepeatLength=35 seed=TAATTCCGGC Num.seqs=6 Similarity=0.916191
 74 AATT--A--AA-AA-TTTCGGCAAACGGC-AAATTGCCG-G-
 WB235_3:12636128-12637282 Satlength=1155 Nr of Repeats=29 RepeatLength=35
 seed=GGCAAACCGG Num.seqs=25 Similarity=0.815309
 83 AATT--A--AN-AA-TTTCGGCAAACGGC-AAATTGCCG-G-
 Rev.of_WB235_3:12692942-12693363 Satlength=422 Nr of Repeats=8
 RepeatLength=35 seed=GGAAATTTTA Num.seqs=5 Similarity=0.820952
 83 AATT--T--AA-AA-TTTCGGCAAACGGC-AAATTGCCG-G-
 WB235_5:775870-776051 Satlength=182 Nr of Repeats=5 RepeatLength=35
 seed=TTTCGGCAA Num.seqs=3 Similarity=0.834921
 78 AATT--G--AA-GA-TTTCGGCAAACGGC-NAATTGCCG-G-
 Rev.of_WB235_1:13800189-13800502 Satlength=314 Nr of Repeats=9
 RepeatLength=35 seed=AATTCCGGCA Num.seqs=7 Similarity=0.756173
 73 AATT--T--AA-AT-TTTCGGCAAATNGGC-AAATTGCCG-G-
 WB235_3:3030347-3030891 Satlength=545 Nr of Repeats=14 RepeatLength=35
 seed=AATTGCCGGA Num.seqs=11 Similarity=0.836537
 95 AATT--T--AA-AA-TTTCGGCAAATTGGC-AAATTGCCG-G-
 WB235_3:11152069-11152305 Satlength=237 Nr of Repeats=6 RepeatLength=35
 seed=AATTGCCGGA Num.seqs=4 Similarity=0.720635
 95 AATT--A--AA-AA-TTTCGGCAAATTGGC-AAATTGCCG-G-
 WB235_3:11924167-11924393 Satlength=227 Nr of Repeats=6 RepeatLength=35
 seed=TTCCGGCAAA Num.seqs=4 Similarity=0.676190
 114 AATT--G--AA-AA-TTTCGGCAAATTGGC-AAATTGCCG-G-
 Rev.of_WB235_5:2654959-2655536 Satlength=578 Nr of Repeats=16
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=10 Similarity=0.790053
 124 AATT--G--AA-AA-TTTCGGCAAATTGGC-AAATTGNCG-G-

WB235_3:3542667-3542838 Satlength=172 Nr of Repeats=5 RepeatLength=34
 seed=AATTGAAATT Num.seqs=4 Similarity=0.800794
 34 AATT--G--AA--A-TTTCCGGCAAAGCGGC-AAATTGTCG-G-
 Rev.of_WB235_1:3602994-3603167 Satlength=174 Nr of Repeats=5
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.822222
 54 AATT--G--AA-CA-TTTCCGGCAAACCGGC-AAATTGTCG-G-
 WB235_1:11186372-11187503 Satlength=1132 Nr of Repeats=15 RepeatLength=35
 seed=TTCCGGCAAA Num.seqs=9 Similarity=0.743915
 44 AACT--G--AA-AA-TTTCCGGCAAATCGGC-AAATTGCCN-G-
 WB235_3:11546762-11547752 Satlength=991 Nr of Repeats=24 RepeatLength=35
 seed=CGGCAAATCG Num.seqs=16 Similarity=0.809524
 47 AACT--G--AA-AA-TTTCCGGCAAATCGGC-AAATTGCCA-A-
 Rev.of_WB235_2:12757809-12758089 Satlength=281 Nr of Repeats=8
 RepeatLength=35 seed=ATTTTCAGGCA Num.seqs=8 Similarity=0.791832
 73 AAAT--G--AA-AA-TTTCTGGCAAATCGGC-AAATTGCCT-G-
 Rev.of_WB235_2:12757828-12758945 Satlength=1118 Nr of Repeats=16
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=10 Similarity=0.752804
 89 AAAT--G--AA-AA-TTTCCGGCAAATCGGC-AAATTGCCN-G-
 WB235_2:4296664-4296988 Satlength=325 Nr of Repeats=8 RepeatLength=35
 seed=TTCCGGCAAA Num.seqs=5 Similarity=0.790476
 44 AATT--G--AA-AA-TTTCCGGCAAACCGGC-AAATTGCCA-A-
 WB235_3:12004285-12004750 Satlength=466 Nr of Repeats=12 RepeatLength=35
 seed=AAAATTTCCG Num.seqs=9 Similarity=0.877249
 74 AATT--G--AA-AA-TTTCCGGCAAATCAGC-TAATTGCCA-G-
 WB235_3:12289600-12291140 Satlength=1541 Nr of Repeats=44 RepeatLength=35
 seed=TTGCCAGAAT Num.seqs=44 Similarity=0.791362
 97 AATT--G--AA-AA-ATTCCGGNAAATCGGC-AAATTGCCA-G-
 Rev.of_WB235_5:1273379-1274003 Satlength=625 Nr of Repeats=14
 RepeatLength=35 seed=AATTCTGGCA Num.seqs=12 Similarity=0.883983
 108 AATT--G--AA-AA-TTTCCGGCAAATCGGT-AATTTGCCA-G-
 Rev.of_WB235_5:1273379-1274654 Satlength=1276 Nr of Repeats=15
 RepeatLength=35 seed=AATTCTGGCA Num.seqs=12 Similarity=0.883983
 108 AATT--G--AA-AA-TTTCCGGCAAATCGGT-AATTTGCCA-G-
 WB235_2:14780596-14780942 Satlength=347 Nr of Repeats=4 RepeatLength=35
 seed=TCCGGCAAAT Num.seqs=3 Similarity=0.586420
 45 AATT--T--AN-AA-TNTCCGGCAAATCGGC-AAATTGCCG-A-
 WB235_5:19799341-19799769 Satlength=429 Nr of Repeats=12 RepeatLength=35
 seed=AATTTCCGGC Num.seqs=11 Similarity=0.926580
 76 AATT--T--AA-AA-TTTCCGGCAAATCGGC-AAATAACCG-G-
 Rev.of_WB235_1:14764447-14764676 Satlength=230 Nr of Repeats=5
 RepeatLength=34 seed=GAAATTTCAA Num.seqs=4 Similarity=0.901961
 46 AGTT--G--AA--A-TTTCCGGCAAATTGGC-TAATTGCCG-G-
 WB235_2:14137014-14137524 Satlength=511 Nr of Repeats=14 RepeatLength=34
 seed=CGGAATTGAA Num.seqs=13 Similarity=0.833082
 65 AATT--G--AA--A-TTTCCGGCAAATTGGT-AAAATGCCG-G-
 Rev.of_WB235_3:12532752-12533511 Satlength=760 Nr of Repeats=21
 RepeatLength=34 seed=TTTCAATTCC Num.seqs=15 Similarity=0.747664
 76 AATT--G--AA--A-NTTCCGGCAAATTGGT-AAATTGCCG-G-
 Rev.of_WB235_3:133200-133804 Satlength=605 Nr of Repeats=7
 RepeatLength=34 seed=AATTCCGGCA Num.seqs=5 Similarity=0.976471
 72 AATT--G--AA--A-TTTTTGGCAAATTGGT-AAATTGCCG-G-
 WB235_4:1348897-1349230 Satlength=334 Nr of Repeats=9 RepeatLength=34
 seed=ATTGCCGGAA Num.seqs=7 Similarity=0.886088
 94 AATT--G--AA--A-TTTCTGGCAAATTGGC-AAATTGCCG-G-

WB235_5:4685532-4685994 Satlength=463 Nr of Repeats=10 RepeatLength=35
 seed=GCAAAATCGGC Num.seqs=6 Similarity=0.837460
 15 -ATTC-G--AA-AA-TGTCCGGCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_2:13831950-13832774 Satlength=825 Nr of Repeats=18
 RepeatLength=34 seed=AATTCCGGCA Num.seqs=12 Similarity=0.803922
 4 AATT--G--AA--A-TTTCCGATAAATCAGC-AAATTGCCG-G-
 WB235_3:10489911-10490082 Satlength=172 Nr of Repeats=5 RepeatLength=34
 seed=TTTCCGGCAA Num.seqs=4 Similarity=0.819841
 8 AATC-----AA-AA-TTTCCGGCAAATTGAC-AAATTGCCG-G-
 WB235_5:3702753-3703068 Satlength=316 Nr of Repeats=9 RepeatLength=35
 seed=AAAATTTCCG Num.seqs=9 Similarity=0.834921
 5 AATT--G--AA-AA-TTTCCGGCAAACAGGC-AAATTTCTG-G-
 WB235_1:2557777-2557986 Satlength=210 Nr of Repeats=6 RepeatLength=35
 seed=TTGCCGGAAT Num.seqs=5 Similarity=0.794286
 28 AATT--G--AA-AA-TTTTTGGNAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_1:2844921-2845096 Satlength=176 Nr of Repeats=4
 RepeatLength=35 seed=TTTGCCGATT Num.seqs=3 Similarity=0.733333
 28 AATT--A--AA-AA-TTTTGNCAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_1:11425096-11425445 Satlength=350 Nr of Repeats=9
 RepeatLength=35 seed=ATTCCGGCAA Num.seqs=6 Similarity=0.888254
 38 AATT--G--AA-AA-TTTCTGGAAAATCGGC-AAATTGCCG-G-
 Rev.of_WB235_1:14811659-14812009 Satlength=351 Nr of Repeats=10
 RepeatLength=35 seed=AATTCCGGCA Num.seqs=10 Similarity=0.804115
 39 AATT--G--AA-AA-TTTCAGGAAAATCGGC-AAATTGCCG-G-
 WB235_3:3037879-3038500 Satlength=622 Nr of Repeats=13 RepeatLength=35
 seed=AAATCGGCAA Num.seqs=8 Similarity=0.885714
 52 AATT--G--AA-AA-TTTCAGAAAATCGGC-AAATTGCCG-G-
 WB235_2:13761268-13762971 Satlength=1704 Nr of Repeats=50 RepeatLength=35
 seed=CCGGAATTGA Num.seqs=37 Similarity=0.869813
 66 AATT--G--AA-AA-TTTCTGGAAAATCAAC-AAATTGCCG-G-
 Rev.of_WB235_5:1239922-1240281 Satlength=360 Nr of Repeats=10
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=8 Similarity=0.842177
 48 AATT--G--AA-AA-TTTCTGGCAATTTGGC-AAATTGCCG-G-
 WB235_2:10713445-10714142 Satlength=698 Nr of Repeats=8 RepeatLength=35
 seed=TTTCTGGCAA Num.seqs=5 Similarity=0.900952
 44 AAAT--T--AA-AA-TTTCTGGCAAACCGGC-AAATTGCCG-A-
 WB235_3:12341199-12341722 Satlength=524 Nr of Repeats=7 RepeatLength=35
 seed=TTGCCGGAAT Num.seqs=5 Similarity=0.729630
 63 AATT--G--NA-AA-TTTCTGGCAAACCGGC-AAATTGCCG-G-
 WB235_2:15211519-15211997 Satlength=479 Nr of Repeats=9 RepeatLength=35
 seed=TTGCCGGAAT Num.seqs=6 Similarity=0.720635
 63 AATT--T--AA-AA-TTTCTGGCAAACCGCC-AAATTGCCG-G-
 Rev.of_WB235_3:11311767-11311976 Satlength=210 Nr of Repeats=6
 RepeatLength=35 seed=GATTTGCCGG Num.seqs=5 Similarity=0.850926
 22 ATTT----TAA-TA-TTTCCGGCAAATCGAT-AAATTGCCG-G-
 Rev.of_WB235_5:4443918-4444112 Satlength=195 Nr of Repeats=5
 RepeatLength=35 seed=ATTCCGGCAA Num.seqs=3 Similarity=0.822222
 38 AATT----TAA-TA-GTTCCGGCAAATCGGC-AAATTGCCG-G-
 WB235_5:19762622-19764008 Satlength=1387 Nr of Repeats=40 RepeatLength=35
 seed=CCGGCAAATC Num.seqs=26 Similarity=0.887707
 47 ATTT--G-TAA--A-TTTCCGGCAAATCGAN-AAATTACCG-G-
 Rev.of_WB235_4:2851958-2852560 Satlength=603 Nr of Repeats=7
 RepeatLength=35 seed=TTTTCAATTC Num.seqs=5 Similarity=0.801905
 9 AATT--G--AA-AA-ATTCAGGCAAATCTGC-AAATTGCTT-G-

Rev.of_WB235_5:3763703-3764133 Satlength=431 Nr of Repeats=4
 RepeatLength=35 seed=GCCGATTTGC Num.seqs=3 Similarity=0.743827
 25 ANTT--G--AA-CA-TTTCAGGCAAATCGGC-AAATTGNCA-G-
 WB235_1:1211856-1212413 Satlength=558 Nr of Repeats=15 RepeatLength=35
 seed=AAATCGGCAA Num.seqs=12 Similarity=0.802020
 17 AAAT--G--AA-AG-ATTCCGGCAAATCGGC-AATTTGCCN-A-
 Rev.of_WB235_1:1919828-1922029 Satlength=2202 Nr of Repeats=58
 RepeatLength=35 seed=TTGCCGATTT Num.seqs=42 Similarity=0.889475
 27 AAAT--G--AA-AA-TTTCGGCAAATCGGC-AATTTGCNA-A-
 WB235_5:4190322-4190733 Satlength=412 Nr of Repeats=11 RepeatLength=35
 seed=TTCCGGCAAA Num.seqs=7 Similarity=0.865760
 45 AAAT--G--AA-AA-TTTCGGCAAACCGGC-AATTTGCCA-A-
 Rev.of_WB235_3:11422288-11422568 Satlength=281 Nr of Repeats=6
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=4 Similarity=0.790476
 55 AAAT--C--AA-AA-TTTCGGCAAATCGGC-AATTTGCCA-G-
 WB235_3:12823844-12823984 Satlength=141 Nr of Repeats=4 RepeatLength=35
 seed=CGGCAATTTG Num.seqs=4 Similarity=0.936508
 56 AAAT--C--AA-AA-TTTCGGCAAATCGGC-AATTTGCCA-A-
 Rev.of_WB235_5:1388994-1389344 Satlength=351 Nr of Repeats=8
 RepeatLength=35 seed=TGCCGGAAAT Num.seqs=5 Similarity=0.790476
 88 AAAT--C--AA-AA-TTTCGGCAAATCGGC-AATTTGCCA-A-
 Rev.of_WB235_3:12722182-12722605 Satlength=424 Nr of Repeats=13
 RepeatLength=35 seed=AAATTTTGAT Num.seqs=9 Similarity=0.900529
 82 AAAT--C--AA-AA-TTTCGGCAAATCGGC-AAATTGCCA-A-
 Rev.of_WB235_5:4146424-4146572 Satlength=149 Nr of Repeats=4
 RepeatLength=35 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.682540
 55 AAAT--N--AA-AA-TTTCGGCAAAACCGGC-AATTTACCA-A-
 Rev.of_WB235_5:5215493-5215916 Satlength=424 Nr of Repeats=9
 RepeatLength=35 seed=CGATTTGCCG Num.seqs=6 Similarity=0.576768
 58 AAAT--A--AA-AA-TTTCGGCAAATCGGC-AATTTGCC-GA-
 WB235_6:209349-209653 Satlength=305 Nr of Repeats=8 RepeatLength=36
 seed=ATAAAAATTT Num.seqs=7 Similarity=0.865961
 73 AAAT--A--AA-AA-TTTCGGCAAATCGGC-AATTTGCCAGA-
 Rev.of_WB235_4:1295080-1295440 Satlength=361 Nr of Repeats=9
 RepeatLength=36 seed=TTATTTTCTG Num.seqs=8 Similarity=0.838624
 77 AAAT--A--AA-AA-TTTCGGCAAATGGGC-AATTTGTCAGA-
 Rev.of_WB235_4:1299931-1300254 Satlength=324 Nr of Repeats=8
 RepeatLength=36 seed=TTTGCCGGAA Num.seqs=5 Similarity=0.859259
 91 AAAT--A--AA-AA-TTTCGGCAAATCGGC-AATTTGTCAGA-
 Rev.of_WB235_1:1935250-1936853 Satlength=1604 Nr of Repeats=40
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=33 Similarity=0.890620
 48 AACT--G--AA-AA-TTTCGGCAAATCGGC-AATTTGCCG-A-
 Rev.of_WB235_1:1935250-1938219 Satlength=2970 Nr of Repeats=70
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=48 Similarity=0.836375
 48 AACT--G--AA-AA-TTTCGGCAAATCGGC-AATTTGCCG-A-
 WB235_1:14449256-14449536 Satlength=281 Nr of Repeats=8 RepeatLength=35
 seed=AAAAATTTCCG Num.seqs=8 Similarity=0.952381
 75 AAGT--G--AA-AA-TTTCGGCAAATCGGC-AATTTACCG-A-
 Rev.of_WB235_1:14452267-14454642 Satlength=2376 Nr of Repeats=68
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=67 Similarity=0.938593
 83 AAGT--G--AA-AA-TTTCGGCAAATCGGC-AATTTACCG-A-
 WB235_5:1940104-1940384 Satlength=281 Nr of Repeats=8 RepeatLength=35
 seed=GGCAAATCGG Num.seqs=8 Similarity=0.914286
 84 AAAT--G--AA-AA-TTTCGGCAAATCGGC-AATTTTCCG-A-

WB235_4:1654913-1655123 Satlength=211 Nr of Repeats=6 RepeatLength=35
 seed=ATTTCCGGCA Num.seqs=6 Similarity=0.819683
 78 AAAT--G--AA-AA-TTTCCGGCAAATCGGC-AATATGCCG-A-
 WB235_4:16403739-16404089 Satlength=351 Nr of Repeats=10 RepeatLength=35
 seed=CAAATCGGCA Num.seqs=8 Similarity=0.824490
 86 AATT--G--AA-AA-TTTCCGGCAAATCGGC-AATATGCCA-A-
 WB235_4:16409693-16409938 Satlength=246 Nr of Repeats=7 RepeatLength=35
 seed=GCAAATCGGC Num.seqs=7 Similarity=0.842177
 120 AATT--G--AA-AA-TTTCCGGCAAATCGGC-AATATGCCA-A-
 Rev.of_WB235_4:16408366-16409098 Satlength=733 Nr of Repeats=21
 RepeatLength=35 seed=TTTGCCATAT Num.seqs=16 Similarity=0.860000
 106 AATT--G--AA-AT-TTTCCGGCAAATCGGC-AATATGCCA-A-
 Rev.of_WB235_2:4569011-4569221 Satlength=211 Nr of Repeats=5
 RepeatLength=35 seed=TTTGCCGAA Num.seqs=4 Similarity=0.757716
 55 AAAT--G--AA-AT-TTTCCGGCAAATCGGT-AATTTGCCG-A-
 Rev.of_WB235_5:19795837-19797364 Satlength=1528 Nr of Repeats=40
 RepeatLength=35 seed=GAAATTTTCA Num.seqs=29 Similarity=0.756979
 83 AAAT--G--AA-AA-TTTCCGGCAAATCNGT-AATTTGCCG-A-
 WB235_1:11190690-11191449 Satlength=760 Nr of Repeats=4 RepeatLength=35
 seed=TCGGCAAATT Num.seqs=3 Similarity=1.000000
 20 AAAT--G--AA-AA-TTTCCGGCAAATCGGC-AAATTACGG-A-
 Rev.of_WB235_2:2529567-2530441 Satlength=875 Nr of Repeats=24
 RepeatLength=35 seed=CCGGAAATTT Num.seqs=16 Similarity=0.798413
 51 AAAT--G--AA-AA-TTTCCGGCAAATCGGC-AAATCGCCG-A-
 Rev.of_WB235_5:967850-968138 Satlength=289 Nr of Repeats=7
 RepeatLength=35 seed=TGCCGATTTG Num.seqs=5 Similarity=0.809524
 26 AAAT--G--AA-CA-TTTCCGGCAAATCGGC-AAATTCTCG-A-
 Rev.of_WB235_2:13422904-13423919 Satlength=1016 Nr of Repeats=29
 RepeatLength=35 seed=GAATTTTGA Num.seqs=29 Similarity=0.850622
 48 AAAT--C--AA-AA-ATTCCGGCAAATCGGC-AAATTGCCG-A-
 Rev.of_WB235_3:12731873-12732374 Satlength=502 Nr of Repeats=16
 RepeatLength=35 seed=ATTTGCCGGA Num.seqs=10 Similarity=0.867936
 56 AAAT--C--AA-AA-TTTCCGGCAAATCGGC-ATATTGCCG-G-
 Rev.of_WB235_5:5117986-5118371 Satlength=386 Nr of Repeats=10
 RepeatLength=35 seed=TGCCGGAAT Num.seqs=6 Similarity=0.730794
 88 AAAT--C--AA-AA-TTTCCGGCAAATCGGC-ATTTGCCG-G-
 WB235_4:4355433-4355651 Satlength=219 Nr of Repeats=5 RepeatLength=35
 seed=TTCCGGCAAA Num.seqs=3 Similarity=0.675676
 45 AAAT--C--AG-AG-TTTCCGGCAAATCGAC-AATTTGCCG-A-
 WB235_2:13681580-13681759 Satlength=180 Nr of Repeats=5 RepeatLength=36
 seed=TTGCCATAAA Num.seqs=4 Similarity=0.938272
 29 AAAT--T--AA-AA-TTTCCGGCAAATCAGCAAATTTGCCT-A-
 Rev.of_WB235_4:1931275-1932180 Satlength=906 Nr of Repeats=26
 RepeatLength=35 seed=CATTTTCGCC Num.seqs=20 Similarity=0.946867
 40 AAAT--G--GA-AA-TTTCCGGCAAACCGGC-AATTCGGCG-A-
 Rev.of_WB235_4:1931275-1933389 Satlength=2115 Nr of Repeats=50
 RepeatLength=35 seed=CATTTTCGCC Num.seqs=38 Similarity=0.954101
 40 AAAT--G--GA-AA-TTTCCGGCAAACCGGC-AATTCGGCG-A-
 Rev.of_WB235_1:3028822-3029013 Satlength=192 Nr of Repeats=5
 RepeatLength=35 seed=TTGCCGAAA Num.seqs=3 Similarity=0.808642
 19 AATT-AC--AA--A-TTTCCGGCAAATCGGC-AATTTGTGCG-G-
 WB235_5:18042826-18043263 Satlength=438 Nr of Repeats=10 RepeatLength=35
 seed=TTTCCGGCAA Num.seqs=6 Similarity=0.790432
 45 AATT-TG--AA--AGTTTCCGGCAAATCGGC-ATTTTGCCG-G-

Rev.of_WB235_1:3114471-3114865 Satlength=395 Nr of Repeats=8
RepeatLength=35 seed=CGATTTGCCG Num.seqs=6 Similarity=0.862857
23 AAAT--G--AA-TA-TTTCGGCAAATCGGC-AGTTTGCCG-G-
WB235_3:11314293-11314573 Satlength=281 Nr of Repeats=6 RepeatLength=35
seed=TTGCCGGATT Num.seqs=4 Similarity=0.815873
28 ATTG--G--AA-TA-TTTCGGCAAATCGGC-AATTGCGG-G-
WB235_1:3459203-3459616 Satlength=414 Nr of Repeats=8 RepeatLength=35
seed=TCCGGCAAAT Num.seqs=5 Similarity=0.939048
46 AAGT--C--AA-AA-ATTCCGGCAAATCGGA-AATCTGCCG-G-
Rev.of_WB235_4:4792114-4792760 Satlength=647 Nr of Repeats=17
RepeatLength=35 seed=TTGCCGGAAA Num.seqs=13 Similarity=0.909646
54 AAAC--C--AA-AA-TTTCGGCAAATCGGA-AACTTGCCG-G-
WB235_1:2111857-2112268 Satlength=412 Nr of Repeats=7 RepeatLength=35
seed=CAAACCGGCA Num.seqs=5 Similarity=0.675926
15 AATT-----AA-CA-TTNGAGCAAACCGGC-AANTTGCCG-AA

* *
Consensus:

AAAtGgAAaATTTCCGGCAAATCGGCAAaTTGCCGg

>WB235_Fam_2_12_169 Nr. of seq. 169 Alignment length(with gaps) = 14
Alignment score = 0.769942
WB235_3:2455329-2456409 Satlength=1081 Nr of Repeats=40 RepeatLength=10
seed=AGGCAGGCTT Num.seqs=27 Similarity=0.883001
0 AG-GC---AGGCTT
Rev.of_WB235_1:1-835 Satlength=835 Nr of Repeats=55 RepeatLength=12
seed=CTAAGCCTAA Num.seqs=50 Similarity=0.958639
2 AG-GCTT-AGGCTT
Rev.of_WB235_1:556995-557143 Satlength=149 Nr of Repeats=8
RepeatLength=12 seed=CTAAGCCTAA Num.seqs=5 Similarity=0.811111
2 AG-GCTT-AGGCTT
WB235_1:566943-567081 Satlength=139 Nr of Repeats=8 RepeatLength=12
seed=AGGCTTAGGC Num.seqs=5 Similarity=0.844444
12 AG-GCTT-AGGCTT
Rev.of_WB235_1:640909-641017 Satlength=109 Nr of Repeats=6
RepeatLength=12 seed=TAAGCCTAAG Num.seqs=4 Similarity=0.759259
13 AG-GCTT-AGGCTT
WB235_1:727038-727274 Satlength=237 Nr of Repeats=5 RepeatLength=12
seed=GCTTAGGCTT Num.seqs=3 Similarity=0.777778
2 AG-GCTT-AGGCTT
Rev.of_WB235_1:779157-779331 Satlength=175 Nr of Repeats=12
RepeatLength=12 seed=GCCTAAGCCT Num.seqs=10 Similarity=0.933333
10 AG-GCTT-AGGCTT
Rev.of_WB235_1:806422-806644 Satlength=223 Nr of Repeats=16
RepeatLength=12 seed=GCCTAAGCCT Num.seqs=10 Similarity=0.782716
10 AG-GCTT-AGGCTT
WB235_1:814462-814642 Satlength=181 Nr of Repeats=13 RepeatLength=12
seed=GCTTAGGCTT Num.seqs=9 Similarity=0.895062
2 AG-GCTT-AGGCTT
WB235_1:833515-834452 Satlength=938 Nr of Repeats=48 RepeatLength=12
seed=CTTAGGCTTA Num.seqs=32 Similarity=0.819668
9 AG-GCTT-AGGCTT

WB235_1:846174-846372 Satlength=199 Nr of Repeats=12 RepeatLength=12
 seed=GCTTAGGCTT Num.seqs=8 Similarity=0.888889
 2 AG-GCTT-AGGCTT
 Rev.of_WB235_1:942559-942637 Satlength=79 Nr of Repeats=6 RepeatLength=12
 seed=AGCCTAAGCC Num.seqs=5 Similarity=0.866667
 11 AG-GCTT-AGGCTT
 Rev.of_WB235_1:1000380-1000606 Satlength=227 Nr of Repeats=14
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=9 Similarity=0.854938
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_1:1126721-1126876 Satlength=156 Nr of Repeats=10
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=6 Similarity=0.866667
 9 AG-GCTT-AGGCTT
 WB235_1:2269401-2269479 Satlength=79 Nr of Repeats=6 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=5 Similarity=0.844444
 11 AG-GCTT-AGGCTT
 WB235_1:2276437-2276626 Satlength=190 Nr of Repeats=5 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=3 Similarity=0.703704
 12 AG-GCTT-AGGCTT
 Rev.of_WB235_1:2370746-2370842 Satlength=97 Nr of Repeats=6
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=4 Similarity=0.839744
 12 AG-GCTT-AGGCTT
 WB235_1:2840215-2840304 Satlength=90 Nr of Repeats=5 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=4 Similarity=0.833333
 11 AG-GCTT-AGGCTT
 Rev.of_WB235_1:3115944-3116232 Satlength=289 Nr of Repeats=21
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=15 Similarity=0.766138
 2 AG-GCTT-AGGCTT
 WB235_1:3280164-3280242 Satlength=79 Nr of Repeats=6 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=5 Similarity=0.888889
 12 AG-GCTT-AGGCTT
 WB235_1:3384983-3385061 Satlength=79 Nr of Repeats=6 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=5 Similarity=0.788889
 13 AG-GCTT-AGGCTT
 WB235_1:10404549-10404632 Satlength=84 Nr of Repeats=6 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=4 Similarity=0.777778
 11 AG-GCTT-AGGCTT
 Rev.of_WB235_1:11450427-11450505 Satlength=79 Nr of Repeats=6
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=5 Similarity=1.000000
 12 AG-GCTT-AGGCTT
 WB235_1:11451202-11451316 Satlength=115 Nr of Repeats=9 RepeatLength=12
 seed=GCTTAGGCTT Num.seqs=8 Similarity=0.813492
 2 AG-GCTT-AGGCTT
 WB235_1:11470915-11470999 Satlength=85 Nr of Repeats=7 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=7 Similarity=0.968254
 13 AG-GCTT-AGGCTT
 WB235_1:11933362-11933554 Satlength=193 Nr of Repeats=15 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=11 Similarity=0.838695
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_1:12119896-12120034 Satlength=139 Nr of Repeats=10
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=6 Similarity=0.859259
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_1:12223508-12223556 Satlength=49 Nr of Repeats=4
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=4 Similarity=0.796296
 10 AG-GCTT-AGGCTT

Rev.of_WB235_1:13927845-13927905 Satlength=61 Nr of Repeats=5
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=5 Similarity=0.866667
 10 AG-GCTT-AGGCTT
 WB235_1:15072265-15072421 Satlength=157 Nr of Repeats=13 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=13 Similarity=0.982906
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_2:0-161 Satlength=162 Nr of Repeats=13 RepeatLength=12
 seed=CCTAAGCCTA Num.seqs=12 Similarity=1.000000
 9 AG-GCTT-AGGCTT
 WB235_2:573638-573888 Satlength=251 Nr of Repeats=20 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=18 Similarity=0.816993
 11 AG-GCTT-AGGCTT
 WB235_2:2550207-2550279 Satlength=73 Nr of Repeats=6 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=6 Similarity=0.785185
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_2:2633519-2633585 Satlength=67 Nr of Repeats=5
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=4 Similarity=0.833333
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_2:2731022-2731082 Satlength=61 Nr of Repeats=4
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=3 Similarity=0.777778
 10 AG-GCTT-AGGCTT
 WB235_2:3136277-3136467 Satlength=191 Nr of Repeats=8 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=6 Similarity=0.785185
 13 AG-GCTT-AGGCTT
 WB235_2:4081925-4082141 Satlength=217 Nr of Repeats=14 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=10 Similarity=0.748148
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_2:4312357-4312429 Satlength=73 Nr of Repeats=4
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=3 Similarity=0.851852
 11 AG-GCTT-AGGCTT
 WB235_2:11733044-11733122 Satlength=79 Nr of Repeats=6 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=5 Similarity=0.844444
 9 AG-GCTT-AGGCTT
 WB235_2:11905368-11905475 Satlength=108 Nr of Repeats=8 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=6 Similarity=0.748148
 12 AG-GCTT-AGGCTT
 Rev.of_WB235_2:11930277-11930409 Satlength=133 Nr of Repeats=10
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=6 Similarity=0.792593
 12 AG-GCTT-AGGCTT
 WB235_2:11932324-11932498 Satlength=175 Nr of Repeats=10 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=6 Similarity=0.822222
 12 AG-GCTT-AGGCTT
 Rev.of_WB235_2:12247672-12247768 Satlength=97 Nr of Repeats=7
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=5 Similarity=0.741026
 9 AG-GCTT-AGGCTT
 WB235_2:12322418-12322496 Satlength=79 Nr of Repeats=5 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=4 Similarity=0.777778
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_2:12381010-12381194 Satlength=185 Nr of Repeats=13
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=8 Similarity=0.884921
 11 AG-GCTT-AGGCTT
 WB235_2:12467214-12467281 Satlength=68 Nr of Repeats=5 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=4 Similarity=0.944444
 13 AG-GCTT-AGGCTT

WB235_2:13650128-13650200 Satlength=73 Nr of Repeats=6 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=6 Similarity=0.962963
 11 AG-GCTT-AGGCTT
 Rev.of_WB235_2:13715389-13715533 Satlength=145 Nr of Repeats=10
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=6 Similarity=0.725926
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_2:13796378-13796708 Satlength=331 Nr of Repeats=23
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=15 Similarity=0.803175
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_2:13806123-13806285 Satlength=163 Nr of Repeats=10
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=7 Similarity=0.798942
 10 AG-GCTT-AGGCTT
 WB235_2:13809662-13809758 Satlength=97 Nr of Repeats=7 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=6 Similarity=0.755556
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_2:13934639-13934753 Satlength=115 Nr of Repeats=7
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=5 Similarity=0.733333
 11 AG-GCTT-AGGCTT
 WB235_2:13974202-13974430 Satlength=229 Nr of Repeats=14 RepeatLength=12
 seed=GCTTAGGCTT Num.seqs=11 Similarity=0.711888
 2 AG-GCTT-AGGCTT
 WB235_2:14006879-14006969 Satlength=91 Nr of Repeats=5 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=3 Similarity=0.851852
 11 AG-GCTT-AGGCTT
 WB235_2:14023987-14024052 Satlength=66 Nr of Repeats=4 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=3 Similarity=0.925926
 11 AG-GCTT-AGGCTT
 WB235_2:14893703-14893787 Satlength=85 Nr of Repeats=6 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=4 Similarity=0.814815
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_2:14955292-14955352 Satlength=61 Nr of Repeats=5
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=5 Similarity=0.888889
 12 AG-GCTT-AGGCTT
 WB235_2:15279229-15279409 Satlength=181 Nr of Repeats=15 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=15 Similarity=0.970370
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_3:0-119 Satlength=120 Nr of Repeats=10 RepeatLength=12
 seed=CCTAAGCCTA Num.seqs=10 Similarity=1.000000
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_3:118094-118166 Satlength=73 Nr of Repeats=5 RepeatLength=12
 seed=GCCTAAGCCT Num.seqs=3 Similarity=0.851852
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_3:209292-209524 Satlength=233 Nr of Repeats=8
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=5 Similarity=0.822222
 12 AG-GCTT-AGGCTT
 Rev.of_WB235_3:1052407-1052587 Satlength=181 Nr of Repeats=10
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=7 Similarity=0.841270
 12 AG-GCTT-AGGCTT
 Rev.of_WB235_3:1714052-1714520 Satlength=469 Nr of Repeats=35
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=27 Similarity=0.758492
 2 AG-GCTT-AGGCTT
 WB235_3:1964229-1964835 Satlength=607 Nr of Repeats=30 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=18 Similarity=0.824256
 11 AG-GCTT-AGGCTT

WB235_3:3346751-3346936 Satlength=186 Nr of Repeats=12 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=9 Similarity=0.901235
 11 AG-GCTT-AGGCTT
 Rev.of_WB235_3:3684600-3684680 Satlength=81 Nr of Repeats=5
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=3 Similarity=0.777778
 13 AG-GCTT-AGGCTT
 WB235_3:10924768-10924858 Satlength=91 Nr of Repeats=6 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=5 Similarity=0.822222
 13 AG-GCTT-AGGCTT
 WB235_3:10975223-10975307 Satlength=85 Nr of Repeats=5 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=3 Similarity=0.777778
 13 AG-GCTT-AGGCTT
 WB235_3:11207917-11208073 Satlength=157 Nr of Repeats=10 RepeatLength=12
 seed=GCTTAGGCTT Num.seqs=6 Similarity=0.755556
 2 AG-GCTT-AGGCTT
 WB235_3:11424870-11425146 Satlength=277 Nr of Repeats=12 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=8 Similarity=0.916667
 10 AG-GCTT-AGGCTT
 WB235_3:11475036-11475156 Satlength=121 Nr of Repeats=10 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=8 Similarity=0.797619
 9 AG-GCTT-AGGCTT
 WB235_3:11707265-11707854 Satlength=590 Nr of Repeats=30 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=20 Similarity=0.774854
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_3:11722253-11722390 Satlength=138 Nr of Repeats=8
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=5 Similarity=0.822222
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_3:11737191-11737281 Satlength=91 Nr of Repeats=6
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=5 Similarity=0.833333
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_3:11784840-11785090 Satlength=251 Nr of Repeats=9
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=7 Similarity=0.936508
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_3:12130507-12130633 Satlength=127 Nr of Repeats=9
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=6 Similarity=0.814815
 13 AG-GCTT-AGGCTT
 WB235_3:12143931-12144015 Satlength=85 Nr of Repeats=7 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=7 Similarity=0.968254
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_3:12944421-12944571 Satlength=151 Nr of Repeats=9
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=7 Similarity=0.830688
 13 AG-GCTT-AGGCTT
 WB235_3:13783590-13783788 Satlength=199 Nr of Repeats=16 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=15 Similarity=1.000000
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_4:0-137 Satlength=138 Nr of Repeats=11 RepeatLength=12
 seed=CCTAAGCCTA Num.seqs=10 Similarity=1.000000
 9 AG-GCTT-AGGCTT
 WB235_4:545946-546072 Satlength=127 Nr of Repeats=9 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=7 Similarity=0.788360
 11 AG-GCTT-AGGCTT
 Rev.of_WB235_4:1069432-1069486 Satlength=55 Nr of Repeats=4
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=3 Similarity=0.851852
 11 AG-GCTT-AGGCTT

WB235_4:1071381-1071429 Satlength=49 Nr of Repeats=4 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.888889
 12 AG-GCTT-AGGCTT
 WB235_4:1355992-1356408 Satlength=417 Nr of Repeats=8 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=5 Similarity=0.822222
 11 AG-GCTT-AGGCTT
 WB235_4:1494116-1494472 Satlength=357 Nr of Repeats=5 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.740741
 12 AG-GCTT-AGGCTT
 WB235_4:1628395-1628484 Satlength=90 Nr of Repeats=6 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=4 Similarity=0.888889
 10 AG-GCTT-AGGCTT
 Rev.of_WB235_4:1689083-1689293 Satlength=211 Nr of Repeats=11
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=7 Similarity=0.777778
 2 AG-GCTT-AGGCTT
 Rev.of_WB235_4:1752199-1752289 Satlength=91 Nr of Repeats=5
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=4 Similarity=0.796296
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_4:3166479-3166602 Satlength=124 Nr of Repeats=7
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=5 Similarity=0.800000
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_4:3991189-3991890 Satlength=702 Nr of Repeats=6
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=4 Similarity=0.759259
 13 AG-GCTT-AGGCTT
 WB235_4:17493616-17493814 Satlength=199 Nr of Repeats=16 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=15 Similarity=1.000000
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_5:6-311 Satlength=306 Nr of Repeats=25 RepeatLength=12
 seed=TAAGCCTAAG Num.seqs=24 Similarity=0.964573
 13 AG-GCTT-AGGCTT
 WB235_5:1129473-1129617 Satlength=145 Nr of Repeats=10 RepeatLength=12
 seed=GGCTTAGGCT Num.seqs=7 Similarity=0.814815
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_5:1142352-1142454 Satlength=103 Nr of Repeats=5
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=3 Similarity=0.851852
 2 AG-GCTT-AGGCTT
 Rev.of_WB235_5:1227227-1227275 Satlength=49 Nr of Repeats=4
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=4 Similarity=0.944444
 12 AG-GCTT-AGGCTT
 Rev.of_WB235_5:1230606-1230858 Satlength=253 Nr of Repeats=19
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=14 Similarity=0.804640
 12 AG-GCTT-AGGCTT
 Rev.of_WB235_5:1236678-1236956 Satlength=279 Nr of Repeats=15
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=9 Similarity=0.836420
 2 AG-GCTT-AGGCTT
 WB235_5:1243605-1243701 Satlength=97 Nr of Repeats=7 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=6 Similarity=0.822222
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_5:1341430-1341604 Satlength=175 Nr of Repeats=13
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=11 Similarity=0.826263
 2 AG-GCTT-AGGCTT
 Rev.of_WB235_5:1423375-1423735 Satlength=361 Nr of Repeats=24
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=17 Similarity=0.861928
 9 AG-GCTT-AGGCTT

Rev.of_WB235_5:1481682-1481898 Satlength=217 Nr of Repeats=10
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=7 Similarity=0.788360
 11 AG-GCTT-AGGCTT
 Rev.of_WB235_5:2586211-2586358 Satlength=148 Nr of Repeats=6
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=4 Similarity=0.833333
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_5:2712581-2712737 Satlength=157 Nr of Repeats=13
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=13 Similarity=0.839031
 2 AG-GCTT-AGGCTT
 WB235_5:15615355-15615426 Satlength=72 Nr of Repeats=5 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=3 Similarity=0.925926
 9 AG-GCTT-AGGCTT
 WB235_5:18566411-18566663 Satlength=253 Nr of Repeats=16 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=10 Similarity=0.935802
 12 AG-GCTT-AGGCTT
 Rev.of_WB235_5:18581399-18581759 Satlength=361 Nr of Repeats=22
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=15 Similarity=0.860317
 11 AG-GCTT-AGGCTT
 Rev.of_WB235_5:18588013-18588271 Satlength=259 Nr of Repeats=18
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=13 Similarity=0.874644
 13 AG-GCTT-AGGCTT
 Rev.of_WB235_5:18616302-18616398 Satlength=97 Nr of Repeats=6
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=4 Similarity=0.888889
 2 AG-GCTT-AGGCTT
 Rev.of_WB235_5:18632668-18632722 Satlength=55 Nr of Repeats=4
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=3 Similarity=0.851852
 13 AG-GCTT-AGGCTT
 WB235_5:18639700-18639844 Satlength=145 Nr of Repeats=9 RepeatLength=12
 seed=GCTTAGGCTT Num.seqs=6 Similarity=0.925926
 2 AG-GCTT-AGGCTT
 Rev.of_WB235_5:19232598-19232808 Satlength=211 Nr of Repeats=15
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=11 Similarity=0.818182
 10 AG-GCTT-AGGCTT
 WB235_5:19517965-19518323 Satlength=359 Nr of Repeats=22 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=15 Similarity=0.813757
 9 AG-GCTT-AGGCTT
 WB235_5:19528638-19528776 Satlength=139 Nr of Repeats=11 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=10 Similarity=0.938272
 9 AG-GCTT-AGGCTT
 Rev.of_WB235_5:19801650-19801767 Satlength=118 Nr of Repeats=5
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=3 Similarity=0.851852
 12 AG-GCTT-AGGCTT
 WB235_5:20923994-20924168 Satlength=175 Nr of Repeats=14 RepeatLength=12
 seed=GCTTAGGCTT Num.seqs=13 Similarity=1.000000
 2 AG-GCTT-AGGCTT
 Rev.of_WB235_6:0-251 Satlength=252 Nr of Repeats=21 RepeatLength=12
 seed=CTAAGCCTAA Num.seqs=21 Similarity=1.000000
 2 AG-GCTT-AGGCTT
 WB235_6:2563170-2563230 Satlength=61 Nr of Repeats=5 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=5 Similarity=0.888889
 12 AG-GCTT-AGGCTT
 WB235_6:17718013-17718930 Satlength=918 Nr of Repeats=12 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=11 Similarity=0.979798
 10 AG-GCTT-AGGCTT

WB235_1:477877-478046 Satlength=170 Nr of Repeats=13 RepeatLength=12
 seed=TAGGCTTAGG Num.seqs=8 Similarity=0.813492
 11 AG-GCNT-AGGCTT
 Rev.of_WB235_1:1000379-1000469 Satlength=91 Nr of Repeats=5
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=3 Similarity=0.740741
 11 AG-GCNT-AGGCTT
 Rev.of_WB235_1:12175889-12176021 Satlength=133 Nr of Repeats=9
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=7 Similarity=0.767196
 10 AG-GCTT-AGGCNT
 Rev.of_WB235_2:2817169-2817253 Satlength=85 Nr of Repeats=6
 RepeatLength=12 seed=CCTAAGCCTA Num.seqs=4 Similarity=0.754274
 21 AG-GCTT-AGGCGT
 Rev.of_WB235_4:4459427-4459589 Satlength=163 Nr of Repeats=12
 RepeatLength=12 seed=GCCTAAGCCT Num.seqs=11 Similarity=0.751515
 22 AG-GCTT-AGGCGT
 Rev.of_WB235_1:12277734-12277806 Satlength=73 Nr of Repeats=5
 RepeatLength=12 seed=AAGCCTAAGC Num.seqs=3 Similarity=0.777778
 12 AG-GCTT-CGGCTT
 WB235_2:1224948-1225028 Satlength=81 Nr of Repeats=5 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=3 Similarity=0.925926
 10 AG-GCTT-AGGTTT
 WB235_4:3608664-3608778 Satlength=115 Nr of Repeats=7 RepeatLength=12
 seed=TTAGGCTTAG Num.seqs=5 Similarity=0.866667
 10 AG-GCTT-AGGATT
 WB235_4:1632727-1632835 Satlength=109 Nr of Repeats=9 RepeatLength=12
 seed=CTTAAGCTTA Num.seqs=9 Similarity=0.975309
 9 AA-GCTT-AGGCTT
 Rev.of_WB235_4:1890247-1890331 Satlength=85 Nr of Repeats=5
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=3 Similarity=0.851852
 13 AA-GCTT-AGGCTT
 Rev.of_WB235_4:3455422-3455812 Satlength=391 Nr of Repeats=27
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=21 Similarity=0.808059
 13 AA-GCTT-AGGCTT
 WB235_5:365726-365780 Satlength=55 Nr of Repeats=4 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=3 Similarity=1.000000
 12 AG-GCTT-AGGCTA
 Rev.of_WB235_2:4365202-4365284 Satlength=83 Nr of Repeats=4
 RepeatLength=12 seed=TAAGCCTAAG Num.seqs=3 Similarity=0.925926
 13 AG-TCTT-AGGCTT
 WB235_2:12239992-12240106 Satlength=115 Nr of Repeats=7 RepeatLength=12
 seed=TTAGTCTTAG Num.seqs=5 Similarity=0.833333
 22 AG-TCTT-AGGCTT
 Rev.of_WB235_6:1509783-1509855 Satlength=73 Nr of Repeats=5
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=4 Similarity=0.851852
 14 AG-TCTT-TGGCTT
 Rev.of_WB235_2:2632149-2632578 Satlength=430 Nr of Repeats=33
 RepeatLength=13 seed=AGCCTAAGCT Num.seqs=33 Similarity=0.987568
 12 AGAGCTT-AGGCTT
 Rev.of_WB235_1:11984232-11984346 Satlength=115 Nr of Repeats=7
 RepeatLength=12 seed=CTAAGCCTAA Num.seqs=5 Similarity=0.766667
 2 AG-GTTT-AGGCTT
 WB235_4:13007463-13008066 Satlength=604 Nr of Repeats=12 RepeatLength=12
 seed=GCTTGGGTTT Num.seqs=9 Similarity=0.907407
 8 GG-GTTT-AGGCTT

WB235_4:13007463-13008198 Satlength=736 Nr of Repeats=17 RepeatLength=12
 seed=GCTTGGGTTT Num.seqs=11 Similarity=0.903030
 8 GG-GTTT-AGGCTT
 Rev.of_WB235_1:1653240-1653360 Satlength=121 Nr of Repeats=7
 RepeatLength=12 seed=AGCCTAAACC Num.seqs=5 Similarity=0.702564
 11 AG-GTTT-AGGCTC
 WB235_3:1256230-1256326 Satlength=97 Nr of Repeats=5 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=3 Similarity=0.925926
 12 AG-GCTT-AGGCTC
 WB235_3:1264671-1264767 Satlength=97 Nr of Repeats=5 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=3 Similarity=0.925926
 12 AG-GCTT-AGGCTC
 WB235_3:1761961-1762051 Satlength=91 Nr of Repeats=6 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.668803
 12 AG-GCTT-AGGCTC
 WB235_5:1305908-1306004 Satlength=97 Nr of Repeats=7 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=5 Similarity=1.000000
 12 AG-GCTT-AGGCTC
 Rev.of_WB235_5:1825303-1825405 Satlength=103 Nr of Repeats=7
 RepeatLength=12 seed=AGCCTGAGCC Num.seqs=5 Similarity=0.955556
 17 AG-GCTT-AGGCTC
 WB235_5:2394729-2394777 Satlength=49 Nr of Repeats=4 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.870370
 12 AG-GCTT-AGGCTC
 WB235_5:2503008-2503056 Satlength=49 Nr of Repeats=4 RepeatLength=12
 seed=AGGCTTAGGC Num.seqs=4 Similarity=0.870370
 12 AG-GCTT-AGGCTC
 Rev.of_WB235_5:18597908-18598040 Satlength=133 Nr of Repeats=9
 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=7 Similarity=0.841270
 23 AG-GCTT-AGGCTC
 WB235_1:11655695-11656421 Satlength=727 Nr of Repeats=60 RepeatLength=12
 seed=AGGCTCAGGC Num.seqs=59 Similarity=0.880322
 18 AG-GCTC-AGGCTC
 WB235_2:645177-645231 Satlength=55 Nr of Repeats=4 RepeatLength=12
 seed=GGCTCAGGCT Num.seqs=3 Similarity=1.000000
 19 AG-GCTC-AGGCTC
 Rev.of_WB235_3:1656487-1657087 Satlength=601 Nr of Repeats=50
 RepeatLength=12 seed=TGAGCCTGAG Num.seqs=50 Similarity=0.966440
 19 AG-GCTC-AGGCTC
 Rev.of_WB235_3:11783258-11783348 Satlength=91 Nr of Repeats=4
 RepeatLength=12 seed=AGCCTGAGCC Num.seqs=3 Similarity=0.851852
 23 AG-GCTC-AGGCTC
 WB235_5:18678760-18678838 Satlength=79 Nr of Repeats=6 RepeatLength=12
 seed=GGCTCAGGCT Num.seqs=5 Similarity=0.955556
 19 AG-GCTC-AGGCTC
 Rev.of_WB235_5:18722989-18723101 Satlength=113 Nr of Repeats=7
 RepeatLength=12 seed=AGCCTGAGCC Num.seqs=6 Similarity=1.000000
 23 AG-GCTC-AGGCTC
 WB235_5:19229130-19229634 Satlength=505 Nr of Repeats=37 RepeatLength=12
 seed=AGGCTCAGGC Num.seqs=32 Similarity=0.903226
 18 AG-GCTC-AGGCTC
 WB235_2:13353644-13353730 Satlength=87 Nr of Repeats=6 RepeatLength=12
 seed=CTTAGGCTTA Num.seqs=4 Similarity=0.743590
 10 AG-GCTTAAGNCTT

WB235_4:1785293-1785383 Satlength=91 Nr of Repeats=7 RepeatLength=12
seed=TTAGGATTAG Num.seqs=6 Similarity=0.962963
10 AG-GATT-AGGATT
Rev.of_WB235_1:11540263-11540521 Satlength=259 Nr of Repeats=16
RepeatLength=12 seed=AAGCCAAAGC Num.seqs=13 Similarity=0.854701
12 TG-GCTT-TGGCTT
WB235_2:13974189-13974267 Satlength=79 Nr of Repeats=6 RepeatLength=12
seed=GGCTTTGGCT Num.seqs=5 Similarity=1.000000
19 TG-GCTT-TGGCTT
Rev.of_WB235_3:2456635-2456707 Satlength=73 Nr of Repeats=5
RepeatLength=12 seed=CCAAGCCCAA Num.seqs=3 Similarity=0.851852
20 GG-GCTT-GGGCTT
WB235_5:20001413-20002864 Satlength=1452 Nr of Repeats=51 RepeatLength=12
seed=GCTTGGGCTT Num.seqs=38 Similarity=0.904694
20 GG-GCTT-GGGCTT
Rev.of_WB235_5:3767901-3768001 Satlength=101 Nr of Repeats=6
RepeatLength=10 seed=TAGCCATGCC Num.seqs=4 Similarity=0.933333
1 AG-GCAT--GGC-T
Rev.of_WB235_1:11032650-11032782 Satlength=133 Nr of Repeats=12
RepeatLength=11 seed=TATGCCTAGC Num.seqs=12 Similarity=1.000000
7 AG-GCAT-AGGC-T
Rev.of_WB235_2:1250454-1251360 Satlength=907 Nr of Repeats=73
RepeatLength=12 seed=CTATGCCTAT Num.seqs=70 Similarity=0.936784
14 AG-GCAT-AGGCAT
Rev.of_WB235_2:1252963-1253498 Satlength=536 Nr of Repeats=44
RepeatLength=12 seed=CTATGCCTAT Num.seqs=42 Similarity=0.937798
14 AG-GCAT-AGGCAT
Rev.of_WB235_2:1421457-1422023 Satlength=567 Nr of Repeats=41
RepeatLength=12 seed=CCTATGCCTA Num.seqs=30 Similarity=0.874585
21 AG-GCAT-AGGCAT
WB235_2:2957411-2957495 Satlength=85 Nr of Repeats=7 RepeatLength=12
seed=ATAGGCATAG Num.seqs=7 Similarity=1.000000
22 AG-GCAT-AGGCAT
WB235_2:14166594-14166830 Satlength=237 Nr of Repeats=18 RepeatLength=12
seed=ATAGGCATAG Num.seqs=11 Similarity=0.834343
22 AG-GCAT-AGGCAT
WB235_3:12302154-12302292 Satlength=139 Nr of Repeats=9 RepeatLength=12
seed=TAGGCATAGG Num.seqs=6 Similarity=0.829630
23 AG-GCAT-AGGCAT
WB235_4:1429990-1430044 Satlength=55 Nr of Repeats=4 RepeatLength=12
seed=CATAGGCATA Num.seqs=3 Similarity=0.925926
21 AG-GCAT-AGGCAT
WB235_6:14126276-14126426 Satlength=151 Nr of Repeats=12 RepeatLength=12
seed=ATAGGCATAG Num.seqs=11 Similarity=0.979798
22 AG-GCAT-AGGCAT

*

Consensus:

AGGCTTAGGCTT

>WB235_Fam_3_15_136 Nr. of seq. 136 Alignment length(with gaps) = 15
Alignment score = 0.942162

WB235_1:222749-222854 Satlength=106 Nr of Repeats=5 RepeatLength=15
 seed=AGACCCATCG Num.seqs=4 Similarity=0.911111
 0 AGACCCATCGTGGTG
 WB235_1:281468-282278 Satlength=811 Nr of Repeats=52 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=48 Similarity=0.862569
 7 AGACCCATCGTGGTG
 WB235_1:689715-689895 Satlength=181 Nr of Repeats=12 RepeatLength=15
 seed=GGTGAGACCC Num.seqs=12 Similarity=0.900337
 11 AGACCCATCGTGGTG
 Rev.of_WB235_1:4574052-4574607 Satlength=556 Nr of Repeats=34
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=31 Similarity=0.896583
 6 AGACCCATCGTGGTG
 WB235_1:7868293-7868548 Satlength=256 Nr of Repeats=17 RepeatLength=15
 seed=ACCCATCGTG Num.seqs=17 Similarity=0.847712
 2 AGACCCATCGTGGTG
 Rev.of_WB235_1:9819851-9820331 Satlength=481 Nr of Repeats=31
 RepeatLength=15 seed=CACGATGGGT Num.seqs=30 Similarity=0.857982
 12 AGACCCATCGTGGTG
 WB235_1:11144860-11145055 Satlength=196 Nr of Repeats=13 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=13 Similarity=0.842735
 7 AGACCCATCGTGGTG
 WB235_1:11480157-11480277 Satlength=121 Nr of Repeats=8 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=8 Similarity=0.930159
 7 AGACCCATCGTGGTG
 Rev.of_WB235_2:451705-452550 Satlength=846 Nr of Repeats=32
 RepeatLength=15 seed=TCTCACCACG Num.seqs=30 Similarity=0.884138
 3 AGACCCATCGTGGTG
 Rev.of_WB235_2:633057-633477 Satlength=421 Nr of Repeats=27
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=26 Similarity=0.898256
 6 AGACCCATCGTGGTG
 WB235_2:694364-699056 Satlength=4693 Nr of Repeats=287 RepeatLength=15
 seed=GAGACCCATC Num.seqs=267 Similarity=0.890323
 14 AGACCCATCGTGGTG
 WB235_2:694391-699449 Satlength=5059 Nr of Repeats=247 RepeatLength=15
 seed=GGTGAGACCC Num.seqs=190 Similarity=0.923290
 11 AGACCCATCGTGGTG
 WB235_2:1037817-1039287 Satlength=1471 Nr of Repeats=95 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=92 Similarity=0.911069
 7 AGACCCATCGTGGTG
 WB235_2:3365918-3365978 Satlength=61 Nr of Repeats=4 RepeatLength=15
 seed=GGTGAGACCC Num.seqs=4 Similarity=0.911111
 11 AGACCCATCGTGGTG
 WB235_2:4684295-4684838 Satlength=544 Nr of Repeats=21 RepeatLength=15
 seed=TGGTGAGACC Num.seqs=13 Similarity=0.879202
 10 AGACCCATCGTGGTG
 Rev.of_WB235_2:8460726-8460801 Satlength=76 Nr of Repeats=4
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=3 Similarity=0.822222
 6 AGACCCATCGTGGTG
 Rev.of_WB235_2:9633989-9634259 Satlength=271 Nr of Repeats=17
 RepeatLength=15 seed=CCACGATGGG Num.seqs=16 Similarity=0.891852
 13 AGACCCATCGTGGTG
 WB235_2:12649559-12650818 Satlength=1260 Nr of Repeats=83 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=82 Similarity=0.874683
 7 AGACCCATCGTGGTG

WB235_2:12649559-12651613 Satlength=2055 Nr of Repeats=136
 RepeatLength=15 seed=TCGTGGTGAG Num.seqs=133 Similarity=0.866505
 7 AGACCCATCGTGGTG
 WB235_2:14836705-14836840 Satlength=136 Nr of Repeats=9 RepeatLength=15
 seed=AGACCCATCG Num.seqs=9 Similarity=0.881481
 0 AGACCCATCGTGGTG
 Rev.of_WB235_2:14878607-14878727 Satlength=121 Nr of Repeats=7
 RepeatLength=15 seed=CCACGATGGG Num.seqs=6 Similarity=0.881481
 13 AGACCCATCGTGGTG
 Rev.of_WB235_3:2502140-2502620 Satlength=481 Nr of Repeats=29
 RepeatLength=15 seed=GGTCTCACCA Num.seqs=26 Similarity=0.920957
 5 AGACCCATCGTGGTG
 WB235_3:3896301-3896751 Satlength=451 Nr of Repeats=30 RepeatLength=15
 seed=CGTGGTGAGA Num.seqs=30 Similarity=0.932158
 8 AGACCCATCGTGGTG
 Rev.of_WB235_3:13448299-13448524 Satlength=226 Nr of Repeats=15
 RepeatLength=15 seed=CCACGATGGG Num.seqs=15 Similarity=0.930582
 13 AGACCCATCGTGGTG
 WB235_3:13750231-13751043 Satlength=813 Nr of Repeats=52 RepeatLength=15
 seed=GTGGTGAGAC Num.seqs=46 Similarity=0.862158
 9 AGACCCATCGTGGTG
 WB235_3:13753764-13754664 Satlength=901 Nr of Repeats=60 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=60 Similarity=0.880778
 7 AGACCCATCGTGGTG
 WB235_4:281265-281745 Satlength=481 Nr of Repeats=32 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=32 Similarity=0.882258
 7 AGACCCATCGTGGTG
 Rev.of_WB235_4:1154252-1154492 Satlength=241 Nr of Repeats=16
 RepeatLength=15 seed=GGTCTCACCA Num.seqs=16 Similarity=0.880741
 5 AGACCCATCGTGGTG
 WB235_4:1440391-1440556 Satlength=166 Nr of Repeats=11 RepeatLength=15
 seed=AGACCCATCG Num.seqs=11 Similarity=0.880404
 0 AGACCCATCGTGGTG
 Rev.of_WB235_4:2096897-2096972 Satlength=76 Nr of Repeats=5
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=5 Similarity=0.840000
 6 AGACCCATCGTGGTG
 Rev.of_WB235_4:2244962-2245187 Satlength=226 Nr of Repeats=15
 RepeatLength=15 seed=CGATGGGTCT Num.seqs=15 Similarity=0.914497
 10 AGACCCATCGTGGTG
 Rev.of_WB235_4:3052982-3053132 Satlength=151 Nr of Repeats=8
 RepeatLength=15 seed=CACGATGGGT Num.seqs=7 Similarity=0.843386
 12 AGACCCATCGTGGTG
 WB235_4:3670737-3670797 Satlength=61 Nr of Repeats=4 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=4 Similarity=0.940741
 7 AGACCCATCGTGGTG
 WB235_4:4898047-4898612 Satlength=566 Nr of Repeats=18 RepeatLength=15
 seed=GAGACCCATC Num.seqs=15 Similarity=0.903492
 14 AGACCCATCGTGGTG
 Rev.of_WB235_4:4921570-4922365 Satlength=796 Nr of Repeats=47
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=41 Similarity=0.943631
 6 AGACCCATCGTGGTG
 Rev.of_WB235_4:4923839-4924634 Satlength=796 Nr of Repeats=47
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=41 Similarity=0.943631
 6 AGACCCATCGTGGTG

Rev.of_WB235_4:4926108-4926918 Satlength=811 Nr of Repeats=48
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=42 Similarity=0.944767
 6 AGACCCATCGTGGTG
 Rev.of_WB235_4:5456641-5456776 Satlength=136 Nr of Repeats=9
 RepeatLength=15 seed=CCACGATGGG Num.seqs=7 Similarity=0.898413
 13 AGACCCATCGTGGTG
 Rev.of_WB235_4:8073709-8073979 Satlength=271 Nr of Repeats=18
 RepeatLength=15 seed=CTCACCACGA Num.seqs=18 Similarity=0.902977
 2 AGACCCATCGTGGTG
 Rev.of_WB235_4:8469615-8470279 Satlength=665 Nr of Repeats=41
 RepeatLength=15 seed=TCTCACCACG Num.seqs=39 Similarity=0.951297
 3 AGACCCATCGTGGTG
 Rev.of_WB235_4:9066182-9067563 Satlength=1382 Nr of Repeats=81
 RepeatLength=15 seed=CTCACCACGA Num.seqs=60 Similarity=0.961833
 2 AGACCCATCGTGGTG
 Rev.of_WB235_4:9410150-9411415 Satlength=1266 Nr of Repeats=46
 RepeatLength=15 seed=ACGATGGGTC Num.seqs=43 Similarity=0.911013
 11 AGACCCATCGTGGTG
 WB235_4:10262913-10263301 Satlength=389 Nr of Repeats=26 RepeatLength=15
 seed=GACCCATCGT Num.seqs=25 Similarity=0.898074
 1 AGACCCATCGTGGTG
 WB235_4:13462457-13462800 Satlength=344 Nr of Repeats=22 RepeatLength=15
 seed=ACCCATCGTG Num.seqs=19 Similarity=0.894997
 2 AGACCCATCGTGGTG
 Rev.of_WB235_4:13884400-13884820 Satlength=421 Nr of Repeats=24
 RepeatLength=15 seed=ACGATGGGTC Num.seqs=21 Similarity=0.916191
 11 AGACCCATCGTGGTG
 WB235_4:13922430-13922519 Satlength=90 Nr of Repeats=6 RepeatLength=15
 seed=ACCCATCGTG Num.seqs=5 Similarity=0.946667
 2 AGACCCATCGTGGTG
 WB235_4:14476805-14480237 Satlength=3433 Nr of Repeats=67 RepeatLength=15
 seed=CGTGGTGAGA Num.seqs=53 Similarity=0.889437
 8 AGACCCATCGTGGTG
 WB235_4:15188409-15188529 Satlength=121 Nr of Repeats=8 RepeatLength=15
 seed=GGTGAGACCC Num.seqs=8 Similarity=0.926984
 11 AGACCCATCGTGGTG
 WB235_4:15319979-15320069 Satlength=91 Nr of Repeats=6 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=6 Similarity=0.887407
 7 AGACCCATCGTGGTG
 Rev.of_WB235_4:15375074-15376143 Satlength=1070 Nr of Repeats=51
 RepeatLength=15 seed=CCACGATGGG Num.seqs=44 Similarity=0.911299
 13 AGACCCATCGTGGTG
 Rev.of_WB235_4:15766277-15766397 Satlength=121 Nr of Repeats=8
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=8 Similarity=0.939683
 6 AGACCCATCGTGGTG
 Rev.of_WB235_4:15766300-15766555 Satlength=256 Nr of Repeats=17
 RepeatLength=15 seed=CCACGATGGG Num.seqs=17 Similarity=0.875163
 13 AGACCCATCGTGGTG
 WB235_4:15826645-15826960 Satlength=316 Nr of Repeats=21 RepeatLength=15
 seed=CCCATCGTGG Num.seqs=21 Similarity=0.916191
 3 AGACCCATCGTGGTG
 Rev.of_WB235_4:15971205-15972491 Satlength=1287 Nr of Repeats=15
 RepeatLength=15 seed=CACGATGGGT Num.seqs=13 Similarity=0.863248
 12 AGACCCATCGTGGTG

Rev.of_WB235_4:16458853-16459033 Satlength=181 Nr of Repeats=10
 RepeatLength=15 seed=TGGGTCTCAC Num.seqs=8 Similarity=0.895238
 7 AGACCCATCGTGGTG
 WB235_4:16880641-16880761 Satlength=121 Nr of Repeats=8 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=8 Similarity=0.866667
 7 AGACCCATCGTGGTG
 WB235_4:16910542-16910677 Satlength=136 Nr of Repeats=9 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=9 Similarity=0.980247
 7 AGACCCATCGTGGTG
 WB235_4:17140454-17141354 Satlength=901 Nr of Repeats=60 RepeatLength=15
 seed=ACCCATCGTG Num.seqs=60 Similarity=0.889768
 2 AGACCCATCGTGGTG
 Rev.of_WB235_4:17147999-17148449 Satlength=451 Nr of Repeats=28
 RepeatLength=15 seed=TCTCACCACG Num.seqs=25 Similarity=0.847111
 3 AGACCCATCGTGGTG
 Rev.of_WB235_5:1403881-1404196 Satlength=316 Nr of Repeats=21
 RepeatLength=15 seed=CGATGGGTCT Num.seqs=21 Similarity=0.927196
 10 AGACCCATCGTGGTG
 Rev.of_WB235_5:2676568-2676778 Satlength=211 Nr of Repeats=14
 RepeatLength=15 seed=CTCACCACGA Num.seqs=14 Similarity=0.840316
 2 AGACCCATCGTGGTG
 WB235_5:3621266-3621341 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=CGTGGTGAGA Num.seqs=5 Similarity=0.840000
 8 AGACCCATCGTGGTG
 Rev.of_WB235_5:5010548-5010653 Satlength=106 Nr of Repeats=7
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=7 Similarity=0.898413
 6 AGACCCATCGTGGTG
 WB235_5:6071658-6071958 Satlength=301 Nr of Repeats=20 RepeatLength=15
 seed=ACCCATCGTG Num.seqs=20 Similarity=0.901287
 2 AGACCCATCGTGGTG
 WB235_5:6091617-6091992 Satlength=376 Nr of Repeats=25 RepeatLength=15
 seed=CCCATCGTGG Num.seqs=25 Similarity=0.889185
 3 AGACCCATCGTGGTG
 Rev.of_WB235_5:6299893-6299998 Satlength=106 Nr of Repeats=7
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=7 Similarity=0.881481
 6 AGACCCATCGTGGTG
 WB235_5:6587809-6587899 Satlength=91 Nr of Repeats=6 RepeatLength=15
 seed=GGTGAGACCC Num.seqs=6 Similarity=0.917037
 11 AGACCCATCGTGGTG
 Rev.of_WB235_5:7914059-7914224 Satlength=166 Nr of Repeats=11
 RepeatLength=15 seed=CCACGATGGG Num.seqs=11 Similarity=0.877172
 13 AGACCCATCGTGGTG
 WB235_5:7915927-7916107 Satlength=181 Nr of Repeats=11 RepeatLength=15
 seed=ACCCATCGTG Num.seqs=10 Similarity=0.907161
 2 AGACCCATCGTGGTG
 Rev.of_WB235_5:8316057-8316570 Satlength=514 Nr of Repeats=17
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=16 Similarity=0.932593
 6 AGACCCATCGTGGTG
 Rev.of_WB235_5:9439276-9439441 Satlength=166 Nr of Repeats=11
 RepeatLength=15 seed=CGATGGGTCT Num.seqs=11 Similarity=0.899798
 10 AGACCCATCGTGGTG
 Rev.of_WB235_5:15295547-15296333 Satlength=787 Nr of Repeats=8
 RepeatLength=15 seed=TCTCACCACG Num.seqs=7 Similarity=0.923810
 3 AGACCCATCGTGGTG

Rev.of_WB235_5:15321484-15322280 Satlength=797 Nr of Repeats=53
 RepeatLength=15 seed=CCACGATGGG Num.seqs=50 Similarity=0.875935
 13 AGACCCATCGTGGTG
 WB235_5:15582778-15582853 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=AGACCCATCG Num.seqs=5 Similarity=0.928889
 0 AGACCCATCGTGGTG
 Rev.of_WB235_6:161586-161691 Satlength=106 Nr of Repeats=7
 RepeatLength=15 seed=GTCTCACCAC Num.seqs=7 Similarity=0.932275
 4 AGACCCATCGTGGTG
 Rev.of_WB235_6:169222-169627 Satlength=406 Nr of Repeats=27
 RepeatLength=15 seed=ACGATGGGTC Num.seqs=27 Similarity=0.913897
 11 AGACCCATCGTGGTG
 Rev.of_WB235_6:943488-943966 Satlength=479 Nr of Repeats=11
 RepeatLength=15 seed=CACGATGGGT Num.seqs=10 Similarity=0.887407
 12 AGACCCATCGTGGTG
 Rev.of_WB235_6:1376205-1376549 Satlength=345 Nr of Repeats=23
 RepeatLength=15 seed=CGATGGGTCT Num.seqs=22 Similarity=0.845695
 10 AGACCCATCGTGGTG
 Rev.of_WB235_6:3075483-3075588 Satlength=106 Nr of Repeats=7
 RepeatLength=15 seed=TCACCACGAT Num.seqs=7 Similarity=0.923810
 1 AGACCCATCGTGGTG
 WB235_6:5227815-5227935 Satlength=121 Nr of Repeats=8 RepeatLength=15
 seed=TGGTGAGACC Num.seqs=8 Similarity=0.860317
 10 AGACCCATCGTGGTG
 Rev.of_WB235_6:15635841-15636081 Satlength=241 Nr of Repeats=15
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=14 Similarity=0.906227
 6 AGACCCATCGTGGTG
 Rev.of_WB235_6:16852072-16852162 Satlength=91 Nr of Repeats=6
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=6 Similarity=0.922963
 6 AGACCCATCGTGGTG
 Rev.of_WB235_2:15138506-15140272 Satlength=1767 Nr of Repeats=38
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=35 Similarity=0.915593
 6 AGACCCNTCGTGGTG
 WB235_5:16273937-16274402 Satlength=466 Nr of Repeats=31 RepeatLength=15
 seed=TGGTGAGACC Num.seqs=31 Similarity=0.865806
 10 AGACCCNTCGTGGTG
 Rev.of_WB235_6:12521171-12522034 Satlength=864 Nr of Repeats=10
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=9 Similarity=0.920988
 6 AGACCCNTCGTGGTG
 WB235_1:6647571-6647736 Satlength=166 Nr of Repeats=11 RepeatLength=15
 seed=GAGACCCATC Num.seqs=11 Similarity=0.883636
 14 AGACCCATCGTGGCG
 Rev.of_WB235_2:857683-857758 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=ATGGGTCTCG Num.seqs=3 Similarity=1.000000
 23 AGACCCATCGTGGCG
 WB235_2:2002012-2002087 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=TCGTGGCGAG Num.seqs=5 Similarity=0.928889
 22 AGACCCATCGTGGCG
 WB235_2:2386288-2386363 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=TCGTGGCGAG Num.seqs=5 Similarity=0.928889
 22 AGACCCATCGTGGCG
 WB235_2:4684299-4684389 Satlength=91 Nr of Repeats=6 RepeatLength=15
 seed=GAGACCCATC Num.seqs=6 Similarity=0.899259
 14 AGACCCATCGTGGCG

WB235_2:14991646-14991736 Satlength=91 Nr of Repeats=6 RepeatLength=15
 seed=TCGTGGCGAG Num.seqs=6 Similarity=0.940741
 22 AGACCCATCGTGGCG
 WB235_2:15000612-15000786 Satlength=175 Nr of Repeats=9 RepeatLength=15
 seed=AGACCCATCG Num.seqs=8 Similarity=0.895238
 15 AGACCCATCGTGGCG
 WB235_3:8335590-8336085 Satlength=496 Nr of Repeats=32 RepeatLength=15
 seed=ACCCATCGTG Num.seqs=31 Similarity=0.914170
 17 AGACCCATCGTGGCG
 WB235_4:13846283-13847033 Satlength=751 Nr of Repeats=45 RepeatLength=15
 seed=CCCATCGTGG Num.seqs=40 Similarity=0.901766
 18 AGACCCATCGTGGCG
 WB235_4:15166280-15166460 Satlength=181 Nr of Repeats=11 RepeatLength=15
 seed=GAGACCCATC Num.seqs=10 Similarity=0.917037
 14 AGACCCATCGTGGCG
 Rev.of_WB235_6:9607653-9607728 Satlength=76 Nr of Repeats=5
 RepeatLength=15 seed=ATGGGTCTCG Num.seqs=3 Similarity=1.000000
 23 AGACCCATCGTGGCG
 WB235_6:14362236-14362311 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=TCGTGGCGAG Num.seqs=5 Similarity=0.928889
 22 AGACCCATCGTGGCG
 WB235_6:17311002-17311107 Satlength=106 Nr of Repeats=7 RepeatLength=15
 seed=GAGACCCATC Num.seqs=7 Similarity=0.847619
 14 AGACCCATCGTGGCG
 Rev.of_WB235_4:1345560-1345725 Satlength=166 Nr of Repeats=11
 RepeatLength=15 seed=CCACGATGGG Num.seqs=11 Similarity=0.880404
 28 AGACCCATCGTGGNG
 Rev.of_WB235_4:13464499-13464709 Satlength=211 Nr of Repeats=14
 RepeatLength=15 seed=CCACGATGGG Num.seqs=14 Similarity=0.902320
 28 AGACCCATCGTGGNG
 WB235_4:14476813-14476978 Satlength=166 Nr of Repeats=11 RepeatLength=15
 seed=GACCCATCGT Num.seqs=11 Similarity=0.878788
 16 AGACCCATCGTGGNG
 Rev.of_WB235_6:516173-516819 Satlength=647 Nr of Repeats=15
 RepeatLength=15 seed=CCACGATGGG Num.seqs=14 Similarity=0.873016
 28 AGACCCATCGTGGNG
 Rev.of_WB235_6:5229858-5230323 Satlength=466 Nr of Repeats=31
 RepeatLength=15 seed=CCACGATGGG Num.seqs=27 Similarity=0.802469
 28 AGACCCATCGTGGNG
 Rev.of_WB235_1:14668547-14668607 Satlength=61 Nr of Repeats=4
 RepeatLength=15 seed=CCACGATGGG Num.seqs=4 Similarity=0.881481
 28 AGACCCATCGTGGAG
 Rev.of_WB235_1:3389969-3393329 Satlength=3361 Nr of Repeats=224
 RepeatLength=15 seed=CTCACCACGA Num.seqs=206 Similarity=0.875278
 2 AGACCCTTCGTGGTG
 WB235_1:3980324-3980429 Satlength=106 Nr of Repeats=7 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=7 Similarity=0.949206
 7 AGACCCTTCGTGGTG
 WB235_1:5144853-5145677 Satlength=825 Nr of Repeats=51 RepeatLength=15
 seed=CGTGGTGAGA Num.seqs=47 Similarity=0.827485
 8 AGACCCTTCGTGGTG
 WB235_1:7740676-7740751 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=5 Similarity=0.911111
 7 AGACCCTTCGTGGTG

WB235_2:1034465-1036445 Satlength=1981 Nr of Repeats=125 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=119 Similarity=0.915200
 7 AGACCCTTCGTGGTG
 Rev.of_WB235_2:4260577-4261267 Satlength=691 Nr of Repeats=40
 RepeatLength=15 seed=GTCTCACCAC Num.seqs=34 Similarity=0.828821
 4 AGACCCTTCGTGGTG
 WB235_2:9202102-9202507 Satlength=406 Nr of Repeats=27 RepeatLength=15
 seed=TGGTGAGACC Num.seqs=25 Similarity=0.902519
 10 AGACCCTTCGTGGTG
 WB235_2:14993591-14993681 Satlength=91 Nr of Repeats=6 RepeatLength=15
 seed=GGTGAGACCC Num.seqs=6 Similarity=0.905185
 11 AGACCCTTCGTGGTG
 WB235_3:1320777-1320837 Satlength=61 Nr of Repeats=4 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=4 Similarity=0.955556
 7 AGACCCTTCGTGGTG
 WB235_3:3446010-3446749 Satlength=740 Nr of Repeats=47 RepeatLength=15
 seed=GTGGTGAGAC Num.seqs=44 Similarity=0.837350
 9 AGACCCTTCGTGGTG
 Rev.of_WB235_4:1477450-1477555 Satlength=106 Nr of Repeats=7
 RepeatLength=15 seed=CTCACCACGA Num.seqs=7 Similarity=0.873016
 2 AGACCCTTCGTGGTG
 Rev.of_WB235_4:14218012-14218147 Satlength=136 Nr of Repeats=9
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=9 Similarity=0.930864
 6 AGACCCTTCGTGGTG
 Rev.of_WB235_4:15060108-15060798 Satlength=691 Nr of Repeats=39
 RepeatLength=15 seed=GGTCTACCA Num.seqs=32 Similarity=0.917921
 5 AGACCCTTCGTGGTG
 Rev.of_WB235_4:16128108-16129641 Satlength=1534 Nr of Repeats=16
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=11 Similarity=0.935354
 6 AGACCCTTCGTGGTG
 WB235_4:16153344-16153449 Satlength=106 Nr of Repeats=7 RepeatLength=15
 seed=GTGGTGAGAC Num.seqs=7 Similarity=0.898413
 9 AGACCCTTCGTGGTG
 Rev.of_WB235_4:16223761-16224157 Satlength=397 Nr of Repeats=25
 RepeatLength=15 seed=TCTCACCACG Num.seqs=21 Similarity=0.820106
 3 AGACCCTTCGTGGTG
 WB235_5:1254384-1254459 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=5 Similarity=0.911111
 7 AGACCCTTCGTGGTG
 WB235_5:1254384-1256245 Satlength=1862 Nr of Repeats=31 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=29 Similarity=0.903667
 7 AGACCCTTCGTGGTG
 WB235_5:1254387-1257024 Satlength=2638 Nr of Repeats=44 RepeatLength=15
 seed=TGGTGAGACC Num.seqs=41 Similarity=0.901138
 10 AGACCCTTCGTGGTG
 WB235_5:5005844-5006744 Satlength=901 Nr of Repeats=59 RepeatLength=15
 seed=TCGTGGTGAG Num.seqs=50 Similarity=0.805823
 7 AGACCCTTCGTGGTG
 WB235_5:5640056-5640116 Satlength=61 Nr of Repeats=4 RepeatLength=15
 seed=CGTGGTGAGA Num.seqs=4 Similarity=0.911111
 8 AGACCCTTCGTGGTG
 Rev.of_WB235_5:7720637-7720787 Satlength=151 Nr of Repeats=10
 RepeatLength=15 seed=GGGTCTCACC Num.seqs=10 Similarity=0.934815
 6 AGACCCTTCGTGGTG

WB235_5:9601934-9602249 Satlength=316 Nr of Repeats=21 RepeatLength=15
seed=GGTGAGACCC Num.seqs=21 Similarity=0.928889
11 AGACCCCTTCGTGGTG
WB235_5:13882296-13882386 Satlength=91 Nr of Repeats=6 RepeatLength=15
seed=TCGTGGTGAG Num.seqs=6 Similarity=0.857778
7 AGACCCCTTCGTGGTG
WB235_5:14124319-14124409 Satlength=91 Nr of Repeats=6 RepeatLength=15
seed=CGTGGTGAGA Num.seqs=6 Similarity=0.893333
8 AGACCCCTTCGTGGTG
Rev.of_WB235_5:14156207-14156297 Satlength=91 Nr of Repeats=6
RepeatLength=15 seed=GGGTCTCACC Num.seqs=6 Similarity=0.917037
6 AGACCCCTTCGTGGTG
WB235_6:13560726-13560906 Satlength=181 Nr of Repeats=11 RepeatLength=15
seed=TCGTGGTGAG Num.seqs=10 Similarity=0.857778
7 AGACCCCTTCGTGGTG
Rev.of_WB235_6:15482468-15483998 Satlength=1531 Nr of Repeats=97
RepeatLength=15 seed=GTCTCACCAC Num.seqs=92 Similarity=0.888135
4 AGACCCCTTCGTGGTG
Rev.of_WB235_6:16505118-16505433 Satlength=316 Nr of Repeats=18
RepeatLength=15 seed=TCACCACGAA Num.seqs=15 Similarity=0.947513
16 AGACCCCTTCGTGGTG
WB235_6:14121147-14122257 Satlength=1111 Nr of Repeats=73 RepeatLength=15
seed=TCGTGGTGAG Num.seqs=70 Similarity=0.770484
7 AGACCTATCGTGGTG
WB235_1:308028-308148 Satlength=121 Nr of Repeats=7 RepeatLength=15
seed=GAGACCCATC Num.seqs=6 Similarity=0.764583
14 AGACCCATCGTGACG
WB235_3:690245-690736 Satlength=492 Nr of Repeats=19 RepeatLength=15
seed=TGAGACCCAT Num.seqs=13 Similarity=0.851852
28 AGACCCATCGTGATG

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Consensus:

AGACCCaTCGTGGTG

>WB235_Fam_4_35_115 Nr. of seq. 115 Alignment length(with gaps) = 45
Alignment score = 0.601883
WB235_1:1136040-1136228 Satlength=189 Nr of Repeats=5 RepeatLength=31
seed=ATTCCCGCCA Num.seqs=3 Similarity=0.628472
0 ATT--CCCGCC--AATT-----TT-TT-CT-CAGGAAATTGA--
Rev.of_WB235_3:1320896-1321023 Satlength=128 Nr of Repeats=4
RepeatLength=31 seed=AATTCAAATT Num.seqs=3 Similarity=0.885305
3 ATT--CCCGCC--AAAA-----TT-TT-TT-GAAGAAATTGA--
WB235_4:6664978-6665286 Satlength=309 Nr of Repeats=9 RepeatLength=31
seed=CCCGCCAAAA Num.seqs=7 Similarity=0.897593
3 ATT--CCCGCC--AAAA-----TT-TT-TT-GAAAAAATTGA--
Rev.of_WB235_4:13478657-13478875 Satlength=219 Nr of Repeats=6
RepeatLength=31 seed=AATTCAAATT Num.seqs=4 Similarity=0.942652
3 ATT--CCCGCC--AAAA-----TT-TT-TT-GAGGAAATTGA--
Rev.of_WB235_5:19052161-19052388 Satlength=228 Nr of Repeats=7
RepeatLength=33 seed=GGAATTCAAA Num.seqs=5 Similarity=0.967677
6 AT-T-CCCGCC--AAAATT---TT-TT-TT-GAATAAATTGA--

Rev.of_WB235_3:12141791-12142267 Satlength=477 Nr of Repeats=10
 RepeatLength=32 seed=ATTCAAATTT Num.seqs=6 Similarity=0.602694
 34 ATT--TTCGCC--AAAA-N---TT-TT-CT-GAAGAAATTTGA--
 WB235_4:17262649-17262776 Satlength=128 Nr of Repeats=4 RepeatLength=32
 seed=GAAGAAATTT Num.seqs=3 Similarity=0.861111
 52 ATT--TGCACC--AAAA-T---TT-TT-CT-GAAGAAATTTGA--
 Rev.of_WB235_1:669658-671715 Satlength=2058 Nr of Repeats=63
 RepeatLength=32 seed=GAATTCAAAT Num.seqs=41 Similarity=0.870732
 4 ATT-C-CCGCC--AAAA-T---TT-TT-CT-CAGAAAATTTGA--
 WB235_1:1362690-1362850 Satlength=161 Nr of Repeats=5 RepeatLength=32
 seed=TCAGAAAATT Num.seqs=5 Similarity=0.983333
 19 ATT-C-CCGCC--AAAA-T---TT-TT-CT-CAGAAAATTTGA--
 WB235_4:15708521-15708971 Satlength=451 Nr of Repeats=14 RepeatLength=32
 seed=TTGAATTCCC Num.seqs=13 Similarity=0.905983
 28 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 WB235_5:4053377-4053861 Satlength=485 Nr of Repeats=15 RepeatLength=32
 seed=TTTCACAGAA Num.seqs=11 Similarity=0.921212
 47 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 WB235_6:14723633-14724049 Satlength=417 Nr of Repeats=13 RepeatLength=32
 seed=TTGAATTCCC Num.seqs=13 Similarity=0.927885
 28 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 WB235_5:19993167-19993682 Satlength=516 Nr of Repeats=14 RepeatLength=32
 seed=AAATTTGAAT Num.seqs=9 Similarity=0.806958
 24 ATT-T-CCGCC--AAAA-T---TT-TT-CT-CAGAAAATTTGA--
 WB235_1:13610087-13613799 Satlength=3713 Nr of Repeats=116
 RepeatLength=32 seed=TGAATTCCCG Num.seqs=116 Similarity=0.922301
 29 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 Rev.of_WB235_2:4555047-4555687 Satlength=641 Nr of Repeats=20
 RepeatLength=32 seed=CGGGAATTCA Num.seqs=20 Similarity=0.921491
 39 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 Rev.of_WB235_3:11160967-11161287 Satlength=321 Nr of Repeats=10
 RepeatLength=32 seed=TTTCTGTGAA Num.seqs=10 Similarity=0.896296
 58 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 WB235_4:8467114-8467274 Satlength=161 Nr of Repeats=5 RepeatLength=32
 seed=TTGAATTCCC Num.seqs=5 Similarity=0.891667
 60 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 Rev.of_WB235_4:12023094-12025460 Satlength=2367 Nr of Repeats=74
 RepeatLength=32 seed=CGGGAATTCA Num.seqs=72 Similarity=0.926774
 39 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 Rev.of_WB235_5:3520923-3521917 Satlength=995 Nr of Repeats=31
 RepeatLength=32 seed=CGGGAATTCA Num.seqs=29 Similarity=0.920874
 39 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 Rev.of_WB235_6:9008356-9008996 Satlength=641 Nr of Repeats=20
 RepeatLength=32 seed=CGGGAATTCA Num.seqs=20 Similarity=0.894298
 39 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 WB235_6:14723638-14724190 Satlength=553 Nr of Repeats=16 RepeatLength=32
 seed=TTCCCGCCAA Num.seqs=11 Similarity=0.947727
 33 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAGAAAATTTGA--
 Rev.of_WB235_5:6984815-6985177 Satlength=363 Nr of Repeats=11
 RepeatLength=32 seed=AATTCAAATT Num.seqs=7 Similarity=0.908730
 35 ATT-C-CCGCC--AAAA-T---TT-TT-CA-CAAAAAATTTGA--
 WB235_2:1968841-1969602 Satlength=762 Nr of Repeats=23 RepeatLength=32
 seed=AATTCCTGCC Num.seqs=16 Similarity=0.855208
 31 ATT-C-CCGCC--AAAA-A---TT-TT-CA-NAGAAAATTTGA--

WB235_2:1976612-1976897 Satlength=286 Nr of Repeats=8 RepeatLength=32
 seed=AATTCCCGCC Num.seqs=5 Similarity=0.858333
 31 ATT-C-CCGCC--AAAA-A--TT-TT-CA-NAGAAAAATTTGA--
 WB235_2:1985022-1985847 Satlength=826 Nr of Repeats=25 RepeatLength=32
 seed=AATTCCCGCC Num.seqs=18 Similarity=0.860566
 31 ATT-C-CCGCC--AAAA-A--TT-TT-CA-NAGAAAAATTTGA--
 Rev.of_WB235_2:2002110-2002460 Satlength=351 Nr of Repeats=10
 RepeatLength=32 seed=GGCGGGAATT Num.seqs=7 Similarity=0.843675
 41 ATT-C-CCGCC--AAAA-A--TT-TT-CA-AAGAAAAATTTGA--
 WB235_6:9605306-9607639 Satlength=2334 Nr of Repeats=65 RepeatLength=32
 seed=TCCCGCCAAA Num.seqs=47 Similarity=0.846978
 66 ATT-C-CCGCC--AAAA-A--TT-TT-CA-AAGAAAAATTTGA--
 Rev.of_WB235_2:14991755-14991977 Satlength=223 Nr of Repeats=7
 RepeatLength=32 seed=TTTTGGCGGG Num.seqs=5 Similarity=0.841667
 45 ATT-C-CCGCC--AAAA-A--TT-TT-CA-NAGAAAAATTTGA--
 WB235_2:6434384-6434544 Satlength=161 Nr of Repeats=5 RepeatLength=32
 seed=AAAAATTTTC Num.seqs=5 Similarity=0.916667
 41 ATT-C-CCGCC--AAAA-A--TT-TT-CA-CAGAAAAATTTGA--
 WB235_2:6434384-6435137 Satlength=754 Nr of Repeats=6 RepeatLength=32
 seed=AAAAATTTTC Num.seqs=5 Similarity=0.916667
 41 ATT-C-CCGCC--AAAA-A--TT-TT-CA-CAGAAAAATTTGA--
 WB235_5:20471611-20471894 Satlength=284 Nr of Repeats=9 RepeatLength=32
 seed=CCGCCAAAAT Num.seqs=7 Similarity=0.853175
 4 ATT-C-CCGCC--AAAA-T--TT-TT-CT-TTGAAAAATTTGA--
 WB235_1:994259-994677 Satlength=419 Nr of Repeats=4 RepeatLength=32
 seed=CAAAATTTT Num.seqs=3 Similarity=0.888889
 9 A-T-CGCCGCC--AAAA-T--TT-TT-CT-CAGAAAAATTTGA--
 Rev.of_WB235_5:18473949-18474108 Satlength=160 Nr of Repeats=4
 RepeatLength=32 seed=GAATTCAAAT Num.seqs=3 Similarity=0.888889
 4 ATT-C-ACGCC--AAAA-A--TT-TT-TT-CAGAAAAATTTGA--
 WB235_2:2599830-2600053 Satlength=224 Nr of Repeats=7 RepeatLength=32
 seed=AATTCCCGCC Num.seqs=6 Similarity=0.855556
 31 ATT-C-CCGCC--AAAA-A--AT-TT-CA-AAGAAAAATTTAA--
 WB235_2:2599867-2600422 Satlength=556 Nr of Repeats=7 RepeatLength=32
 seed=CCGCCAAAAA Num.seqs=5 Similarity=0.866667
 36 ATT-C-CCGCC--AAAA-A--AT-TT-CA-AAGAAAAATTTAA--
 WB235_2:13906504-13906669 Satlength=166 Nr of Repeats=5 RepeatLength=33
 seed=AAAATTTGAA Num.seqs=5 Similarity=0.749495
 24 ATT-TCCCGCC--AAAA-T--T-T-TT-CT-CAGAAAAATTTGA--
 Rev.of_WB235_5:1368467-1368669 Satlength=203 Nr of Repeats=6
 RepeatLength=34 seed=AAATTCAAAT Num.seqs=5 Similarity=0.823529
 37 ATT-TCCCGCC--AAAA-T--TAT-TT-CT-CAGAAAAATTTGA--
 WB235_1:759087-759538 Satlength=452 Nr of Repeats=13 RepeatLength=34
 seed=TTTCTCAGAA Num.seqs=8 Similarity=0.787245
 50 ATT-TCCCACC--AAAA-T--TTT-TT-CT-CAGAAAAATTTGA--
 WB235_5:2716232-2716355 Satlength=124 Nr of Repeats=4 RepeatLength=35
 seed=TTTCTCAGAA Num.seqs=3 Similarity=0.923810
 51 ATT-TCCCGCC--AAAA-T-GTTT-TT-CT-CAGAAAAATTTGA--
 WB235_1:14257569-14258742 Satlength=1174 Nr of Repeats=31 RepeatLength=34
 seed=AAATTTGAAT Num.seqs=19 Similarity=0.788556
 25 ATT-TCCCGCC--AAAA-A-GT-T-TT-CT-CAGAAAAATTTGA--
 WB235_3:12480633-12480804 Satlength=172 Nr of Repeats=5 RepeatLength=35
 seed=AATTTGAATT Num.seqs=3 Similarity=0.923810
 26 ATT-TCCCGCC--AAAA-TCAT-T-TT-CT-GAGAAAAATTTGA--

WB235_2:1793298-1793504 Satlength=207 Nr of Repeats=6 RepeatLength=34
 seed=ATTTGAATTT Num.seqs=4 Similarity=0.980392
 27 ATT-TCCCGCC--AAAA--TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_2:1796656-1797032 Satlength=377 Nr of Repeats=11
 RepeatLength=34 seed=CGGGAAATTC Num.seqs=9 Similarity=0.956427
 41 ATT-TCCCGCC--AAAA--TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_2:14993697-14994076 Satlength=380 Nr of Repeats=11
 RepeatLength=34 seed=TTGGCGGGAA Num.seqs=7 Similarity=0.880511
 45 ATT-TCCCGCC--AAAA--TTTT-TT-CA-CTGAAAATTTGA--
 WB235_4:1344791-1345475 Satlength=685 Nr of Repeats=20 RepeatLength=34
 seed=ATTTCCCGCC Num.seqs=16 Similarity=0.995098
 33 ATT-TCCCGCC--AAAA--TTTT-TT-CA-CTGAAAATTTGA--
 WB235_4:1477245-1477418 Satlength=174 Nr of Repeats=5 RepeatLength=34
 seed=GAAAATTTGA Num.seqs=3 Similarity=0.828571
 57 ATT-TCCCGCC--AAAA--TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_4:15188545-15190957 Satlength=2413 Nr of Repeats=70
 RepeatLength=34 seed=TTGGCGGGAA Num.seqs=46 Similarity=0.965786
 45 ATT-TCCCGCC--AAAA--TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_5:10268112-10269248 Satlength=1137 Nr of Repeats=33
 RepeatLength=34 seed=TTGGCGGGAA Num.seqs=20 Similarity=0.915765
 45 ATT-TCCCGCC--AAAA--TTTT-TT-CA-CTGAAAATTTGA--
 WB235_1:1429375-1430301 Satlength=927 Nr of Repeats=24 RepeatLength=35
 seed=AAATTTGAAT Num.seqs=15 Similarity=0.827628
 60 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_1:7740774-7741690 Satlength=917 Nr of Repeats=26
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=17 Similarity=0.870370
 77 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_1:11480313-11481528 Satlength=1216 Nr of Repeats=24
 RepeatLength=35 seed=TGGCGGGAAA Num.seqs=17 Similarity=0.860771
 79 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_2:9202534-9203060 Satlength=527 Nr of Repeats=15
 RepeatLength=35 seed=ATTCAAATTT Num.seqs=10 Similarity=0.900952
 70 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_2:9202525-9203501 Satlength=977 Nr of Repeats=16
 RepeatLength=35 seed=TGGCGGGAAA Num.seqs=10 Similarity=0.909418
 79 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_4:1476030-1477123 Satlength=1094 Nr of Repeats=29
 RepeatLength=35 seed=AAAAAATTTT Num.seqs=18 Similarity=0.995767
 88 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_4:10263336-10264889 Satlength=1554 Nr of Repeats=42
 RepeatLength=35 seed=AATTCAAATT Num.seqs=30 Similarity=0.878991
 71 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 WB235_4:12155676-12156286 Satlength=611 Nr of Repeats=8 RepeatLength=35
 seed=AAATTTGAAT Num.seqs=5 Similarity=0.847619
 60 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 WB235_4:14740489-14741012 Satlength=524 Nr of Repeats=15 RepeatLength=35
 seed=AAATTTGAAT Num.seqs=9 Similarity=0.935450
 60 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_4:15320096-15321040 Satlength=945 Nr of Repeats=27
 RepeatLength=35 seed=GAAATTCAAA Num.seqs=18 Similarity=0.936508
 73 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 WB235_4:15971109-15972271 Satlength=1163 Nr of Repeats=29 RepeatLength=35
 seed=TTCCCGCCAA Num.seqs=20 Similarity=0.886717
 70 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--

Rev.of_WB235_5:1254505-1257773 Satlength=3269 Nr of Repeats=35
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=21 Similarity=0.865809
 77 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 WB235_5:5009264-5010522 Satlength=1259 Nr of Repeats=36 RepeatLength=35
 seed=AAATTTGAAT Num.seqs=26 Similarity=0.926974
 60 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 WB235_5:6296625-6296906 Satlength=282 Nr of Repeats=8 RepeatLength=35
 seed=AATTTCCCGC Num.seqs=7 Similarity=0.909297
 67 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 WB235_5:6297848-6298284 Satlength=437 Nr of Repeats=5 RepeatLength=35
 seed=TTTCCCGCCA Num.seqs=3 Similarity=0.916667
 69 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_5:9602338-9603453 Satlength=1116 Nr of Repeats=32
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=21 Similarity=0.936327
 77 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_5:13882409-13882690 Satlength=282 Nr of Repeats=8
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=5 Similarity=0.946667
 77 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_5:14124469-14125286 Satlength=818 Nr of Repeats=21
 RepeatLength=35 seed=GGAAATTCAA Num.seqs=14 Similarity=0.914181
 74 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 Rev.of_WB235_5:15582889-15584265 Satlength=1377 Nr of Repeats=36
 RepeatLength=35 seed=TTCAAATTTT Num.seqs=30 Similarity=0.828501
 69 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 WB235_6:9188817-9189060 Satlength=244 Nr of Repeats=7 RepeatLength=35
 seed=AAAAATTTGAA Num.seqs=5 Similarity=0.908571
 94 ATT-TCCCGCC--AAAA-T-TTTT-TT-CA-CTGAAAATTTGA--
 WB235_3:10678429-10678847 Satlength=419 Nr of Repeats=11 RepeatLength=35
 seed=CCGCCAAAAT Num.seqs=10 Similarity=0.943280
 38 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CTAAAAATTTGA--
 Rev.of_WB235_3:10683224-10684272 Satlength=1049 Nr of Repeats=30
 RepeatLength=35 seed=AAATTCAAAT Num.seqs=28 Similarity=0.892702
 72 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CTAAAAATTTGA--
 Rev.of_WB235_4:15201340-15201723 Satlength=384 Nr of Repeats=11
 RepeatLength=35 seed=GGGAAATTCA Num.seqs=7 Similarity=0.941950
 40 ATT-TCCCGCC--AAAA-T-ATTT-TT-TA-CTAAAAATTTGA--
 Rev.of_WB235_4:15201392-15202170 Satlength=779 Nr of Repeats=9
 RepeatLength=35 seed=GTAAAAAATA Num.seqs=7 Similarity=0.929252
 57 ATT-TCCCGCC--AAAA-T-ATTT-TT-TA-CTAAAAATTTGA--
 Rev.of_WB235_1:7868653-7868828 Satlength=176 Nr of Repeats=5
 RepeatLength=35 seed=GGGAAATTTA Num.seqs=5 Similarity=0.946667
 40 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 WB235_2:14878167-14878554 Satlength=388 Nr of Repeats=11 RepeatLength=35
 seed=CAGAAAATTT Num.seqs=9 Similarity=0.949206
 56 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_4:13462892-13463563 Satlength=672 Nr of Repeats=18
 RepeatLength=35 seed=GAAATTTAAA Num.seqs=15 Similarity=0.948481
 73 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_4:13462893-13464435 Satlength=1543 Nr of Repeats=25
 RepeatLength=35 seed=AAATTTAAAT Num.seqs=19 Similarity=0.791694
 72 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_4:13922549-13923902 Satlength=1354 Nr of Repeats=39
 RepeatLength=35 seed=GGGAAATTTA Num.seqs=27 Similarity=0.939655
 40 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--

Rev.of_WB235_4:15166547-15166687 Satlength=141 Nr of Repeats=4
 RepeatLength=35 seed=AAATTTTCTG Num.seqs=4 Similarity=0.904762
 66 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_4:16910719-16910928 Satlength=210 Nr of Repeats=6
 RepeatLength=35 seed=GAAATTTAAA Num.seqs=5 Similarity=0.900952
 73 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_4:17141438-17141648 Satlength=211 Nr of Repeats=6
 RepeatLength=35 seed=AAATTTTCTG Num.seqs=6 Similarity=0.928889
 66 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_5:6071995-6072240 Satlength=246 Nr of Repeats=7
 RepeatLength=35 seed=ATTTTGGCGG Num.seqs=7 Similarity=0.952834
 48 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 WB235_5:7913711-7913991 Satlength=281 Nr of Repeats=8 RepeatLength=35
 seed=CAGAAAATTT Num.seqs=8 Similarity=0.964626
 56 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_5:7916137-7916840 Satlength=704 Nr of Repeats=20
 RepeatLength=35 seed=GGGAAATTTA Num.seqs=17 Similarity=0.971429
 40 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 WB235_6:1375505-1376170 Satlength=666 Nr of Repeats=19 RepeatLength=35
 seed=CCCGCCAAAA Num.seqs=19 Similarity=0.932275
 72 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 WB235_6:13795780-13795990 Satlength=211 Nr of Repeats=6 RepeatLength=35
 seed=CAGAAAATTT Num.seqs=6 Similarity=0.949206
 56 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 WB235_6:15482252-15482427 Satlength=176 Nr of Repeats=5 RepeatLength=35
 seed=ATTTAAATTT Num.seqs=5 Similarity=0.939048
 62 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_6:17311164-17311479 Satlength=316 Nr of Repeats=9
 RepeatLength=35 seed=AAATTTTCTG Num.seqs=7 Similarity=0.909297
 66 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_4:15826993-15827272 Satlength=280 Nr of Repeats=8
 RepeatLength=35 seed=AATTTAAATT Num.seqs=7 Similarity=0.896599
 71 ATT-TCCCGCC--AAAA-T-ATTT-TT-CN-CAGAAAATTTAA--
 WB235_2:632106-632999 Satlength=894 Nr of Repeats=4 RepeatLength=35
 seed=GAAAATTTAA Num.seqs=3 Similarity=0.923810
 58 ATT-TCCCTCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_2:14836894-14837772 Satlength=879 Nr of Repeats=25
 RepeatLength=35 seed=TTAAATTTTC Num.seqs=22 Similarity=0.939312
 68 ATT-TCCCTCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_3:8336113-8336287 Satlength=175 Nr of Repeats=5
 RepeatLength=35 seed=GGGAAATTTA Num.seqs=4 Similarity=0.974603
 75 ATT-TCCCTCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTAA--
 Rev.of_WB235_1:14403308-14403517 Satlength=210 Nr of Repeats=6
 RepeatLength=35 seed=AATTTAAATT Num.seqs=5 Similarity=0.859048
 71 ATT-TCCCGCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--
 WB235_3:13447979-13448227 Satlength=249 Nr of Repeats=7 RepeatLength=35
 seed=AATTTCCCGC Num.seqs=5 Similarity=0.885714
 102 ATT-TCCCGCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--
 WB235_4:7441316-7441526 Satlength=211 Nr of Repeats=6 RepeatLength=35
 seed=CAGAAAATTT Num.seqs=6 Similarity=0.926349
 91 ATT-TCCCGCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--
 WB235_5:9439011-9439221 Satlength=211 Nr of Repeats=6 RepeatLength=35
 seed=AGAAAATTTA Num.seqs=6 Similarity=0.888254
 92 ATT-TCCCGCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--

WB235_5:18777092-18777231 Satlength=140 Nr of Repeats=4 RepeatLength=35
 seed=TCAGAAAATT Num.seqs=3 Similarity=0.923810
 90 ATT-TCCCGCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--
 WB235_6:14937379-14937623 Satlength=245 Nr of Repeats=7 RepeatLength=35
 seed=CAGAAAATTT Num.seqs=6 Similarity=0.893333
 91 ATT-TCCCGCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--
 WB235_4:8469359-8469569 Satlength=211 Nr of Repeats=6 RepeatLength=35
 seed=GAAAATTTAA Num.seqs=6 Similarity=0.898413
 93 ATT-TCCCTCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--
 WB235_6:15635446-15635796 Satlength=351 Nr of Repeats=10 RepeatLength=35
 seed=CAGAAAATTT Num.seqs=10 Similarity=0.875556
 126 ATT-TCCCTCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--
 WB235_4:15765291-15766235 Satlength=945 Nr of Repeats=8 RepeatLength=35
 seed=AAAATTTAAA Num.seqs=7 Similarity=0.883900
 94 ATT-TCCCNCC--AAAA-T-ATTT-TT-CT-CAGAAAATTTAA--
 Rev.of_WB235_2:15000726-15000995 Satlength=270 Nr of Repeats=5
 RepeatLength=35 seed=ATTTTGGCGG Num.seqs=4 Similarity=0.904762
 83 ATT-TCCCGCC--AAAA-T-ATTT-TT-CT-CCGAAAATTTAA--
 WB235_4:16675832-16676039 Satlength=208 Nr of Repeats=6 RepeatLength=35
 seed=TTGAATTTCC Num.seqs=4 Similarity=0.917460
 64 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAGAAAATTTGA--
 Rev.of_WB235_6:142149-142814 Satlength=666 Nr of Repeats=19
 RepeatLength=35 seed=GCGGGAAATT Num.seqs=15 Similarity=0.805405
 77 ATT-TCCCGCC--AAAA-T-ATTT-TT-CA-CAAAAAATTTGA--
 WB235_2:9633206-9633906 Satlength=701 Nr of Repeats=20 RepeatLength=35
 seed=CCAAAATATT Num.seqs=20 Similarity=0.928822
 41 ATT-TCCCTCC--AAAA-T-ATTT-TT-TT-CAGAAAATTTAA--
 WB235_4:1153661-1154193 Satlength=533 Nr of Repeats=4 RepeatLength=35
 seed=AAAATATTTT Num.seqs=3 Similarity=0.898413
 43 ATT-TCCCTCC--AAAA-T-ATTT-TT-TT-CAGAAAATTTAA--
 Rev.of_WB235_3:3896794-3897038 Satlength=245 Nr of Repeats=7
 RepeatLength=35 seed=AATTTAAATT Num.seqs=6 Similarity=0.890794
 71 ATT-TCCCGCC--AAAA-T-ATTT-TT-TT-CAGAAAATTTAA--
 WB235_4:4920980-4921503 Satlength=524 Nr of Repeats=15 RepeatLength=35
 seed=TTTTCAGAAA Num.seqs=13 Similarity=0.973626
 52 ATT-TCCCTCC--AAAA-T-ATTT-TT-TT-CAGAAAATTTAA--
 WB235_4:4923556-4923766 Satlength=211 Nr of Repeats=6 RepeatLength=35
 seed=AATATTTTTT Num.seqs=6 Similarity=0.964444
 80 ATT-TCCCTCC--AAAA-T-ATTT-TT-TT-CAGAAAATTTAA--
 WB235_4:4925825-4926035 Satlength=211 Nr of Repeats=6 RepeatLength=35
 seed=AATATTTTTT Num.seqs=6 Similarity=0.939048
 80 ATT-TCCCTCC--AAAA-T-ATTT-TT-TT-CAGAAAATTTAA--
 Rev.of_WB235_3:12485043-12485356 Satlength=314 Nr of Repeats=8
 RepeatLength=35 seed=TTCAAATTTT Num.seqs=5 Similarity=0.658559
 34 ATT-TNCCGCC--AAAA-T-GTCT-TT-CA-CAGAAAATTTGA--
 WB235_5:19866564-19867301 Satlength=738 Nr of Repeats=21 RepeatLength=33
 seed=TTTGAATTTT Num.seqs=17 Similarity=0.722086
 26 -TT-TCCCACC--AAAA-T---TT-TC--T-CAAAAAATTTGAA-
 WB235_5:19755742-19756252 Satlength=511 Nr of Repeats=14 RepeatLength=34
 seed=TTTCCCGCCA Num.seqs=12 Similarity=0.859774
 32 -TT-TCCCGCC--AAAA-T---AT-TCACT-CNAAAAATTTGAA-
 Rev.of_WB235_3:12762055-12762649 Satlength=595 Nr of Repeats=17
 RepeatLength=35 seed=AAATTCAAAT Num.seqs=16 Similarity=0.851746
 35 -TT-TCCCGCCATAAAA-T---AT-TT-CT-CAATAATTTGAA-

Rev.of_WB235_3:12345927-12348234 Satlength=2308 Nr of Repeats=63
RepeatLength=35 seed=CGGGAAAATT Num.seqs=39 Similarity=0.947253
40 -TT-TCCCGCC--AAAA-T--TTGTT--TCCAAAAAATTTGAAT
Rev.of_WB235_5:17817728-17818258 Satlength=531 Nr of Repeats=13
RepeatLength=34 seed=TCAAATTTTC Num.seqs=8 Similarity=0.860204
0 ATT-T-CCGCC--AAAG-T-TTTT-TT-AA-AAGAAAAATTTGA--

* * * * *

Consensus:

ATTtcCCGCCAAAAtnTtTTTTCaCaGAAAATTTgA

>WB235_Fam_5_40_94 Nr. of seq. 94 Alignment length(with gaps) = 41
Alignment score = 0.668164
WB235_1:334679-335159 Satlength=481 Nr of Repeats=12 RepeatLength=40
seed=AATTTTCTCG Num.seqs=12 Similarity=0.914646
0 AATTTTCTCGAATTTCCAGAAGGTTCTAGAACATTTCa-G
Rev.of_WB235_5:1352314-1352754 Satlength=441 Nr of Repeats=9
RepeatLength=40 seed=AATGTTCTAG Num.seqs=6 Similarity=0.738753
36 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTTCa-G
WB235_1:14668659-14668849 Satlength=191 Nr of Repeats=5 RepeatLength=40
seed=CCAGAAGGTT Num.seqs=4 Similarity=0.800000
16 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTCa-G
WB235_1:13613895-13615295 Satlength=1401 Nr of Repeats=35 RepeatLength=40
seed=GAATTTTCTC Num.seqs=35 Similarity=0.957535
39 AATTTTCTCGAATTTTCCAGAAGGTTCTGGAGCATTCa-G
Rev.of_WB235_6:16100718-16101792 Satlength=1075 Nr of Repeats=13
RepeatLength=40 seed=ATGTTCCAGA Num.seqs=12 Similarity=0.873676
75 AATTTTCTCGAATTTTCCAGAAGGTTCTGGAACATTCa-G
WB235_4:2135958-2136208 Satlength=251 Nr of Repeats=6 RepeatLength=40
seed=TTCCAGAATT Num.seqs=5 Similarity=0.866667
74 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTCa-G
Rev.of_WB235_4:13668023-13668625 Satlength=603 Nr of Repeats=12
RepeatLength=40 seed=AAAATTCTGG Num.seqs=9 Similarity=0.870370
86 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTCa-G
Rev.of_WB235_6:443181-444059 Satlength=879 Nr of Repeats=19
RepeatLength=40 seed=AAAATTCTGG Num.seqs=12 Similarity=0.943434
86 AATTTTCTCGAATTTTCCAGAAGGTTCTAGAACATTCa-G
Rev.of_WB235_4:13861930-13862600 Satlength=671 Nr of Repeats=11
RepeatLength=40 seed=CTGGAATGTT Num.seqs=9 Similarity=0.940741
40 AATTTTCTCAAATTTTCCAGAAGGTTCTGGAACATTCa-G
Rev.of_WB235_5:16547704-16548504 Satlength=801 Nr of Repeats=18
RepeatLength=40 seed=CTGGAATGTT Num.seqs=16 Similarity=0.952222
40 AATTTTCTCAAATTTTCCAGAAGGTTCTGGAACATTCa-G
Rev.of_WB235_5:16547704-16548822 Satlength=1119 Nr of Repeats=19
RepeatLength=40 seed=CTGGAATGTT Num.seqs=16 Similarity=0.952222
40 AATTTTCTCAAATTTTCCAGAAGGTTCTGGAACATTCa-G
Rev.of_WB235_5:17043954-17044434 Satlength=481 Nr of Repeats=12
RepeatLength=40 seed=AAAATTCTGG Num.seqs=12 Similarity=0.900000
46 AATTTTCTCAAATTTTCCAAAAGGCTCTAGAACATTCa-G
WB235_6:17288074-17288675 Satlength=602 Nr of Repeats=6 RepeatLength=40
seed=TTTCTCGAAT Num.seqs=4 Similarity=0.866667
43 AAATTTCTCGAATCTTCCAGAAGGTTCTAGAACATTCa-G

WB235_1:4573284-4573803 Satlength=520 Nr of Repeats=13 RepeatLength=40
 seed=CATTCAGAA Num.seqs=12 Similarity=0.966667
 22 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G
 WB235_3:2501737-2501917 Satlength=181 Nr of Repeats=5 RepeatLength=40
 seed=TTCCAGAATT Num.seqs=4 Similarity=0.966667
 24 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G
 WB235_4:15765625-15765904 Satlength=280 Nr of Repeats=6 RepeatLength=40
 seed=GATTTTCTA Num.seqs=4 Similarity=0.911111
 39 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G
 Rev.of_WB235_5:6088840-6089240 Satlength=401 Nr of Repeats=10
 RepeatLength=40 seed=TGGAATGTTC Num.seqs=10 Similarity=0.916622
 29 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G
 Rev.of_WB235_5:13440191-13440658 Satlength=468 Nr of Repeats=12
 RepeatLength=40 seed=TCTGGAATGT Num.seqs=11 Similarity=0.922424
 31 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G
 Rev.of_WB235_6:142874-143634 Satlength=761 Nr of Repeats=19
 RepeatLength=40 seed=GAAAATTCTG Num.seqs=19 Similarity=0.974269
 37 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCCC-G
 Rev.of_WB235_4:16910953-16911111 Satlength=159 Nr of Repeats=4
 RepeatLength=40 seed=AAAATTCTGG Num.seqs=3 Similarity=0.977778
 36 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 WB235_5:15320778-15321338 Satlength=561 Nr of Repeats=14 RepeatLength=40
 seed=CGATTTTCT Num.seqs=14 Similarity=0.947985
 38 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 WB235_6:1375049-1375406 Satlength=358 Nr of Repeats=9 RepeatLength=40
 seed=ATTTTCTAG Num.seqs=6 Similarity=0.937778
 40 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 Rev.of_WB235_1:6647885-6648325 Satlength=441 Nr of Repeats=11
 RepeatLength=40 seed=TTCTGGAATG Num.seqs=11 Similarity=0.960000
 32 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 Rev.of_WB235_1:7868937-7869457 Satlength=521 Nr of Repeats=13
 RepeatLength=40 seed=GAATGTTCCA Num.seqs=11 Similarity=0.935758
 67 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 WB235_2:9631891-9633131 Satlength=1241 Nr of Repeats=31 RepeatLength=40
 seed=TTCTGGAACA Num.seqs=31 Similarity=0.949462
 54 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 WB235_3:424780-427345 Satlength=2566 Nr of Repeats=43 RepeatLength=40
 seed=ACATTCCAGA Num.seqs=41 Similarity=0.892358
 61 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 Rev.of_WB235_3:3897112-3897672 Satlength=561 Nr of Repeats=14
 RepeatLength=40 seed=GTTCAGAAC Num.seqs=14 Similarity=0.942857
 63 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 WB235_4:7441099-7441297 Satlength=199 Nr of Repeats=5 RepeatLength=40
 seed=TCCAGAATTT Num.seqs=4 Similarity=0.966667
 65 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 WB235_4:7441099-7441714 Satlength=616 Nr of Repeats=6 RepeatLength=40
 seed=TCCAGAATTT Num.seqs=4 Similarity=0.966667
 65 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 WB235_4:8467091-8469338 Satlength=2248 Nr of Repeats=33 RepeatLength=40
 seed=TCCAGAATTT Num.seqs=27 Similarity=0.869136
 65 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G
 Rev.of_WB235_4:13847379-13847579 Satlength=201 Nr of Repeats=5
 RepeatLength=40 seed=AATGTTCCAG Num.seqs=5 Similarity=0.973333
 66 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTCTC-G

Rev.of_WB235_4:15166752-15167072 Satlength=321 Nr of Repeats=8
 RepeatLength=40 seed=GAATGTTCCA Num.seqs=8 Similarity=0.897619
 67 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G
 WB235_4:16458486-16458684 Satlength=199 Nr of Repeats=5 RepeatLength=40
 seed=TTCCAGAATT Num.seqs=4 Similarity=0.966667
 64 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G
 WB235_6:168652-168890 Satlength=239 Nr of Repeats=6 RepeatLength=40
 seed=TTCCAGAATT Num.seqs=5 Similarity=0.986667
 64 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G
 WB235_6:2002759-2003439 Satlength=681 Nr of Repeats=17 RepeatLength=40
 seed=GAATTTTCTC Num.seqs=17 Similarity=0.955392
 69 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G
 WB235_6:2057847-2058368 Satlength=522 Nr of Repeats=13 RepeatLength=40
 seed=TTTTCTCGAT Num.seqs=12 Similarity=0.960606
 32 ATTTTCTAGAAAGTTCTGGAACATTCCAGAATTTTCTC-G
 Rev.of_WB235_1:13231021-13231669 Satlength=649 Nr of Repeats=15
 RepeatLength=40 seed=GAAAATTCTG Num.seqs=13 Similarity=0.967949
 37 ATTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCTC-G
 Rev.of_WB235_6:17310825-17311809 Satlength=985 Nr of Repeats=10
 RepeatLength=40 seed=AATGTTCCAG Num.seqs=9 Similarity=0.879630
 66 ATTTTCTAGAAAGTTCTGGAACATTTCCAGAATTTTCTC-G
 WB235_4:16675606-16675766 Satlength=161 Nr of Repeats=4 RepeatLength=40
 seed=TTCCAGAATT Num.seqs=4 Similarity=0.950000
 64 ATTTTCTAGAAAGTTCTGGAACGTTCCAGAATTTTCCC-G
 WB235_5:4052517-4053360 Satlength=844 Nr of Repeats=21 RepeatLength=40
 seed=CTAGAAAGTT Num.seqs=18 Similarity=0.796514
 46 AATTCCTAGAAAGTTCTGGAACATTCCAGAATTTTCTT-G
 Rev.of_WB235_3:8344363-8344643 Satlength=281 Nr of Repeats=7
 RepeatLength=40 seed=TCTGGAATGT Num.seqs=7 Similarity=0.971429
 31 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCC-A
 WB235_4:1153760-1154039 Satlength=280 Nr of Repeats=7 RepeatLength=40
 seed=ATTTTCTAG Num.seqs=6 Similarity=0.911111
 40 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCC-A
 WB235_4:1153773-1154667 Satlength=895 Nr of Repeats=10 RepeatLength=40
 seed=GTTCTGGAAC Num.seqs=7 Similarity=0.844444
 53 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCC-A
 WB235_5:1403527-1403806 Satlength=280 Nr of Repeats=7 RepeatLength=40
 seed=ATTTTCTAG Num.seqs=6 Similarity=0.880000
 40 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCC-A
 Rev.of_WB235_5:7916966-7925007 Satlength=8042 Nr of Repeats=201
 RepeatLength=40 seed=TTCTAGAAAA Num.seqs=194 Similarity=0.914186
 52 ATTTTCTAGAAAGTTCTGGAACATTCCAGACTTTTCCC-A
 Rev.of_WB235_1:778056-778335 Satlength=280 Nr of Repeats=6
 RepeatLength=40 seed=GAACCTTCTG Num.seqs=4 Similarity=0.850000
 7 AAGGTTCTAGAACATTCCAGAATTTTCTCAAATTTTCCA-G
 Rev.of_WB235_2:4554394-4554914 Satlength=521 Nr of Repeats=13
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=13 Similarity=0.958120
 11 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G
 WB235_4:8467000-8468026 Satlength=1027 Nr of Repeats=15 RepeatLength=40
 seed=TTCTGGAACA Num.seqs=14 Similarity=0.912088
 44 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G
 WB235_6:14723559-14724409 Satlength=851 Nr of Repeats=5 RepeatLength=40
 seed=TTCTGGAACA Num.seqs=4 Similarity=0.866667
 44 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G

Rev.of_WB235_6:16100682-16101122 Satlength=441 Nr of Repeats=11
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=11 Similarity=0.950303
 11 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G
 Rev.of_WB235_3:11160584-11160784 Satlength=201 Nr of Repeats=5
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=5 Similarity=0.960000
 11 AAGGTTCTGGAACATTCCAGCATTTTCTCAAATTTTCCA-G
 WB235_4:15709349-15709549 Satlength=201 Nr of Repeats=5 RepeatLength=40
 seed=ATTTTCCAGA Num.seqs=5 Similarity=0.920000
 31 AAGGTTCTGGAACATTCCAGAATTTTCTCAAATTTTCCA-G
 WB235_2:633567-633717 Satlength=151 Nr of Repeats=4 RepeatLength=40
 seed=CAGAAAGTTC Num.seqs=3 Similarity=0.800000
 37 AAGGTTCTGGAACATTCCAGAATTTTCTAGAATTTTCCA-G
 Rev.of_WB235_3:3895928-3896228 Satlength=301 Nr of Repeats=8
 RepeatLength=40 seed=AGAACCTTCT Num.seqs=6 Similarity=0.824444
 48 AAGGTTCTGGAACATTCCAGAATTTTCTAGAATTTTCCA-G
 Rev.of_WB235_3:9534180-9534500 Satlength=321 Nr of Repeats=8
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=8 Similarity=0.945238
 51 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G
 Rev.of_WB235_3:9534215-9534836 Satlength=622 Nr of Repeats=9
 RepeatLength=40 seed=AATGTTCCAG Num.seqs=8 Similarity=0.903571
 56 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G
 Rev.of_WB235_4:12022575-12022894 Satlength=320 Nr of Repeats=8
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=7 Similarity=0.946032
 51 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G
 Rev.of_WB235_4:13861901-13862381 Satlength=481 Nr of Repeats=12
 RepeatLength=40 seed=CAGAACCTTC Num.seqs=12 Similarity=0.914646
 89 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G
 Rev.of_WB235_5:3520502-3520742 Satlength=241 Nr of Repeats=6
 RepeatLength=40 seed=TCCAGAACCT Num.seqs=6 Similarity=0.931111
 51 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G
 Rev.of_WB235_6:9007668-9008148 Satlength=481 Nr of Repeats=12
 RepeatLength=40 seed=CTTCTGGAAA Num.seqs=12 Similarity=0.953030
 83 AAGGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCCA-G
 WB235_1:780732-781012 Satlength=281 Nr of Repeats=7 RepeatLength=40
 seed=TCTAGAACAT Num.seqs=7 Similarity=0.838095
 45 AAGGTTCTAGAACATTCCAGAATTTTCTCGAATTTTCCA-A
 WB235_5:1355392-1355652 Satlength=261 Nr of Repeats=6 RepeatLength=40
 seed=CTAGAACATT Num.seqs=5 Similarity=0.712195
 46 AANGTTCTAGAACATTCCAGAATTTTCTCGAATTTTCCA-G
 Rev.of_WB235_1:14033367-14034207 Satlength=841 Nr of Repeats=24
 RepeatLength=40 seed=TTCTGGAAAA Num.seqs=18 Similarity=0.755338
 82 AAGGTTCTAGAACATTCCAGAATTTTATCGAATTTTCCA-G
 Rev.of_WB235_4:2754821-2756571 Satlength=1751 Nr of Repeats=49
 RepeatLength=40 seed=TTCTGGAAAA Num.seqs=36 Similarity=0.839524
 82 AAGGTTCTAGAACATTCCAGAATTTTTCGAATTTTCCA-G
 Rev.of_WB235_5:4050682-4051242 Satlength=561 Nr of Repeats=14
 RepeatLength=40 seed=GAACCTTCTG Num.seqs=12 Similarity=0.857071
 47 AAGGTTCAAAAACATTCCAGAATTTTCTCGAATTTTCCA-G
 WB235_5:1530916-1531076 Satlength=161 Nr of Repeats=4 RepeatLength=40
 seed=GTTCTAGAAC Num.seqs=4 Similarity=0.875339
 84 AAGGTTCTAGAACATTCCAGAATTTTCTCGAATTTTACCAGG
 WB235_3:12001471-12001873 Satlength=403 Nr of Repeats=10 RepeatLength=40
 seed=ATTCAGAAAT Num.seqs=8 Similarity=0.860714
 13 AAGGTTCTAGAACATTCCAGAATTTTTTAAAATTTTCCA-G

Rev.of_WB235_5:7115024-7115184 Satlength=161 Nr of Repeats=4
 RepeatLength=40 seed=TTCTAGAACC Num.seqs=4 Similarity=0.794444
 52 AAGGTTCTAGAACATTCCAGAATTTTCTNAACTTTCCA-G
 WB235_5:7442929-7443089 Satlength=161 Nr of Repeats=4 RepeatLength=40
 seed=GAAGGTTCTA Num.seqs=4 Similarity=0.794444
 79 AAGGTTCTAGAACATTCCAGAATTTTCTNAAAATTCCA-G
 WB235_4:2694935-2695125 Satlength=191 Nr of Repeats=5 RepeatLength=40
 seed=GAATTTTCCA Num.seqs=4 Similarity=0.822222
 29 AAAGTTCTAGAAAATTCCAGAATTTTTCGAATTTTCCA-G
 Rev.of_WB235_1:3980821-3981021 Satlength=201 Nr of Repeats=6
 RepeatLength=40 seed=TTTCTAGAAA Num.seqs=4 Similarity=0.816667
 43 AAAATTCTGGACCATTCCGGAATTTTCTCGAATTTTCTA-G
 Rev.of_WB235_4:3671203-3671723 Satlength=521 Nr of Repeats=15
 RepeatLength=40 seed=TTTCTAGAAA Num.seqs=11 Similarity=0.820606
 43 AAAATTCTGGACCATTCCNGAATTTTCTCGAATTTTCTA-G
 Rev.of_WB235_1:7741780-7742262 Satlength=483 Nr of Repeats=13
 RepeatLength=40 seed=TTTCTAGAAA Num.seqs=9 Similarity=0.834259
 43 AAAGTTCTGGAATATTCCAGANTTTTCCCGAATTTTCTA-G
 WB235_4:14740244-14740404 Satlength=161 Nr of Repeats=5 RepeatLength=40
 seed=TTTCTAGAA Num.seqs=3 Similarity=0.755556
 72 AAAGTTCTGGAACATTCCAGAATTTTCCCGAATTTTCTA-G
 Rev.of_WB235_5:9603508-9604068 Satlength=561 Nr of Repeats=15
 RepeatLength=40 seed=TTTCTAGAAA Num.seqs=13 Similarity=0.855128
 83 AAAATTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G
 WB235_6:16851316-16851756 Satlength=441 Nr of Repeats=13 RepeatLength=40
 seed=TTTCTAGAAA Num.seqs=9 Similarity=0.814815
 113 AAANTTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G
 Rev.of_WB235_5:13882781-13883141 Satlength=361 Nr of Repeats=10
 RepeatLength=40 seed=TTTCTAGAAA Num.seqs=8 Similarity=0.826190
 83 AAAGTTCTGGAACATTCCAGAATTTTCTCGAATTTTCTA-G
 WB235_1:14686490-14687331 Satlength=842 Nr of Repeats=22 RepeatLength=40
 seed=TCTAGAAAGT Num.seqs=19 Similarity=0.888304
 75 AAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTCTA-G
 WB235_4:13463828-13464877 Satlength=1050 Nr of Repeats=12 RepeatLength=40
 seed=GTTCTGGAAC Num.seqs=10 Similarity=0.891111
 83 AAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTCTA-G
 WB235_6:2057868-2059356 Satlength=1489 Nr of Repeats=20 RepeatLength=40
 seed=GTTCTGGAAC Num.seqs=15 Similarity=0.890159
 83 AAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTCTA-G
 WB235_6:13795118-13795677 Satlength=560 Nr of Repeats=14 RepeatLength=40
 seed=GAACATTCCA Num.seqs=13 Similarity=0.911111
 89 AAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTCTA-G
 WB235_6:13795118-13796907 Satlength=1790 Nr of Repeats=19 RepeatLength=40
 seed=GAACATTCCA Num.seqs=16 Similarity=0.884722
 89 AAAGTTCTGGAACATTCCAGAATTTTCTCGATTTTCTA-G
 WB235_4:15895865-15896183 Satlength=319 Nr of Repeats=8 RepeatLength=40
 seed=GAACATTCCA Num.seqs=6 Similarity=0.922222
 89 AAAGTTCTGGAACATTCCAGAATTTTCTCAATTTTCTA-G
 WB235_2:632493-632813 Satlength=321 Nr of Repeats=8 RepeatLength=40
 seed=TTTCTAGAAA Num.seqs=8 Similarity=0.917857
 113 AAAATTCTGGAACATTCCAGAATTTTCCCGATTTTCTA-G
 WB235_3:424806-426326 Satlength=1521 Nr of Repeats=38 RepeatLength=40
 seed=TAGAAAGTTC Num.seqs=38 Similarity=0.903556
 117 AAAGTTCTGGAACATTCCAGAATTTTCCCGATTTTCTA-G

Rev.of_WB235_4:15826528-15827586 Satlength=1059 Nr of Repeats=8
RepeatLength=40 seed=GTTCAGAAC Num.seqs=7 Similarity=0.814286
133 AAAGTTCTGGAACATTCCAGAATTTTCCCGATTTTCTA-G
Rev.of_WB235_5:6072277-6072797 Satlength=521 Nr of Repeats=13
RepeatLength=40 seed=TTCCAGAACT Num.seqs=13 Similarity=0.959829
132 AAAGTTCTGGAACATTCCAGAATTTTCCCGATTTTCTA-G
WB235_4:4920724-4920924 Satlength=201 Nr of Repeats=5 RepeatLength=40
seed=TTCTAGAAAG Num.seqs=5 Similarity=0.913333
154 AAAGTTCTGGAACATTTCNAGAATTTTCCCGATTTTCTA-G
WB235_2:8460034-8460434 Satlength=401 Nr of Repeats=10 RepeatLength=40
seed=AAAGTTCTGG Num.seqs=10 Similarity=0.901482
80 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G
WB235_3:13447046-13447886 Satlength=841 Nr of Repeats=21 RepeatLength=40
seed=ATTTTCTAG Num.seqs=21 Similarity=0.903175
110 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G
WB235_4:15374013-15374693 Satlength=681 Nr of Repeats=17 RepeatLength=40
seed=GAACATTCCA Num.seqs=17 Similarity=0.919608
89 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G
WB235_5:7912986-7913626 Satlength=641 Nr of Repeats=16 RepeatLength=40
seed=TCTGGAACAT Num.seqs=16 Similarity=0.859790
85 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G
WB235_6:15635133-15635373 Satlength=241 Nr of Repeats=6 RepeatLength=40
seed=AAAGTTCTGG Num.seqs=6 Similarity=0.904444
80 AAAGTTCTGGAACATTCCAGAATTTTCCCAATTTTCTA-G
WB235_4:15059144-15059784 Satlength=641 Nr of Repeats=16 RepeatLength=40
seed=TTTCTAGAA Num.seqs=16 Similarity=0.900000
112 AAAGTTCTGGAACATTCCAGAAATTTCCCGATTTTCTA-G

* * * * *

Consensus:

AannTTCTnGAaCaTTCcaGAAttTTCtnGAaTTTTTcCaG

>WB235_Fam_6_11_75 Nr. of seq. 75 Alignment length(with gaps) = 12
Alignment score = 0.809099
WB235_1:562402-562457 Satlength=56 Nr of Repeats=5 RepeatLength=11
seed=GTACTCCTAC Num.seqs=5 Similarity=0.830303
0 GTACTC-CTACC
Rev.of_WB235_1:1214097-1214254 Satlength=158 Nr of Repeats=7
RepeatLength=11 seed=GTACTGTAGG Num.seqs=6 Similarity=0.870707
4 GTACTC-CTACA
Rev.of_WB235_1:13230567-13230940 Satlength=374 Nr of Repeats=12
RepeatLength=11 seed=GTACTGTAGG Num.seqs=9 Similarity=0.952862
4 GTACTC-CTACA
Rev.of_WB235_1:14402777-14402900 Satlength=124 Nr of Repeats=4
RepeatLength=11 seed=GTACTGTAGG Num.seqs=3 Similarity=0.919192
4 GTACTC-CTACA
WB235_2:633813-633947 Satlength=135 Nr of Repeats=4 RepeatLength=11
seed=GTACTCCTAC Num.seqs=3 Similarity=0.838384
11 GTACTC-CTACA
WB235_2:9634505-9634639 Satlength=135 Nr of Repeats=5 RepeatLength=11
seed=GTACTCCTAC Num.seqs=4 Similarity=0.878788
11 GTACTC-CTACA

Rev.of_WB235_2:13989510-13989877 Satlength=368 Nr of Repeats=11
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=8 Similarity=0.878788
 4 GTACTC-CTACA
 WB235_3:427473-427977 Satlength=505 Nr of Repeats=18 RepeatLength=11
 seed=CTACAGTACT Num.seqs=12 Similarity=0.773779
 6 GTACTC-CTACA
 Rev.of_WB235_3:1320466-1320612 Satlength=147 Nr of Repeats=5
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=3 Similarity=0.919192
 4 GTACTC-CTACA
 Rev.of_WB235_3:9533702-9534094 Satlength=393 Nr of Repeats=13
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=8 Similarity=0.796537
 4 GTACTC-CTACA
 WB235_4:1154757-1155014 Satlength=258 Nr of Repeats=8 RepeatLength=11
 seed=GTACTCCTAC Num.seqs=5 Similarity=0.854545
 11 GTACTC-CTACA
 WB235_4:2245441-2245572 Satlength=132 Nr of Repeats=4 RepeatLength=11
 seed=GTACTCCTAC Num.seqs=3 Similarity=0.838384
 11 GTACTC-CTACA
 Rev.of_WB235_4:2754343-2754722 Satlength=380 Nr of Repeats=12
 RepeatLength=11 seed=TACTGTAGGA Num.seqs=8 Similarity=0.787698
 14 GTACTC-CTACA
 Rev.of_WB235_4:4305710-4305967 Satlength=258 Nr of Repeats=5
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=3 Similarity=1.000000
 4 GTACTC-CTACA
 WB235_4:4325075-4325582 Satlength=508 Nr of Repeats=13 RepeatLength=11
 seed=CTACAGTACT Num.seqs=9 Similarity=0.878788
 6 GTACTC-CTACA
 WB235_4:4554554-4555060 Satlength=507 Nr of Repeats=13 RepeatLength=11
 seed=CTACAGTACT Num.seqs=9 Similarity=0.878788
 6 GTACTC-CTACA
 WB235_4:9411725-9412004 Satlength=280 Nr of Repeats=10 RepeatLength=11
 seed=GTACTCCTAC Num.seqs=8 Similarity=0.883117
 11 GTACTC-CTACA
 Rev.of_WB235_4:13845937-13846071 Satlength=135 Nr of Repeats=6
 RepeatLength=11 seed=AGTACTGTAG Num.seqs=4 Similarity=0.939394
 5 GTACTC-CTACA
 Rev.of_WB235_4:13922018-13922152 Satlength=135 Nr of Repeats=6
 RepeatLength=11 seed=AGTACTGTAG Num.seqs=4 Similarity=0.939394
 5 GTACTC-CTACA
 WB235_4:15766783-15767403 Satlength=621 Nr of Repeats=19 RepeatLength=11
 seed=GTACTCCTAC Num.seqs=13 Similarity=0.888112
 11 GTACTC-CTACA
 Rev.of_WB235_4:16094815-16095563 Satlength=749 Nr of Repeats=18
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=12 Similarity=0.878788
 4 GTACTC-CTACA
 Rev.of_WB235_4:16910220-16910354 Satlength=135 Nr of Repeats=6
 RepeatLength=11 seed=AGTACTGTAG Num.seqs=4 Similarity=0.939394
 5 GTACTC-CTACA
 WB235_4:17076321-17076588 Satlength=268 Nr of Repeats=10 RepeatLength=11
 seed=CCTACAGTAC Num.seqs=6 Similarity=0.716667
 5 GTACTC-CTACA
 Rev.of_WB235_5:3520159-3520417 Satlength=259 Nr of Repeats=7
 RepeatLength=11 seed=TACTGTAGGA Num.seqs=5 Similarity=0.763889
 14 GTACTC-CTACA

Rev.of_WB235_5:5004204-5005690 Satlength=1487 Nr of Repeats=35
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=22 Similarity=0.888233
 4 GTACTC-CTACA
 WB235_5:9439666-9439923 Satlength=258 Nr of Repeats=8 RepeatLength=11
 seed=GTACTCCTAC Num.seqs=6 Similarity=0.870707
 11 GTACTC-CTACA
 WB235_5:15322538-15322672 Satlength=135 Nr of Repeats=5 RepeatLength=11
 seed=GTACTCCTAC Num.seqs=4 Similarity=0.878788
 11 GTACTC-CTACA
 Rev.of_WB235_5:16547005-16547587 Satlength=583 Nr of Repeats=10
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=6 Similarity=0.846465
 4 GTACTC-CTACA
 WB235_5:17495404-17495538 Satlength=135 Nr of Repeats=5 RepeatLength=11
 seed=CCTACAGTAC Num.seqs=3 Similarity=0.919192
 5 GTACTC-CTACA
 WB235_5:20588792-20588997 Satlength=206 Nr of Repeats=5 RepeatLength=11
 seed=CCTACAGTAC Num.seqs=3 Similarity=1.000000
 5 GTACTC-CTACA
 WB235_6:1376859-1377239 Satlength=381 Nr of Repeats=13 RepeatLength=11
 seed=GTACTCCTAC Num.seqs=10 Similarity=0.886869
 11 GTACTC-CTACA
 WB235_6:5230547-5230804 Satlength=258 Nr of Repeats=10 RepeatLength=11
 seed=CTACAGTACT Num.seqs=7 Similarity=0.849928
 6 GTACTC-CTACA
 WB235_6:11489369-11489615 Satlength=247 Nr of Repeats=7 RepeatLength=11
 seed=TCCTACAGTA Num.seqs=5 Similarity=0.854545
 4 GTACTC-CTACA
 WB235_6:13797037-13797540 Satlength=504 Nr of Repeats=19 RepeatLength=11
 seed=CTACAGTACT Num.seqs=14 Similarity=0.771368
 6 GTACTC-CTACA
 WB235_6:14724532-14724801 Satlength=270 Nr of Repeats=10 RepeatLength=11
 seed=CCTACAGTAC Num.seqs=6 Similarity=0.738889
 5 GTACTC-CTACA
 WB235_1:1430568-1430936 Satlength=369 Nr of Repeats=14 RepeatLength=11
 seed=CTACAGTACT Num.seqs=10 Similarity=0.753704
 6 GTACTN-CTACA
 Rev.of_WB235_2:1033777-1034280 Satlength=504 Nr of Repeats=17
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=11 Similarity=0.819284
 4 GTACTN-CTACA
 WB235_2:2348715-2349106 Satlength=392 Nr of Repeats=13 RepeatLength=11
 seed=CTACAGTACC Num.seqs=9 Similarity=0.763889
 6 GTACTN-CTACA
 WB235_2:12701130-12701355 Satlength=226 Nr of Repeats=7 RepeatLength=11
 seed=CTACAGTACC Num.seqs=5 Similarity=0.775000
 6 GTACTN-CTACA
 WB235_4:8565636-8566140 Satlength=505 Nr of Repeats=13 RepeatLength=11
 seed=CTACAGTACT Num.seqs=9 Similarity=0.865320
 6 GTACTN-CTACA
 Rev.of_WB235_4:12022220-12022489 Satlength=270 Nr of Repeats=10
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=7 Similarity=0.832612
 4 GTACTN-CTACA
 WB235_4:16511822-16512828 Satlength=1007 Nr of Repeats=39 RepeatLength=11
 seed=CTACAGTACT Num.seqs=30 Similarity=0.778225
 6 GTACTN-CTACA

WB235_5:1911033-1911178 Satlength=146 Nr of Repeats=7 RepeatLength=11
 seed=CTACAGTACT Num.seqs=6 Similarity=0.723148
 6 GTACTN-CTACA
 WB235_5:16878345-16878591 Satlength=247 Nr of Repeats=7 RepeatLength=11
 seed=CTACAGTACC Num.seqs=5 Similarity=0.786111
 6 GTACTN-CTACA
 WB235_5:20260289-20260916 Satlength=628 Nr of Repeats=16 RepeatLength=11
 seed=CTACAGTACT Num.seqs=11 Similarity=0.854545
 6 GTACTN-CTACA
 WB235_6:944053-944332 Satlength=280 Nr of Repeats=13 RepeatLength=11
 seed=CTACAGTACT Num.seqs=11 Similarity=0.823691
 6 GTACTN-CTACA
 Rev.of_WB235_6:1610992-1611280 Satlength=289 Nr of Repeats=10
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=6 Similarity=0.790741
 4 GTACTN-CTACA
 Rev.of_WB235_6:9007305-9007574 Satlength=270 Nr of Repeats=10
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=7 Similarity=0.832612
 4 GTACTN-CTACA
 Rev.of_WB235_6:16100349-16100596 Satlength=248 Nr of Repeats=8
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=5 Similarity=0.755556
 4 GTACTN-CTACA
 Rev.of_WB235_2:10832628-10833651 Satlength=1024 Nr of Repeats=24
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=16 Similarity=0.896970
 4 GTACTA-CTACA
 WB235_5:1404428-1404696 Satlength=269 Nr of Repeats=8 RepeatLength=11
 seed=CTACAGTACC Num.seqs=6 Similarity=0.798148
 6 GTACTA-CTACA
 Rev.of_WB235_6:28398-28532 Satlength=135 Nr of Repeats=5 RepeatLength=11
 seed=GTACTGTAGT Num.seqs=3 Similarity=1.000000
 4 GTACTA-CTACA
 Rev.of_WB235_1:11420316-11421039 Satlength=724 Nr of Repeats=15
 RepeatLength=11 seed=GTACTGTAGG Num.seqs=9 Similarity=0.841751
 4 GTACCC-CTACA
 Rev.of_WB235_2:882370-882522 Satlength=153 Nr of Repeats=5
 RepeatLength=11 seed=TGTAGGGGTA Num.seqs=3 Similarity=1.000000
 11 GTACCC-CTACA
 WB235_2:12350820-12350876 Satlength=57 Nr of Repeats=5 RepeatLength=11
 seed=CTACAGTACC Num.seqs=4 Similarity=0.919192
 6 GTACCC-CTACA
 WB235_2:13415355-13415629 Satlength=275 Nr of Repeats=20 RepeatLength=11
 seed=CCTACAGTAC Num.seqs=12 Similarity=0.853076
 5 GTACCC-CTACA
 WB235_3:259921-260355 Satlength=435 Nr of Repeats=11 RepeatLength=11
 seed=CCTACAGTAC Num.seqs=7 Similarity=0.965368
 5 GTACCC-CTACA
 Rev.of_WB235_3:1326908-1327395 Satlength=488 Nr of Repeats=33
 RepeatLength=11 seed=GGTACTGTAG Num.seqs=21 Similarity=0.844156
 5 GTACCC-CTACA
 Rev.of_WB235_3:1633390-1634249 Satlength=860 Nr of Repeats=41
 RepeatLength=11 seed=TACTGTAGG Num.seqs=30 Similarity=0.811076
 14 GTACCC-CTACA
 WB235_4:9433776-9433910 Satlength=135 Nr of Repeats=4 RepeatLength=11
 seed=CCCTACAGTA Num.seqs=3 Similarity=0.919192
 4 GTACCC-CTACA

WB235_4:16522968-16523369 Satlength=402 Nr of Repeats=28 RepeatLength=11
seed=CCCCTACAGT Num.seqs=17 Similarity=0.887701
14 GTACCC-CTACA
WB235_5:14057570-14057714 Satlength=145 Nr of Repeats=6 RepeatLength=11
seed=CTACAGTACC Num.seqs=4 Similarity=0.818182
6 GTACCC-CTACA
Rev.of_WB235_5:15823540-15823605 Satlength=66 Nr of Repeats=4
RepeatLength=11 seed=GTACTGTAGG Num.seqs=3 Similarity=0.919192
4 GTACCC-CTACA
WB235_5:17619161-17619418 Satlength=258 Nr of Repeats=8 RepeatLength=11
seed=CCTACAGTAC Num.seqs=6 Similarity=0.886869
5 GTACCC-CTACA
Rev.of_WB235_2:4094407-4094663 Satlength=257 Nr of Repeats=13
RepeatLength=11 seed=GTACTGTAGG Num.seqs=9 Similarity=0.735043
4 GTACNC-CTACA
WB235_3:520005-520140 Satlength=136 Nr of Repeats=6 RepeatLength=11
seed=CTACAGTACC Num.seqs=4 Similarity=0.858586
6 GTACCA-CTACA
WB235_3:2035722-2035981 Satlength=260 Nr of Repeats=20 RepeatLength=11
seed=CTACAGTACC Num.seqs=14 Similarity=0.795788
6 GTACCN-CTACA
WB235_5:2141423-2141937 Satlength=515 Nr of Repeats=18 RepeatLength=11
seed=CTACAGTACC Num.seqs=14 Similarity=0.742063
6 GTACCN-CTACA
Rev.of_WB235_4:10025402-10025894 Satlength=493 Nr of Repeats=10
RepeatLength=11 seed=TACTGTAGG Num.seqs=6 Similarity=0.935354
14 GTAACC-CTACA
Rev.of_WB235_5:3731028-3731508 Satlength=481 Nr of Repeats=23
RepeatLength=11 seed=AGGATTACTG Num.seqs=15 Similarity=0.843001
19 GTAATC-CTACA
WB235_3:11331372-11331497 Satlength=126 Nr of Repeats=4 RepeatLength=11
seed=CTACAGTACT Num.seqs=3 Similarity=0.838384
6 GTACTT-CTACA
Rev.of_WB235_3:11700371-11700706 Satlength=336 Nr of Repeats=7
RepeatLength=11 seed=GTACTGTAGA Num.seqs=5 Similarity=0.854545
15 GTACNT-CTACA
WB235_5:7443218-7444716 Satlength=1499 Nr of Repeats=50 RepeatLength=11
seed=CTACAGTACC Num.seqs=38 Similarity=0.685961
6 GTACCT-CTACA
WB235_4:2136323-2136466 Satlength=144 Nr of Repeats=5 RepeatLength=11
seed=CTACAGTACC Num.seqs=4 Similarity=0.796296
6 GTACCTACTACA
Rev.of_WB235_1:11763187-11763333 Satlength=147 Nr of Repeats=6
RepeatLength=11 seed=AGTACTGTAG Num.seqs=4 Similarity=0.731481
16 GTACTNACTACA

*** ****

Consensus:

GTACTcCTACA

>WB235_Fam_7_15_70 Nr. of seq. 70 Alignment length(with gaps) = 15
Alignment score = 0.826961

WB235_1:902260-902411 Satlength=152 Nr of Repeats=8 RepeatLength=15
 seed=ATCTTCTTTT Num.seqs=5 Similarity=0.911111
 0 ATCTTCTTTTCGTAG
 WB235_1:2144021-2144187 Satlength=167 Nr of Repeats=10 RepeatLength=15
 seed=AGATCTTGTT Num.seqs=8 Similarity=0.831746
 13 ATCTTGTTTTTCGTAG
 Rev.of_WB235_2:12002438-12002513 Satlength=76 Nr of Repeats=4
 RepeatLength=15 seed=AAAACAAGAT Num.seqs=3 Similarity=0.792593
 25 ATCTTGTTTTTNGTAG
 WB235_2:690749-690809 Satlength=61 Nr of Repeats=4 RepeatLength=15
 seed=GTAGATCTTG Num.seqs=4 Similarity=0.675347
 26 ATCTTGTTTTGGTAG
 WB235_2:7475407-7475467 Satlength=61 Nr of Repeats=4 RepeatLength=15
 seed=GTAGATCTTG Num.seqs=4 Similarity=0.675347
 26 ATCTTGTTTTGGTAG
 WB235_4:17285019-17285079 Satlength=61 Nr of Repeats=4 RepeatLength=15
 seed=GTAGATCTTG Num.seqs=4 Similarity=0.675347
 26 ATCTTGTTTTGGTAG
 Rev.of_WB235_5:100578-100668 Satlength=91 Nr of Repeats=6 RepeatLength=15
 seed=AAAAGGAGAA Num.seqs=6 Similarity=0.822222
 10 TTCTCCTTTTCGTNG
 WB235_5:100901-100991 Satlength=91 Nr of Repeats=6 RepeatLength=15
 seed=TTCTCCTTTT Num.seqs=6 Similarity=0.792593
 15 TTCTCCTTTTCGTNG
 Rev.of_WB235_1:4958855-4958932 Satlength=78 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.807407
 12 CTCCCCTTTTCGTAT
 WB235_1:4959104-4959196 Satlength=93 Nr of Repeats=5 RepeatLength=15
 seed=CTCCCCTTTT Num.seqs=3 Similarity=0.847222
 15 CTCCCCTTTTCGTAT
 WB235_1:4961695-4961802 Satlength=108 Nr of Repeats=6 RepeatLength=15
 seed=CTCCCCTTTT Num.seqs=4 Similarity=0.869792
 15 CTCCCCTTTTCGTAT
 Rev.of_WB235_2:1134516-1134593 Satlength=78 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.777778
 12 CTCCCCTTTTCGTAT
 Rev.of_WB235_3:6551383-6551520 Satlength=138 Nr of Repeats=9
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=8 Similarity=0.847619
 12 CTCCCCTTTTCGTAT
 Rev.of_WB235_3:12878018-12878110 Satlength=93 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.881481
 12 CTCCCCTTTTCGTAT
 WB235_4:1447227-1447319 Satlength=93 Nr of Repeats=6 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.840000
 16 CTCCCCTTTTCGTAT
 Rev.of_WB235_4:4702090-4702167 Satlength=78 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.777778
 12 CTCCCCTTTTCGTAT
 Rev.of_WB235_4:8015849-8015941 Satlength=93 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.881481
 12 CTCCCCTTTTCGTAT
 WB235_4:12621744-12621836 Satlength=93 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=3 Similarity=0.881481
 16 CTCCCCTTTTCGTAT

WB235_1:5176308-5176383 Satlength=76 Nr of Repeats=5 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
Rev.of_WB235_1:10468958-10469050 Satlength=93 Nr of Repeats=6
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889
27 CTCCCCCTTTTCGTAG
WB235_1:10469225-10469317 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
WB235_2:1134783-1134875 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
Rev.of_WB235_2:7894727-7894819 Satlength=93 Nr of Repeats=6
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889
27 CTCCCCCTTTTCGTAG
WB235_2:7894995-7895087 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=CCCCTTTTCG Num.seqs=5 Similarity=0.733333
17 CTCCCCCTTTTCGTAG
WB235_2:10248425-10248517 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.733333
16 CTCCCCCTTTTCGTAG
Rev.of_WB235_2:11534628-11534720 Satlength=93 Nr of Repeats=6
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889
27 CTCCCCCTTTTCGTAG
WB235_2:11534895-11534970 Satlength=76 Nr of Repeats=5 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
Rev.of_WB235_2:14346267-14346344 Satlength=78 Nr of Repeats=5
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148
27 CTCCCCCTTTTCGTAG
WB235_3:7708901-7708993 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
WB235_3:10436489-10436581 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
WB235_4:628375-628467 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
Rev.of_WB235_4:3050503-3050595 Satlength=93 Nr of Repeats=6
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.760000
27 CTCCCCCTTTTCGTAG
WB235_4:3050770-3050862 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
Rev.of_WB235_4:4401664-4401741 Satlength=78 Nr of Repeats=5
RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148
27 CTCCCCCTTTTCGTAG
WB235_4:4702342-4702434 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG
WB235_4:8016116-8016208 Satlength=93 Nr of Repeats=6 RepeatLength=15
seed=TCCCCCTTTTC Num.seqs=5 Similarity=0.768889
16 CTCCCCCTTTTCGTAG

Rev.of_WB235_4:11178974-11179067 Satlength=94 Nr of Repeats=6
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148
 27 CTCCCCTTTTCGTAG
 Rev.of_WB235_4:12621478-12621570 Satlength=93 Nr of Repeats=6
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889
 27 CTCCCCTTTTCGTAG
 Rev.of_WB235_4:15199553-15199645 Satlength=93 Nr of Repeats=6
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889
 27 CTCCCCTTTTCGTAG
 Rev.of_WB235_5:1197262-1197339 Satlength=78 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148
 27 CTCCCCTTTTCGTAG
 WB235_5:1197514-1197589 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889
 16 CTCCCCTTTTCGTAG
 Rev.of_WB235_5:5754995-5755070 Satlength=76 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889
 27 CTCCCCTTTTCGTAG
 WB235_5:5755255-5755347 Satlength=93 Nr of Repeats=6 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.733333
 16 CTCCCCTTTTCGTAG
 WB235_5:14444028-14444120 Satlength=93 Nr of Repeats=6 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889
 16 CTCCCCTTTTCGTAG
 Rev.of_WB235_5:15770931-15771023 Satlength=93 Nr of Repeats=6
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=5 Similarity=0.768889
 27 CTCCCCTTTTCGTAG
 Rev.of_WB235_5:16552748-16552808 Satlength=61 Nr of Repeats=4
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.748148
 27 CTCCCCTTTTCGTAG
 WB235_4:17345179-17345256 Satlength=78 Nr of Repeats=5 RepeatLength=15
 seed=TTCCCCTTTT Num.seqs=4 Similarity=0.866667
 15 TTCCCCTTTTCGTAT
 WB235_1:5621701-5621793 Satlength=93 Nr of Repeats=6 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889
 16 ATCCCCTTTTCGCAG
 WB235_2:14346519-14346611 Satlength=93 Nr of Repeats=6 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.768889
 16 ATCCCCTTTTCGCAG
 Rev.of_WB235_3:6013025-6013087 Satlength=63 Nr of Repeats=4
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.762963
 27 ATCCCCTTTTCGCAG
 WB235_3:6013262-6013339 Satlength=78 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.748148
 16 ATCCCCTTTTCGCAG
 WB235_3:6551695-6551771 Satlength=77 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.748148
 16 ATCCCCTTTTCGCAG
 Rev.of_WB235_3:7708654-7708716 Satlength=63 Nr of Repeats=4
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.762963
 27 ATCCCCTTTTCGCAG
 WB235_3:10123694-10123786 Satlength=93 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=3 Similarity=0.762963
 16 ATCCCCTTTTCGCAG

Rev.of_WB235_3:10436267-10436329 Satlength=63 Nr of Repeats=4
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.762963
 27 ATCCCCTTTTCGCAG
 WB235_3:10811336-10811411 Satlength=76 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=5 Similarity=0.751111
 16 ATCCCCTTTTCGCAG
 WB235_3:12878285-12878362 Satlength=78 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.777778
 16 ATCCCCTTTTCGCAG
 WB235_4:385463-385525 Satlength=63 Nr of Repeats=4 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=3 Similarity=0.762963
 16 ATCCCCTTTTCGCAG
 Rev.of_WB235_4:1715069-1715131 Satlength=63 Nr of Repeats=4
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.703704
 27 ATCCCCTTTTCGCAG
 WB235_4:11179242-11179304 Satlength=63 Nr of Repeats=4 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=3 Similarity=0.762963
 16 ATCCCCTTTTCGCAG
 WB235_4:15199820-15199897 Satlength=78 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.748148
 16 ATCCCCTTTTCGCAG
 WB235_5:4553148-4553225 Satlength=78 Nr of Repeats=5 RepeatLength=15
 seed=CCCCTTTTCG Num.seqs=4 Similarity=0.748148
 17 ATCCCCTTTTCGCAG
 WB235_5:16553018-16553153 Satlength=136 Nr of Repeats=7 RepeatLength=15
 seed=GCAGATCCCC Num.seqs=6 Similarity=0.946667
 26 ATCCCCTTTTCGCAG
 Rev.of_WB235_5:20839492-20839569 Satlength=78 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.822222
 27 ATCCCCTTTTCGCAG
 WB235_5:20839745-20839822 Satlength=78 Nr of Repeats=5 RepeatLength=15
 seed=CCCCTTTTCG Num.seqs=4 Similarity=0.748148
 17 ATCCCCTTTTCGCAG
 Rev.of_WB235_6:256843-256905 Satlength=63 Nr of Repeats=4 RepeatLength=15
 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.762963
 27 ATCCCCTTTTCGCAG
 Rev.of_WB235_3:10123441-10123519 Satlength=79 Nr of Repeats=5
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=3 Similarity=0.733333
 27 ATCCCCTTTTCGNAG
 WB235_6:257079-257156 Satlength=78 Nr of Repeats=5 RepeatLength=15
 seed=TCCCCTTTTC Num.seqs=4 Similarity=0.762963
 16 ATCCCCTTTTCGTAG
 Rev.of_WB235_1:12899142-12899606 Satlength=465 Nr of Repeats=31
 RepeatLength=15 seed=AAAAGGGGAT Num.seqs=28 Similarity=0.945444
 25 ATCCCCTTTTTCGAG
 Rev.of_WB235_1:7003581-7003641 Satlength=61 Nr of Repeats=4
 RepeatLength=15 seed=CGAAAAGGGG Num.seqs=4 Similarity=0.807407
 27 ATCCCCTTTTCGCTG

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Consensus:

cTCCCCTTTTCGtAG

>WB235_Fam_8_16_50 Nr. of seq. 50 Alignment length(with gaps) = 16
 Alignment score = 0.867364
 WB235_1:11273722-11273834 Satlength=113 Nr of Repeats=7 RepeatLength=16
 seed=CTACATGCCT Num.seqs=7 Similarity=0.805556
 0 CTACATGCCTACATGC
 WB235_1:11273722-11274842 Satlength=1121 Nr of Repeats=68 RepeatLength=16
 seed=CTACATGCCT Num.seqs=64 Similarity=0.868304
 0 CTACATGCCTACATGC
 Rev.of_WB235_1:11656920-11657791 Satlength=872 Nr of Repeats=54
 RepeatLength=16 seed=GCATGTAGGC Num.seqs=52 Similarity=0.946833
 0 CTACATGCCTACATGC
 WB235_2:12978404-12978548 Satlength=145 Nr of Repeats=9 RepeatLength=16
 seed=GCCTACATGC Num.seqs=7 Similarity=0.861111
 6 CTACATGCCTACATGC
 Rev.of_WB235_2:13304324-13304580 Satlength=257 Nr of Repeats=15
 RepeatLength=16 seed=GGCATGTAGG Num.seqs=13 Similarity=0.840812
 1 CTACATGCCTACATGC
 Rev.of_WB235_2:13310035-13310356 Satlength=322 Nr of Repeats=20
 RepeatLength=16 seed=GGCATGTAGG Num.seqs=19 Similarity=0.773879
 1 CTACATGCCTACATGC
 WB235_2:13507307-13507403 Satlength=97 Nr of Repeats=6 RepeatLength=16
 seed=ACATGCCTAC Num.seqs=6 Similarity=0.888889
 2 CTACATGCCTACATGC
 WB235_2:13631132-13631348 Satlength=217 Nr of Repeats=13 RepeatLength=16
 seed=ACATGCCTAC Num.seqs=12 Similarity=0.958333
 2 CTACATGCCTACATGC
 Rev.of_WB235_3:3746895-3747055 Satlength=161 Nr of Repeats=10
 RepeatLength=16 seed=TAGGCATGTA Num.seqs=10 Similarity=0.920370
 3 CTACATGCCTACATGC
 Rev.of_WB235_4:594389-594607 Satlength=219 Nr of Repeats=10
 RepeatLength=16 seed=AGGCATGTAG Num.seqs=9 Similarity=0.796296
 2 CTACATGCCTACATGC
 Rev.of_WB235_4:2953071-2953413 Satlength=343 Nr of Repeats=19
 RepeatLength=16 seed=TAGGCATGTA Num.seqs=16 Similarity=0.859028
 3 CTACATGCCTACATGC
 WB235_4:3184703-3185093 Satlength=391 Nr of Repeats=5 RepeatLength=16
 seed=TACATGCCTA Num.seqs=4 Similarity=0.958333
 1 CTACATGCCTACATGC
 WB235_4:3189159-3189343 Satlength=185 Nr of Repeats=11 RepeatLength=16
 seed=CATGCCTACA Num.seqs=10 Similarity=0.816667
 3 CTACATGCCTACATGC
 WB235_4:3193096-3194818 Satlength=1723 Nr of Repeats=67 RepeatLength=16
 seed=ATGCCTACAT Num.seqs=46 Similarity=0.819565
 4 CTACATGCCTACATGC
 Rev.of_WB235_4:3211749-3211845 Satlength=97 Nr of Repeats=6
 RepeatLength=16 seed=AGGCATGTAG Num.seqs=6 Similarity=0.872222
 2 CTACATGCCTACATGC
 WB235_4:3568013-3568493 Satlength=481 Nr of Repeats=28 RepeatLength=16
 seed=TGCCTACATG Num.seqs=23 Similarity=0.914032
 5 CTACATGCCTACATGC
 Rev.of_WB235_4:3825814-3826008 Satlength=195 Nr of Repeats=12
 RepeatLength=16 seed=TAGGCATGTA Num.seqs=10 Similarity=0.983333
 3 CTACATGCCTACATGC

WB235_5:335210-335330 Satlength=121 Nr of Repeats=7 RepeatLength=16
 seed=CATGCCTACA Num.seqs=6 Similarity=0.972222
 3 CTACATGCCTACATGC
 Rev.of_WB235_5:342974-343198 Satlength=225 Nr of Repeats=14
 RepeatLength=16 seed=GGCATGTAGG Num.seqs=14 Similarity=0.928571
 1 CTACATGCCTACATGC
 WB235_5:777315-777395 Satlength=81 Nr of Repeats=5 RepeatLength=16
 seed=CTACATGCCT Num.seqs=5 Similarity=0.933333
 0 CTACATGCCTACATGC
 Rev.of_WB235_5:777834-778359 Satlength=526 Nr of Repeats=12
 RepeatLength=16 seed=AGGCATGTAG Num.seqs=9 Similarity=0.907407
 2 CTACATGCCTACATGC
 Rev.of_WB235_5:779287-779455 Satlength=169 Nr of Repeats=10
 RepeatLength=16 seed=AGGCATGTAG Num.seqs=9 Similarity=0.944444
 2 CTACATGCCTACATGC
 WB235_5:885274-885474 Satlength=201 Nr of Repeats=12 RepeatLength=16
 seed=ATGCCTACAT Num.seqs=11 Similarity=0.956061
 4 CTACATGCCTACATGC
 WB235_5:2164618-2164730 Satlength=113 Nr of Repeats=6 RepeatLength=16
 seed=ATGCCTACAT Num.seqs=4 Similarity=0.875000
 4 CTACATGCCTACATGC
 Rev.of_WB235_5:4784597-4784789 Satlength=193 Nr of Repeats=11
 RepeatLength=16 seed=TAGGCATGTA Num.seqs=9 Similarity=0.944444
 3 CTACATGCCTACATGC
 Rev.of_WB235_5:3085214-3085707 Satlength=494 Nr of Repeats=4
 RepeatLength=16 seed=GCATGTAGGC Num.seqs=3 Similarity=0.944444
 0 CTACAAGCCTACATGC
 WB235_3:11475344-11475488 Satlength=145 Nr of Repeats=7 RepeatLength=16
 seed=TACAAGCCTA Num.seqs=5 Similarity=0.866667
 1 CTACAAGCCTACAAGC
 WB235_2:674091-674259 Satlength=169 Nr of Repeats=9 RepeatLength=16
 seed=CCTACGTGCC Num.seqs=6 Similarity=0.844444
 7 CTACGTGCCTACGTGC
 Rev.of_WB235_2:2761987-2762171 Satlength=185 Nr of Repeats=11
 RepeatLength=16 seed=CACGTAGGCA Num.seqs=10 Similarity=0.966667
 7 CTACGTGCCTACGTGC
 Rev.of_WB235_2:3124197-3124357 Satlength=161 Nr of Repeats=9
 RepeatLength=16 seed=TAGGCACGTA Num.seqs=7 Similarity=0.849206
 11 CTACGTGCCTACGTGC
 WB235_2:3125607-3125959 Satlength=353 Nr of Repeats=18 RepeatLength=16
 seed=TACGTGCCTA Num.seqs=12 Similarity=0.845960
 9 CTACGTGCCTACGTGC
 Rev.of_WB235_2:3179723-3180290 Satlength=568 Nr of Repeats=21
 RepeatLength=16 seed=GTAGGCACGT Num.seqs=18 Similarity=0.936819
 12 CTACGTGCCTACGTGC
 Rev.of_WB235_2:3271556-3272244 Satlength=689 Nr of Repeats=42
 RepeatLength=16 seed=CGTAGGCACG Num.seqs=38 Similarity=0.966809
 13 CTACGTGCCTACGTGC
 Rev.of_WB235_2:3420081-3420246 Satlength=166 Nr of Repeats=5
 RepeatLength=16 seed=GCACGTAGGC Num.seqs=3 Similarity=0.944444
 8 CTACGTGCCTACGTGC
 Rev.of_WB235_2:3512519-3512671 Satlength=153 Nr of Repeats=9
 RepeatLength=16 seed=GTAGGCACGT Num.seqs=8 Similarity=0.958333
 12 CTACGTGCCTACGTGC

WB235_2:4030891-4031711 Satlength=821 Nr of Repeats=4 RepeatLength=16
seed=TGCCTACGTG Num.seqs=3 Similarity=1.000000
13 CTACGTGCCTACGTGC
Rev.of_WB235_2:13061749-13061893 Satlength=145 Nr of Repeats=8
RepeatLength=16 seed=TAGGCACGTA Num.seqs=6 Similarity=0.916667
11 CTACGTGCCTACGTGC
Rev.of_WB235_3:8334779-8334979 Satlength=201 Nr of Repeats=12
RepeatLength=16 seed=AGGCACGTAG Num.seqs=11 Similarity=0.887879
10 CTACGTGCCTACGTGC
Rev.of_WB235_3:10480990-10481350 Satlength=361 Nr of Repeats=14
RepeatLength=16 seed=TAGGCACGTA Num.seqs=13 Similarity=0.961538
11 CTACGTGCCTACGTGC
Rev.of_WB235_3:12190449-12190847 Satlength=399 Nr of Repeats=13
RepeatLength=16 seed=ACGTAGGCAC Num.seqs=10 Similarity=0.916667
14 CTACGTGCCTACGTGC
Rev.of_WB235_4:1762607-1762703 Satlength=97 Nr of Repeats=5
RepeatLength=16 seed=CACGTAGGCA Num.seqs=4 Similarity=0.916667
7 CTACGTGCCTACGTGC
Rev.of_WB235_4:1787801-1788241 Satlength=441 Nr of Repeats=26
RepeatLength=16 seed=TAGGCACGTA Num.seqs=23 Similarity=0.944005
11 CTACGTGCCTACGTGC
WB235_4:5060074-5060274 Satlength=201 Nr of Repeats=12 RepeatLength=16
seed=CTACGTGCCT Num.seqs=11 Similarity=0.969697
8 CTACGTGCCTACGTGC
WB235_4:12326778-12327098 Satlength=321 Nr of Repeats=18 RepeatLength=16
seed=GTGCCCTACGT Num.seqs=14 Similarity=0.887363
12 CTACGTGCCTACGTGC
Rev.of_WB235_2:3152725-3152861 Satlength=137 Nr of Repeats=8
RepeatLength=16 seed=AGGCACGTAG Num.seqs=7 Similarity=0.853175
10 CTACGTGCCTACNTGC
Rev.of_WB235_2:14108714-14108890 Satlength=177 Nr of Repeats=10
RepeatLength=16 seed=TAGGCATATA Num.seqs=9 Similarity=0.842593
3 CTATATGCCTATATGC
WB235_3:3647083-3647155 Satlength=73 Nr of Repeats=4 RepeatLength=16
seed=CCTACATACC Num.seqs=3 Similarity=0.888889
7 CTACATACCTACATAC
WB235_5:16699106-16699538 Satlength=433 Nr of Repeats=26 RepeatLength=16
seed=ACATACCTAC Num.seqs=24 Similarity=0.960145
10 CTACATACCTACATAC
Rev.of_WB235_3:206747-206867 Satlength=121 Nr of Repeats=7
RepeatLength=16 seed=TAGGCATCTA Num.seqs=6 Similarity=0.827778
3 CTAGGTGCATAGATGC
Rev.of_WB235_4:2981693-2981773 Satlength=81 Nr of Repeats=4
RepeatLength=16 seed=AGGTAGGAAG Num.seqs=3 Similarity=0.722222
2 CTACCTACCTTCCTAC

*** * * *

Consensus:

CTACaTGCCTACaTGC

>WB235_Fam_9_20_46 Nr. of seq. 46 Alignment length(with gaps) = 20
Alignment score = 0.797488

WB235_1:2542918-2543982 Satlength=1065 Nr of Repeats=56 RepeatLength=19
 seed=TGTTACACGA Num.seqs=56 Similarity=0.965915
 0 TGTTACACG-AAAAATAGAT
 Rev.of_WB235_1:4465416-4465569 Satlength=154 Nr of Repeats=8
 RepeatLength=19 seed=TTTTTCGTGT Num.seqs=7 Similarity=0.900000
 14 TGTTACACG-AAAAATAGAT
 Rev.of_WB235_1:14128159-14128469 Satlength=311 Nr of Repeats=16
 RepeatLength=19 seed=AACAATCTAT Num.seqs=10 Similarity=1.000000
 4 TGTTACACG-AAAAATAGAT
 WB235_3:3987076-3987676 Satlength=601 Nr of Repeats=31 RepeatLength=19
 seed=AAAAATAGAT Num.seqs=20 Similarity=1.000000
 9 TGTTACACG-AAAAATAGAT
 WB235_3:6185212-6186090 Satlength=879 Nr of Repeats=42 RepeatLength=19
 seed=AAAAATAGAT Num.seqs=38 Similarity=0.969155
 9 TGTTACACG-AAAAATAGAT
 Rev.of_WB235_3:7668665-7669197 Satlength=533 Nr of Repeats=28
 RepeatLength=19 seed=AATCTATTTT Num.seqs=28 Similarity=0.920040
 1 TGTTACACG-AAAAATAGAT
 Rev.of_WB235_3:7678163-7678429 Satlength=267 Nr of Repeats=14
 RepeatLength=19 seed=CAATCTATTT Num.seqs=14 Similarity=0.974552
 2 TGTTACACG-AAAAATAGAT
 WB235_3:13243432-13245239 Satlength=1808 Nr of Repeats=95 RepeatLength=19
 seed=AAAAATAGAT Num.seqs=93 Similarity=0.938765
 9 TGTTACACG-AAAAATAGAT
 WB235_4:10681773-10682153 Satlength=381 Nr of Repeats=20 RepeatLength=19
 seed=ATTGTTACAC Num.seqs=20 Similarity=0.974146
 17 TGTTACACG-AAAAATAGAT
 WB235_4:16963408-16964890 Satlength=1483 Nr of Repeats=77 RepeatLength=19
 seed=AAAAATAGAT Num.seqs=58 Similarity=0.957844
 9 TGTTACACG-AAAAATAGAT
 Rev.of_WB235_5:6937435-6937626 Satlength=192 Nr of Repeats=10
 RepeatLength=19 seed=AACAATCTAT Num.seqs=9 Similarity=1.000000
 4 TGTTACACG-AAAAATAGAT
 WB235_5:13365913-13366445 Satlength=533 Nr of Repeats=28 RepeatLength=19
 seed=GTTCACGAA Num.seqs=28 Similarity=0.981064
 1 TGTTACACG-AAAAATAGAT
 Rev.of_WB235_5:17412072-17412375 Satlength=304 Nr of Repeats=16
 RepeatLength=19 seed=TTTTTCGTGTA Num.seqs=15 Similarity=0.934503
 13 TGTTACACG-AAAAATAGAT
 Rev.of_WB235_6:3007216-3008016 Satlength=801 Nr of Repeats=42
 RepeatLength=19 seed=GTGTAACAAT Num.seqs=31 Similarity=0.982192
 8 TGTTACACG-AAAAATAGAT
 WB235_6:12276123-12276239 Satlength=117 Nr of Repeats=6 RepeatLength=19
 seed=ATAGATTGTT Num.seqs=4 Similarity=1.000000
 13 TGTTACACG-AAAAATAGAT
 WB235_6:12502706-12502822 Satlength=117 Nr of Repeats=6 RepeatLength=19
 seed=AAAAATAGAT Num.seqs=4 Similarity=0.894737
 9 TGTTACACG-AAAAATAGAT
 WB235_4:16244112-16245385 Satlength=1274 Nr of Repeats=65 RepeatLength=19
 seed=AAATAGATTG Num.seqs=45 Similarity=0.932093
 11 TGTTACACG-GAAAATAGAT
 WB235_1:11357272-11357373 Satlength=102 Nr of Repeats=5 RepeatLength=20
 seed=AATAGATTGT Num.seqs=4 Similarity=0.933333
 13 TGTTACACGAAAAATAGAT

WB235_1:13276960-13277319 Satlength=360 Nr of Repeats=18 RepeatLength=20
 seed=AAAAATAGATT Num.seqs=17 Similarity=0.992157
 31 TGTTACACGAAAAAATAGAT
 WB235_3:10796467-10796566 Satlength=100 Nr of Repeats=5 RepeatLength=20
 seed=GTTACACGAA Num.seqs=4 Similarity=1.000000
 21 TGTTACACGAAAAAATAGAT
 WB235_4:15859222-15859379 Satlength=158 Nr of Repeats=8 RepeatLength=20
 seed=TGTTACACGA Num.seqs=5 Similarity=1.000000
 20 TGTTACACGAAAAAATAGAT
 WB235_5:18400360-18401785 Satlength=1426 Nr of Repeats=72 RepeatLength=20
 seed=AAAAATAGAT Num.seqs=57 Similarity=0.937761
 30 TGTTACACGAAAAAATAGAT
 WB235_5:18727688-18728599 Satlength=912 Nr of Repeats=46 RepeatLength=20
 seed=AAAAATAGAT Num.seqs=37 Similarity=1.000000
 30 TGTTACACGAAAAAATAGAT
 WB235_6:1945521-1946157 Satlength=637 Nr of Repeats=32 RepeatLength=20
 seed=GTTACACGAA Num.seqs=28 Similarity=1.000000
 21 TGTTACACGAAAAAATAGAT
 WB235_6:1954050-1954308 Satlength=259 Nr of Repeats=13 RepeatLength=20
 seed=GTTACACGAA Num.seqs=11 Similarity=1.000000
 21 TGTTACACGAAAAAATAGAT
 Rev.of_WB235_6:14154417-14154672 Satlength=256 Nr of Repeats=13
 RepeatLength=20 seed=TAACAATCTA Num.seqs=8 Similarity=0.966667
 25 TGTTACACGAAAAAATAGAT
 Rev.of_WB235_6:15811201-15811280 Satlength=80 Nr of Repeats=4
 RepeatLength=20 seed=TAACAATCTA Num.seqs=3 Similarity=0.955556
 25 TGTTACACGAAAAAATAGAT
 WB235_2:3994649-3994788 Satlength=140 Nr of Repeats=7 RepeatLength=20
 seed=AAATAGATTG Num.seqs=6 Similarity=0.964444
 32 TGTTACACTAAAAAATAGAT
 WB235_4:6210092-6210227 Satlength=136 Nr of Repeats=7 RepeatLength=19
 seed=ATTGACAGAC Num.seqs=5 Similarity=0.971930
 17 TGACAGACG-AAAAATAGAT
 WB235_4:12584972-12585067 Satlength=96 Nr of Repeats=5 RepeatLength=19
 seed=AAAAATAGAT Num.seqs=5 Similarity=0.971930
 28 TGACAGACG-AAAAATAGAT
 Rev.of_WB235_5:3098854-3099539 Satlength=686 Nr of Repeats=35
 RepeatLength=19 seed=AATCTATTTT Num.seqs=24 Similarity=0.944826
 20 TGACAGACG-AAAAATAGAT
 WB235_5:5646992-5647147 Satlength=156 Nr of Repeats=8 RepeatLength=19
 seed=AAAAATAGAT Num.seqs=5 Similarity=1.000000
 28 TGGCAGACG-AAAAATAGAT
 WB235_3:1260242-1261618 Satlength=1377 Nr of Repeats=70 RepeatLength=20
 seed=AAAAATAGAT Num.seqs=42 Similarity=0.907822
 29 TGACAGACGAAAAAATAGAT
 WB235_3:12009165-12009381 Satlength=217 Nr of Repeats=11 RepeatLength=20
 seed=AAATAGATTG Num.seqs=7 Similarity=0.904762
 31 TGACAGACGAAAAAATAGAT
 WB235_6:4285394-4285533 Satlength=140 Nr of Repeats=7 RepeatLength=20
 seed=ACAGACGAAA Num.seqs=6 Similarity=0.937778
 41 TGACAGACGAAAAAATAGAT
 Rev.of_WB235_6:7081038-7081216 Satlength=179 Nr of Repeats=9
 RepeatLength=20 seed=TTTTTCGTCT Num.seqs=7 Similarity=0.961905
 33 TGACAGACGAAAAAATAGAT

WB235_6:7895537-7895652 Satlength=116 Nr of Repeats=6 RepeatLength=19
seed=CAGACGAAAA Num.seqs=5 Similarity=0.887719
22 TGGCAGACG-AAAAATATAT
WB235_1:3485156-3487576 Satlength=2421 Nr of Repeats=121 RepeatLength=20
seed=AAAAAATAGA Num.seqs=121 Similarity=0.970083
28 TGACATACCAAAAAATAGAT
WB235_1:13925940-13926100 Satlength=161 Nr of Repeats=8 RepeatLength=20
seed=AAAAAATAGA Num.seqs=8 Similarity=0.900000
28 TGACATACCAAAAAATAGAT
WB235_3:9940544-9940665 Satlength=122 Nr of Repeats=6 RepeatLength=20
seed=TGACATACCA Num.seqs=5 Similarity=0.973333
39 TGACATACCAAAAAATAGAT
Rev.of_WB235_3:11004687-11006367 Satlength=1681 Nr of Repeats=84
RepeatLength=20 seed=TCTATTTTTT Num.seqs=84 Similarity=0.960031
38 TGACATACCAAAAAATAGAT
WB235_6:3924546-3924685 Satlength=140 Nr of Repeats=7 RepeatLength=20
seed=AAAATAGATT Num.seqs=6 Similarity=0.955556
30 TGACATACCAAAAAATAGAT
Rev.of_WB235_2:887413-887570 Satlength=158 Nr of Repeats=8
RepeatLength=20 seed=CAATCTATTT Num.seqs=6 Similarity=0.902222
41 TGNCATACCAAAAAATAGAT
WB235_6:15806999-15807439 Satlength=441 Nr of Repeats=22 RepeatLength=20
seed=CATACCAAAA Num.seqs=22 Similarity=0.934488
42 TGGCATACCAAAAAATAGAT
WB235_2:11423462-11423661 Satlength=200 Nr of Repeats=9 RepeatLength=20
seed=AAAAAATAGA Num.seqs=8 Similarity=0.892857
28 TGGCATACGAAAAAATAGAT
WB235_1:14321889-14321969 Satlength=81 Nr of Repeats=4 RepeatLength=20
seed=ATATCAAAAA Num.seqs=4 Similarity=0.855556
43 TGGCATATCAAAAAATAAAT

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Consensus:

TGttAcACGaAAAAATAGAT

>WB235_Fam_10_25_40 Nr. of seq. 40 Alignment length(with gaps) = 28
Alignment score = 0.748245
WB235_1:3763157-3765957 Satlength=2801 Nr of Repeats=112 RepeatLength=25
seed=TTTACTCTCT Num.seqs=112 Similarity=0.895307
0 TTTACTCTCT--GGC-TTCACCAAATAT
Rev.of_WB235_6:10361494-10369166 Satlength=7673 Nr of Repeats=299
RepeatLength=25 seed=GTGAAGCCAG Num.seqs=291 Similarity=0.913572
18 TTTACTCTCT--GGC-TTCACCAAATAT
Rev.of_WB235_2:5144410-5146766 Satlength=2357 Nr of Repeats=80
RepeatLength=25 seed=AGCCAGAGAG Num.seqs=74 Similarity=0.877056
14 TTTACTCTCT--GGC-TTCACCAATTAT
Rev.of_WB235_3:1299759-1303117 Satlength=3359 Nr of Repeats=134
RepeatLength=25 seed=CAGAGAGTAA Num.seqs=126 Similarity=0.920857
36 TTTACTCTCT--GGC-TTCACCAATTAT
Rev.of_WB235_2:4259952-4260552 Satlength=601 Nr of Repeats=24
RepeatLength=25 seed=GAGAGTAAAA Num.seqs=24 Similarity=0.932560
9 TTTACTCTCT--GGC-TTCACCGTATAT

WB235_4:17492409-17493609 Satlength=1201 Nr of Repeats=48 RepeatLength=25
 seed=ACTCTCTGGC Num.seqs=48 Similarity=0.888227
 28 TTTACTCTCT--GGC-TTCACCGTATAT
 Rev.of_WB235_3:2497037-2501716 Satlength=4680 Nr of Repeats=187
 RepeatLength=25 seed=GTGAAGCCAG Num.seqs=184 Similarity=0.887060
 18 TTTACTCTCT--GGC-TTCACCATATAT
 WB235_2:9404845-9405392 Satlength=548 Nr of Repeats=22 RepeatLength=25
 seed=GGCTTCACAG Num.seqs=20 Similarity=0.925053
 10 TTTACTCTCT--GGC-TTCACAGTATAT
 WB235_4:5299099-5299474 Satlength=376 Nr of Repeats=15 RepeatLength=25
 seed=TTTACTCTCT Num.seqs=15 Similarity=0.890286
 25 TTTACTCTCT--GGC-TTCACAGTATAT
 Rev.of_WB235_5:7993172-7993472 Satlength=301 Nr of Repeats=12
 RepeatLength=25 seed=CCAGAGAGTA Num.seqs=12 Similarity=0.873131
 12 TTTACTCTCT--GGC-TTCACAGTATAT
 WB235_5:10449424-10450674 Satlength=1251 Nr of Repeats=50 RepeatLength=25
 seed=TTTACTCTCT Num.seqs=50 Similarity=0.898601
 25 TTTACTCTCT--GGC-TTCACAGTATAT
 Rev.of_WB235_6:9184992-9188750 Satlength=3759 Nr of Repeats=150
 RepeatLength=25 seed=CAGAGAGTAA Num.seqs=149 Similarity=0.922331
 11 TTTACTCTCT--GGC-TTCACAGTATAT
 WB235_6:2055472-2055647 Satlength=176 Nr of Repeats=7 RepeatLength=25
 seed=TATATTTTAC Num.seqs=7 Similarity=0.852698
 20 TTTACTCTCT--GGC-TTCACANTATAT
 WB235_6:2056950-2057275 Satlength=326 Nr of Repeats=12 RepeatLength=25
 seed=TCTGGCTTCA Num.seqs=11 Similarity=0.885576
 32 TTTACTCTCT--GGC-TTCACACTATAT
 WB235_6:14908166-14909416 Satlength=1251 Nr of Repeats=49 RepeatLength=25
 seed=TGGCTTCACA Num.seqs=48 Similarity=0.906856
 34 TTTACTCTCT--GGC-TTCACAATATAT
 WB235_6:11886530-11888254 Satlength=1725 Nr of Repeats=68 RepeatLength=25
 seed=TTCAACATAT Num.seqs=64 Similarity=0.956852
 13 TTTACTCTCT--GGC-TTCACCATATAT
 Rev.of_WB235_1:6771968-6773943 Satlength=1976 Nr of Repeats=79
 RepeatLength=25 seed=GTGAAGCCAG Num.seqs=69 Similarity=0.904109
 18 TTTACTCTCT--GGC-TTCACAGAATAA
 WB235_4:6090427-6090577 Satlength=151 Nr of Repeats=6 RepeatLength=25
 seed=TTTACTCTCT Num.seqs=6 Similarity=0.882667
 25 TTTACTCTCT--GGC-TTCACAGAATAA
 Rev.of_WB235_5:14750559-14751884 Satlength=1326 Nr of Repeats=53
 RepeatLength=25 seed=TGTGAAGCCA Num.seqs=53 Similarity=0.918336
 19 TTTACTCTCT--GGC-TTCACAGAATAA
 WB235_4:13360500-13361979 Satlength=1480 Nr of Repeats=59 RepeatLength=25
 seed=TTTACTCTCT Num.seqs=56 Similarity=0.877229
 25 TTTACTCTCT--GGC-TTCACAGAATAT
 Rev.of_WB235_5:4333269-4336644 Satlength=3376 Nr of Repeats=135
 RepeatLength=25 seed=AGAGTAAAAT Num.seqs=135 Similarity=0.922491
 33 TTTACTCTCT--GGC-TTCACAGAATAT
 WB235_6:13981254-13981504 Satlength=251 Nr of Repeats=10 RepeatLength=25
 seed=TCTCTGGCTT Num.seqs=10 Similarity=0.913481
 30 TTTACTCTCT--GGC-TTCACAGAATAT
 WB235_2:12844903-12846136 Satlength=1234 Nr of Repeats=49 RepeatLength=25
 seed=GGCTTCCCAC Num.seqs=45 Similarity=0.990626
 10 TTTACTCTCT--GGC-TTCCCACTATAT

WB235_1:933478-934899 Satlength=1422 Nr of Repeats=52 RepeatLength=27
seed=TATTTTACTC Num.seqs=46 Similarity=0.859742
22 TTTACTCTCTGTGGC-TTCCCACTATAT
WB235_2:3290648-3290783 Satlength=136 Nr of Repeats=5 RepeatLength=27
seed=TTTACTCTCT Num.seqs=5 Similarity=1.000000
25 TTTACTCTCTGTGGC-TTCCCACTATAT
WB235_2:14337687-14339240 Satlength=1554 Nr of Repeats=57 RepeatLength=27
seed=GGCTTCCCAC Num.seqs=48 Similarity=0.918571
37 TTTACTCTCTGTGGC-TTCCCACTATAT
Rev.of_WB235_3:931250-931684 Satlength=435 Nr of Repeats=16
RepeatLength=27 seed=AGAGAGTAAA Num.seqs=15 Similarity=0.926631
35 TTTACTCTCTGTGGC-TTCCCACTATAT
Rev.of_WB235_3:7444445-7448204 Satlength=3760 Nr of Repeats=143
RepeatLength=27 seed=ACAGAGAGTA Num.seqs=126 Similarity=0.934432
37 TTTACTCTCTGTGGC-TTCCCACTATAT
Rev.of_WB235_6:109717-114226 Satlength=4510 Nr of Repeats=167
RepeatLength=27 seed=CACAGAGAGT Num.seqs=167 Similarity=0.846944
38 TTTACTCTCTGTGGC-TTCCCACTATAT
WB235_6:5056273-5057278 Satlength=1006 Nr of Repeats=38 RepeatLength=27
seed=TATTTTACTC Num.seqs=31 Similarity=0.933897
22 TTTACTCTCTGTGGC-TTCCCACTATAT
WB235_5:14754513-14757536 Satlength=3024 Nr of Repeats=84 RepeatLength=27
seed=CTGTGGCTTC Num.seqs=77 Similarity=0.911293
33 TTTACTCTCTGTGGC-TTCCCACCATAT
WB235_6:1752278-1755168 Satlength=2891 Nr of Repeats=107 RepeatLength=27
seed=ACTCTCTGTG Num.seqs=106 Similarity=0.943527
55 TTTACTCTCTGTGGC-TTCCCACCATAT
Rev.of_WB235_2:12843822-12844875 Satlength=1054 Nr of Repeats=39
RepeatLength=27 seed=GTGGGAAGCC Num.seqs=39 Similarity=0.975075
47 TTTACTCTCTATGGC-TTCCCACTATAT
Rev.of_WB235_5:14768011-14769734 Satlength=1724 Nr of Repeats=59
RepeatLength=27 seed=GGAAGCCACA Num.seqs=57 Similarity=0.946781
17 TTTACTCTCTGTGGC-TTCCAACCATAT
WB235_5:1104557-1105016 Satlength=460 Nr of Repeats=17 RepeatLength=27
seed=TTACTCTCTG Num.seqs=17 Similarity=0.900145
26 TTTACTCTCTGTGGC-TTCACAGTATAT
WB235_3:3334358-3337083 Satlength=2726 Nr of Repeats=109 RepeatLength=25
seed=ACTCTCTGGC Num.seqs=109 Similarity=0.899274
28 TTTACTCTCT--GGC-TTCCCATCATAT
Rev.of_WB235_4:5878242-5878392 Satlength=151 Nr of Repeats=6
RepeatLength=25 seed=CCAGAGAGTA Num.seqs=6 Similarity=0.875556
37 TTTACTCTCT--GGT-TTCCCACTATAT
Rev.of_WB235_2:5144313-5144565 Satlength=253 Nr of Repeats=9
RepeatLength=25 seed=AGAGTAAAAT Num.seqs=6 Similarity=0.823932
8 TTTACTCTCT--GGCTTTCCCAAT-TAT
WB235_1:4544868-4547696 Satlength=2829 Nr of Repeats=104 RepeatLength=27
seed=ACTCTCTGTG Num.seqs=100 Similarity=0.845700
3 TTTACTCTCTGTGGC-TTCACCGATNAT
Rev.of_WB235_4:2828548-2830536 Satlength=1989 Nr of Repeats=74
RepeatLength=27 seed=CAGAGAGTAA Num.seqs=69 Similarity=0.869860
11 TTTACTCTCTGTGGC-TTCACCAATTAT

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Consensus :

TTTACTCTCTGGCTTCaCantATAT

>WB235_Fam_11_20_29 Nr. of seq. 29 Alignment length(with gaps) = 25
Alignment score = 0.605057
WB235_1:354705-355291 Satlength=587 Nr of Repeats=29 RepeatLength=19
seed=TATCGATTTT Num.seqs=25 Similarity=0.914854
0 TATCGATTTT-C---TG-G-AATT
Rev.of_WB235_5:19026746-19027590 Satlength=845 Nr of Repeats=33
RepeatLength=20 seed=AAAATCGATA Num.seqs=22 Similarity=0.814643
10 TATCGATTTT-C---TG-GAAATT
WB235_5:18984459-18985309 Satlength=851 Nr of Repeats=31 RepeatLength=20
seed=ATTTATTGAT Num.seqs=20 Similarity=0.886667
17 TATCGATTTT-C---TG-GAAATT
WB235_5:19112578-19114304 Satlength=1727 Nr of Repeats=66 RepeatLength=20
seed=TATCGATTTT Num.seqs=59 Similarity=0.867212
20 TATCGATTTT-C---TG-GAAATT
WB235_5:18993608-18993851 Satlength=244 Nr of Repeats=8 RepeatLength=20
seed=TATCGATTTT Num.seqs=5 Similarity=0.900000
20 TATCGATTTT-C---TG-CAAATT
WB235_5:19909526-19910097 Satlength=572 Nr of Repeats=12 RepeatLength=20
seed=TTATTGATTT Num.seqs=8 Similarity=0.876190
19 TATTGATTTT-A---TG-GAAATT
Rev.of_WB235_1:1815369-1815789 Satlength=421 Nr of Repeats=18
RepeatLength=19 seed=AAAATCAATA Num.seqs=14 Similarity=0.796414
10 TATTGATTTT--C---TT-AGAATT
Rev.of_WB235_1:1815369-1817144 Satlength=1776 Nr of Repeats=44
RepeatLength=19 seed=AAAATCAATA Num.seqs=32 Similarity=0.769949
10 TATTGATTTT--C---TN-NGAATT
Rev.of_WB235_4:1740517-1740917 Satlength=401 Nr of Repeats=20
RepeatLength=20 seed=CAGAAAAATC Num.seqs=20 Similarity=0.835088
14 TATTGATTTT-C---TG-AGAATT
WB235_5:18632123-18632283 Satlength=161 Nr of Repeats=8 RepeatLength=20
seed=GATTTTCTG Num.seqs=8 Similarity=0.871429
24 TATTGATTTT-C---TG-AAAATT
Rev.of_WB235_5:18675402-18675828 Satlength=427 Nr of Repeats=12
RepeatLength=20 seed=AGAAAAATCA Num.seqs=8 Similarity=0.902381
33 TATTGATTTT-C---TG-AAAATT
Rev.of_WB235_5:18986276-18986397 Satlength=122 Nr of Repeats=6
RepeatLength=20 seed=ATAAATTTTC Num.seqs=5 Similarity=0.960000
43 TATTGATTTT-C---TG-AAAATT
Rev.of_WB235_5:19099300-19100374 Satlength=1075 Nr of Repeats=31
RepeatLength=20 seed=AAAAATCAAT Num.seqs=22 Similarity=0.750066
31 TATTGATTTT-C---TG-AAAATT
WB235_5:19100422-19100868 Satlength=447 Nr of Repeats=10 RepeatLength=20
seed=ATTGATTTT Num.seqs=8 Similarity=0.861905
41 TATTGATTTT-C---TG-AAAATT
WB235_5:19129872-19130673 Satlength=802 Nr of Repeats=34 RepeatLength=20
seed=GATTTTCTG Num.seqs=28 Similarity=0.875661
24 TATTGATTTT-C---TG-AAAATT
Rev.of_WB235_5:19101640-19102041 Satlength=402 Nr of Repeats=17
RepeatLength=20 seed=CAGAAAAATC Num.seqs=12 Similarity=0.905051
14 TATTGATTTT-C---TG-GAAATT

WB235_5:19901870-19902110 Satlength=241 Nr of Repeats=10 RepeatLength=20
seed=TTATTGATTT Num.seqs=8 Similarity=0.866667
19 TATTGATTTTT-C---TG-GAAATT
Rev.of_WB235_5:19907460-19907660 Satlength=201 Nr of Repeats=9
RepeatLength=20 seed=CAGAAAAATC Num.seqs=8 Similarity=0.873810
14 TATTGATTTTT-C---TG-GAAATT
WB235_5:19121195-19121753 Satlength=559 Nr of Repeats=25 RepeatLength=20
seed=AATTTATTGA Num.seqs=16 Similarity=0.823333
16 TATTGATTTTT-T---TG-GAAATT
Rev.of_WB235_6:190303-190811 Satlength=509 Nr of Repeats=10
RepeatLength=20 seed=AAAAATCAAT Num.seqs=9 Similarity=0.907407
31 TATTGATTTTT-N---TG-GAAATT
Rev.of_WB235_1:11485772-11485879 Satlength=108 Nr of Repeats=5
RepeatLength=19 seed=TCAAAAATCA Num.seqs=4 Similarity=0.873611
12 -ATTGATTTTT-GA--TG--AAATT
Rev.of_WB235_1:11383715-11384049 Satlength=335 Nr of Repeats=14
RepeatLength=20 seed=AAAAATCAAT Num.seqs=11 Similarity=0.883636
29 -ATTGATTTTTCGA--TG--AAATT
Rev.of_WB235_1:11485735-11486997 Satlength=1263 Nr of Repeats=20
RepeatLength=19 seed=AAAAATCGAT Num.seqs=12 Similarity=0.725830
29 -ATCGATTTTT-GA--NG--AAATT
Rev.of_WB235_2:2623068-2623182 Satlength=115 Nr of Repeats=6
RepeatLength=19 seed=AAAATCGATA Num.seqs=6 Similarity=0.601058
47 -ATCGATTTTC-GA--TG--AAATT
Rev.of_WB235_1:11532642-11533117 Satlength=476 Nr of Repeats=17
RepeatLength=19 seed=TTTCACAAAA Num.seqs=12 Similarity=0.943647
17 -ATTGATTTTT-G---TGA-AAATT
Rev.of_WB235_1:11531919-11534041 Satlength=2123 Nr of Repeats=45
RepeatLength=19 seed=AAAATCGATA Num.seqs=29 Similarity=0.730706
29 -ATCGATTTTT-N---TGA-AAATT
Rev.of_WB235_4:977829-978532 Satlength=704 Nr of Repeats=35
RepeatLength=19 seed=CAATAATTTTC Num.seqs=27 Similarity=0.905233
24 -ATTGATTTTT-T-G-GG--AAATT
WB235_1:11384374-11386353 Satlength=1980 Nr of Repeats=95 RepeatLength=20
seed=ATTGATTTTT Num.seqs=91 Similarity=0.879707
40 -ATTGATTTTT-T-GAGG--AAATT
WB235_1:2364706-2365240 Satlength=535 Nr of Repeats=20 RepeatLength=20
seed=TTATTGATTT Num.seqs=12 Similarity=0.816162
38 -ATTGATTTTT-C-TAGG--ACATT

** *****

Consensus:

tATtGATTTTTcTGnAAATT

>WB235_Fam_12_45_28 Nr. of seq. 28 Alignment length(with gaps) = 46

Alignment score = 0.807319

WB235_2:11230254-11230477 Satlength=224 Nr of Repeats=5 RepeatLength=44

seed=AAGGATCAGA Num.seqs=3 Similarity=0.696296

0 AAGGATCAGAACATCA-GGAAG-AGCCTCGTGATCCTTTGGAGCTG

Rev.of_WB235_1:3553785-3554055 Satlength=271 Nr of Repeats=6

RepeatLength=45 seed=CTGAATCTTC Num.seqs=6 Similarity=0.990123

9 AAGATTCAGATCATAAAGGAGG-ATCCTTGTGATCCTTTGGAGCTG

WB235_5:18314435-18314705 Satlength=271 Nr of Repeats=6 RepeatLength=45
 seed=TTTGGAGCTG Num.seqs=6 Similarity=0.928889
 35 AAGATTCAGTTCATAAGGGGGG-ACCCTTATGATCCTTTGGAGCTG
 Rev.of_WB235_1:676497-676765 Satlength=269 Nr of Repeats=6
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=4 Similarity=0.792593
 10 AAGGATCAGACCATCA-GGAGGTACCCTTGTGATCCTTCTTATCTG
 Rev.of_WB235_3:7602309-7602577 Satlength=269 Nr of Repeats=6
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=4 Similarity=0.841975
 10 AAGGATCAGACCATCA-GGAGGTACCCTTGTGATCCTTCTTATCTG
 Rev.of_WB235_5:14348178-14348446 Satlength=269 Nr of Repeats=6
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=4 Similarity=0.812346
 10 AAGGATCAGACCATCA-GGAGGTACCCTTGTGATCCTTCTTATCTG
 WB235_1:5977228-5977451 Satlength=224 Nr of Repeats=5 RepeatLength=45
 seed=AAGGATCAGA Num.seqs=3 Similarity=0.841975
 45 AAGGATCAGACCATCA-GAAGGTACCCTTACGATCCTTCTTATCTG
 Rev.of_WB235_5:11108155-11108378 Satlength=224 Nr of Repeats=5
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=3 Similarity=0.822222
 55 AAGGATCAGACCATCA-GGAGGTACCCTTACGATCCTTCTTATCTG
 Rev.of_WB235_1:1664772-1664951 Satlength=180 Nr of Repeats=4
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=3 Similarity=0.743210
 10 AAGGATCAGAACATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG
 WB235_5:14348461-14348640 Satlength=180 Nr of Repeats=4 RepeatLength=45
 seed=CTGAAGGATC Num.seqs=3 Similarity=0.841975
 42 AAGGATCAGAACATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG
 Rev.of_WB235_1:3746094-3746497 Satlength=404 Nr of Repeats=9
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=7 Similarity=0.825044
 10 AAGGATCAGANCATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG
 WB235_1:3746917-3747230 Satlength=314 Nr of Repeats=7 RepeatLength=45
 seed=CTGAAGGATC Num.seqs=5 Similarity=0.792593
 42 AAGGATCAGANCATCA-GAAGGTACCCATGTGATCCTTCGGAGCTG
 Rev.of_WB235_1:5975024-5975828 Satlength=805 Nr of Repeats=18
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=12 Similarity=0.835690
 10 AAGGATCAGAACATCA-GAAGGTACCCTTGTGATCCTTCGGATCTG
 Rev.of_WB235_2:11527871-11528452 Satlength=582 Nr of Repeats=13
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=9 Similarity=0.846914
 10 AAGGATCAGANCATCA-GAAGGTACCCATGTGATCCTTCGGATCTG
 WB235_2:11530067-11530424 Satlength=358 Nr of Repeats=8 RepeatLength=45
 seed=GAAGGATCAG Num.seqs=5 Similarity=0.828148
 44 AAGGATCAGANCATCA-GAAGGTACCCATGTGATCCTTCGGATCTG
 Rev.of_WB235_3:2496715-2496983 Satlength=269 Nr of Repeats=6
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=4 Similarity=0.802469
 10 AAGGATCAGACCATCA-GGAGGTACCCATGTGATCCTTCGGATCTG
 WB235_3:7602873-7603364 Satlength=492 Nr of Repeats=11 RepeatLength=45
 seed=GAAGGATCAG Num.seqs=7 Similarity=0.820811
 44 AAGGATCAGANCATCA-GGAGGTACCCATGTGATCCTTCGGATCTG
 Rev.of_WB235_3:10792337-10792694 Satlength=358 Nr of Repeats=8
 RepeatLength=45 seed=TCTGATCCTT Num.seqs=5 Similarity=0.801481
 10 AAGGATCAGANCATCA-GGAGGTACCCATGTGATCCTTCGGATCTG
 WB235_4:349715-350206 Satlength=492 Nr of Repeats=11 RepeatLength=45
 seed=GAAGGATCAG Num.seqs=7 Similarity=0.826455
 44 AAGGATCAGANCATCA-GGAGGTACCCATGTGATCCTTCGGATCTG
 WB235_2:6082023-6082291 Satlength=269 Nr of Repeats=6 RepeatLength=45
 seed=CTGAAGGATC Num.seqs=4 Similarity=0.797531
 42 AAGGATCAGAACATCA-GAAGGTACCCATACGATCCTTCGGAGCTG

WB235_5:11108491-11108983 Satlength=493 Nr of Repeats=11 RepeatLength=45
seed=CTGAAGGATC Num.seqs=8 Similarity=0.864550
42 AAGGATCAGAACATCA-GAAGGTACCCATACGATCCTTCGGAGCTG
Rev.of_WB235_4:8255934-8256202 Satlength=269 Nr of Repeats=6
RepeatLength=45 seed=TCTGATCCTT Num.seqs=4 Similarity=0.851852
55 AAGGATCAGACCATCA-GGAGGTACCCTTACGATCCTTCGGAGCTG
WB235_2:3937888-3938177 Satlength=290 Nr of Repeats=6 RepeatLength=45
seed=AAGGATCAGA Num.seqs=5 Similarity=0.643210
45 AAGGATCAGATCANCA-GGAGGTACCCTTCTGATCCTTCGGAGCTG
Rev.of_WB235_2:12749754-12749935 Satlength=182 Nr of Repeats=4
RepeatLength=45 seed=ATCTGATCCT Num.seqs=3 Similarity=0.950617
56 AAGGATCAGATCACCA-GGAGGTACCCTTNTGATCCTTCGGAGCTG
WB235_4:3366659-3367988 Satlength=1330 Nr of Repeats=24 RepeatLength=45
seed=TCTGATCCTT Num.seqs=17 Similarity=0.598811
72 AAGGATCAGATCANCA-GGAGGTACCCTTCTGATCCTTCGNAGCTG
Rev.of_WB235_4:10943462-10944138 Satlength=677 Nr of Repeats=14
RepeatLength=45 seed=AGCTCCGAAG Num.seqs=11 Similarity=0.932121
89 AAGGATCAGATCACCA-GGAGGTACCCTTCTGATCCTTCGGAGCTT
WB235_4:10945693-10946234 Satlength=542 Nr of Repeats=12 RepeatLength=45
seed=CTTCGGAGCT Num.seqs=11 Similarity=0.945050
124 AAGGATCAGATCACCA-GGAGGTACCCTTCTGATCCTTCGGAGCTT
WB235_2:13598710-13599880 Satlength=1171 Nr of Repeats=26 RepeatLength=45
seed=ACCAGGAGGT Num.seqs=26 Similarity=0.929709
57 AATGATCAGATCACCA-GGAGGTACCCTTCTTATCCTTCGGAGCTG

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Consensus:

AAGGATCAGAnCAtCAGgAGGTACCCTgTGATCCTTCGgAgCTG

>WB235_Fam_13_43_26 Nr. of seq. 26 Alignment length(with gaps) = 47
Alignment score = 0.705990
WB235_1:1322604-1322925 Satlength=322 Nr of Repeats=5 RepeatLength=42
seed=TTTGCCGGAA Num.seqs=3 Similarity=0.705426
0 TTTGCCGGAAAT--TTTCATTTCCGGCAA-ATTGCCGATTTGNCG--
WB235_2:12951422-12951594 Satlength=173 Nr of Repeats=4 RepeatLength=43
seed=CGGCAAATTA Num.seqs=4 Similarity=0.803618
21 TTTGCCGGAAAT--TTTCATTTCCGGCAA-ATTACCAATTTGCCGA-
Rev.of_WB235_1:1796469-1796919 Satlength=451 Nr of Repeats=9
RepeatLength=43 seed=AAATCGGCAA Num.seqs=7 Similarity=0.793282
3 TTTGCCGGAAAT--TTTCAATTCCGGCAA-ATTGCCGTTTGCCGA-
WB235_2:12905369-12905758 Satlength=390 Nr of Repeats=5 RepeatLength=43
seed=GATTTGCCGG Num.seqs=3 Similarity=0.875969
41 TTTGCCGGAAAT--TTTCAATCCCGCAA-ATTGCAGTTTGCCGA-
WB235_4:2140998-2141533 Satlength=536 Nr of Repeats=8 RepeatLength=43
seed=TTGCCGGAAA Num.seqs=5 Similarity=0.868148
44 TTTGCCGGAAAT--TTTCAATCCCGGCAT-TTTGCCGTTTGCCGA-
Rev.of_WB235_1:3424298-3424548 Satlength=251 Nr of Repeats=6
RepeatLength=43 seed=TTGAAAATTT Num.seqs=5 Similarity=0.810853
18 TTTGCCGGAAAT--TTTCAATTCCGCCAA-TTTGCCGTTTGCCGA-
Rev.of_WB235_2:3111494-3112267 Satlength=774 Nr of Repeats=16
RepeatLength=43 seed=TTGCCGGAAT Num.seqs=13 Similarity=0.825084
27 TTTACAGGAAAT--TTTCAATTCCGGCAA-GTTGCCGTTTGCCGA-

Rev.of_WB235_4:2964807-2965022 Satlength=216 Nr of Repeats=4
 RepeatLength=43 seed=TTTGCCGGAA Num.seqs=3 Similarity=0.739899
 28 TTTNCAGGAAAT--TTTCAATTCCGGCAA-ACTGCCGGTTTGCCAGA-
 Rev.of_WB235_1:2263541-2264092 Satlength=552 Nr of Repeats=13
 RepeatLength=43 seed=ATTTCCGGCA Num.seqs=12 Similarity=0.752353
 12 TTTGCCGGAAAT--TTTTATTTTCGGCAA-NTTGCCGGTTTGCCGA-
 Rev.of_WB235_1:11474410-11474625 Satlength=216 Nr of Repeats=5
 RepeatLength=43 seed=CGGCAAATCG Num.seqs=5 Similarity=0.801550
 50 TTTGCCGGAAAT--TTTCATTTTCGGCAA-NTTGCCGGTTTGCCGA-
 Rev.of_WB235_2:12402768-12404058 Satlength=1291 Nr of Repeats=30
 RepeatLength=43 seed=TTTCCGGCAA Num.seqs=30 Similarity=0.867914
 54 TTTGCCGGAAAT--TTTCATTTTCGGCAA-ATTGCCGGTTTGCCGA-
 WB235_3:12017198-12017750 Satlength=553 Nr of Repeats=10 RepeatLength=43
 seed=AATTGCCGGT Num.seqs=7 Similarity=0.748854
 69 TTTGCCGGAAAA--TTTCATTTTCGGCAA-ATTGCCGGTTTGCCGA-
 WB235_3:13094103-13095343 Satlength=1241 Nr of Repeats=25 RepeatLength=43
 seed=CGGAAATTTT Num.seqs=17 Similarity=0.776106
 48 TTTGCCGGAAAT--TTTNATTTTCGGCAA-TTGCCNGTTTGCCGA-
 WB235_2:12719695-12719880 Satlength=186 Nr of Repeats=5 RepeatLength=43
 seed=TATTTTCATT Num.seqs=3 Similarity=0.979328
 52 TTTGCCGGGTAT--TTTCATTTTCGGCAA-ATTGCCGGTTTGCCGA-
 WB235_1:687047-687860 Satlength=814 Nr of Repeats=14 RepeatLength=44
 seed=TTTGCCGGTT Num.seqs=9 Similarity=0.927609
 28 TTTGCCCGAAAT--TTTCAATTTTCGGCAA-TTTGCCGGTTTGCCGA-
 Rev.of_WB235_1:1797802-1798215 Satlength=414 Nr of Repeats=9
 RepeatLength=43 seed=GCCGGAATTG Num.seqs=7 Similarity=0.864157
 25 TTTGCCAGAAAT--TTTCAATTCCGGCTA-TGTGCCGGTTTGCCGA-
 WB235_1:2817881-2818157 Satlength=277 Nr of Repeats=5 RepeatLength=43
 seed=TTGCCGATTT Num.seqs=3 Similarity=0.834625
 29 TTTGCCGGAAAT--TTACAATTCC-ACTATTTTGCCGGTTTGCCGA-
 Rev.of_WB235_1:1209321-1210686 Satlength=1366 Nr of Repeats=32
 RepeatLength=43 seed=CCAGAAATTA Num.seqs=22 Similarity=0.892882
 24 TTTGCCGAAAAT--TCTAATTTCTGGCAA-TTTGCCGGTTTGCTGA-
 Rev.of_WB235_1:2858185-2858357 Satlength=173 Nr of Repeats=4
 RepeatLength=43 seed=AAATCGGCAA Num.seqs=4 Similarity=0.906977
 46 TTTGCCGGGAAT--TTTCATTTTTTGCAA-TTTGCCGGATTGCCGA-
 Rev.of_WB235_3:12581020-12581289 Satlength=270 Nr of Repeats=5
 RepeatLength=43 seed=GGCAAATCGG Num.seqs=3 Similarity=0.689394
 49 TTTGCCGGAAAT--TTTNATATTTNACAA-ATTGCCGGTTTGCCGA-
 WB235_1:2653859-2654031 Satlength=173 Nr of Repeats=4 RepeatLength=43
 seed=TTGCCGATTT Num.seqs=4 Similarity=0.798450
 36 TTTGCCGGAAAT-GTTT-ATTTCCGACAA-TTGGCAGATTTGCCGA-
 WB235_1:14554105-14554484 Satlength=380 Nr of Repeats=9 RepeatLength=43
 seed=TTTGCCGGTT Num.seqs=8 Similarity=0.931340
 27 TTCGACGGAAAT--TTTTATTTTCGGCAC-TTGCCGGTTTGCCGG-
 Rev.of_WB235_5:3679665-3679834 Satlength=170 Nr of Repeats=4
 RepeatLength=42 seed=TTTCCAGCAA Num.seqs=3 Similarity=0.767196
 11 TTTGCTGGAAA--TCTCAATTCCGGCAA-TTCGCTGATTTGCCGA-
 Rev.of_WB235_1:2233376-2233627 Satlength=252 Nr of Repeats=6
 RepeatLength=43 seed=CAAATCGGCA Num.seqs=5 Similarity=0.795349
 47 TTTGCTGGAAAT--TTTTAATTTTCGAAA-TTGCCGAGTTGCCGA-
 WB235_5:17885285-17887191 Satlength=1907 Nr of Repeats=37 RepeatLength=44
 seed=TTGCCGAAA Num.seqs=31 Similarity=0.808472
 1 TTTGCCGGAAAT--ATTCAATTTTGCAA-ATTGNCCGGTTTGCTGAA

WB235_1:11113480-11113648 Satlength=169 Nr of Repeats=4 RepeatLength=42
seed=TGCCGGAAAT Num.seqs=4 Similarity=0.788360
2 GCTGCCGGAAAT---TTCAAACCCGGCAA-TTTGCCCATTTGCCGA-

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Consensus:

TTTGCCGGAAATTTTcAaTTcCGGCAAtTTGCCGgTTTGCCGA

>WB235_Fam_14_11_23 Nr. of seq. 23 Alignment length(with gaps) = 12
Alignment score = 0.800725

WB235_1:11694858-11694997 Satlength=140 Nr of Repeats=13 RepeatLength=11
seed=TTTTGCACAT Num.seqs=9 Similarity=0.838384

0 TTTTGCACAT-T

WB235_1:12093567-12094297 Satlength=731 Nr of Repeats=59 RepeatLength=11
seed=CACATTTTTT Num.seqs=45 Similarity=0.854790

5 TTTTGCACAT-T

WB235_1:12129305-12129768 Satlength=464 Nr of Repeats=41 RepeatLength=11
seed=TTGCACATTT Num.seqs=32 Similarity=0.962854

2 TTTTGCACAT-T

WB235_2:4442528-4442746 Satlength=219 Nr of Repeats=20 RepeatLength=11
seed=TGCACATTTT Num.seqs=18 Similarity=0.986532

3 TTTTGCACAT-T

WB235_3:1245524-1246875 Satlength=1352 Nr of Repeats=116 RepeatLength=11
seed=TTTTTGCACA Num.seqs=73 Similarity=0.910060

10 TTTTGCACAT-T

Rev.of_WB235_3:1671460-1671581 Satlength=122 Nr of Repeats=11
RepeatLength=11 seed=GCAAAAAATG Num.seqs=11 Similarity=0.960331

6 TTTTGCACAT-T

WB235_3:1809979-1810419 Satlength=441 Nr of Repeats=36 RepeatLength=11
seed=ATTTTTTGCA Num.seqs=32 Similarity=0.920088

8 TTTTGCACAT-T

Rev.of_WB235_3:1985833-1986090 Satlength=258 Nr of Repeats=24
RepeatLength=11 seed=TGTGCAAAAA Num.seqs=17 Similarity=0.959002

9 TTTTGCACAT-T

WB235_3:12172469-12173356 Satlength=888 Nr of Repeats=63 RepeatLength=11
seed=TTTTTGCACA Num.seqs=46 Similarity=1.000000

10 TTTTGCACAT-T

Rev.of_WB235_3:13116308-13116374 Satlength=67 Nr of Repeats=5
RepeatLength=11 seed=AAAAATGTGC Num.seqs=4 Similarity=1.000000

3 TTTTGCACAT-T

WB235_4:15648768-15648845 Satlength=78 Nr of Repeats=6 RepeatLength=11
seed=TGCACATTTT Num.seqs=5 Similarity=0.903030

3 TTTTGCACAT-T

WB235_5:2886582-2886789 Satlength=208 Nr of Repeats=19 RepeatLength=11
seed=GCACATTTTT Num.seqs=17 Similarity=0.908200

4 TTTTGCACAT-T

Rev.of_WB235_5:3629745-3629789 Satlength=45 Nr of Repeats=4
RepeatLength=11 seed=CAAAAAATGT Num.seqs=4 Similarity=0.878788

5 TTTTGCACAT-T

WB235_5:11057749-11057963 Satlength=215 Nr of Repeats=10 RepeatLength=11
seed=CACATTTTTT Num.seqs=9 Similarity=0.946128

5 TTTTGCACAT-T

Rev.of_WB235_6:8602386-8602451 Satlength=66 Nr of Repeats=5
RepeatLength=11 seed=GCAAAAATG Num.seqs=4 Similarity=0.878788
6 TTTTGCACAT-T
WB235_3:11862696-11862861 Satlength=166 Nr of Repeats=15 RepeatLength=11
seed=ACATTTTTTG Num.seqs=13 Similarity=0.919192
6 TTTTGNACAT-T
Rev.of_WB235_1:11840154-11840231 Satlength=78 Nr of Repeats=7
RepeatLength=11 seed=CAAAAATGT Num.seqs=7 Similarity=0.942280
5 TTTTGGACAT-T
WB235_4:13547778-13547822 Satlength=45 Nr of Repeats=4 RepeatLength=11
seed=CACATTTTTT Num.seqs=4 Similarity=0.919192
5 TTTTCCACAT-T
WB235_4:13575701-13576041 Satlength=341 Nr of Repeats=30 RepeatLength=11
seed=GCACATTTTTT Num.seqs=22 Similarity=0.772787
4 TTTAGCACAT-T
Rev.of_WB235_6:3261930-3262051 Satlength=122 Nr of Repeats=11
RepeatLength=11 seed=AAAATGTGCT Num.seqs=7 Similarity=0.826720
13 TTTAGCACAT-T
Rev.of_WB235_4:15034367-15034488 Satlength=122 Nr of Repeats=9
RepeatLength=11 seed=TGTGCAAAAA Num.seqs=7 Similarity=0.838384
9 TTTTGCACAA-T
Rev.of_WB235_5:3092621-3092687 Satlength=67 Nr of Repeats=5
RepeatLength=11 seed=TTTGGCAAGA Num.seqs=4 Similarity=0.818182
10 TCTTGCCCAA-T
WB235_2:144001-144084 Satlength=84 Nr of Repeats=6 RepeatLength=12
seed=ATTCTTGCA Num.seqs=5 Similarity=0.844444
21 TCTTGCAAAAT

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Consensus:

TTTTGCACATT

>WB235_Fam_15_31_22 Nr. of seq. 22 Alignment length(with gaps) = 33
Alignment score = 0.785911
WB235_3:78610-79849 Satlength=1240 Nr of Repeats=39 RepeatLength=31
seed=TAAATAATTA Num.seqs=37 Similarity=0.866835
0 TAAATAATTAGCAGA-CCAAAGTTGGG-TCTGC
WB235_3:85304-85614 Satlength=311 Nr of Repeats=9 RepeatLength=31
seed=TGCTAAATAA Num.seqs=8 Similarity=0.907834
28 TAAATAATTAGCAGA-CCAAAGTTGGG-TATGC
Rev.of_WB235_3:498249-499054 Satlength=806 Nr of Repeats=26
RepeatLength=31 seed=GGTCTGCTAA Num.seqs=19 Similarity=0.861661
48 TAAATAATTAGCAGA-CCAAAGTTGGG-TATGC
WB235_3:587989-588144 Satlength=156 Nr of Repeats=5 RepeatLength=31
seed=TGGGTATGCT Num.seqs=5 Similarity=1.000000
53 TAAATAATTAGCAGA-CCAAAGTTGGG-TATGC
Rev.of_WB235_3:584894-585235 Satlength=342 Nr of Repeats=11
RepeatLength=31 seed=GGTCTGCTAA Num.seqs=11 Similarity=0.968719
17 TAAATAATTAGCAGA-CCGAAGTTGGG-TATGC
Rev.of_WB235_3:334126-334653 Satlength=528 Nr of Repeats=17
RepeatLength=31 seed=TGGTCTGCTA Num.seqs=15 Similarity=0.868920
18 TAAATATTTAGCAGA-CCAAAGTTGGG-TATGC

WB235_3:346580-346716 Satlength=137 Nr of Repeats=5 RepeatLength=31
seed=AATATTTAGC Num.seqs=3 Similarity=0.885305
33 TAAATATTTAGCAGA-CCAAAGTTGGG-TATGC
WB235_3:470472-471505 Satlength=1034 Nr of Repeats=16 RepeatLength=31
seed=TTAGCAGAC Num.seqs=10 Similarity=0.931183
37 TAAATATTTAGCAGA-CCAAAGTTGGG-TATGC
WB235_3:492131-493485 Satlength=1355 Nr of Repeats=34 RepeatLength=31
seed=TTAGCAGACC Num.seqs=25 Similarity=0.924301
38 TAAATATTTAGCAGA-CCAAAGATGGG-TATGC
WB235_3:855590-855838 Satlength=249 Nr of Repeats=7 RepeatLength=31
seed=TAAATATTTA Num.seqs=6 Similarity=0.862366
31 TAAATATTTAGCAGA-CCAAAGTTAGG-TATGC
Rev.of_WB235_3:187630-188214 Satlength=585 Nr of Repeats=4
RepeatLength=31 seed=TTAGCAGACC Num.seqs=3 Similarity=0.942652
3 TAAATAATTAGCAGA-CCATAGTTGGG-TCTGC
WB235_3:410715-410901 Satlength=187 Nr of Repeats=6 RepeatLength=31
seed=TTGGGTCTGC Num.seqs=6 Similarity=0.868100
21 TAAATAATTAGCAGA-CCATAATTGGG-TCTGC
Rev.of_WB235_3:423133-423737 Satlength=605 Nr of Repeats=6
RepeatLength=31 seed=TATTTAGCAG Num.seqs=5 Similarity=0.901075
37 TAAATAATTAGCAGA-CCATAATTGGG-TCTGC
Rev.of_WB235_3:189539-190145 Satlength=607 Nr of Repeats=5
RepeatLength=31 seed=TTAGCAGACC Num.seqs=3 Similarity=0.971326
3 TAATTATTTAGCAGA-CCATACTTGGG-TCTGC
Rev.of_WB235_3:191259-191627 Satlength=369 Nr of Repeats=7
RepeatLength=31 seed=GGTCTGCTAA Num.seqs=6 Similarity=0.868100
17 TAAATATTTAGCAGA-CCATACTTGGG-TCTGC
Rev.of_WB235_3:193180-193459 Satlength=280 Nr of Repeats=9
RepeatLength=31 seed=ACCCAAGTAT Num.seqs=9 Similarity=0.906810
27 TAAACATTTAGCAGA-CCATACTTGGG-TCTGC
WB235_3:9853874-9853997 Satlength=124 Nr of Repeats=4 RepeatLength=31
seed=TCTGCTAAAT Num.seqs=3 Similarity=0.971326
26 TAAATAATTAGCAGA-CCATACTTGAT-TCTGC
WB235_3:337086-337644 Satlength=559 Nr of Repeats=17 RepeatLength=31
seed=TATGCTAAAT Num.seqs=16 Similarity=0.883154
26 TAAATATTTAGCAGA-CCAAAAGTAGG-TATGC
WB235_3:340719-342118 Satlength=1400 Nr of Repeats=23 RepeatLength=31
seed=TTAGCAGACC Num.seqs=22 Similarity=0.867430
38 TAAATATTTAGCAGA-CCAAAANTAGG-TATGC
Rev.of_WB235_3:345158-345375 Satlength=218 Nr of Repeats=7
RepeatLength=31 seed=CTGCTAAATA Num.seqs=7 Similarity=0.938556
45 TAAATATTTAGCAGA-CCCAAAGTTGG-TATGC
WB235_3:9958568-9958766 Satlength=199 Nr of Repeats=4 RepeatLength=31
seed=TATGCTAAAT Num.seqs=3 Similarity=0.812500
26 TAAATATTTAGCAGA-CCCAANGT-GGNTATGC
WB235_3:633852-634044 Satlength=193 Nr of Repeats=6 RepeatLength=31
seed=TTAGCAGACC Num.seqs=4 Similarity=0.781250
7 TAAATAATTAGCAGACCCATAGGTAGG-TATGC

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Consensus:

TAAATAtTTAGCAGACCAaAgtTgGGTaTGC

>WB235_Fam_16_26_20 Nr. of seq. 20 Alignment length(with gaps) = 26
 Alignment score = 0.760324
 WB235_1:3171655-3172409 Satlength=755 Nr of Repeats=29 RepeatLength=26
 seed=CAGAGTCACT Num.seqs=29 Similarity=0.926235
 0 CAGAGTCACTATTTTTGGGGAACGGC
 WB235_4:15409425-15409737 Satlength=313 Nr of Repeats=12 RepeatLength=26
 seed=CAGAGTCACT Num.seqs=12 Similarity=0.943279
 0 CAGAGTCACTATTTTTGGTGAACGGC
 WB235_5:5283302-5285834 Satlength=2533 Nr of Repeats=98 RepeatLength=26
 seed=CAGAGTCACT Num.seqs=94 Similarity=0.876599
 0 CAGAGTCACTATTTTTGGTGAACGGC
 WB235_6:15807460-15811152 Satlength=3693 Nr of Repeats=142
 RepeatLength=26 seed=GTGAACGGCC Num.seqs=142 Similarity=0.927510
 17 CAGAGTCACTATTTTTGGTGAACGGC
 WB235_6:1636150-1638568 Satlength=2419 Nr of Repeats=93 RepeatLength=26
 seed=GGTGAACGGT Num.seqs=93 Similarity=0.946896
 16 CAGAGTCACTATTTTTGGTGAACGGT
 Rev.of_WB235_6:5542238-5542420 Satlength=183 Nr of Repeats=7
 RepeatLength=26 seed=TAGTGACTCT Num.seqs=7 Similarity=0.836567
 11 CAGAGTCACTAATTTTTGGTGAACGGC
 WB235_3:931109-931213 Satlength=105 Nr of Repeats=4 RepeatLength=26
 seed=CGGCCAGAGT Num.seqs=4 Similarity=0.863248
 22 CAGAGTCACTACTTATGGTGAACGGC
 WB235_5:10446631-10446995 Satlength=365 Nr of Repeats=14 RepeatLength=26
 seed=CCAGAGTCAC Num.seqs=14 Similarity=0.974641
 25 CAGAGTCACTATAATTGGTGAACGGC
 Rev.of_WB235_1:13277345-13277527 Satlength=183 Nr of Repeats=7
 RepeatLength=26 seed=CTCTGGCAGT Num.seqs=7 Similarity=0.941392
 5 CAGAGCCACTTATTTTTAGTGAAGTGC
 WB235_4:10985445-10985549 Satlength=105 Nr of Repeats=4 RepeatLength=26
 seed=CCAGAGTCAC Num.seqs=4 Similarity=0.863248
 25 CAGAGTCACTATTTTTAGTGAAGTGC
 WB235_6:2379254-2380684 Satlength=1431 Nr of Repeats=55 RepeatLength=26
 seed=TTTTAGTGAA Num.seqs=55 Similarity=0.934801
 38 CAGAGTCACTAATTTTTAGTGAAGTGC
 WB235_1:3664200-3666098 Satlength=1899 Nr of Repeats=73 RepeatLength=26
 seed=ATGGTTAGAG Num.seqs=73 Similarity=0.974476
 21 TAGAGTCATATTTTTAGGTGAATGGT
 Rev.of_WB235_2:10336035-10336399 Satlength=365 Nr of Repeats=14
 RepeatLength=26 seed=TATGACTCTA Num.seqs=14 Similarity=0.950409
 36 TAGAGTCATATTTTTAGGTGAATGGT
 Rev.of_WB235_6:1642568-1643478 Satlength=911 Nr of Repeats=35
 RepeatLength=26 seed=GA CTCTAACC Num.seqs=35 Similarity=0.961474
 33 TAGAGTCATATTTTTAGGTGAATGGT
 WB235_1:13404330-13408464 Satlength=4135 Nr of Repeats=159
 RepeatLength=26 seed=TTTTAGGTGA Num.seqs=159 Similarity=0.972965
 37 TAGAGTCATAATTTTTAGGTGAATGGT
 WB235_3:5353177-5358366 Satlength=5190 Nr of Repeats=198 RepeatLength=26
 seed=GTTAGAGTCA Num.seqs=196 Similarity=0.933400
 24 TAGAGTCATTATTTTTAGGTGAATGGT
 Rev.of_WB235_3:5358375-5358505 Satlength=131 Nr of Repeats=5
 RepeatLength=26 seed=ACCATTCACC Num.seqs=5 Similarity=0.917949
 26 TAGAGTCATTATTTTTAGGTGAATGGT

WB235_4:14781306-14781436 Satlength=131 Nr of Repeats=5 RepeatLength=26
seed=TTGGTTAGAGT Num.seqs=5 Similarity=0.958974
48 TAGAGTCATTATTTTAGGTGAATGGT
Rev.of_WB235_5:15170122-15170278 Satlength=157 Nr of Repeats=6
RepeatLength=26 seed=TTACACCTAAA Num.seqs=6 Similarity=0.846154
48 TAGAGTCATTATTTTAGGTGAATGGT
Rev.of_WB235_6:11785744-11787512 Satlength=1769 Nr of Repeats=68
RepeatLength=26 seed=ACCATTACACC Num.seqs=68 Similarity=0.956012
26 TAGAGTCATTATTTTAGGTGAATGGT

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Consensus:

cAGAGTCActatTTTtGGTGAAcGGc

>WB235_Fam_17_37_19 Nr. of seq. 19 Alignment length(with gaps) = 43
Alignment score = 0.743370
WB235_5:16273671-16273852 Satlength=182 Nr of Repeats=5 RepeatLength=36
seed=GGGAATTCAA Num.seqs=4 Similarity=0.962963
25 TTTTAATTTTTT-GAAAAC-ATTTTGGC-GGGAA-TTC--AAA
WB235_3:3023864-3024701 Satlength=838 Nr of Repeats=18 RepeatLength=37
seed=ATTTTGGCGG Num.seqs=16 Similarity=0.920120
54 TTTTAATTTTTTC-GAAAAC-ATTTTGGC-GGGAA-TTC--AAA
WB235_5:17308169-17308466 Satlength=298 Nr of Repeats=8 RepeatLength=37
seed=AAAACATTTT Num.seqs=5 Similarity=0.894737
86 TTTTAATTTTTT-GAAAAC-ATTTTGGC-GGGAA-TTC--AAA
WB235_4:3098171-3098319 Satlength=149 Nr of Repeats=4 RepeatLength=37
seed=TTGGCGGGAAT Num.seqs=4 Similarity=0.867868
58 TTTTAATTTTCC-GAAAAC-ATTTTGGC-GGGAA-TTC--AAA
WB235_2:12649041-12649452 Satlength=412 Nr of Repeats=11 RepeatLength=37
seed=ATTTTGGCGG Num.seqs=7 Similarity=0.951952
54 TTTTAATTTTTT-GAAAAT-ATTTTGGC-GGGAA-TTC--AAA
WB235_3:10943916-10944702 Satlength=787 Nr of Repeats=15 RepeatLength=37
seed=TTGGCGGGAA Num.seqs=10 Similarity=0.935135
57 TTTTAATTTTTT-GAAAAT-ATTTTGGC-GGGAA-TTC--AAA
WB235_4:280698-281177 Satlength=480 Nr of Repeats=13 RepeatLength=37
seed=TTGGCGGGAA Num.seqs=9 Similarity=0.933934
57 TTTTAATTTTTT-GAAAAT-ATTTTGGC-GGGAA-TTC--AAA
Rev.of_WB235_4:17147932-17148762 Satlength=831 Nr of Repeats=9
RepeatLength=37 seed=ATTCCCGCCA Num.seqs=6 Similarity=0.896697
68 TTTTAATTTTTT-GAAAAT-ATTTTGGC-GGGAA-TTC--AAA
WB235_6:14119472-14121076 Satlength=1605 Nr of Repeats=43 RepeatLength=37
seed=TTTAATTTTTT Num.seqs=26 Similarity=0.924934
74 TTTTAATTTTTT-GAAAAT-ATTTTGGC-GGGAA-TTC--AAA
Rev.of_WB235_4:1681168-1681390 Satlength=223 Nr of Repeats=6
RepeatLength=37 seed=CGCCAAAATG Num.seqs=6 Similarity=0.894294
63 TTTTAATTTTTT-GAAAAC-ATTTTGGC-GGGAA-TTC--AAA
WB235_4:16471145-16471947 Satlength=803 Nr of Repeats=4 RepeatLength=37
seed=ATTCAAATTT Num.seqs=3 Similarity=0.951952
66 TTTTAATTTTTT-GAAAAT-ACTTTGGC-GGGAA-TTC--AAA
Rev.of_WB235_5:20153934-20154193 Satlength=260 Nr of Repeats=7
RepeatLength=37 seed=AATTTGAATT Num.seqs=7 Similarity=0.941656
75 TTTTAATTTTTC-AAAAT-ATTTTGGC-GGGAA-TTC--AAA

WB235_4:15842446-15843519 Satlength=1074 Nr of Repeats=16 RepeatLength=37
seed=CGGGAATTCA Num.seqs=13 Similarity=0.831370
61 TTTTAATTTTTT-G-AAATCATTTTGGC-GGGAA-TTC--AAA
WB235_5:15941558-15942466 Satlength=909 Nr of Repeats=7 RepeatLength=37
seed=GCGGGAATTC Num.seqs=5 Similarity=0.877477
97 TTTTAATTATTT-G-AAATCATTTTGGC-GGGAA-TTC--AAA
WB235_1:1317490-1319274 Satlength=1785 Nr of Repeats=47 RepeatLength=38
seed=GGGAATTCAA Num.seqs=45 Similarity=0.939890
25 TTTTAATTTTTTTTGAAAAC-ATTTTGGC-GGGAA-TTC--AAA
WB235_3:12698391-12698580 Satlength=190 Nr of Repeats=5 RepeatLength=38
seed=TTTGTGCGGG Num.seqs=4 Similarity=0.844017
56 ATTTAATTTTTTTTGAAAAT-ATTTTGGC-GGGAA-TTC--AAA
WB235_1:280525-281393 Satlength=869 Nr of Repeats=23 RepeatLength=38
seed=AAATTTTAAT Num.seqs=17 Similarity=0.995872
34 TTTTAATTTTTT-GAAAAT-ATTTTGGC-GGGAATTTA--AAA
WB235_3:2113231-2114730 Satlength=1500 Nr of Repeats=39 RepeatLength=39
seed=TTTTTGGCGG Num.seqs=29 Similarity=0.914530
55 TTCAA-TTTTTC-AAATAT-TTTTTGGCGGGAAA-TTCAAAAA
Rev.of_WB235_3:2117069-2117228 Satlength=160 Nr of Repeats=4
RepeatLength=40 seed=TCCCGCCAAA Num.seqs=3 Similarity=0.866667
67 TTTAAATTTTTT-GAATAT-TTTTTGGCGGGAAA-TTCAAAAA

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Consensus:

GGGAATTCAAATTTTAATTTTTtGAAAAtATTTTGGC

>WB235_Fam_18_19_17 Nr. of seq. 17 Alignment length(with gaps) = 19
Alignment score = 0.859649
WB235_1:12955954-12956201 Satlength=248 Nr of Repeats=13 RepeatLength=19
seed=CAAGGCACTA Num.seqs=13 Similarity=0.816464
0 CAAGGCACTAGAAATGCGC
Rev.of_WB235_5:18575312-18575616 Satlength=305 Nr of Repeats=15
RepeatLength=19 seed=TAGTGCCTTG Num.seqs=12 Similarity=0.808612
10 CAAGGCACTAGAAATGCGC
Rev.of_WB235_5:18684513-18684741 Satlength=229 Nr of Repeats=8
RepeatLength=19 seed=TTCTAGTGCC Num.seqs=5 Similarity=0.817544
13 CAAGGCACTAGAAATGCGC
WB235_5:19373212-19373421 Satlength=210 Nr of Repeats=9 RepeatLength=19
seed=TTGCGCCAAG Num.seqs=7 Similarity=0.744444
13 CAAGGCACTAGAAATGCGC
Rev.of_WB235_3:3233988-3234755 Satlength=768 Nr of Repeats=13
RepeatLength=19 seed=CTTGGCGCAA Num.seqs=8 Similarity=0.764411
4 CAAGGCACGAGAATTGCGC
WB235_5:19379891-19380043 Satlength=153 Nr of Repeats=5 RepeatLength=19
seed=AGAATTGCGC Num.seqs=3 Similarity=0.859649
9 CAAGGCACGAGAATTGCGC
Rev.of_WB235_5:19148365-19148726 Satlength=362 Nr of Repeats=16
RepeatLength=19 seed=TGGCGCATTT Num.seqs=14 Similarity=0.787160
21 CAAGGCACGAGAAATGCGC
WB235_5:18388249-18388686 Satlength=438 Nr of Repeats=22 RepeatLength=19
seed=CAAGGCACTA Num.seqs=21 Similarity=0.750042
0 CAAGGCACTANAATTGCGT

Rev.of_WB235_5:18389794-18390302 Satlength=509 Nr of Repeats=18
 RepeatLength=19 seed=TGACGCAATT Num.seqs=14 Similarity=0.787931
 2 CAAGGCACTAGAAATTGCGT
 Rev.of_WB235_5:18676328-18676917 Satlength=590 Nr of Repeats=23
 RepeatLength=19 seed=TGACGCAATT Num.seqs=15 Similarity=0.830476
 2 CAAGGCACTAGAAATTGCGT
 WB235_5:18677260-18677830 Satlength=571 Nr of Repeats=26 RepeatLength=19
 seed=ACTAGAAATTG Num.seqs=23 Similarity=0.820539
 6 CAAGGCACTAGAAATTGCGT
 Rev.of_WB235_5:19380090-19380527 Satlength=438 Nr of Repeats=16
 RepeatLength=19 seed=GCCTTGACGC Num.seqs=11 Similarity=0.888995
 6 CAAGGCACTAGAAATTGCGT
 Rev.of_WB235_5:19821185-19822021 Satlength=837 Nr of Repeats=37
 RepeatLength=19 seed=TAGTGCCTTG Num.seqs=30 Similarity=0.844807
 10 CAAGGCACTAGAAATTGCGT
 Rev.of_WB235_5:18573477-18573762 Satlength=286 Nr of Repeats=11
 RepeatLength=19 seed=TTGACGCAAT Num.seqs=9 Similarity=0.666667
 3 CAANGCACTAGAAATTGCGT
 Rev.of_WB235_5:18619123-18619731 Satlength=609 Nr of Repeats=29
 RepeatLength=19 seed=GTGCCTTGAC Num.seqs=26 Similarity=0.876923
 8 CAAGGCACTAGAAANTGCGT
 WB235_2:3036430-3037140 Satlength=711 Nr of Repeats=18 RepeatLength=19
 seed=GCCAAGGCAC Num.seqs=11 Similarity=0.680606
 17 CAAGGCACTNGAAANGCGC
 Rev.of_WB235_5:19022623-19023690 Satlength=1068 Nr of Repeats=10
 RepeatLength=19 seed=TGGCGCATTT Num.seqs=6 Similarity=0.714620
 2 CAACTCACCAAATGCGC

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Consensus:

CAAGGCACTAGAAATGCGC

>WB235_Fam_19_14_17 Nr. of seq. 17 Alignment length(with gaps) = 14
 Alignment score = 0.892682
 WB235_2:11306986-11307037 Satlength=52 Nr of Repeats=4 RepeatLength=12
 seed=ACTATAACTA Num.seqs=3 Similarity=0.851852
 0 ACTATA-ACTACA-
 WB235_1:11155001-11155099 Satlength=99 Nr of Repeats=7 RepeatLength=14
 seed=AACTACTAAC Num.seqs=7 Similarity=0.803175
 6 ACTACTAACTACTA
 Rev.of_WB235_1:13019817-13020208 Satlength=392 Nr of Repeats=8
 RepeatLength=14 seed=AGTTTGTAGT Num.seqs=5 Similarity=0.885714
 10 ACTACAAACTACAA
 Rev.of_WB235_1:13499215-13500226 Satlength=1012 Nr of Repeats=11
 RepeatLength=14 seed=TAGTTTGTAG Num.seqs=7 Similarity=0.845805
 18 ACTACAAACTACAA
 WB235_1:13500544-13500919 Satlength=376 Nr of Repeats=11 RepeatLength=14
 seed=TACAAACTAC Num.seqs=7 Similarity=0.918367
 23 ACTACAAACTACAA
 Rev.of_WB235_1:14324192-14324420 Satlength=229 Nr of Repeats=4
 RepeatLength=14 seed=TGTAGTTTGT Num.seqs=3 Similarity=0.936508
 20 ACTACAAACTACAA

WB235_2:2629919-2630440 Satlength=522 Nr of Repeats=10 RepeatLength=14
seed=CTACAAACTA Num.seqs=6 Similarity=0.796825
22 ACTACAAACTACAA
WB235_2:12761888-12762610 Satlength=723 Nr of Repeats=9 RepeatLength=14
seed=AACTACAAAC Num.seqs=6 Similarity=0.841270
20 ACTACAAACTACAA
Rev.of_WB235_2:13303475-13303853 Satlength=379 Nr of Repeats=13
RepeatLength=14 seed=TAGTTTGTAG Num.seqs=8 Similarity=0.829932
18 ACTACAAACTACAA
WB235_2:13962702-13964354 Satlength=1653 Nr of Repeats=47 RepeatLength=14
seed=TACAAACTAC Num.seqs=31 Similarity=0.870968
23 ACTACAAACTACAA
Rev.of_WB235_2:14006143-14006320 Satlength=178 Nr of Repeats=5
RepeatLength=14 seed=GTAGTTTGTGTA Num.seqs=3 Similarity=0.809524
19 ACTACAAACTACAA
Rev.of_WB235_4:15294619-15295382 Satlength=764 Nr of Repeats=4
RepeatLength=14 seed=TTGTAGTTTG Num.seqs=3 Similarity=0.936508
21 ACTACAAACTACAA
WB235_5:18354225-18354524 Satlength=300 Nr of Repeats=14 RepeatLength=14
seed=ACAAACTACA Num.seqs=10 Similarity=0.942857
10 ACTACAAACTACAA
Rev.of_WB235_5:19550939-19551875 Satlength=937 Nr of Repeats=7
RepeatLength=14 seed=TTTGTAGTTT Num.seqs=5 Similarity=0.804444
22 ACTACAAACTACAA
WB235_5:19551915-19552281 Satlength=367 Nr of Repeats=11 RepeatLength=14
seed=ACAAACTACA Num.seqs=7 Similarity=0.931973
10 ACTACANACTACAA
Rev.of_WB235_1:13600712-13601694 Satlength=983 Nr of Repeats=52
RepeatLength=14 seed=TGTAGTATGT Num.seqs=42 Similarity=0.960511
20 ACTACATACTACAT
WB235_4:1624502-1624593 Satlength=92 Nr of Repeats=6 RepeatLength=14
seed=ACTACACACT Num.seqs=5 Similarity=1.000000
21 ACTACACACTACAC

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Consensus:

ACTACAaACTACAA

>WB235_Fam_20_12_15 Nr. of seq. 15 Alignment length(with gaps) = 14
Alignment score = 0.745805
WB235_4:15410980-15411070 Satlength=91 Nr of Repeats=8 RepeatLength=10
seed=TGTTATGATA Num.seqs=5 Similarity=0.763636
0 TG-T-TATG--ATA
Rev.of_WB235_1:11145522-11145582 Satlength=61 Nr of Repeats=5
RepeatLength=12 seed=TATACATATA Num.seqs=5 Similarity=1.000000
0 TG-TATATG-TATA
WB235_1:11342672-11342750 Satlength=79 Nr of Repeats=6 RepeatLength=12
seed=TATATGTATA Num.seqs=5 Similarity=1.000000
8 TG-TATATG-TATA
WB235_1:14430493-14430609 Satlength=117 Nr of Repeats=10 RepeatLength=12
seed=ATATGTATAT Num.seqs=6 Similarity=0.888889
9 TG-TATATG-TATA

WB235_2:2000885-2001197 Satlength=313 Nr of Repeats=26 RepeatLength=12
seed=ATGTATATGT Num.seqs=26 Similarity=0.950769
11 TG-TATATG-TATA
Rev.of_WB235_2:3471040-3471110 Satlength=71 Nr of Repeats=4
RepeatLength=12 seed=ATACATATAC Num.seqs=3 Similarity=1.000000
11 TG-TATATG-TATA
Rev.of_WB235_3:12538530-12538668 Satlength=139 Nr of Repeats=11
RepeatLength=12 seed=TATACATATA Num.seqs=10 Similarity=1.000000
0 TG-TATATG-TATA
WB235_4:1438688-1438742 Satlength=55 Nr of Repeats=4 RepeatLength=12
seed=TATATGTATA Num.seqs=3 Similarity=1.000000
8 TG-TATATG-TATA
WB235_5:18475570-18475679 Satlength=110 Nr of Repeats=6 RepeatLength=12
seed=GTATATGTAT Num.seqs=5 Similarity=0.955556
7 TG-TATATG-TATA
Rev.of_WB235_5:19038887-19039001 Satlength=115 Nr of Repeats=9
RepeatLength=12 seed=ATACATATAC Num.seqs=8 Similarity=1.000000
11 TG-TATATG-TATA
WB235_5:19957566-19957879 Satlength=314 Nr of Repeats=8 RepeatLength=12
seed=TATGTATATG Num.seqs=6 Similarity=1.000000
10 TG-TATATG-TATA
Rev.of_WB235_5:19966309-19966447 Satlength=139 Nr of Repeats=11
RepeatLength=12 seed=ATATACATAT Num.seqs=10 Similarity=1.000000
7 TG-TATATG-TATA
WB235_5:19043595-19043791 Satlength=197 Nr of Repeats=8 RepeatLength=12
seed=ATATGTATAT Num.seqs=5 Similarity=0.777778
11 TA-TNTATA-TNTA
WB235_5:19047920-19048249 Satlength=330 Nr of Repeats=23 RepeatLength=14
seed=TATATGTTAT Num.seqs=22 Similarity=0.960421
10 TGTTATATGTTATA
Rev.of_WB235_6:16158526-16158670 Satlength=145 Nr of Repeats=9
RepeatLength=14 seed=TACCATATAC Num.seqs=7 Similarity=0.841270
12 TGGTATATGGTATA

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Consensus:

TGTATATGTATA

>WB235_Fam_21_18_14 Nr. of seq. 14 Alignment length(with gaps) = 18
Alignment score = 0.786121
WB235_2:4210804-4210907 Satlength=104 Nr of Repeats=5 RepeatLength=18
seed=TGCAAGACTA Num.seqs=3 Similarity=0.950617
0 TGCAAGACTAATAGAGAC
WB235_3:922387-922734 Satlength=348 Nr of Repeats=8 RepeatLength=18
seed=TGCAAGACTA Num.seqs=5 Similarity=0.822222
0 TGCAAGACTAATAGAGAC
Rev.of_WB235_2:14355352-14355470 Satlength=119 Nr of Repeats=5
RepeatLength=18 seed=TAGTCTTGCA Num.seqs=3 Similarity=0.901235
10 TGCAAGACTAATAGAGGC
WB235_6:13423594-13423926 Satlength=333 Nr of Repeats=8 RepeatLength=18
seed=TGCAAGACTA Num.seqs=5 Similarity=0.851852
18 TGCAAGACTAATAGAGGC

WB235_5:3332437-3332702 Satlength=266 Nr of Repeats=4 RepeatLength=18
seed=TGCAAGACTA Num.seqs=3 Similarity=0.876543
18 TGCAAGACTANTAGAGGC
Rev.of_WB235_6:7574716-7575007 Satlength=292 Nr of Repeats=5
RepeatLength=18 seed=TAGTCTTGCA Num.seqs=3 Similarity=0.901235
10 TGCAAGACTATTAGAGGC
WB235_6:14323895-14325001 Satlength=1107 Nr of Repeats=10 RepeatLength=18
seed=TGCAAGACTA Num.seqs=6 Similarity=0.841975
0 TGCAAGACTAATAAAGGC
Rev.of_WB235_4:3834124-3834445 Satlength=322 Nr of Repeats=5
RepeatLength=18 seed=ATTAGTATTG Num.seqs=3 Similarity=0.802469
12 TGCAATACTAATAGGGAG
WB235_6:11859496-11859817 Satlength=322 Nr of Repeats=5 RepeatLength=18
seed=TGCAATACTA Num.seqs=3 Similarity=0.901235
18 TGCAAGACTAATAGGGAG
Rev.of_WB235_4:17134995-17135342 Satlength=348 Nr of Repeats=5
RepeatLength=18 seed=GCACTCCCTA Num.seqs=3 Similarity=0.950617
21 TGCAAGACTATTAGGGAG
Rev.of_WB235_5:12370870-12371218 Satlength=349 Nr of Repeats=5
RepeatLength=18 seed=GCACTCCCTA Num.seqs=3 Similarity=0.950617
21 TGCAAGACTATTAGGGAG
Rev.of_WB235_6:16135006-16135334 Satlength=329 Nr of Repeats=5
RepeatLength=18 seed=ATTAGTTTGT Num.seqs=3 Similarity=0.950617
12 TGCAAACTAATAGAGAG
Rev.of_WB235_3:922819-923128 Satlength=310 Nr of Repeats=5
RepeatLength=18 seed=TAGTGCTGCA Num.seqs=3 Similarity=0.777778
10 TGCAGCACTANTAGAGAC
WB235_3:3794723-3795033 Satlength=311 Nr of Repeats=5 RepeatLength=18
seed=TGCAGCACTA Num.seqs=3 Similarity=0.851852
18 TGCAGCACTATTAGAGAC

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Consensus:

TGCAAGACTAaTAGaGac

>WB235_Fam_22_59_11 Nr. of seq. 11 Alignment length(with gaps) = 62
Alignment score = 0.794330
WB235_1:3990050-3990699 Satlength=650 Nr of Repeats=11 RepeatLength=59
seed=AAAACCACTG Num.seqs=11 Similarity=0.799486
0 AAAACCACTGCACATTTGAAATT-CCATA--TTCTCCATAATTTTCAGTTTAAATATTTTG
Rev.of_WB235_3:8958876-8960427 Satlength=1552 Nr of Repeats=21
RepeatLength=59 seed=TTCAAACTT Num.seqs=20 Similarity=0.972643
2 AAAACCACTGCACATTTGAAATT-CCATA--TTCTCCATAAATCTCAGTTTAAAAAGTTTTG
Rev.of_WB235_5:6219658-6220602 Satlength=945 Nr of Repeats=16
RepeatLength=59 seed=ATGTGCACTG Num.seqs=16 Similarity=0.951601
15 AAAACCACTGCACATTTGAAATT-CCATA--TTCTCCATTATTCTCAGTTTAAAAATTTTTG
WB235_3:13074772-13086747 Satlength=11976 Nr of Repeats=206
RepeatLength=59 seed=TCTCCATAAT Num.seqs=197 Similarity=0.927617
29 AAAACAGTGCACATTTGAAATT-CCATA--TTCTCCATAATTCTCAGTTTAAAAAATTTTG
Rev.of_WB235_3:10224644-10226007 Satlength=1364 Nr of Repeats=23
RepeatLength=59 seed=AAATGTGCAC Num.seqs=20 Similarity=0.928397
17 AAAACCACTGCACATTT-AAATTTCCATA--TTCTCCATAATTCTCAGTTTAAAAAATTTTG

Rev.of_WB235_5:3056063-3056653 Satlength=591 Nr of Repeats=10
RepeatLength=59 seed=AATTTCAAAT Num.seqs=10 Similarity=0.895123
23 AAAACCAAGTGCACATTTGAAATTNCCATA--TTTCCATAATTCTCAGTTTAAAAATTTTG
Rev.of_WB235_5:17384240-17394505 Satlength=10266 Nr of Repeats=173
RepeatLength=59 seed=ATGGTGAATA Num.seqs=165 Similarity=0.936880
36 AAAACCAAGTGCACATTTGAATTT-CCATA--TTCACCATAATTCTCGGTTTTAAAAATTTTG
Rev.of_WB235_2:891126-892012 Satlength=887 Nr of Repeats=12
RepeatLength=59 seed=CAAATTTTTT Num.seqs=11 Similarity=0.987673
0 AAAACCAAGTTTCATTTAAAAAT-CCATA--TTTCCATAATTCTCAGTTTAAAAAATTTG
Rev.of_WB235_3:1017334-1020579 Satlength=3246 Nr of Repeats=55
RepeatLength=59 seed=TGTGCACTGG Num.seqs=55 Similarity=0.955928
14 AAAACCAAGTGCACATTT-AAATT--TATATTTTTTCCATAATTCTCAGTTTAAAAAGTTTTG
WB235_4:12169299-12171242 Satlength=1944 Nr of Repeats=24 RepeatLength=59
seed=TTTTAAAAAT Num.seqs=23 Similarity=0.964628
45 AAAACCAAGTGAAGTCTTGATATT-CCATA--TTCTCCATAATTCTCGGTTTTAAAAATTTTG
Rev.of_WB235_5:6942140-6942965 Satlength=826 Nr of Repeats=14
RepeatLength=59 seed=AATTCAAGAC Num.seqs=13 Similarity=0.956541
81 AAAACCAAGTGAAGTCTTGATTT-CCATA--TTCCCATAATTCTCGGTTTTAAATTTTTTG

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Consensus:

AAAACCAAGTGCACATTTgAAATTCCATATTcTCCATAATTCTCaGTTTaAAAAaTTTTG

>WB235_Fam_23_32_11 Nr. of seq. 11 Alignment length(with gaps) = 35
Alignment score = 0.789437
WB235_5:20268029-20268566 Satlength=538 Nr of Repeats=15 RepeatLength=31
seed=CTACAAACTA Num.seqs=9 Similarity=0.899642
0 CTACAAACTACG-A-G-TTTTGGGCGCTGCTAAG-
Rev.of_WB235_5:18888872-18889346 Satlength=475 Nr of Repeats=14
RepeatLength=32 seed=TTGTAGTTTG Num.seqs=9 Similarity=0.939815
13 CTACAAACTACA-A-A-TTTTGGGCGCTGCTTAGA
WB235_5:19933050-19934036 Satlength=987 Nr of Repeats=29 RepeatLength=32
seed=ACTACAAACT Num.seqs=22 Similarity=0.934365
31 CTACAAACTACA-A-G-TTTTGGGCGCTGCTTAGA
WB235_5:20101712-20102976 Satlength=1265 Nr of Repeats=44 RepeatLength=32
seed=TTTGGGCGC Num.seqs=27 Similarity=0.907170
14 CTACAAACTACA-A-T-TTTTGGGCGCTGCTTAGA
WB235_6:188398-190104 Satlength=1707 Nr of Repeats=53 RepeatLength=32
seed=CGCTGCTAAG Num.seqs=43 Similarity=0.970561
21 CTACAAACTACA-AG--TTTGGGCGCTGCTAAGA
Rev.of_WB235_5:19117969-19118122 Satlength=154 Nr of Repeats=5
RepeatLength=33 seed=TTAGCAGCGC Num.seqs=4 Similarity=0.979798
30 CTACAAACTACA-AGA-TTTTGGGCGCTGCTAAGA
Rev.of_WB235_5:19122509-19124474 Satlength=1966 Nr of Repeats=65
RepeatLength=33 seed=AGCAGCGCCC Num.seqs=49 Similarity=0.900143
61 CTACAAACTACA-AGA-TTTTGGGCGCTGCTAAGA
WB235_5:20273044-20275266 Satlength=2223 Nr of Repeats=68 RepeatLength=31
seed=GGCGCTGCTA Num.seqs=43 Similarity=0.966992
19 CTACAAACTACA-A-G-ATTTGGGCGCTGCTAA-A
Rev.of_WB235_6:161009-161190 Satlength=182 Nr of Repeats=5
RepeatLength=32 seed=TGTAGTTTGT Num.seqs=4 Similarity=0.881944
44 CTACAAACTACA-A-G-ATTTGGGCGCTGCTAACA

Rev.of_WB235_5:20263899-20264125 Satlength=227 Nr of Repeats=7
RepeatLength=32 seed=TTAGCAGCGC Num.seqs=5 Similarity=0.931313
30 CTACAAACTACA-A-GTTTTTGGGCGCTGCTAA-A
Rev.of_WB235_5:18989479-18989970 Satlength=492 Nr of Repeats=14
RepeatLength=32 seed=TGTAGTTTGT Num.seqs=9 Similarity=0.905443
12 CTACAAACTACACA-A-TTTTGGGCGCTGCTAA-A

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Consensus:

CTACAAACTACAAnTTTTGGGCGCTGCTaAgA

>WB235_Fam_24_20_11 Nr. of seq. 11 Alignment length(with gaps) = 21
Alignment score = 0.822222
WB235_1:1852567-1852667 Satlength=101 Nr of Repeats=5 RepeatLength=20
seed=CTAGGCAGAC Num.seqs=5 Similarity=1.000000
0 CTAGGCAG-ACTTAGCCTACC
WB235_1:3427447-3429127 Satlength=1681 Nr of Repeats=81 RepeatLength=20
seed=GGCAGACCTA Num.seqs=78 Similarity=0.844356
3 CTAGGCAG-ACCTAGCCTACC
Rev.of_WB235_3:5285020-5285610 Satlength=591 Nr of Repeats=28
RepeatLength=20 seed=CTAGGTCTGC Num.seqs=25 Similarity=0.872444
14 CTAGGCAG-ACCTAGCCTACC
Rev.of_WB235_3:5285044-5285922 Satlength=879 Nr of Repeats=40
RepeatLength=20 seed=GGTAGGCTAG Num.seqs=28 Similarity=0.844293
20 CTAGGCAG-ACCTAGCCTACC
WB235_6:1508523-1508943 Satlength=421 Nr of Repeats=18 RepeatLength=20
seed=AGGCAGACCT Num.seqs=16 Similarity=0.885556
22 CTAGGCAG-ACCTAGCCTACC
WB235_5:904415-904569 Satlength=155 Nr of Repeats=8 RepeatLength=20
seed=GGCAGACCTA Num.seqs=7 Similarity=0.809524
3 CTAGGCAG-ACCTAGTCTACC
WB235_3:2470723-2471262 Satlength=540 Nr of Repeats=27 RepeatLength=20
seed=GACCCAGCCT Num.seqs=26 Similarity=0.980718
7 CCAGGCAG-ACCCAGCCTACC
WB235_3:2470728-2471526 Satlength=799 Nr of Repeats=40 RepeatLength=20
seed=AGCCTACCCC Num.seqs=38 Similarity=0.909815
12 CCAGGCAG-ACCCAGCCTACC
WB235_5:904306-904460 Satlength=155 Nr of Repeats=7 RepeatLength=20
seed=CCTACCCCAG Num.seqs=6 Similarity=0.871111
14 CCAGGCAG-ACCTAGCCTACC
WB235_1:1852477-1852561 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=CCTACTCTAG Num.seqs=4 Similarity=1.000000
15 CTAGGCAGCCCCTAGCCTACT
Rev.of_WB235_6:15738820-15738988 Satlength=169 Nr of Repeats=8
RepeatLength=21 seed=GGCTGCCGAG Num.seqs=8 Similarity=0.916100
31 CTCGGCAGCCCCTAGCCTACC

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Consensus:

CtAGGCAGACCTAGCCTACC

>WB235_Fam_25_12_11 Nr. of seq. 11 Alignment length(with gaps) = 12
Alignment score = 0.746970
WB235_2:2151844-2151904 Satlength=61 Nr of Repeats=4 RepeatLength=11
seed=ACCGCAACGC Num.seqs=3 Similarity=1.000000
0 AC-CGCAACGCA
Rev.of_WB235_5:20605796-20606242 Satlength=447 Nr of Repeats=40
RepeatLength=11 seed=GTTGCGGTTG Num.seqs=39 Similarity=0.965976
8 AC-CGCAACGCA
Rev.of_WB235_3:1976102-1976245 Satlength=144 Nr of Repeats=11
RepeatLength=11 seed=GTCGCGTTGC Num.seqs=9 Similarity=0.885522
2 AC-CGCAACGCG
Rev.of_WB235_1:565592-565664 Satlength=73 Nr of Repeats=6 RepeatLength=12
seed=GCGTTGCGTG Num.seqs=6 Similarity=0.896296
4 ACGCGGCACGCA
WB235_1:2254186-2255835 Satlength=1650 Nr of Repeats=87 RepeatLength=12
seed=CACGCAACGC Num.seqs=80 Similarity=0.934001
6 ACGCAGCACGCA
Rev.of_WB235_1:11253589-11254333 Satlength=745 Nr of Repeats=60
RepeatLength=12 seed=CGTTGCGTGT Num.seqs=58 Similarity=0.901727
15 ACGCGACACGCA
WB235_3:12987113-12987245 Satlength=133 Nr of Repeats=7 RepeatLength=12
seed=CGCGACACGC Num.seqs=5 Similarity=0.822222
25 ACGCGACACGCA
Rev.of_WB235_4:4166741-4166830 Satlength=90 Nr of Repeats=7
RepeatLength=12 seed=GTTGCGTGTC Num.seqs=6 Similarity=0.962963
26 ACGCGACACGCA
Rev.of_WB235_4:4166744-4167306 Satlength=563 Nr of Repeats=46
RepeatLength=12 seed=GCGTGTCGCG Num.seqs=44 Similarity=0.893587
23 ACGCGACACGCA
WB235_5:17587204-17587343 Satlength=140 Nr of Repeats=10 RepeatLength=12
seed=ACGCGACACG Num.seqs=8 Similarity=0.972222
24 ACGCGACACGCA
WB235_5:17364710-17364818 Satlength=109 Nr of Repeats=9 RepeatLength=12
seed=CGCAACGCGA Num.seqs=9 Similarity=0.907407
8 ACGCGATACGCA

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Consensus:

ACgCGacACGCA

>WB235_Fam_26_26_10 Nr. of seq. 10 Alignment length(with gaps) = 27
Alignment score = 0.768999
WB235_2:5097197-5097899 Satlength=703 Nr of Repeats=27 RepeatLength=26
seed=TTAGACCATT Num.seqs=27 Similarity=0.928117
0 TTAGACCATTAGATGAATTTTCAAAG
Rev.of_WB235_4:4416113-4421995 Satlength=5883 Nr of Repeats=213
RepeatLength=26 seed=GTCTAACTTT Num.seqs=207 Similarity=0.933392
6 TTAGACCATTAGATGAATTTTCAAAG
WB235_4:13115382-13116006 Satlength=625 Nr of Repeats=24 RepeatLength=26
seed=ATTAGATGAA Num.seqs=24 Similarity=0.974173
7 TTAGACCATTAGATGAATTTTCAAAG

WB235_5:5073280-5076759 Satlength=3480 Nr of Repeats=131 RepeatLength=26
seed=AAAGTTAGAC Num.seqs=113 Similarity=0.928636
22 TTAGACCATTAGATGAATTTC-CAAAG
WB235_3:7594698-7597267 Satlength=2570 Nr of Repeats=98 RepeatLength=26
seed=ATTAGATGAA Num.seqs=93 Similarity=0.955479
7 TTAGACCATTAGATGAATTCC-CAAAG
Rev.of_WB235_6:15687867-15688727 Satlength=861 Nr of Repeats=33
RepeatLength=26 seed=AATTCATCTA Num.seqs=32 Similarity=0.950269
19 TTAGACCAGTAGATGAATTCC-CAAAG
WB235_6:11787527-11789550 Satlength=2024 Nr of Repeats=75 RepeatLength=26
seed=AAAGTTAGAC Num.seqs=72 Similarity=0.907026
22 TTAGACCATTAGATGAATTTA-TAAAG
Rev.of_WB235_6:15597064-15597272 Satlength=209 Nr of Repeats=8
RepeatLength=26 seed=GGTCTAACTT Num.seqs=8 Similarity=0.899267
7 TTAGACCGTCAGATCCATTTA-TAAAG
Rev.of_WB235_6:5913335-5915857 Satlength=2523 Nr of Repeats=97
RepeatLength=26 seed=TTCTAAATTT Num.seqs=97 Similarity=0.940589
6 TTAGAACGGTAGATGAATTTT-CAAAAT
Rev.of_WB235_4:13464747-13465805 Satlength=1059 Nr of Repeats=13
RepeatLength=27 seed=TTTTTAAAT Num.seqs=11 Similarity=0.892256
26 TTAGAACGGTATATGAATTTTAAAAAG

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Consensus:

TTAGAcCatTAGATGAATTtccAAAG

>WB235_Fam_27_21_10 Nr. of seq. 10 Alignment length(with gaps) = 23
Alignment score = 0.611433
WB235_6:920806-920909 Satlength=104 Nr of Repeats=5 RepeatLength=20
seed=ATGCACTGAC Num.seqs=3 Similarity=0.866667
0 AT-GCACTGACCAAAAATATG--
Rev.of_WB235_6:954503-954587 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=CAGTGCAATTC Num.seqs=4 Similarity=0.830688
8 AT-GCACTGACCAAAAGTTCTGA-
Rev.of_WB235_6:954523-954714 Satlength=192 Nr of Repeats=6
RepeatLength=21 seed=TCAGTGCAAT Num.seqs=4 Similarity=0.735450
9 AT-GCACTGACCAAACTTCTGA-
Rev.of_WB235_6:1016701-1016827 Satlength=127 Nr of Repeats=6
RepeatLength=21 seed=GTCAGTGCAAT Num.seqs=6 Similarity=0.944974
10 AT-GCACTGACCGAAACTATCA-
Rev.of_WB235_6:1022677-1022779 Satlength=103 Nr of Repeats=5
RepeatLength=20 seed=TTGGTCAGTG Num.seqs=3 Similarity=0.955556
13 AT-GCACTGACCAAGACTA-AA-
Rev.of_WB235_6:3693989-3694090 Satlength=102 Nr of Repeats=5
RepeatLength=20 seed=TTTGGTCAGT Num.seqs=4 Similarity=0.933333
14 AA-GCACTGACCAAA-ATA-GAA
WB235_6:863878-863962 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=ACTGACCAAA Num.seqs=4 Similarity=0.936508
25 AT-GCACTGACCAAAAATA-GAT
WB235_6:1296886-1296996 Satlength=111 Nr of Repeats=5 RepeatLength=22
seed=TCGCACTGAC Num.seqs=5 Similarity=0.915152
22 ATCGCACTGACCAAACTTA-GAA

Rev.of_WB235_6:703442-703568 Satlength=127 Nr of Repeats=5
RepeatLength=21 seed=GGTCAGTGCA Num.seqs=4 Similarity=0.904762
32 AT-GCACTGACCAAAATTG-GTA
Rev.of_WB235_6:1058514-1058619 Satlength=106 Nr of Repeats=4
RepeatLength=21 seed=GTCAGTGCAA Num.seqs=3 Similarity=0.661376
10 TT-GCACTGACCANNACTCTAA-

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Consensus:

ATGCACTGACCAAAanTatga

>WB235_Fam_28_163_9 Nr. of seq. 9 Alignment length(with gaps) = 170
Alignment score = 0.739924
WB235_1:976735-977538 Satlength=804 Nr of Repeats=5 RepeatLength=162
seed=ATCATATGAA Num.seqs=4 Similarity=0.781893
0 ATCATATGAAGCGATTCTTTTTCTTTTATAAACCTGTTTCAAGATTGGCAAACTACCAGAAAATAC-
TAAACAAATTAGGCTAGCATGAACGGAAGTA-TTTTTT-A-AAAATTGAT-AAAAATA-ATGAAAAGCTG-A-
TATTTTCAAAATTCAGAAATGACGGAAAA
Rev.of_WB235_2:2050346-2051160 Satlength=815 Nr of Repeats=5
RepeatLength=162 seed=AGTTTTATGA Num.seqs=3 Similarity=0.983539
36
ATCATATAGAGTCATTCTTTTTTATTTTCATAAACTCTTCAGCATAGTCAAAAATACCAGAAAATGC-
TAAACAAAGTATAATAGTTTGTACGGAAGTA-TTTTTT-A-AAAATGGAT-AAAAATATAT-AAAAGCTG-A-
TTTTTTCAAAAATTCAAAAGTATGGGAAA
WB235_1:10851626-10855375 Satlength=3750 Nr of Repeats=23
RepeatLength=163 seed=GCATAGTCAA Num.seqs=23 Similarity=0.935660
41
ATCATATGGAGTCATTCTTTTTTATCTCAAAAACTGTTTCAAGCATAGTCAAAAATACCAGCAAATAC-
CAAACAGAGTATATTAGCTTGTACGGAAGTA-TTTTTT-AGAAAATTGAT-AAAAATATAT-AAAAGCTG-A-
TTTTTTCAAAAATTCAAAAGTATGGGAAA
Rev.of_WB235_2:15186190-15187654 Satlength=1465 Nr of Repeats=9
RepeatLength=163 seed=AAATAAAAAA Num.seqs=8 Similarity=0.966696
190
ATCATATGGAGTCATTCTTTTTTATTTTCATAAACTGTTTCAAGCATAGTTAAAATTACCAGAATATGC-
CAATCAAAGTATATTAGCTTGTACGGAAGTATTTTTTT-A-AAAATTGAT-AAAAATATAT-AAAAGCTG-A-
TTTTTTCAAAAATTCAAAAGTATGGGAAA
WB235_3:10226211-10227863 Satlength=1653 Nr of Repeats=11
RepeatLength=164 seed=TATGGGAAAA Num.seqs=9 Similarity=0.973351
318
ATCATATGGAGTCATTCTTTTTTATTGCATAAACTGTTTCAAGTATAGTCAAAAATACCAGAATATGC-
CAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTT-A-AAAATTGATAAAAAATATAT-AAAAGCTG-A-
TTTTTTCAAAAATTCAAAAGTATGGGAAA
Rev.of_WB235_5:16330598-16333224 Satlength=2627 Nr of Repeats=16
RepeatLength=164 seed=AAAAAATCAG Num.seqs=12 Similarity=0.959226
303
ATCATATGGAGTCATTCTTTTTTATTTTCATAAAAATGTTTCAAGCATAGTCAAAAACACCAGAATATGC-
CAATCAAAGTATAATAGCTTGTACGGAAGTATTTTTTT-A-AAAATTGAT-AAAAATATAT-AAAATCTG-
ATTTTTTTCAAAAATTCAAAAGTCCTAGAAA
Rev.of_WB235_5:14586076-14591096 Satlength=5021 Nr of Repeats=31
RepeatLength=162 seed=TTCCGTACAA Num.seqs=29 Similarity=0.941779
95
ATCATATGAAGTCATTCTTTTTTATTTTATAGAACTGTTTCAAGCACAACCAAATATACCAGAAAATGC-

CAAAACAAAGTATGCTAGCTTGTACGGAAGTTAATTTTT-A-AAAATTCAG--AAATTAACCAGAAGCTA-T-TATTTTTCAAAAATTCAAAAGTAAGGGAAA

Rev.of_WB235_2:2361743-2363537 Satlength=1795 Nr of Repeats=9
RepeatLength=163 seed=TGAATTTTTG Num.seqs=7 Similarity=0.906387
150

ATCATATGAAGTCATTCTTTTTTATTTTATAAACTGTTTACGATAGTCAAATGTACCAGAAAATACTTAAAA
AAAG-GTGCTAGCTCGTACGGAAGTTTATTTTAA-AAAATGCAG--AATTTAACCAAAAGCTG-T-
TATTTTCAAAAATTCAAAAGTACCTCAA

WB235_4:2573920-2576033 Satlength=2114 Nr of Repeats=13 RepeatLength=164
seed=CTTTTTCTT Num.seqs=12 Similarity=0.979921
180

ATCATAAAAAAGTGCTTCTTTTTTCTTTTATAACACTGTTTAGCATAGTCAAATATACCAGAAAATAC-
CAAAACAAAGTATGCTATCTTGTACGAAAGATTATTTTA-A-AAAATTCAG--AAAATGCATCTAAAGCGGTT-
TTTTTTCAAAAATTCAAAAGTACCGGAAA

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Consensus:

ATCATATggAGTcATTCTTTTTTaTTTcATAAACTGTTTcAGcATAGtCAAAaATACCAGAAaATgCcAAaCA
AAGTATanTAGCTTGTACGGAAGTattTTTTTAAAAATtgAtaaAAATatAtAAAAGCTGaTtTTTTCAAAA
TTCAAAAGTAngggAAA

>WB235_Fam_29_42_9 Nr. of seq. 9 Alignment length(with gaps) = 42
Alignment score = 0.733686

WB235_1:961892-962564 Satlength=673 Nr of Repeats=16 RepeatLength=42
seed=CCGGAATTT Num.seqs=16 Similarity=0.888889

0 CCGGAATTTTCGAAAACCGGCAATTGCCGAAATTGCCGATTG

WB235_2:3572146-3572433 Satlength=288 Nr of Repeats=6 RepeatLength=42
seed=TTTGAAAACC Num.seqs=4 Similarity=0.851852

8 CCGGAATTTTGAAAACCGGCAATAGCCGAAATTGCCGAGTG

Rev.of_WB235_5:20315897-20316651 Satlength=755 Nr of Repeats=12
RepeatLength=42 seed=ATTGCCGTT Num.seqs=9 Similarity=0.803351

24 CCGAAAATTTTAAAAACCGGCAATTGCCGAAATTGCCGATTG

WB235_5:3816982-3817234 Satlength=253 Nr of Repeats=6 RepeatLength=42
seed=ACCGCAATT Num.seqs=6 Similarity=0.881481

15 CTGAAAATTTCCAAAACCGGCAATTGCCAAAATTGCCGATTG

WB235_2:14192423-14193096 Satlength=674 Nr of Repeats=16 RepeatLength=42
seed=AAAACCGGCA Num.seqs=10 Similarity=0.749832

12 CCGGNAATATTAAAAACCGGCAATTGCCGAAATTGCCGATTG

Rev.of_WB235_2:1630503-1630898 Satlength=396 Nr of Repeats=5
RepeatLength=42 seed=TTGCCGTTG Num.seqs=3 Similarity=0.809524

23 CAAAAAATTTTCGGCAACCGGCAATTGCCGAAGTTGCCGAACC

WB235_2:1635206-1635601 Satlength=396 Nr of Repeats=5 RepeatLength=42
seed=CAACCGGCAA Num.seqs=3 Similarity=0.809524

55 CAAAAAATTTTCGGCAACCGGCAATTGCCGAAGTTGCCGAACC

WB235_5:16191704-16191915 Satlength=212 Nr of Repeats=6 RepeatLength=42
seed=TTTCGGCAAC Num.seqs=4 Similarity=0.899471

49 CGAAAAATTTTCGGCAACCGGCAATTGCCGATGTTGCCGAACC

WB235_2:12577021-12577399 Satlength=379 Nr of Repeats=8 RepeatLength=42
seed=TTGCCGAACC Num.seqs=7 Similarity=0.797619

32 GTAAAAATTTTCGGCAACCGGCAATTGCCAAAGTTGCCGAACC

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Consensus:

CngaAAATTTcgaaAACCGGCAATTGCCgAAaTTGCCGAntg

>WB235_Fam_30_31_9 Nr. of seq. 9 Alignment length(with gaps) = 37
Alignment score = 0.708709
WB235_3:2110682-2111451 Satlength=770 Nr of Repeats=22 RepeatLength=31
seed=ATTTCCCGCC Num.seqs=14 Similarity=0.922486
0 ATTTCCCGCCAAAAATA---TTT---GAAAATTTGA
Rev.of_WB235_5:18169395-18171299 Satlength=1905 Nr of Repeats=61
RepeatLength=31 seed=GTCAATTTTT Num.seqs=48 Similarity=0.882004
20 ATTTCCCGCCAAAAATTG---ACT---GAAAATTTGA
WB235_5:19535226-19535475 Satlength=250 Nr of Repeats=6 RepeatLength=31
seed=AATTTCCCGC Num.seqs=5 Similarity=0.756250
30 ATTTCCCGCCAAAAATTG---ACT---GAAAATTTGA
Rev.of_WB235_5:19630875-19631274 Satlength=400 Nr of Repeats=12
RepeatLength=31 seed=GGCGGGAAAT Num.seqs=8 Similarity=0.930876
41 ATTTCCCGCCAAAAATTG---ACT---GAAAATTTGA
WB235_5:19689942-19690431 Satlength=490 Nr of Repeats=10 RepeatLength=31
seed=AAAATTTGAA Num.seqs=9 Similarity=0.942652
22 ATTTCCCGCCAAAAATTG---ACT---GAAAATTTGA
Rev.of_WB235_5:19376610-19376889 Satlength=280 Nr of Repeats=9
RepeatLength=31 seed=CGGGAAATTC Num.seqs=7 Similarity=0.774706
39 ATTTCCCGCCAAAAATTA---ACT---GAAAATTTGA
Rev.of_WB235_5:19615691-19616051 Satlength=361 Nr of Repeats=8
RepeatLength=31 seed=TTCAAATTTT Num.seqs=7 Similarity=0.819764
32 AATTTCCCGCCAAAAATTG---ACT---GAAAATTTGA
WB235_5:19863556-19864754 Satlength=1199 Nr of Repeats=28 RepeatLength=31
seed=TTCCCGCCTA Num.seqs=17 Similarity=0.854243
2 ATTTCCCGCCTAAACT---ACTC---GAAAATTCAA
Rev.of_WB235_5:18666434-18666663 Satlength=230 Nr of Repeats=6
RepeatLength=35 seed=GGAAATTCAA Num.seqs=4 Similarity=0.776235
6 ATTTTCCGCCAAAAATATTTTCT-CCGAAAATTTGA

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Consensus:

ATTTCCCGCCAAAAATgACTGAAAATTTGA

>WB235_Fam_31_26_9 Nr. of seq. 9 Alignment length(with gaps) = 26
Alignment score = 0.798789
WB235_4:11610541-11615517 Satlength=4977 Nr of Repeats=199
RepeatLength=25 seed=CATTACGGCA Num.seqs=198 Similarity=0.948255
0 CATTACGGCAGATTCTA-TAAATTGG
Rev.of_WB235_4:14209284-14209609 Satlength=326 Nr of Repeats=13
RepeatLength=25 seed=TAATGCCAAT Num.seqs=13 Similarity=0.948034
5 CATTACGGCAGATTCTA-TAAATTGG
Rev.of_WB235_6:11441051-11442751 Satlength=1701 Nr of Repeats=68
RepeatLength=25 seed=CCGTAATGCC Num.seqs=68 Similarity=0.907381
8 CATTACGGCAGATTCTA-TAAATTGG

Rev.of_WB235_1:4540371-4544820 Satlength=4450 Nr of Repeats=169
RepeatLength=26 seed=AAATCCGCCG Num.seqs=166 Similarity=0.908932
15 CATTGCGGCGGATTTTAGAAAAATGG
Rev.of_WB235_6:1644418-1644678 Satlength=261 Nr of Repeats=10
RepeatLength=26 seed=GCCGCAATGC Num.seqs=10 Similarity=0.971510
35 CATTGCGGCGGATTTTAGAAAAATGG
WB235_6:11442777-11443790 Satlength=1014 Nr of Repeats=39 RepeatLength=26
seed=CGGCGGATTT Num.seqs=38 Similarity=0.921509
31 CATTGCGGCGGATTTTAGAAAAATGG
WB235_1:10953026-10953491 Satlength=466 Nr of Repeats=4 RepeatLength=26
seed=TTTTTGAAAA Num.seqs=3 Similarity=0.931624
38 CATTGCGGCGGATTTTGAAAAATGG
WB235_4:12730503-12732683 Satlength=2181 Nr of Repeats=84 RepeatLength=26
seed=CATTGCGGCG Num.seqs=80 Similarity=0.917965
26 CATTGCGGCGGATTTTCAGAAAAATGG
WB235_6:12607668-12607975 Satlength=308 Nr of Repeats=5 RepeatLength=26
seed=AAAAATGGCA Num.seqs=4 Similarity=0.897436
44 CATTGCGGCGGATTTTCAGAAAAATGG

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Consensus:

CATTgCGGcGgATTttAgaAAAaTGG

>WB235_Fam_32_18_9 Nr. of seq. 9 Alignment length(with gaps) = 23
Alignment score = 0.628019
WB235_1:11485772-11485879 Satlength=108 Nr of Repeats=5 RepeatLength=19
seed=TCAAAAATCA Num.seqs=4 Similarity=0.873611
21 CA--TC-AAAAATCAATAA-TTT
WB235_1:11383715-11384049 Satlength=335 Nr of Repeats=14 RepeatLength=20
seed=AAAAATCAAT Num.seqs=11 Similarity=0.883636
24 CA--TCGAAAAATCAATAA-TTT
WB235_1:11485735-11486997 Satlength=1263 Nr of Repeats=20 RepeatLength=19
seed=AAAAATCGAT Num.seqs=12 Similarity=0.725830
23 CN--TC-AAAAATCGATAA-TTT
WB235_2:2623068-2623182 Satlength=115 Nr of Repeats=6 RepeatLength=19
seed=AAAAATCGATA Num.seqs=6 Similarity=0.601058
24 CA--TC-GAAAATCGATAA-TTT
WB235_1:11532642-11533117 Satlength=476 Nr of Repeats=17 RepeatLength=19
seed=TTTCACAAAA Num.seqs=12 Similarity=0.943647
35 CA---C-AAAAATCAATAATTTT
WB235_1:11531919-11534041 Satlength=2123 Nr of Repeats=45 RepeatLength=19
seed=AAAAATCGATA Num.seqs=29 Similarity=0.730706
42 CA---N-AAAAATCGATAATTTT
WB235_4:977829-978532 Satlength=704 Nr of Repeats=35 RepeatLength=19
seed=CAATAATTTT Num.seqs=27 Similarity=0.905233
28 CC-C-A-AAAAATCAATAA-TTT
Rev.of_WB235_1:11384374-11386353 Satlength=1980 Nr of Repeats=95
RepeatLength=20 seed=ATTGATTTTT Num.seqs=91 Similarity=0.879707
32 CCTC-A-AAAAATCAATAA-TTT
Rev.of_WB235_1:2364706-2365240 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

>WB235_Fam_33_18_9 Nr. of seq. 9 Alignment length(with gaps) = 19

Alignment score = 0.838207

WB235_5:18881944-18883813 Satlength=1870 Nr of Repeats=74 RepeatLength=17

seed=ATTAGCAGCG Num.seqs=48 Similarity=0.873325

0 -ATTAGCAGCGCCCCAAA-

WB235_5:18966918-18967045 Satlength=128 Nr of Repeats=5 RepeatLength=18

seed=GCAGCGCCCA Num.seqs=3 Similarity=0.950617

4 -ATTAGCAGCGCCCCAAA

Rev.of_WB235_5:18970132-18970454 Satlength=323 Nr of Repeats=18

RepeatLength=18 seed=TGCTAATTTT Num.seqs=16 Similarity=0.939506

7 -ATTAGCAGCGCCCCAAA

Rev.of_WB235_5:18979816-18980485 Satlength=670 Nr of Repeats=37

RepeatLength=18 seed=GCGCTGCTAA Num.seqs=25 Similarity=0.926420

11 -ATTAGCAGCGCCCCAAA

WB235_5:18987130-18987201 Satlength=72 Nr of Repeats=4 RepeatLength=18

seed=TAGCAGCGCC Num.seqs=3 Similarity=0.901235

2 -ATTAGCAGCGCCCAAGAA

WB235_5:18886295-18887294 Satlength=1000 Nr of Repeats=12 RepeatLength=18

seed=AATTAGCAGC Num.seqs=10 Similarity=0.960494

0 AATTAGCAGCGACCAAAA-

WB235_5:19106243-19106368 Satlength=126 Nr of Repeats=6 RepeatLength=18

seed=ATTAGCAGCG Num.seqs=4 Similarity=1.000000

1 AATTAGCAGCGACCAAAA-

Rev.of_WB235_5:19193880-19195207 Satlength=1328 Nr of Repeats=74

RepeatLength=18 seed=GCTGCTAATT Num.seqs=61 Similarity=0.900627

10 AATTAGCAGCGACCAAAA-

WB235_5:18964514-18964623 Satlength=110 Nr of Repeats=6 RepeatLength=18

seed=AGCAGCGCCC Num.seqs=5 Similarity=0.896296

3 -AATAGCAGCGCCCCAAA

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Consensus:

ATTAGCAGCGcCCAAAAa

>WB235_Fam_34_12_9 Nr. of seq. 9 Alignment length(with gaps) = 15

Alignment score = 0.680247

WB235_6:2263547-2263756 Satlength=210 Nr of Repeats=16 RepeatLength=11

seed=CCATACCTAT Num.seqs=13 Similarity=1.000000

0 -CC-ATACCT-ATA-

WB235_1:12620508-12620574 Satlength=67 Nr of Repeats=5 RepeatLength=12

seed=TACCTATACC Num.seqs=4 Similarity=0.944444

3 -CT-ATACCT-ATAC

WB235_1:13689387-13689549 Satlength=163 Nr of Repeats=13 RepeatLength=12

seed=TATACCTATA Num.seqs=10 Similarity=0.955556

7 -CT-ATACCT-ATAC

Rev.of_WB235_1:13689822-13689960 Satlength=139 Nr of Repeats=11
RepeatLength=12 seed=ATAGGTATAG Num.seqs=10 Similarity=0.955556
4 -CT-ATACCT-ATAC
Rev.of_WB235_2:3490327-3491001 Satlength=675 Nr of Repeats=54
RepeatLength=12 seed=TAGGTATAGG Num.seqs=45 Similarity=0.881481
3 -CT-ATACCT-ATAC
WB235_2:12353539-12353707 Satlength=169 Nr of Repeats=14 RepeatLength=12
seed=CCTATACCTA Num.seqs=14 Similarity=0.968254
5 -CT-ATACCT-ATAC
WB235_4:13222198-13222342 Satlength=145 Nr of Repeats=12 RepeatLength=12
seed=TATACCTATA Num.seqs=12 Similarity=0.944444
7 -CT-ATACCT-ATAC
WB235_2:3048248-3048472 Satlength=225 Nr of Repeats=15 RepeatLength=14
seed=CTTATACCTT Num.seqs=14 Similarity=0.947671
1 CCTTATACCTTATA-
WB235_3:1334409-1335297 Satlength=889 Nr of Repeats=40 RepeatLength=14
seed=ATACCTAATA Num.seqs=28 Similarity=0.877047
4 CCTAATACCTAATA-

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Consensus:

CTATACCTATAC

>WB235_Fam_35_14_9 Nr. of seq. 9 Alignment length(with gaps) = 14
Alignment score = 0.904762
WB235_1:10291633-10291724 Satlength=92 Nr of Repeats=6 RepeatLength=14
seed=GCTATACGCT Num.seqs=5 Similarity=1.000000
0 GCTATACGCTATAC
WB235_2:1455578-1455634 Satlength=57 Nr of Repeats=4 RepeatLength=14
seed=TACGCTATAC Num.seqs=4 Similarity=0.952381
4 GCTATACGCTATAC
WB235_2:6185280-6186470 Satlength=1191 Nr of Repeats=85 RepeatLength=14
seed=ACGCTATACG Num.seqs=85 Similarity=1.000000
5 GCTATACGCTATAC
Rev.of_WB235_4:14209637-14209721 Satlength=85 Nr of Repeats=6
RepeatLength=14 seed=AGCGTATAGC Num.seqs=6 Similarity=1.000000
3 GCTATACGCTATAC
Rev.of_WB235_6:316974-317093 Satlength=120 Nr of Repeats=8
RepeatLength=14 seed=ATAGCGTATA Num.seqs=7 Similarity=0.891156
5 GCTATACGCTATAC
WB235_6:11440976-11441039 Satlength=64 Nr of Repeats=4 RepeatLength=14
seed=CTATACGCTA Num.seqs=3 Similarity=0.936508
1 GCTATACGCTATAC
WB235_5:12510458-12510577 Satlength=120 Nr of Repeats=8 RepeatLength=14
seed=CTATACGCTA Num.seqs=7 Similarity=0.891156
1 GCTATACGCTATGC
Rev.of_WB235_6:16886473-16886932 Satlength=460 Nr of Repeats=20
RepeatLength=14 seed=ATAGCGCATA Num.seqs=18 Similarity=0.808279
5 GCTATGCGCTATGC
WB235_4:14208040-14209239 Satlength=1200 Nr of Repeats=70 RepeatLength=14
seed=GCTATGCGCT Num.seqs=52 Similarity=0.786869
0 GCTATGCGCTGTAC

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Consensus:

GCTATaCGCTATaC

>WB235_Fam_36_12_9 Nr. of seq. 9 Alignment length(with gaps) = 12
Alignment score = 0.876543
WB235_1:765668-765992 Satlength=325 Nr of Repeats=27 RepeatLength=12
seed=TCTAGGTCTA Num.seqs=27 Similarity=0.944286
0 TCTAGGTCTAGG
WB235_1:991239-991341 Satlength=103 Nr of Repeats=8 RepeatLength=12
seed=GGTCTAGGTC Num.seqs=7 Similarity=0.936508
4 TCTAGGTCTAGG
WB235_1:11484951-11485029 Satlength=79 Nr of Repeats=6 RepeatLength=12
seed=TAGGTCTAGG Num.seqs=5 Similarity=1.000000
2 TCTAGGTCTAGG
Rev.of_WB235_2:878150-878348 Satlength=199 Nr of Repeats=15
RepeatLength=12 seed=ACCTAGACCT Num.seqs=12 Similarity=0.858586
1 TCTAGGTCTAGG
WB235_1:942750-943044 Satlength=295 Nr of Repeats=24 RepeatLength=12
seed=CTAAGTCTAA Num.seqs=23 Similarity=1.000000
1 TCTAAGTCTAAG
WB235_1:942557-943381 Satlength=825 Nr of Repeats=46 RepeatLength=12
seed=TAAGCCTAAG Num.seqs=40 Similarity=0.768310
2 TCTAAGTCTAAG
WB235_1:3258597-3259299 Satlength=703 Nr of Repeats=58 RepeatLength=12
seed=CTAAGTCTAA Num.seqs=57 Similarity=0.888053
1 TCTAAGTCTAAG
Rev.of_WB235_3:12196315-12196495 Satlength=181 Nr of Repeats=14
RepeatLength=12 seed=CTTAGACTTA Num.seqs=12 Similarity=0.929293
6 TCTAAGTCTAAG
WB235_5:15009961-15010009 Satlength=49 Nr of Repeats=4 RepeatLength=12
seed=TCTAAGTCTA Num.seqs=4 Similarity=0.944444
6 TCTAAGTCTAAG

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Consensus:

TCTAaGTCTAaG

>WB235_Fam_37_21_8 Nr. of seq. 8 Alignment length(with gaps) = 23
Alignment score = 0.616977
WB235_2:463793-464368 Satlength=576 Nr of Repeats=9 RepeatLength=20
seed=CAATTTTTGA Num.seqs=7 Similarity=0.942857
17 TT-TTTGAGTTAAAAAT-T-CAA
Rev.of_WB235_2:13318641-13320189 Satlength=1549 Nr of Repeats=49
RepeatLength=20 seed=TTTGAATTTT Num.seqs=35 Similarity=0.825770
21 AT-TTTGACTTAAAAAT-T-CAA
Rev.of_WB235_3:1934627-1936118 Satlength=1492 Nr of Repeats=61
RepeatLength=21 seed=TGGAAATTTT Num.seqs=49 Similarity=0.853795
19 TT-TTTGGGTAAAAATT-TCCAA

WB235_3:1560064-1560620 Satlength=557 Nr of Repeats=7 RepeatLength=21
seed=CCTAAAAATT Num.seqs=5 Similarity=0.695238
27 TT-TTNACCTAAAAAT-TNCAA
WB235_3:1536002-1536441 Satlength=440 Nr of Repeats=21 RepeatLength=20
seed=TTTCACTAAA Num.seqs=20 Similarity=0.889265
22 AA-TTTCAC-TAAAAATCT-CAA
Rev.of_WB235_4:16425000-16425220 Satlength=221 Nr of Repeats=8
RepeatLength=20 seed=TTTTAGTGAA Num.seqs=5 Similarity=1.000000
33 AT-TTTCAC-TAAAAATCT-CAA
WB235_5:20494724-20495104 Satlength=381 Nr of Repeats=15 RepeatLength=20
seed=TTTCACTAAA Num.seqs=11 Similarity=0.741991
22 AT-TTTCAC-TAAAAATTT-CAA
Rev.of_WB235_2:2897150-2899742 Satlength=2593 Nr of Repeats=100
RepeatLength=21 seed=CCAAAAATTG Num.seqs=87 Similarity=0.735669
26 TTTTGGAC-TAAAAATCT-CAA

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Consensus:

CAAaTTTgAcnTAAAAATnT

>WB235_Fam_38_18_8 Nr. of seq. 8 Alignment length(with gaps) = 19
Alignment score = 0.681391
WB235_4:640232-640313 Satlength=82 Nr of Repeats=4 RepeatLength=15
seed=TAAGCCTAAG Num.seqs=3 Similarity=1.000000
0 TAAGCCTA-AGCC-CA-C-
WB235_5:1848647-1848932 Satlength=286 Nr of Repeats=14 RepeatLength=17
seed=TAAGCCTAAG Num.seqs=9 Similarity=0.930283
0 TAAGCCTA-AG-CTTAGCT
Rev.of_WB235_3:635824-635934 Satlength=111 Nr of Repeats=6
RepeatLength=18 seed=TAGGCTTAGG Num.seqs=4 Similarity=0.527778
8 TAAGCCTACAG-CTAAGCC
WB235_2:368393-368601 Satlength=209 Nr of Repeats=10 RepeatLength=18
seed=TAAGCCTAAG Num.seqs=6 Similarity=0.619753
12 TAAGCCTA-AGTCTAAGCC
WB235_2:12942997-12943139 Satlength=143 Nr of Repeats=5 RepeatLength=18
seed=CCTAAGCCTA Num.seqs=3 Similarity=0.660819
16 TAAGCCTA-AGNCTAAACC
WB235_5:1047118-1047214 Satlength=97 Nr of Repeats=6 RepeatLength=18
seed=AAGCCTAAGC Num.seqs=4 Similarity=0.691358
19 TAAGCCTA-AGCCTAAACC
WB235_5:1661122-1661200 Satlength=79 Nr of Repeats=5 RepeatLength=18
seed=GCCTAAGCCT Num.seqs=3 Similarity=0.614035
21 TANGCCTA-AGCCTAAGCA
Rev.of_WB235_2:3459359-3459467 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

>WB235_Fam_39_10_8 Nr. of seq. 8 Alignment length(with gaps) = 11
Alignment score = 0.758117
WB235_2:4207582-4207842 Satlength=261 Nr of Repeats=25 RepeatLength=10
seed=GCGTTAGCAG Num.seqs=24 Similarity=0.977778
0 GCGTTAGCAG-
WB235_5:842648-842948 Satlength=301 Nr of Repeats=24 RepeatLength=10
seed=GGCGTCAGCG Num.seqs=18 Similarity=0.893682
9 GCGTCAGCGG-
WB235_5:1850026-1850346 Satlength=321 Nr of Repeats=23 RepeatLength=10
seed=GGGCGTCAGC Num.seqs=15 Similarity=0.949206
18 GCGTCAGCGG-
Rev.of_WB235_2:13790809-13791073 Satlength=265 Nr of Repeats=22
RepeatLength=10 seed=CCGCTACCGC Num.seqs=18 Similarity=1.000000
0 GCGGTAGCGG-
Rev.of_WB235_3:13032223-13032864 Satlength=642 Nr of Repeats=39
RepeatLength=10 seed=TACCGCCCGC Num.seqs=24 Similarity=0.944444
6 GCGGTAGCGG-
Rev.of_WB235_5:2777566-2778653 Satlength=1088 Nr of Repeats=65
RepeatLength=10 seed=TACCGCCCGC Num.seqs=59 Similarity=0.973972
6 GCGGTAGCGG-
WB235_5:3145392-3145472 Satlength=81 Nr of Repeats=6 RepeatLength=10
seed=GCGGGCGGTA Num.seqs=4 Similarity=0.933333
6 GCGGTAGCGG-
Rev.of_WB235_2:13795316-13795382 Satlength=67 Nr of Repeats=5
RepeatLength=11 seed=CCGCTACCGC Num.seqs=4 Similarity=0.919192
0 GCGGTAGCGGT

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Consensus:

GCGgtAGCGG

>WB235_Fam_40_166_7 Nr. of seq. 7 Alignment length(with gaps) = 173
Alignment score = 0.741077
WB235_6:15929033-15929676 Satlength=644 Nr of Repeats=4 RepeatLength=158
seed=TATCAATTTT Num.seqs=3 Similarity=0.924051
0 TATCAATTTTCAGACGCGCTACGGGGTTTTTGTCTTGAATTCCAATTTCAAC-----
AGGCGCAAAAAACAAAAATAAAATTTTTGGATT-TTTGGAAAAGT-TTTT-
ATAGATTTCTATTCTAGATTGTTTAA-AAATATTATTGGTACGTTTTTGTACCAANA
WB235_6:15929110-15929778 Satlength=669 Nr of Repeats=4 RepeatLength=158
seed=CAAAAATAAA Num.seqs=3 Similarity=0.935302
66 TATCAATTTTCAGACGCGCTACGGGGTTTTTGTCTTGAATTCCAATTTCAAC-----
AGGCGCAAAAAACAAAAATAAAATTTTTGGATT-TTTGGAAAAGT-TTTT-
ATAGATTTGTATTCTAGATTGTTTAA-AAATATTATTGGTACGTTTTTGTACCAANA
Rev.of_WB235_3:2077634-2082512 Satlength=4879 Nr of Repeats=29
RepeatLength=168 seed=TTTATTTTTG Num.seqs=28 Similarity=0.979634
86 TATCCATTTTCAGACGCGCTACAGGGGTTTTTGTCTTGAATTCCAATTTCAACAGGTA-
TATGTAGGCACAAAAACAAAAATAAACATTTTGGAAAT-TCTGGA-AA-
TGTTTTGATAGATTTGGATTCTAGATTGTTTAA-AAATATTATTGGTAAGTTTTTGTACCTAGA
WB235_4:15225095-15227378 Satlength=2284 Nr of Repeats=12
RepeatLength=168 seed=AAAAACAAAA Num.seqs=9 Similarity=0.953704
239 TATCAATTTTCAGATGCGCTAGAGGGTTTTTGTCTTGAATTCCAATTTCAACAGATA-
TATACAGGCACAAAAACAAAAATAAAATTTTGGAAATGTTGGGAGAA-T-TTTT-
ATAGATTTGGATTCTAGATT-TTAAACAAATATTTTTGGTAAGTTTCTGGACCTAGA

WB235_4:15225869-15227795 Satlength=1927 Nr of Repeats=11
RepeatLength=168 seed=AACAAAAATA Num.seqs=9 Similarity=0.953704
242 TATCAATTTTCAGATGCGCTAGAGGGGTTTTGTCTTGAATTCCAATTTCAACAGATA-
TATACAGGCACAAAAAACAAAAATAAAATTTTGGGAATGTTGGGAGAA-T-TTTT-
ATAGATTTGGATTCTAGATT-TTTAACAAATATTTTTGGTAAGTTTCTGGACCTAGA
Rev.of_WB235_4:12931758-12932786 Satlength=1029 Nr of Repeats=5
RepeatLength=168 seed=TTTTTAAAAA Num.seqs=3 Similarity=0.984127
141 AAGTAAATTTAAGCCGCGCTAGAGAGGTTTTGTGTGCGAGTTCCAATTTTCACAGGTACTA-
GTAGGCTCAAAAAACAAAAATAAAATTATCGAAT-TCCGGA-AA-
TGTTTTGATAGATTTGGATTCTAGATTTTTTAA-AAATATTATTGGTAAGTTTGTGGGCCAGGA
WB235_4:15511605-15513283 Satlength=1679 Nr of Repeats=10
RepeatLength=168 seed=GAATTCGGGA Num.seqs=8 Similarity=0.944161
261 AAGTAACTTAAAGCCGCGCTAGGAAGGTTTTGTGTGCGAGTTACAATTTTCACAGGTACTA-
GTAGGCGCAAAAAACAAAAATAAAATTATGGAAT-TCCGGA-AA-
TGTTTTGATAGATTTGGATTCTAGATTTTTTAA-AAATATTATAGGTGAGTTTTTTGGGACAGGA

Consensus:

>WB235_Fam_41_95_7 Nr. of seq. 7 Alignment length(with gaps) = 96
Alignment score = 0.868386

0 AGGGCCGCAGGCCCGAATAGTCTTGGAACCT--GGGCTGGCTATAATCCTATTCCAAGCAGGT-
TGTTATTCACTCAAGCCTATCAACCAAGTTTG

RepeatLength=95 seed=TTCTGGGCCTG Num.seqs=6 Similarity=0.981287

WB235_3:3385070-3386871 Satlength=1802 Nr of Repeats=19 RepeatLength=95
seed=TAATCTATT Num.segs=13 Similarity=0.948178

Rev.of WB235 2:13385641-13386400 Satlength=760 Nr of Repeats=8

108 AGGGCCGCAGGCCCCGAATACTCATGGAAACTAAGGGCCAGCTTTAATCCTATTCCAAGCAGAT-
TGTTATTTCGCTCAAGCCTACCAACCAGGTTTG

RepeatLength=96 seed=GGCCTGCGGC Num.seqs=6 Similarity=0.968518

WB235_3:1119657-1120064 Satlength=408 Nr of Repeats=4 RepeatLength=96
seed=GAGGGCCGCA Num.segs=3 Similarity=0.949074

Rev.of_WB235_5:5415371-5416162 Satlength=792 Nr of Repeats=8
RepeatLength=96 seed=TCTGCTTAGA Num.seqs=7 Similarity=0.949735
254
AGGGCCGCAGGCCCCGAACACTCTTGAAACTATGGGCTGGCTTTGATCCTATTCTAAGCAGATATGTTATTCA
CTCAAGCCTAATAACCAGGTTTG

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Consensus:

AGGGCCGCAGGCCCCGAAtACTCtTGAAACTatGGGctgGCTTTaATCCTATTCCaAGCAGATTGTTATTCaC
TCAAGCCTAnnAACCAGGTTtG

>WB235_Fam_42_94_7 Nr. of seq. 7 Alignment length(with gaps) = 94
Alignment score = 0.948666
WB235_1:4281487-4294537 Satlength=13051 Nr of Repeats=139 RepeatLength=94
seed=TCAAAATCTT Num.seqs=123 Similarity=0.961982
0

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAATCAATGGGAAAATCATC
AATTCTGAAGGCAGTAATTC

Rev.of_WB235_3:7405401-7443206 Satlength=37806 Nr of Repeats=414
RepeatLength=94 seed=CAATATTTAG Num.seqs=380 Similarity=0.958602
27

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAATCAATGGGAAAATCATC
AATTCTGGAGGCAGTAATTC

Rev.of_WB235_3:7448277-7452238 Satlength=3962 Nr of Repeats=40
RepeatLength=94 seed=ACCCAATATT Num.seqs=39 Similarity=0.958308
30

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTATGTAGACAAATCAATGGGAAAATCATC
AATTCTGGAGGCAGTAATTC

WB235_1:10913365-10914502 Satlength=1138 Nr of Repeats=5 RepeatLength=94
seed=TGTAGACAAA Num.seqs=4 Similarity=0.971631
46

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGTCCTTTGTAGACAAATCAATGGGAGAATCATC
AATTCTGAAGGCAGTAATTC

Rev.of_WB235_4:1543828-1544203 Satlength=376 Nr of Repeats=4
RepeatLength=94 seed=TCCCATTGAT Num.seqs=3 Similarity=0.924350
65

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTTTGTAGACAAATCAATGGGAAAATTGTC
CATTTCTGAAGGCAGTAATTC

WB235_6:311553-312211 Satlength=659 Nr of Repeats=7 RepeatLength=94
seed=GCAGTAATTC Num.seqs=7 Similarity=0.944613
84

TCAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTTTGTAGACAAATCAATGAGAAAATTGTC
AATTCTGAAGGCAGTAATTC

Rev.of_WB235_6:6826365-6830125 Satlength=3761 Nr of Repeats=40
RepeatLength=94 seed=TGCCTTCAGA Num.seqs=40 Similarity=0.978523
87

TCAAAATCTTCTGTTCTCTAAATATTGAGTGCTTTTCGATGCCCTATGTAGACAAATCAATGGGAAAATTGTC
AATTCTGAAGGCAGTAATTC

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Consensus:

TCAAAAATCTTCTGTTCTCTAAATATTGGGTGCTTTTCGATGCCCTaTGTAGACAAATCAATGGGAAAAATcaTC
AATTTCTGaAGGCAGTAATTC

>WB235_Fam_43_19_7 Nr. of seq. 7 Alignment length(with gaps) = 23
Alignment score = 0.690821
WB235_3:9863897-9863967 Satlength=71 Nr of Repeats=4 RepeatLength=19
seed=TGGTTGAGGC Num.seqs=3 Similarity=0.906433
0 -TGGTTGAGG--CTCTAG-ATTT
Rev.of_WB235_4:180606-180739 Satlength=134 Nr of Repeats=7
RepeatLength=19 seed=CCTCAACCAA Num.seqs=7 Similarity=0.826232
9 -TGGTTGAGG--CTCTNG-ATTT
WB235_4:119859-120107 Satlength=249 Nr of Repeats=13 RepeatLength=19
seed=TGGTTGAGGC Num.seqs=12 Similarity=0.868155
0 -TGGTTGAGG--CTCTCT-ATTT
WB235_3:9869882-9869977 Satlength=96 Nr of Repeats=5 RepeatLength=19
seed=ATTTTGGTTG Num.seqs=5 Similarity=0.818333
15 -TGGTTGAGG--CTCAGG-ATTT
Rev.of_WB235_4:195511-196615 Satlength=1105 Nr of Repeats=53
RepeatLength=20 seed=CTCAACCAAA Num.seqs=32 Similarity=0.882930
27 -TGGTTGAGG--CTCAGGATTTT
WB235_4:124390-125403 Satlength=1014 Nr of Repeats=21 RepeatLength=22
seed=TTGGTTGAGG Num.seqs=16 Similarity=0.915152
0 TTGGTTGAGGCTCTCTGG-ATTT
WB235_4:236164-236448 Satlength=285 Nr of Repeats=12 RepeatLength=22
seed=TGAGGCTCTC Num.seqs=11 Similarity=0.886501
5 TTGGTTGAGGCTCTCTGG-ATTT

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Consensus:

TGGTTGAGGCTCtgATTT

>WB235_Fam_44_226_6 Nr. of seq. 6 Alignment length(with gaps) = 227
Alignment score = 0.831816
WB235_5:9428459-9435308 Satlength=6850 Nr of Repeats=32 RepeatLength=214
seed=GTAACGCTC Num.seqs=31 Similarity=0.958289
0
GTAACGCTCAAAGCTTCTGGCACCTATTGGGATGTTGTTGGTAAATTCTGAAAAAGCTTGAATTTGCAACA
AAGTTTCTGAAAGAAATTTTC-
AAAAAAGTTGATTTGAAGTGATTTGGGAATTTTCAAAGTTTCATAAATTTACCTA-
TTTTGCCTATAAATGGTCGTTTTTCATTTAATAATAAAATACGCAC--AAAGGTA---CTG--TAGGT----
TTTCT
Rev.of_WB235_1:4280022-4281181 Satlength=1160 Nr of Repeats=6
RepeatLength=226 seed=ACAAGAAGCT Num.seqs=5 Similarity=0.915789
22
GTAAC TACGTGAAGCTTCTTGTACCTACTGGAATATTGTTAATATATTCTAAAAGAGCTTAAAATTTACTACA
AAGTTTCTGAAAGACATTTTCGCAAAAAAATTACTTTGAAGAGATTTATGAATTTTCAAATTACGAAAATCCC
TCTA-
TTTTGCCTATAAGTGGTAGTTTTTCATTAAATAATAAAATACGCACTAAAAGGTAGGGCTGAAAATGTACTATT
TCT
WB235_5:6072983-6091328 Satlength=18346 Nr of Repeats=79 RepeatLength=226
seed=CTTTGAAGAG Num.seqs=52 Similarity=0.955813
104

GTAAC TACGTGAAGCTTCTTGTACCTACTGAAATATTGTTAATATATTCTGAAAGAGCTTAAAATTTACTACA
AAGTTTCTGAAAGACATTTTC-

AAAAAAAAATTACTTTGAAGAGATTTATGAATTTTCAAAGTTTGAAAAATCCACCTATTTTTGCCTATTAATGG
TAGTTTTCATTAATAATAAAAATACGCACTAAAAGGTAGGGCTGAAAATGTACTATTTCT

WB235_6:11888285-11889641 Satlength=1357 Nr of Repeats=6 RepeatLength=226
seed=TGTACTATTT Num.seqs=6 Similarity=0.964602
214

GTAAC TACGTGAAGCTTCTTGTACCTACTGAAATATTGTTGGTATATTCTAAAAGAGCTTAAAATTTACTACA
AAGTTTCTAAAAGACATTTTC-

AAAAAAGTTACTTTGAAGAGATTTATGAATTTTCAAAGTTACGAAAATTCGTCTATTTTTGCCTATAAATGG
TAGTTTTCATTAATAATAAAAATACGCATTATAAGGTAGGGCTGAAAATGTACTATTTCT

WB235_6:5045129-5051107 Satlength=5979 Nr of Repeats=23 RepeatLength=226
seed=GAAAATTCAT Num.seqs=17 Similarity=0.593389
136

GTAAC TACGTGAAGCTTCTTGTACCTACTGAAATATTGTTAATATATTCAGAAAGANCTTAAAANTTACTACG
AAGTTTCTGAAAGACATTTTC-

TAAAAAAGTTACTTTGAAGAGATTTATGAATTTTCAAANTTTNGAAAATTCATCTATTTTTGTCTATAAATGG
TAGTTTTCATTTAATAATAAAAATACGCACTAAAAGGTAGGGCTGAAAATGAACTATTTCT

Rev.of_WB235_6:5045783-5053744 Satlength=7962 Nr of Repeats=32
RepeatLength=226 seed=ATGAATTTTC Num.seqs=26 Similarity=0.592515
146

GTAAC TACGTGAAGCTTCTTGTACCTACTGAAATATTGTTAATATATTCAGAAAGANCTTAAAATTTACTACG
AAGTTTCTGAAAGACATTTTC-

TAAAAAAGTTACTTTGAAGAGATTTATGAATTTTCAAANTTTNGAAAATTCATCTATTTTTGTTTATAAATGG
TAGTTTTCATTTAATAATAAAAATACNCACTAAAAGGTAGGGCTGAAAATGTACTATTTCT

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Consensus :

GTAAC TACGTGAAGCTTCTTGTACCTACTGaaATATTGTTaaTATATTCTgAAAGAgCTTAAAATTTACTACa
AAGTTTCTGAAAGACATTTTcaAAAAAAGTTACTTTGAAGAGATTTATGAATTTTCAAAGTTTcgAAAATtCat
CTatTTTGTcCTATAAATGGTAGTTTTCATTaATAATAAAAATACGCACtAAAAGGTAGGGCTGAAAATGTAC
TATTTCT

>WB235_Fam_45_33_6 Nr. of seq. 6 Alignment length(with gaps) = 33
Alignment score = 0.649832

WB235_1:12612870-12613263 Satlength=394 Nr of Repeats=5 RepeatLength=32
seed=GCTGATTGGT Num.seqs=3 Similarity=0.861111

0 GCTGATTGGTTCA-AAAGTGGGCGTGGCTAATC

Rev.of_WB235_3:12740278-12740831 Satlength=554 Nr of Repeats=5
RepeatLength=32 seed=ACCAATCAGC Num.seqs=3 Similarity=0.916667

10 GCTGATTGGTTCA-AAAGTGGGCGGAGCAAATC

Rev.of_WB235_3:12696947-12698148 Satlength=1202 Nr of Repeats=5
RepeatLength=32 seed=GACCAATCAG Num.seqs=3 Similarity=0.861111

11 GCTGATTGG-TCAGAGAGTGGGCGGGGCGAATC

Rev.of_WB235_2:14274983-14275913 Satlength=931 Nr of Repeats=26
RepeatLength=32 seed=AACCAATCAG Num.seqs=18 Similarity=0.796296

11 GCTGATTGGTTCC-AAAATGGGTGGAGCTGAGC

WB235_5:16583907-16584035 Satlength=129 Nr of Repeats=4 RepeatLength=32
seed=GCTGATTGGT Num.seqs=4 Similarity=0.508488

0 GCTGATTGG-TAAGAACTGGGCGTGGCTGAAA

Rev.of_WB235_3:2218366-2219198 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

>WB235_Fam_46_32_6 Nr. of seq. 6 Alignment length(with gaps) = 32
Alignment score = 0.838889
WB235_2:851256-851616 Satlength=361 Nr of Repeats=5 RepeatLength=31
seed=TGTCTAGCGA Num.seqs=3 Similarity=0.799283
0 TGTCTAGCGAGACCTCAGAAG-AGAGCTGAGT
WB235_2:1970474-1970784 Satlength=311 Nr of Repeats=10 RepeatLength=31
seed=AGAGCTGAGT Num.seqs=10 Similarity=0.801505
22 TGTCTAGCGAGACAGCAGAAGAAGAGCTGAGT
WB235_2:2593754-2594002 Satlength=249 Nr of Repeats=8 RepeatLength=31
seed=AGAGCTGAGT Num.seqs=8 Similarity=0.806548
22 TGTCTAGCGAGACAGCAGAAGAAGAGCTGAGT
WB235_2:1962052-1963013 Satlength=962 Nr of Repeats=31 RepeatLength=31
seed=AGAGCTGAGT Num.seqs=31 Similarity=0.809341
21 TGTCTAGCGAGATAGCAGAN-AAGAGCTGAGT
WB235_2:1977769-1979195 Satlength=1427 Nr of Repeats=46 RepeatLength=31
seed=AGAGCTGAGT Num.seqs=46 Similarity=0.811262
21 TGTCTAGCGAGATAGCAGAN-AAGAGCTGAGT
Rev.of_WB235_2:2008283-2009461 Satlength=1179 Nr of Repeats=38
RepeatLength=31 seed=GACAACTCAG Num.seqs=38 Similarity=0.826733
35 TGTCTAGCGAGATAGCAGAA-AAGAGCTGAGT

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Consensus:

TGTCgAGCGAGAcAGCAGAagAAGAGCTGAGT

>WB235_Fam_47_21_6 Nr. of seq. 6 Alignment length(with gaps) = 25
Alignment score = 0.624889
WB235_3:2235593-2235697 Satlength=105 Nr of Repeats=5 RepeatLength=21
seed=CTGACCAAAT Num.seqs=4 Similarity=0.841270
0 CTGACC---AAATTTGT-TTCAGCA
Rev.of_WB235_3:2245221-2245452 Satlength=232 Nr of Repeats=9
RepeatLength=21 seed=GTCAGTGCTG Num.seqs=6 Similarity=0.856085
5 CTGACA---AAATTTGT-TCCAGCA
WB235_3:3272813-3272897 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=TCCAGCACTG Num.seqs=4 Similarity=0.936508
14 CTGACA---AAATTTGT-TCCAGCA
Rev.of_WB235_6:723810-724054 Satlength=245 Nr of Repeats=5
RepeatLength=22 seed=TGGTCAGTGC Num.seqs=4 Similarity=0.777778
7 CTGACC---AAATTGGTCGCCAGCA
Rev.of_WB235_6:988793-988877 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=TGGTCAGTGC Num.seqs=4 Similarity=0.968254
7 CTGACC---AAATTGTT-TCTTGCA

WB235_6:1524262-1524376 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:

CTGACcAAATTTtGTTcCaGCA

>WB235_Fam_48_21_6 Nr. of seq. 6 Alignment length(with gaps) = 22
Alignment score = 0.621212
WB235_6:1008023-1008695 Satlength=673 Nr of Repeats=4 RepeatLength=21
seed=TGACAAAACA Num.seqs=3 Similarity=1.000000
0 TGACAAAA-CATAACTTTGCAC
Rev.of_WB235_6:11745151-11745371 Satlength=221 Nr of Repeats=10
RepeatLength=22 seed=TCAGTGCAA Num.seqs=8 Similarity=0.818182
3 TGACAAAAGTGTCACCTTTGCAC
Rev.of_WB235_6:1062534-1062618 Satlength=85 Nr of Repeats=4
RepeatLength=21 seed=GTCAGTGCAA Num.seqs=4 Similarity=0.841270
4 TGACAATA-TTTGAATTTGCAC
WB235_6:1320585-1320992 Satlength=408 Nr of Repeats=5 RepeatLength=21
seed=TTGCACTGAC Num.seqs=3 Similarity=0.747475
15 TGACAAAA-TTTCGTNTTGCAC
Rev.of_WB235_6:1214446-1215096 Satlength=651 Nr of Repeats=6
RepeatLength=21 seed=GTCAGTGCAA Num.seqs=4 Similarity=0.809524
4 TGACCAAA-AATGCATTTGCAC
WB235_6:1325710-1325901 Satlength=192 Nr of Repeats=7 RepeatLength=21
seed=TTGCACTGAC Num.seqs=6 Similarity=0.630303
15 TGACCAAC-TCTTCATTTGCAC

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Consensus:

TGACaAAAtnThaaTTTGCAC

>WB235_Fam_49_19_6 Nr. of seq. 6 Alignment length(with gaps) = 21
Alignment score = 0.706878
WB235_1:11486089-11486222 Satlength=134 Nr of Repeats=7 RepeatLength=19
seed=TTATCGATTT Num.seqs=5 Similarity=0.873684
46 TCNA--GAAATTATCGATTTT
Rev.of_WB235_3:2836362-2837893 Satlength=1532 Nr of Repeats=45
RepeatLength=19 seed=AAAATCGATA Num.seqs=33 Similarity=0.907895
57 TCCG--GAAATTATCGATTTT
Rev.of_WB235_3:1805381-1807736 Satlength=2356 Nr of Repeats=56
RepeatLength=19 seed=AAAATCGATA Num.seqs=36 Similarity=0.647665
57 CCGA--TAAATTATCGATTTT
Rev.of_WB235_3:1892229-1893089 Satlength=861 Nr of Repeats=44
RepeatLength=19 seed=AAAATCGATA Num.seqs=39 Similarity=0.805668
57 CCGA--GNAATTATCGATTTT
WB235_3:2012861-2014349 Satlength=1489 Nr of Repeats=36 RepeatLength=19
seed=TATCGATTTT Num.seqs=22 Similarity=0.729931
47 TCGT--AAAATTATCGATTTT

WB235_5:18940941-18941109 Satlength=169 Nr of Repeats=8 RepeatLength=21
seed=ATTATTGATT Num.seqs=8 Similarity=0.778409
23 GAAAAATTATTGATTTTCAA

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Consensus:

gaAATTATCGATTTTtCga

>WB235_Fam_50_18_6 Nr. of seq. 6 Alignment length(with gaps) = 19
Alignment score = 0.644444
WB235_1:6089071-6089158 Satlength=88 Nr of Repeats=5 RepeatLength=17
seed=AGGTAGTCAA Num.seqs=3 Similarity=1.000000
0 AGGTAGTCAATGAGCA-A-
Rev.of_WB235_4:7683397-7683518 Satlength=122 Nr of Repeats=6
RepeatLength=17 seed=CTCATTGCCT Num.seqs=4 Similarity=0.764706
14 GGTAGTCAATGAGCA-C-
WB235_5:8314150-8315036 Satlength=887 Nr of Repeats=51 RepeatLength=17
seed=TAGTCAATGA Num.seqs=33 Similarity=0.909685
3 AGGTAGTCAATGATCT-A-
WB235_4:8999493-8999648 Satlength=156 Nr of Repeats=8 RepeatLength=17
seed=AGGCAATGAG Num.seqs=5 Similarity=0.781482
3 -AGTAGGCAATGAGAA-AG
Rev.of_WB235_5:6910515-6910653 Satlength=139 Nr of Repeats=7
RepeatLength=17 seed=CTCATTGCCT Num.seqs=5 Similarity=0.703704
13 -NGTAGGCAATGAGCA-AG
Rev.of_WB235_5:7703008-7703129 Satlength=122 Nr of Repeats=6
RepeatLength=17 seed=CTCATTGCCT Num.seqs=4 Similarity=0.697531
13 -NGTAGGCAATGAGCACAG

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Consensus:

ngGTAGgCAATGAGCAAg

>WB235_Fam_51_16_6 Nr. of seq. 6 Alignment length(with gaps) = 16
Alignment score = 0.697917
WB235_2:875486-875668 Satlength=183 Nr of Repeats=12 RepeatLength=14
seed=TAGGATCTAG Num.seqs=10 Similarity=0.807407
2 TC-TAGGATCT-AGGA
Rev.of_WB235_2:1605126-1605357 Satlength=232 Nr of Repeats=13
RepeatLength=14 seed=GATCCTAGAT Num.seqs=10 Similarity=0.832804
2 TC-TAGGATCT-AGGA
WB235_1:14002210-14002386 Satlength=177 Nr of Repeats=11 RepeatLength=16
seed=ATCTAAGGAT Num.seqs=11 Similarity=0.872727
6 TCTAAGGATCTAAGGA
Rev.of_WB235_1:14005076-14005524 Satlength=449 Nr of Repeats=13
RepeatLength=16 seed=AGATCCTTAG Num.seqs=10 Similarity=0.811111
10 TCTAAGGATCTAAGGA
WB235_1:14006294-14006390 Satlength=97 Nr of Repeats=6 RepeatLength=16
seed=AGGATCTAAG Num.seqs=6 Similarity=0.972222
11 TCTAAGGATCTAAGGA

WB235_4:15636148-15636960 Satlength=813 Nr of Repeats=51 RepeatLength=14
seed=GGACTAGGGA Num.seqs=48 Similarity=0.885234
3 TAGGGACTAGGGA-C-

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Consensus:

TCtaAGGATCTaAGGA

>WB235_Fam_52_15_6 Nr. of seq. 6 Alignment length(with gaps) = 15
Alignment score = 0.952593
WB235_1:14290714-14290861 Satlength=148 Nr of Repeats=8 RepeatLength=15
seed=GGGGGCAACA Num.seqs=5 Similarity=0.822222
0 GGGGGCAACAAAATA
Rev.of_WB235_1:14292866-14293013 Satlength=148 Nr of Repeats=8
RepeatLength=15 seed=TGTTGCCCCC Num.seqs=5 Similarity=0.822222
10 GGGGGCAACAAAATA
Rev.of_WB235_3:705083-705230 Satlength=148 Nr of Repeats=8
RepeatLength=15 seed=TGTTGCCCCC Num.seqs=5 Similarity=0.795556
10 GGGGGCAACAAAATA
WB235_6:17344107-17344254 Satlength=148 Nr of Repeats=8 RepeatLength=15
seed=GGGGGCAACA Num.seqs=5 Similarity=0.822222
0 GGGGGCAACAAAATA
WB235_2:1487465-1487813 Satlength=349 Nr of Repeats=19 RepeatLength=15
seed=GGGGGCAACA Num.seqs=12 Similarity=0.807407
0 GGGGGCAACAAAAA
WB235_3:700450-700543 Satlength=94 Nr of Repeats=5 RepeatLength=15
seed=GGGGGCAACA Num.seqs=3 Similarity=0.822222
0 GGGGGCAACAAAAA

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Consensus:

GGGGGCAACAAAAtA

>WB235_Fam_53_12_6 Nr. of seq. 6 Alignment length(with gaps) = 14
Alignment score = 0.649206
WB235_1:4548525-4548705 Satlength=181 Nr of Repeats=14 RepeatLength=12
seed=TTTTTATTTT Num.seqs=12 Similarity=0.947811
0 TTTTTATTT-TTA-
Rev.of_WB235_2:11122559-11122763 Satlength=205 Nr of Repeats=16
RepeatLength=12 seed=AATAAAAATA Num.seqs=14 Similarity=1.000000
2 TTTTTATTT-TTA-
Rev.of_WB235_3:3334092-3334302 Satlength=211 Nr of Repeats=17
RepeatLength=12 seed=AAAATAAAAA Num.seqs=16 Similarity=0.986111
4 TTTTTATTT-TTA-
WB235_5:6944029-6944530 Satlength=502 Nr of Repeats=36 RepeatLength=12
seed=TTTAATTTTA Num.seqs=31 Similarity=1.000000
1 TTTTAATTT-TAA-
WB235_4:6291557-6291611 Satlength=55 Nr of Repeats=4 RepeatLength=13
seed=TTTCATTTGT Num.seqs=3 Similarity=0.931624
1 TTTTCATTT-GTAA

Rev.of_WB235_6:2010907-2011305 Satlength=399 Nr of Repeats=28
RepeatLength=12 seed=AATAAATAAC Num.seqs=17 Similarity=1.000000
0 TATTTATTTATT--

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Consensus:

TTTTtATTTTA

>WB235_Fam_54_11_6 Nr. of seq. 6 Alignment length(with gaps) = 11
Alignment score = 0.838384
WB235_2:4309186-4309439 Satlength=254 Nr of Repeats=23 RepeatLength=11
seed=CAGTTGTCAC Num.seqs=19 Similarity=0.897927
0 CAGTTGTCAC
WB235_6:3631392-3631893 Satlength=502 Nr of Repeats=43 RepeatLength=11
seed=CAGTTGTCAC Num.seqs=40 Similarity=0.871173
0 CAGTTGTCACC
Rev.of_WB235_4:4599072-4599116 Satlength=45 Nr of Repeats=4
RepeatLength=11 seed=TGACAACTTT Num.seqs=4 Similarity=1.000000
9 AAGTTGTCACA
Rev.of_WB235_4:7128107-7129879 Satlength=1773 Nr of Repeats=156
RepeatLength=11 seed=TGACAACTTC Num.seqs=113 Similarity=0.796811
9 AAGTTGTCACG
WB235_5:4773346-4773621 Satlength=276 Nr of Repeats=22 RepeatLength=11
seed=CACGAAGTTG Num.seqs=19 Similarity=0.914939
18 AAGTTGTCACG
WB235_6:11789572-11789748 Satlength=177 Nr of Repeats=16 RepeatLength=11
seed=CGAAGTTGTC Num.seqs=16 Similarity=0.870707
9 AAGTTGTCACG

Consensus:

aAGTTGTCACg

>WB235_Fam_55_48_5 Nr. of seq. 5 Alignment length(with gaps) = 48
Alignment score = 0.900000
WB235_4:5465022-5467133 Satlength=2112 Nr of Repeats=44 RepeatLength=48
seed=AATTC AATTT Num.seqs=43 Similarity=0.962532
0 AATTC AATTTTTGATTTGCCGTAATTTATATTTTCTGAAGATGAGC
Rev.of_WB235_4:12891406-12891917 Satlength=512 Nr of Repeats=9
RepeatLength=48 seed=TCATCTTCAG Num.seqs=8 Similarity=0.978175
46 AATTTAATTTTTGATTTGCCGTAATTTATAATTTCTGAAGATGAGC
WB235_6:2991583-2991919 Satlength=337 Nr of Repeats=7 RepeatLength=48
seed=AAGATGAGGA Num.seqs=7 Similarity=0.933862
39 AATTTATTTTTTGATTTGCCGTAATTTATATTTTCTGAAGATGAGG
Rev.of_WB235_6:14384735-14389919 Satlength=5185 Nr of Repeats=108
RepeatLength=48 seed=AAATTACGGG Num.seqs=108 Similarity=0.957391
76 AATTTAATTGTTGATTTGCCGTAATTTATATTTTCTGAAGATGAGG
WB235_5:1637931-1639035 Satlength=1105 Nr of Repeats=23 RepeatLength=48
seed=CCCGTAATTT Num.seqs=23 Similarity=0.933685
18 AATTTAAATTTTGAGTTGCCGTAATTTATAAATTTCTGAAGATGAGC

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Consensus:

AATTtAatTtTTGAtTTGCCGTAATTTATAtTTTCTGAAGATGAGc

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>WB235_Fam_56_21_5  Nr. of seq. 5 Alignment length(with gaps) = 25
Alignment score = 0.616000
WB235_2:9719802-9720144 Satlength=343 Nr of Repeats=16 RepeatLength=19
seed=ATAAATATTA  Num.seqs=10 Similarity=0.961014
0  --ATAAATATTAATTAATAA----
Rev.of_WB235_4:1639384-1639487 Satlength=104 Nr of Repeats=5
RepeatLength=23 seed=ATTTAATTAA  Num.seqs=3 Similarity=0.729469
0  AAATAAATATTAATTAATAAAT--
WB235_6:5229333-5229440 Satlength=108 Nr of Repeats=5 RepeatLength=23
seed=AAATAAATATT  Num.seqs=3 Similarity=0.922705
1  AAATAAATATTAATTAATTAAT--
Rev.of_WB235_6:2004050-2004599 Satlength=550 Nr of Repeats=27
RepeatLength=19 seed=ATATTTATTT  Num.seqs=18 Similarity=0.931201
4  --ATAT----TAATTAAATAAATAA
Rev.of_WB235_4:13463617-13463705 Satlength=89 Nr of Repeats=4
RepeatLength=23 seed=AATATTTATT  Num.seqs=3 Similarity=0.961353
4  --ATATTTATTAAATAAATAAATAA
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Consensus:

ATAaatatTAAtTAAaTAAat

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>WB235_Fam_57_25_5  Nr. of seq. 5 Alignment length(with gaps) = 25
Alignment score = 0.946667
WB235_1:10130602-10133102 Satlength=2501 Nr of Repeats=100
RepeatLength=25 seed=TATTTACTCT  Num.seqs=100 Similarity=0.949274
0  TATTTACTCTAATGTTCTGCCAATT
WB235_6:4026010-4030548 Satlength=4539 Nr of Repeats=181 RepeatLength=25
seed=GTTCTGCCAA  Num.seqs=178 Similarity=0.933006
13  TATTTACTCTAATGTTCTGCCAATT
Rev.of_WB235_4:6357804-6361081 Satlength=3278 Nr of Repeats=132
RepeatLength=25 seed=TAGAGTAAAT  Num.seqs=128 Similarity=0.931929
11  TATTTACTCTAATGTTCTGCTAATT
Rev.of_WB235_6:4030571-4031446 Satlength=876 Nr of Repeats=34
RepeatLength=25 seed=ATTGGCAGAA  Num.seqs=33 Similarity=0.891706
24  TATTTACTCTAATGTTCTGCCAATA
Rev.of_WB235_6:10360970-10361186 Satlength=217 Nr of Repeats=4
RepeatLength=25 seed=ATTGGCAGAA  Num.seqs=3 Similarity=0.837607
24  TATTTACTCTAATGTTCTGCCAATA
```

Consensus:

TATTTACTCTAATGTTCTGCcAATt

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>WB235_Fam_58_21_5  Nr. of seq. 5 Alignment length(with gaps) = 23
Alignment score = 0.667391
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WB235_3:83578-83851 Satlength=274 Nr of Repeats=13 RepeatLength=21
seed=CCATTTTAAG Num.seqs=13 Similarity=0.947904
0 CCATTTTAAGCC-AATTTTGGA-
WB235_3:83578-84096 Satlength=519 Nr of Repeats=25 RepeatLength=21
seed=CCATTTTAAG Num.seqs=16 Similarity=0.877588
0 CCATTTTAAGCC-AATTTTGGA-
Rev.of_WB235_3:80880-81257 Satlength=378 Nr of Repeats=14 RepeatLength=21
seed=AAATTTGGCT Num.seqs=11 Similarity=0.774105
18 CCATTTTAAGCCAAATTTTCAA-
Rev.of_WB235_4:1415278-1415575 Satlength=298 Nr of Repeats=15
RepeatLength=21 seed=AAAATTGACT Num.seqs=10 Similarity=0.908289
18 CGATTTTTAGTC-AATTTTGA-
Rev.of_WB235_4:2182563-2182888 Satlength=326 Nr of Repeats=13
RepeatLength=21 seed=AAAATAGCTT Num.seqs=9 Similarity=0.765993
29 CTATTTTTAGTC-AATTT-TAAG

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Consensus:

CcATTTTaAGcCAATTTtngA

>WB235_Fam_59_22_5 Nr. of seq. 5 Alignment length(with gaps) = 22
Alignment score = 0.630303
WB235_5:18201732-18201816 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=GCACTGACCA Num.seqs=4 Similarity=1.000000
0 GCACTGACCAAATGCAATGTT-
Rev.of_WB235_6:1094209-1094314 Satlength=106 Nr of Repeats=5
RepeatLength=21 seed=TTGGTCAGTG Num.seqs=5 Similarity=0.746032
11 GCACTGACCAATTNNAAAATT-
WB235_6:1292997-1293291 Satlength=295 Nr of Repeats=14 RepeatLength=21
seed=TTTGCACTGA Num.seqs=14 Similarity=0.853480
18 GCACTGACCAACACGAAT-TTT
Rev.of_WB235_2:2110299-2110412 Satlength=114 Nr of Repeats=5
RepeatLength=22 seed=TGGTCAGTGC Num.seqs=3 Similarity=0.959596
31 GCACTGACCAATAAAAATGTTT
Rev.of_WB235_6:1278787-1279105 Satlength=319 Nr of Repeats=7
RepeatLength=22 seed=GTCAGTGCAA Num.seqs=5 Similarity=0.692754
8 GCACTGACCATGTGCACAATTT

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Consensus:

GCACTGACCAantnnAatnTTt

>WB235_Fam_60_19_5 Nr. of seq. 5 Alignment length(with gaps) = 21
Alignment score = 0.695238
WB235_2:13799836-13800686 Satlength=851 Nr of Repeats=47 RepeatLength=18
seed=AATTTACCAA Num.seqs=36 Similarity=0.737116
0 AATTTACC-AA-TTTACCAA-
WB235_3:12188657-12188828 Satlength=172 Nr of Repeats=7 RepeatLength=19
seed=CAATTTACCA Num.seqs=5 Similarity=0.791667
7 AATTTGNC-AA-TTTACCAA

WB235_3:12839625-12840128 Satlength=504 Nr of Repeats=16 RepeatLength=19
seed=TTGGCAATTT Num.seqs=10 Similarity=0.809747
22 AATTTGGC-AA-TTTACCAA
Rev.of_WB235_3:1312388-1312777 Satlength=390 Nr of Repeats=16
RepeatLength=21 seed=TTTTTGGTAA Num.seqs=13 Similarity=0.873016
2 AAGTTACCAAATTTTACCAA
WB235_3:1314701-1315015 Satlength=315 Nr of Repeats=12 RepeatLength=21
seed=CAAAAAGTTA Num.seqs=10 Similarity=0.923810
17 AAGTTACCAAATTTTAACAA

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Consensus:

AATTTacCAATTTAcCAAa

>WB235_Fam_61_20_5 Nr. of seq. 5 Alignment length(with gaps) = 21
Alignment score = 0.652381
WB235_2:3246632-3247175 Satlength=544 Nr of Repeats=19 RepeatLength=20
seed=GTAAATCTAC Num.seqs=12 Similarity=0.565197
0 GTAAATCTACACT-AGCTTCC
WB235_2:11906637-11907671 Satlength=1035 Nr of Repeats=44 RepeatLength=20
seed=TAAATCTACA Num.seqs=34 Similarity=0.664092
1 GTAAATCTACACN-GGCTTGC
Rev.of_WB235_4:3652033-3652933 Satlength=901 Nr of Repeats=15
RepeatLength=21 seed=TGTAGATTTA Num.seqs=10 Similarity=0.670875
11 GTAAATCTACANTAGGCTCCC
Rev.of_WB235_2:15194481-15194561 Satlength=81 Nr of Repeats=4
RepeatLength=20 seed=TGTAGATTTA Num.seqs=4 Similarity=0.688889
11 GTAAATCTACATT-GTCCTTT
WB235_5:18584208-18585555 Satlength=1348 Nr of Repeats=50 RepeatLength=20
seed=GTAAATCTAC Num.seqs=35 Similarity=0.635294
20 GTAAATCTACATN-GACCTCC

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Consensus:

GTAAATCTACAntggCttcc

>WB235_Fam_62_17_5 Nr. of seq. 5 Alignment length(with gaps) = 18
Alignment score = 0.848148
WB235_2:1596937-1597005 Satlength=69 Nr of Repeats=4 RepeatLength=17
seed=TCATTCCGTG Num.seqs=4 Similarity=1.000000
0 TCATTCC-GTGATTATTT
WB235_3:4637893-4638151 Satlength=259 Nr of Repeats=5 RepeatLength=17
seed=ATTATTTTCA Num.seqs=4 Similarity=1.000000
10 TCATTCC-GTGATTATTT
Rev.of_WB235_3:12323417-12323485 Satlength=69 Nr of Repeats=4
RepeatLength=17 seed=TGAAAATAAT Num.seqs=4 Similarity=1.000000
3 TCATTCC-GTGATTATTT
WB235_4:8789534-8789636 Satlength=103 Nr of Repeats=6 RepeatLength=17
seed=TTCAATCCGT Num.seqs=6 Similarity=1.000000
16 TCATTCC-GTGATTATTT

Rev.of_WB235_6:6114472-6114558 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

>WB235_Fam_63_11_5 Nr. of seq. 5 Alignment length(with gaps) = 14
Alignment score = 0.697619
WB235_2:4138713-4139388 Satlength=676 Nr of Repeats=4 RepeatLength=11
seed=TGCCTGCCTA Num.seqs=3 Similarity=0.919192
0 TGCCT--GCCTAC-
Rev.of_WB235_2:4140823-4140867 Satlength=45 Nr of Repeats=4
RepeatLength=11 seed=GGCAGGCAGT Num.seqs=4 Similarity=0.898990
8 TGCCT--GCCTAC-
Rev.of_WB235_4:4532759-4533458 Satlength=700 Nr of Repeats=6
RepeatLength=11 seed=GCAGTAGGCA Num.seqs=5 Similarity=0.878788
3 TGCCT--GCCTAC-
Rev.of_WB235_1:733645-734074 Satlength=430 Nr of Repeats=11
RepeatLength=12 seed=GCAGGTAGGT Num.seqs=7 Similarity=0.841270
3 TGCCTA--CCTACC
WB235_2:2966318-2968108 Satlength=1791 Nr of Repeats=54 RepeatLength=14
seed=CTACCTGCCT Num.seqs=35 Similarity=0.800720
9 TGCCTATGCCTACC

Consensus:

TGCCTgCCTAC

>WB235_Fam_64_11_5 Nr. of seq. 5 Alignment length(with gaps) = 11
Alignment score = 0.951515
WB235_1:12684455-12684521 Satlength=67 Nr of Repeats=5 RepeatLength=11
seed=TTTGGAGCGG Num.seqs=4 Similarity=0.777778
0 TTTGGAGCGGA
WB235_3:7452275-7453348 Satlength=1074 Nr of Repeats=91 RepeatLength=11
seed=TGGAGCGGTT Num.seqs=84 Similarity=0.892314
2 TTTGGAGCGGT
WB235_6:1643531-1644396 Satlength=866 Nr of Repeats=34 RepeatLength=11
seed=GGAGCGGTTT Num.seqs=25 Similarity=0.945050
3 TTTGGAGCGGT
WB235_6:8181963-8182276 Satlength=314 Nr of Repeats=28 RepeatLength=11
seed=GAGCGGTTTT Num.seqs=21 Similarity=0.864358
4 TTTGGAGCGGT
WB235_6:10369202-10370313 Satlength=1112 Nr of Repeats=99 RepeatLength=11
seed=TGGAGCGGTT Num.seqs=97 Similarity=0.865250
2 TTTGGAGCGGT

Consensus:

TTTGGAGCGGt

gGTCTGCTAaATCaAAacTTGTAGTTTGTAGtCTAGCAGACCaAatTTcTtcAAaACCaCaTtG

>WB235_Fam_67_39_4 Nr. of seq. 4 Alignment length(with gaps) = 40
Alignment score = 0.856944
WB235_1:4167811-4168323 Satlength=513 Nr of Repeats=13 RepeatLength=39
seed=TATTTTAAAT Num.seqs=8 Similarity=0.954823
0 TA-TTTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACC
WB235_1:13154184-13155089 Satlength=906 Nr of Repeats=19 RepeatLength=39
seed=TTAAAAAGTA Num.seqs=13 Similarity=0.817735
19 TA-ATTTTAAATTTGGCCTACTTAAAAAGTAGGTCATGACC
WB235_1:12892561-12892756 Satlength=196 Nr of Repeats=5 RepeatLength=39
seed=TATTTTAAAT Num.seqs=5 Similarity=0.965812
0 TA-TTTTAAATTTAACCTACTTAAAAAGTAGGTCATGACC
WB235_3:10316800-10317870 Satlength=1071 Nr of Repeats=27 RepeatLength=40
seed=AAAAAGTAGGT Num.seqs=25 Similarity=0.956889
23 TAGTTTTTAAACGTGACCTCCTTAAAAAGTAGGTCATGACC

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Consensus:

TAtTTTAAAtTgacCTaCTTAAAAAGTAGGTCATGACC

>WB235_Fam_68_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
Alignment score = 0.754630
WB235_1:3442604-3443969 Satlength=1366 Nr of Repeats=56 RepeatLength=35
seed=TTTCGGCAAT Num.seqs=35 Similarity=0.808371
0 TTTCGGCAATTTTCGGCAATTGCCGTTTCNTGAAT-
Rev.of_WB235_4:12678404-12678576 Satlength=173 Nr of Repeats=5
RepeatLength=35 seed=AAACCGGCAA Num.seqs=3 Similarity=0.759259
28 TTTCGGCAATTTTCGGCAATTGCCGTTTGTGAGAAT-
WB235_1:14822628-14822877 Satlength=250 Nr of Repeats=7 RepeatLength=35
seed=CGGTTTTGGA Num.seqs=5 Similarity=0.885714
21 -TTTCGGCAATTTTCGATAATTGCCGTTTGTGAAAAAT
WB235_5:18110272-18110517 Satlength=246 Nr of Repeats=7 RepeatLength=35
seed=AAATTTTCGG Num.seqs=7 Similarity=0.945578
30 -TTTCGGCAAATTTGATAATTGCCGTTTGTGAAATT

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Consensus:

tTTTCGGCAAtTTcGacAATTGCCGTTTtggAAAt

>WB235_Fam_69_30_4 Nr. of seq. 4 Alignment length(with gaps) = 30
Alignment score = 0.777778
WB235_2:13990069-13990966 Satlength=898 Nr of Repeats=30 RepeatLength=30
seed=TTTCTAGAAA Num.seqs=24 Similarity=0.857649
0 TTTCTAGAAAAATCTGGAACTTCTAGAAC
Rev.of_WB235_3:3229003-3229241 Satlength=239 Nr of Repeats=7
RepeatLength=30 seed=TAGAACTTTC Num.seqs=5 Similarity=0.786667
26 TTTCTAGAAAAATTTGGAAAGTTCTAGAAAT
Rev.of_WB235_3:3230816-3231055 Satlength=240 Nr of Repeats=8
RepeatLength=30 seed=TAGAACTTTC Num.seqs=6 Similarity=0.925926
26 TTTCTAGAGAAATTTGGAAAGTTCTAGAAAT

Rev.of_WB235_2:14836506-14836646 Satlength=141 Nr of Repeats=5
RepeatLength=30 seed=TTCTGGAAAA Num.seqs=3 Similarity=0.762963
9 TTTCCAGAAGGTTCTGGAACATTCTAGAAT

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Consensus:

TTTCTAGAaaaaTcTGGAAGTTCTAGAAt

>WB235_Fam_70_30_4 Nr. of seq. 4 Alignment length(with gaps) = 30
Alignment score = 0.983333
WB235_2:14878787-14878927 Satlength=141 Nr of Repeats=5 RepeatLength=30
seed=AATTTTCCAG Num.seqs=3 Similarity=0.792593
0 AATTTTCCAGAAGGTTCTGGAACATTCCAG
WB235_4:9411472-9411612 Satlength=141 Nr of Repeats=5 RepeatLength=30
seed=AATTTTCCAG Num.seqs=3 Similarity=0.822222
0 AATTTTCCAGAAGGTTCTGGAACATTCCAG
WB235_6:1376606-1376746 Satlength=141 Nr of Repeats=5 RepeatLength=30
seed=AATTTTCCAG Num.seqs=3 Similarity=0.792593
0 AATTTTCCAGAAGGTTCTGGAACATTCCAG
WB235_6:516878-517017 Satlength=140 Nr of Repeats=5 RepeatLength=30
seed=AATTTTCCAG Num.seqs=3 Similarity=0.807407
0 AATTTTCCAGAAGGTTCTGGAACNTTCCAG

Consensus:

AATTTTCCAGAAGGTTCTGGAACaTTCCAG

>WB235_Fam_71_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.907407
WB235_1:12910137-12910261 Satlength=125 Nr of Repeats=6 RepeatLength=21
seed=AATCCAATAT Num.seqs=5 Similarity=0.790476
0 AATCCAATATGGANGAAATCT
Rev.of_WB235_2:14802929-14803074 Satlength=146 Nr of Repeats=7
RepeatLength=21 seed=ATTGGATTAG Num.seqs=6 Similarity=0.792593
8 AATCCAATATGGAAGAAATCT
WB235_3:6626010-6626226 Satlength=217 Nr of Repeats=6 RepeatLength=21
seed=AAATCTAATC Num.seqs=5 Similarity=0.822727
15 AATCCAATATGGNCGAAATCT
Rev.of_WB235_5:2636817-2636991 Satlength=175 Nr of Repeats=6
RepeatLength=21 seed=GATTAGATTT Num.seqs=5 Similarity=0.841270
25 AATCCAATATGGACNAAATCT

Consensus:

AATCCAATATGGacgAAATCT

>WB235_Fam_72_19_4 Nr. of seq. 4 Alignment length(with gaps) = 20
Alignment score = 0.761111
WB235_4:229906-231132 Satlength=1227 Nr of Repeats=63 RepeatLength=18
seed=CTCAACCAA Num.seqs=43 Similarity=0.898938
0 CTCAACCAA--ACTCTTAGC

WB235_4:238538-239383 Satlength=846 Nr of Repeats=8 RepeatLength=18
seed=AGCCTCAACC Num.seqs=5 Similarity=0.925926
15 CTCAACCAA--ACTCTTAGC
Rev.of_WB235_4:122695-123566 Satlength=872 Nr of Repeats=28
RepeatLength=19 seed=TTGGTTGAGG Num.seqs=19 Similarity=0.809582
9 CTCAACCAA-AATTGTTAGC
WB235_4:215697-216357 Satlength=661 Nr of Repeats=32 RepeatLength=20
seed=CTCAGCCTCA Num.seqs=30 Similarity=0.934713
14 CTCAACCAAAAATTCTCAGC

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Consensus:

CTCAACCAAaAcTcTtAGC

>WB235_Fam_73_20_4 Nr. of seq. 4 Alignment length(with gaps) = 20
Alignment score = 0.744444
WB235_1:14477083-14477203 Satlength=121 Nr of Repeats=6 RepeatLength=20
seed=GTGAAATTTT Num.seqs=6 Similarity=0.705820
0 GTGAAATTTTAAATTTTAA
WB235_2:14984666-14984990 Satlength=325 Nr of Repeats=14 RepeatLength=20
seed=TTCAAGTCAAA Num.seqs=10 Similarity=0.802963
16 GTCAAAATTTAAATTTTCA
WB235_5:19935725-19935960 Satlength=236 Nr of Repeats=11 RepeatLength=20
seed=TTTGAATTTT Num.seqs=7 Similarity=0.936508
7 GTGAAAATTTGAATTTTGA
WB235_5:20406247-20406428 Satlength=182 Nr of Repeats=9 RepeatLength=20
seed=AAAAATTCAAA Num.seqs=6 Similarity=0.778836
3 CTGAAAATTCAAATTTCTGA

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Consensus:

gTgAAAaTTtaAATTTtTgA

>WB235_Fam_74_17_4 Nr. of seq. 4 Alignment length(with gaps) = 18
Alignment score = 0.902778
WB235_2:1659657-1659775 Satlength=119 Nr of Repeats=7 RepeatLength=17
seed=GATGCCCCCT Num.seqs=5 Similarity=0.729630
0 GATGCCCCCTTTGAACG-
Rev.of_WB235_3:4254156-4254274 Satlength=119 Nr of Repeats=7
RepeatLength=17 seed=AGGGGGCATC Num.seqs=5 Similarity=0.749020
10 GATGCCCCCTCTGAACG-
WB235_3:4257044-4257162 Satlength=119 Nr of Repeats=7 RepeatLength=17
seed=GATGCCCCCT Num.seqs=5 Similarity=0.729630
17 GATGCCCCCTCTGAACG-
WB235_4:4198521-4198622 Satlength=102 Nr of Repeats=6 RepeatLength=17
seed=GATGCCCCCT Num.seqs=4 Similarity=0.722222
0 GATGCCCCCTCTGAACGN

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Consensus:

GATGCCCCCTcTGAACG

>WB235_Fam_75_16_4 Nr. of seq. 4 Alignment length(with gaps) = 16
Alignment score = 0.847222
WB235_1:7780058-7780728 Satlength=671 Nr of Repeats=39 RepeatLength=16
seed=AATTTTCCG Num.seqs=31 Similarity=0.814158
0 AATTTTCCGCNGCGA
Rev.of_WB235_2:7449335-7450152 Satlength=818 Nr of Repeats=42
RepeatLength=16 seed=CGGAAAATT Num.seqs=27 Similarity=0.719401
10 AATTTTCCGCNGCNA
Rev.of_WB235_5:13640261-13645859 Satlength=5599 Nr of Repeats=335
RepeatLength=16 seed=GAAAAATTTT Num.seqs=281 Similarity=0.744871
8 AATTTTTCAGCAGCAA
Rev.of_WB235_5:13640261-13646660 Satlength=6400 Nr of Repeats=357
RepeatLength=16 seed=GAAAAATTTT Num.seqs=293 Similarity=0.745623
8 AATTTTCCGCAGCAA

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Consensus:

AATTTTTCcGCaGCaA

>WB235_Fam_76_14_4 Nr. of seq. 4 Alignment length(with gaps) = 15
Alignment score = 0.727778
WB235_2:3033725-3034005 Satlength=281 Nr of Repeats=20 RepeatLength=14
seed=TTAGGGCCTT Num.seqs=20 Similarity=0.947368
0 TTAGGGCCTTGGGC-
Rev.of_WB235_4:154583-154709 Satlength=127 Nr of Repeats=8
RepeatLength=14 seed=CCTAAGCCTA Num.seqs=7 Similarity=0.918367
5 TTAGGGCCTTAGGC-
WB235_6:16199460-16199628 Satlength=169 Nr of Repeats=12 RepeatLength=14
seed=CTTAGGGCCTT Num.seqs=12 Similarity=0.894661
6 TTAGGGCCTTAGGGC-
Rev.of_WB235_2:3153871-3153936 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

>WB235_Fam_77_15_4 Nr. of seq. 4 Alignment length(with gaps) = 15
Alignment score = 0.955556
WB235_1:4185588-4185648 Satlength=61 Nr of Repeats=4 RepeatLength=15
seed=TTCCGGATC Num.seqs=4 Similarity=0.911111
0 TTCCGGATCTACGT
Rev.of_WB235_1:4185829-4185964 Satlength=136 Nr of Repeats=9
RepeatLength=15 seed=AGATCCGGAA Num.seqs=9 Similarity=1.000000
11 TTCCGGATCTACGT
Rev.of_WB235_1:6854524-6854599 Satlength=76 Nr of Repeats=5
RepeatLength=15 seed=AGATCCGGAA Num.seqs=5 Similarity=0.928889
11 TTCCGGATCTACGT

WB235_2:12763248-12763368 Satlength=121 Nr of Repeats=7 RepeatLength=15
seed=ATTTCGGAT Num.seqs=6 Similarity=0.922963
14 TTTCCGGATCTACGA

Consensus:

TTTCCGGATCTACGt

>WB235_Fam_78_13_4 Nr. of seq. 4 Alignment length(with gaps) = 13
Alignment score = 0.897436
WB235_5:1027504-1027725 Satlength=222 Nr of Repeats=11 RepeatLength=13
seed=GCCTATGGCC Num.seqs=7 Similarity=0.912088
0 GCCTATGGCCTAC
Rev.of_WB235_5:1028226-1028460 Satlength=235 Nr of Repeats=18
RepeatLength=13 seed=CGTAGGCCAT Num.seqs=18 Similarity=0.894754
1 GCCTATGGCCTAC
WB235_5:2102635-2102940 Satlength=306 Nr of Repeats=21 RepeatLength=13
seed=GCCTAAGCCT Num.seqs=17 Similarity=0.930618
7 GCCTATGGCCTAA
Rev.of_WB235_6:5125291-5125369 Satlength=79 Nr of Repeats=6
RepeatLength=13 seed=GCCATAGGCG Num.seqs=6 Similarity=0.931624
9 GCCTATGGCTTAC

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Consensus:

GCCTATGGCcTAc

>WB235_Fam_79_12_4 Nr. of seq. 4 Alignment length(with gaps) = 12
Alignment score = 0.840278
WB235_1:2014890-2015108 Satlength=219 Nr of Repeats=13 RepeatLength=11
seed=TTTTGCCGAA Num.seqs=10 Similarity=0.811448
0 TTTTGCCGAAC-
WB235_1:5563061-5563217 Satlength=157 Nr of Repeats=13 RepeatLength=12
seed=GAAATTTTTT Num.seqs=13 Similarity=0.948718
7 TTTTCCGAAAT
WB235_1:12479088-12479300 Satlength=213 Nr of Repeats=16 RepeatLength=12
seed=GAAATTTTTT Num.seqs=12 Similarity=0.915825
7 TTTTCCGAAAT
Rev.of_WB235_1:12479365-12479989 Satlength=625 Nr of Repeats=49
RepeatLength=12 seed=AAAAATTTC Num.seqs=34 Similarity=0.902159
17 TTTTCCGAAAT

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Consensus:

TTTTtCCGAAat

>WB235_Fam_80_12_4 Nr. of seq. 4 Alignment length(with gaps) = 12
Alignment score = 0.662037
WB235_4:5273292-5273664 Satlength=373 Nr of Repeats=18 RepeatLength=12
seed=AGAAGGAGGA Num.seqs=11 Similarity=0.864646
0 AGAAGGAGGAAA

>WB235_Fam_82_167_3 Nr. of seq. 3 Alignment length(with gaps) = 172
Alignment score = 0.656977
WB235_3:449837-453285 Satlength=3449 Nr of Repeats=21 RepeatLength=164
seed=ATATAATGCT Num.seqs=17 Similarity=0.956420
0
ATATAATGCTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAGCCACGTCTGAAAAATACAGATTTTTTCTCGA

AAATTT---CAAAACTTTTGTA-GAAATTCGATTTTTTGAC--
 ATAAATGATCTCTCTTTTTTTCTGACATGTATTTTCAGTGACAAA-TGGANT-AGAAA
 WB235_2:14333431-14337579 Satlength=4149 Nr of Repeats=25
 RepeatLength=166 seed=TCGTAATTAT Num.seqs=23 Similarity=0.971618
 8 -
 TATAATGTTTCGTAATTATTTCATAAGTTTGTGTTGTCTCAGAGCCATGTCTGAAAAACAGATTTTTTTTTTCGAA
 AATTT---TAAAAAGTTCGTA-
 AAAATTGGATTTTTTGACAAATCTATGCTCTCTTTTTTTGTTTAAAATTTAGTTCAGTGACATA-
 CAATTTCAAAAA
 WB235_2:13243398-13244452 Satlength=1055 Nr of Repeats=6 RepeatLength=165
 seed=AAAATTC AAT Num.seqs=5 Similarity=0.933737
 94 TTATAATGCTCGTAATTATTTATAAGTGTGTGTTGTCTCAGAATCAATTCT-
 AAAAAACAGATTTTTTTTT-GAAAGTTTAAAGTAATATCCGCGGAGAAAATTCAATTTTGGACATTTCTAT--
 TATCT-TTTTTTTAAACATGTATTTTCAGTGA-ATAGAAGACTCAAAA-

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Consensus:

nTATAATGcTCGTAATTATTTATAAGTgTGTGTTGTCTCAGAgcCAngTCTgAAAAaACAGATTTTTTTtTcGA
 AAaTTTtAAaAacttcGtAaAAATTcgATTTTTtGACanaTctATgnTcTcTnTTTTTTtTntaAcATgTatTTC
 AGTGAcAtAnaganTcAaAAa

>WB235_Fam_83_90_3 Nr. of seq. 3 Alignment length(with gaps) = 95
 Alignment score = 0.673684
 WB235_5:19466947-19467275 Satlength=329 Nr of Repeats=4 RepeatLength=82
 seed=CCCCGAACGT Num.seqs=4 Similarity=0.948510
 0 CCCCCGAACGTGTCGGCCGCTTCC--AAATAACCACCTCCTTGCACTACGTTGCGCACACA-----
 CTCATTTACGCCAAGCTGCGGAA--
 WB235_5:1539714-1540122 Satlength=409 Nr of Repeats=5 RepeatLength=89
 seed=GCACTACGTT Num.seqs=3 Similarity=0.740741
 38 CCCTGAACGTGTCGGCCGC-TCC--
 AAATAACTACCTTCTNGCACTACGTTGCGCACACACTAAGCTACTCGTTTCACGCCAAGCTACGGAA---
 WB235_3:1643024-1643390 Satlength=367 Nr of Repeats=4 RepeatLength=92
 seed=CTGCGGAACC Num.seqs=3 Similarity=1.000000
 81 ---
 CGAACGTGTCGGCCGCTTCCAAAAACAACCACCTCTTCACACTTCATTGCGCACACACCAAACCTACTAGTTTC
 ACGTCAAACTGCGGAACCC

Consensus:

ccccGAACGTGTCGGCCGCTTCCAAAtAACcACCTccTngCACTaCgTTGCGCACACAcnaanctaCTcgTTT
 CACGcCAAgCTgCGGAA

>WB235_Fam_84_79_3 Nr. of seq. 3 Alignment length(with gaps) = 79
 Alignment score = 0.912799
 WB235_2:3941820-3946547 Satlength=4728 Nr of Repeats=58 RepeatLength=79
 seed=GTGAATCTCC Num.seqs=53 Similarity=0.979228
 0
 GTGAATCTCCTCTCCACCTAATGATTCTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTT
 TCTTCT

Rev.of_WB235_4:11033628-11036077 Satlength=2450 Nr of Repeats=31
RepeatLength=79 seed=GAAACTAAAA Num.seqs=31 Similarity=0.920108
75

GTGAATCTCCTCTCTACCTAATGAGTCCTGACAGAATACCGGCAGTATTCTGGGGTCTCATTAGGTTTTAGTT
TCTTCT

WB235_2:8287652-8292933 Satlength=5282 Nr of Repeats=61 RepeatLength=79
seed=TGAGTCCTGA Num.seqs=58 Similarity=0.902451
21

CTGAATCTCCACTCTTCCTAATGAGTCCTGACAGAATACCGGCAGTATTTTGGGGTCTCATTAGGTTTTNGTT
TCTTTT

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Consensus:

gTGAATCTCCTcCTcTaCCTAATGAgTCCTGACAGAATACCGGCAGTATTcTGGGGTCTCATTAGGTTTTaGTT
TCTTcT

>WB235_Fam_85_76_3 Nr. of seq. 3 Alignment length(with gaps) = 76
Alignment score = 0.906433

WB235_4:14205760-14206748 Satlength=989 Nr of Repeats=13 RepeatLength=76
seed=AATGCTAGAG Num.seqs=13 Similarity=0.967611
0

AATGCTAGAGGACACTCCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTTCGGTGTCTTTGTGCATGC
TCG

Rev.of_WB235_4:14210874-14215456 Satlength=4583 Nr of Repeats=61
RepeatLength=76 seed=TCGTGCAAAG Num.seqs=60 Similarity=0.948617
27

AATGCTAGAGGACATTCTTTGCACGAAAGGAAGTGGGAGAGACTGTGGAGTTGTTCGGTGTCTTTGTGCATGC
TCG

Rev.of_WB235_6:16758347-16761606 Satlength=3260 Nr of Repeats=43
RepeatLength=76 seed=AGCATTAGAG Num.seqs=34 Similarity=0.949620
6

AATGCTAGAAGACACTCCTTTGCACGAAGGAAAGTGGGAGAGACTGTGGTGTTCGGTGTCTGTGTACATGC
TCT

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Consensus:

AATGCTAGAgGACAcTCCTTTGCACGAAGgAAGTGGGAGAGACTGTGGaGTTGTTCGGTGTCTtTGTgCATGC
TCg

>WB235_Fam_86_66_3 Nr. of seq. 3 Alignment length(with gaps) = 68
Alignment score = 0.892157

WB235_1:9821430-9822959 Satlength=1530 Nr of Repeats=23 RepeatLength=66
seed=AATCAACCTA Num.seqs=16 Similarity=0.986869
0

AATCAACCTATTTCAGTTGACAATGGTTTTCTTTTATCAAATTTTTTAAAATTT--TAAAGAAAACACA
WB235_4:17059789-17062957 Satlength=3169 Nr of Repeats=48 RepeatLength=66
seed=CAAATCAACC Num.seqs=48 Similarity=0.956050
64

AATCAACCTATTTCAGTTGACAATGGTTTTCTTTTATCAAATTTTTTAAAATTT--
TAAAGAAAACACA

Rev.of_WB235_1:10204129-10219199 Satlength=15071 Nr of Repeats=223
RepeatLength=68 seed=ACTGAATAGG Num.seqs=140 Similarity=0.978159

16

AATCAACCTATTTCAGTTGACAATGGTTTTCTTTTACCAAAATTTCTTAGAATTTTCAGAAAGAAAACACA

Consensus:

AATCAACCTATTTCAGTTGACAATGGTTTTCTTTTAtCAAAtTTtTTAaAATTTtAAAGAAAACACA

>WB235_Fam_87_64_3 Nr. of seq. 3 Alignment length(with gaps) = 64
Alignment score = 0.954861
WB235_1:13929375-13929595 Satlength=221 Nr of Repeats=5 RepeatLength=63
seed=TTTTTGACTA Num.seqs=3 Similarity=0.876736
0 TTTTTGACTACGGAATGTCTTTTTTCGCTACTGACTG-AAAAATAGCTACATTCGCACTTTTGNC
Rev.of_WB235_1:13935628-13936488 Satlength=861 Nr of Repeats=15
RepeatLength=64 seed=GTAGTCAAAA Num.seqs=10 Similarity=0.982870
11 TTTTTGACTACTGAATGTCTTTTTTCGCTACTGACTGAAAAAATAGCTACATTCGCACTTTTGTC
Rev.of_WB235_5:14204941-14205737 Satlength=797 Nr of Repeats=14
RepeatLength=64 seed=GTAGTCAAAA Num.seqs=9 Similarity=0.983796
11 TTTTTGACTACTGAATGTCTTTTTTCGCTACTGACTGAAAAAATAGCTACATTCGCACTTTTGTC

Consensus:

TTTTTGACTActGAATGTCTTTTTTCGCTACTGACTGaAAAAATAGCTACATTCGCACTTTTGtC

>WB235_Fam_88_34_3 Nr. of seq. 3 Alignment length(with gaps) = 34
Alignment score = 0.980392
WB235_1:11432554-11432811 Satlength=258 Nr of Repeats=6 RepeatLength=34
seed=ATGCACCATG Num.seqs=4 Similarity=0.679739
0 ATGCACCATGTCAAAAAATATATCCAAAAGTACG
WB235_1:11455940-11456197 Satlength=258 Nr of Repeats=6 RepeatLength=34
seed=ATGCACCATG Num.seqs=4 Similarity=0.679739
0 ATGCACCATGTCAAAAAATATATCCAAAAGTACG
WB235_1:12258128-12258286 Satlength=159 Nr of Repeats=5 RepeatLength=34
seed=ATGCACCATG Num.seqs=4 Similarity=0.712418
0 ATGCACCATGTCAAAAAATATATCCAAAANTACG

Consensus:

ATGCACCATGTCAAAAAATATATCCAAAAGTACG

>WB235_Fam_89_32_3 Nr. of seq. 3 Alignment length(with gaps) = 32
Alignment score = 0.972222
WB235_4:13909776-13910308 Satlength=533 Nr of Repeats=19 RepeatLength=32
seed=CGACCTGCGA Num.seqs=14 Similarity=0.994048
0 CGACCTGCGACCTAGCGACCTGGGTCGCTTTG
WB235_6:2307188-2307299 Satlength=112 Nr of Repeats=4 RepeatLength=32
seed=CGACCTGCGA Num.seqs=3 Similarity=0.805556
0 CGACCTGCGACCTAGCGACCTAGGTCGCTTTG
WB235_6:12578040-12578842 Satlength=803 Nr of Repeats=12 RepeatLength=32
seed=CGACCTAGGT Num.seqs=8 Similarity=0.956845
15 CGACCTGCGACCTAGCGACCTAGGTCGCTTTG

Consensus:

CGACCTGCGACCTAGCGACCTaGGTCGCTTTG

>WB235_Fam_90_27_3 Nr. of seq. 3 Alignment length(with gaps) = 27

Alignment score = 0.658436

WB235_4:2967003-2967147 Satlength=145 Nr of Repeats=6 RepeatLength=24

seed=GCGGCCGACA Num.seqs=6 Similarity=0.855556

0 -GCGGCCGACACCTTACGGGTTG--TA

WB235_2:13502158-13503434 Satlength=1277 Nr of Repeats=26 RepeatLength=27

seed=AGCAGCCGAC Num.seqs=20 Similarity=0.791813

0 AGCAGCCGACACCTTGCNGGTTGCTTA

WB235_5:19555359-19555663 Satlength=305 Nr of Repeats=8 RepeatLength=27

seed=GCAGCCGACA Num.seqs=6 Similarity=0.584291

1 AGCAGCCGACACCTCACTGGTCCCTNA

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Consensus:

aGCaGCCGACACCTtaCnGGTtgcttA

>WB235_Fam_91_26_3 Nr. of seq. 3 Alignment length(with gaps) = 26

Alignment score = 0.965812

WB235_2:2157814-2157944 Satlength=131 Nr of Repeats=5 RepeatLength=26

seed=TCAAGGCGAA Num.seqs=5 Similarity=0.979487

0 TCAAGGCGAAACGGGAGGTGAATCGC

Rev.of_WB235_5:8836966-8837173 Satlength=208 Nr of Repeats=8

RepeatLength=26 seed=TTCGCCCTGA Num.seqs=7 Similarity=0.907204

10 TCAGGGCGAAACGGGAGGTGAATCGC

Rev.of_WB235_5:8879060-8879267 Satlength=208 Nr of Repeats=8

RepeatLength=26 seed=TTCGCCCTGA Num.seqs=7 Similarity=0.907204

10 TCAGGGCGAAACGGGAGGTGAATCGC

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Consensus:

TCAgGGCGAAACGGGAGGTGAATCGC

>WB235_Fam_92_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23

Alignment score = 0.801932

WB235_2:13342774-13342879 Satlength=106 Nr of Repeats=5 RepeatLength=21

seed=CTAGAAAAAC Num.seqs=5 Similarity=0.898413

0 CTA-GAAAAACTCGGCCATCAA-

Rev.of_WB235_2:13343764-13344901 Satlength=1138 Nr of Repeats=46

RepeatLength=21 seed=TTTTCTAGTT Num.seqs=34 Similarity=0.794245

8 CTA-GAAAAACTCGGCCATCAA-

WB235_2:642340-642984 Satlength=645 Nr of Repeats=25 RepeatLength=23

seed=GGCCACCAAT Num.seqs=20 Similarity=0.753776

13 CTATAAAAAACTCGGCCACCAAT

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Consensus:

CTAgAAAAAACTCGGCCAtCAA

>WB235_Fam_93_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.608696
WB235_3:2103059-2103647 Satlength=589 Nr of Repeats=25 RepeatLength=21
seed=GCCTAAAAAC Num.seqs=16 Similarity=0.805291
0 GCCTAAAAA--CGTAAATTTTAA
Rev.of_WB235_4:2702010-2702785 Satlength=776 Nr of Repeats=31
RepeatLength=21 seed=TTTGGATTTT Num.seqs=25 Similarity=0.861799
15 GCCTAAAAA--TCCAATTTTAA
WB235_1:898453-898911 Satlength=459 Nr of Repeats=21 RepeatLength=22
seed=TTTtagccAA Num.seqs=17 Similarity=0.862299
16 -CCAAAAAATCCGTTAATTTTAG

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Consensus:

gCcTAAAAAcgtaAATTTTAa

>WB235_Fam_94_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.748792
WB235_4:3754942-3755101 Satlength=160 Nr of Repeats=5 RepeatLength=21
seed=TAGTTTGTAG Num.seqs=3 Similarity=0.661376
0 TAG-TTT-ATAGTTTGcAGTTTG
WB235_5:3651539-3651616 Satlength=78 Nr of Repeats=4 RepeatLength=21
seed=AGTTTGTAGT Num.seqs=3 Similarity=0.640212
1 TAG-TTT-GTAGTTTGTNGTTTG
Rev.of_WB235_1:12893074-12893850 Satlength=777 Nr of Repeats=11
RepeatLength=23 seed=ACTACAAACT Num.seqs=10 Similarity=1.000000
4 TAGTTTTcATAGTTTGTAGTTTG

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Consensus:

TAGTTTaTAGTTTGtaGTTTG

>WB235_Fam_95_20_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.656566
WB235_3:3042951-3043689 Satlength=739 Nr of Repeats=38 RepeatLength=18
seed=GTCGATTTAC Num.seqs=33 Similarity=0.778900
0 GTCGATTTACG-AGA-TTN--T
Rev.of_WB235_2:13737396-13737775 Satlength=380 Nr of Repeats=15
RepeatLength=21 seed=CTCGTAAATC Num.seqs=9 Similarity=0.754630
13 GTCGATTTACGAGGAGTTC-TT
WB235_4:1848441-1848937 Satlength=497 Nr of Repeats=18 RepeatLength=21
seed=TGTCGATTTA Num.seqs=15 Similarity=0.738095
21 GTCGATTTACG-GGAGTTCAGT

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Consensus:

GTCGATTTACGgGAgTTcnT

>WB235_Fam_96_22_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.777778
WB235_2:2733211-2733873 Satlength=663 Nr of Repeats=24 RepeatLength=22
seed=ACTACAGTAA Num.seqs=18 Similarity=0.729847
0 ACTACAGTAACCCTACANTACC
WB235_5:1025021-1025505 Satlength=485 Nr of Repeats=20 RepeatLength=22
seed=ACAGTACTCC Num.seqs=16 Similarity=0.776630
3 ANTACAGTACTCCTACAGTACC
Rev.of_WB235_5:16536032-16536834 Satlength=803 Nr of Repeats=14
RepeatLength=22 seed=GGGTACTGTA Num.seqs=9 Similarity=0.840067
12 ACTACAGTACCCATACAGTACT

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Consensus:

AcTACAGTAccCcTACAgTACc

>WB235_Fam_97_19_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.608466
WB235_1:2524693-2524982 Satlength=290 Nr of Repeats=10 RepeatLength=18
seed=GCCTAGGAAT Num.seqs=8 Similarity=0.772487
0 GCCTAGGAAT-CCAAT--ATG
Rev.of_WB235_1:1278237-1279259 Satlength=1023 Nr of Repeats=33
RepeatLength=19 seed=TTCTAGGCCA Num.seqs=21 Similarity=0.753383
8 GCCTAGAAATCCTCA--GATG
Rev.of_WB235_1:1108035-1108695 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

>WB235_Fam_98_18_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.761905
WB235_6:3338986-3339541 Satlength=556 Nr of Repeats=27 RepeatLength=18
seed=TTTGTGTCAGT Num.seqs=20 Similarity=0.766579
0 TTTGTGTCAGTGCT--ATAGT
WB235_6:3392053-3392273 Satlength=221 Nr of Repeats=10 RepeatLength=18
seed=TTGTCAGTGC Num.seqs=7 Similarity=0.848325
2 TTTGTGTCAGTGCT--ATAGT
Rev.of_WB235_6:1544700-1544784 Satlength=85 Nr of Repeats=4
RepeatLength=21 seed=TCTGAGCACT Num.seqs=4 Similarity=0.925926
17 TTTGTGTCAGTGCTCAGATAAT

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Consensus:

TTTGTGTCAGTGCTATAgT

>WB235_Fam_99_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.767196

WB235_3:1154872-1155214 Satlength=343 Nr of Repeats=4 RepeatLength=21
seed=ACTACAGTAC Num.seqs=3 Similarity=0.788360
0 ACTACAGTACCCCNACNACT
WB235_4:14426797-14427553 Satlength=757 Nr of Repeats=36 RepeatLength=21
seed=CAACTACCAC Num.seqs=36 Similarity=0.943361
10 ACTACCGTACCAACTACCACA
WB235_4:14447004-14447298 Satlength=295 Nr of Repeats=13 RepeatLength=21
seed=ACTACCGTAC Num.seqs=12 Similarity=0.895142
21 ACTACCGTACCAACTACCACA

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Consensus:

ACTACcGTACCaaCtACcACa

>WB235_Fam_100_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.957672
WB235_5:3373171-3373906 Satlength=736 Nr of Repeats=20 RepeatLength=21
seed=CTAACATTTT Num.seqs=12 Similarity=0.927850
0 CTAACATTTTTCAATTTTCGT
WB235_5:16625438-16625585 Satlength=148 Nr of Repeats=7 RepeatLength=21
seed=ATTTTCAAT Num.seqs=7 Similarity=0.848828
5 CTAACATTTTTCAATTTTCGT
WB235_5:3632093-3632198 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=TTTCAGTTTT Num.seqs=5 Similarity=0.911111
8 CTAACATTTTTCAGTTTTCGT

Consensus:

CTAACATTTTTCAaTTTTCGT

>WB235_Fam_101_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.682540
WB235_6:1214446-1215096 Satlength=651 Nr of Repeats=6 RepeatLength=21
seed=GTCAAGTCAA Num.seqs=4 Similarity=0.809524
34 AAATGCATTTTTGGTCAGTGC
Rev.of_WB235_6:1325710-1325901 Satlength=192 Nr of Repeats=7
RepeatLength=21 seed=TTGCACTGAC Num.seqs=6 Similarity=0.630303
44 AAATGAAGAGTTGGTCAGTGC
WB235_6:15295722-15295953 Satlength=232 Nr of Repeats=11 RepeatLength=21
seed=TGAAAGATTG Num.seqs=9 Similarity=0.957672
28 GTGCCTATGAAAGATTGGTCA

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Consensus:

GTgcaaatgnAtnnttGgTca

>WB235_Fam_102_20_3 Nr. of seq. 3 Alignment length(with gaps) = 20
Alignment score = 0.688889
WB235_2:13528439-13528985 Satlength=547 Nr of Repeats=24 RepeatLength=20
seed=GTAAATCGAC Num.seqs=16 Similarity=0.655886
10 ACACNACGTCGTAAATCGAC

Rev.of_WB235_3:2036337-2036525 Satlength=189 Nr of Repeats=9
RepeatLength=20 seed=TGTAGATTTA Num.seqs=6 Similarity=0.697778
21 ATAGAACCCCGTAAATCTAC
Rev.of_WB235_3:12835769-12836969 Satlength=1201 Nr of Repeats=30
RepeatLength=20 seed=TGTAGATTTA Num.seqs=22 Similarity=0.674981
21 ATAGANCTTCGTAAATCTAC

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Consensus:

GTAAATCtACAtAgaaCntC

>WB235_Fam_103_20_3 Nr. of seq. 3 Alignment length(with gaps) = 20
Alignment score = 0.777778
WB235_4:8572647-8581868 Satlength=9222 Nr of Repeats=443 RepeatLength=20
seed=CGATATAGCT Num.seqs=408 Similarity=0.824886
0 CGATATAGCTATTAACGATA
Rev.of_WB235_6:4031472-4056497 Satlength=25026 Nr of Repeats=1238
RepeatLength=20 seed=GCTATATCGT Num.seqs=1039 Similarity=0.874603
9 CGATATAGCTATTTACGATA
Rev.of_WB235_6:7077538-7079254 Satlength=1717 Nr of Repeats=55
RepeatLength=20 seed=TCGTTTATAG Num.seqs=33 Similarity=0.899747
18 CGACACAGCTATAAACGACA

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Consensus:

CGAtAtAGCTATtaACGAtA

>WB235_Fam_104_16_3 Nr. of seq. 3 Alignment length(with gaps) = 16
Alignment score = 0.777778
WB235_1:749263-749839 Satlength=577 Nr of Repeats=36 RepeatLength=16
seed=TTTCAGGCTT Num.seqs=36 Similarity=0.942460
0 TTTCAGGCTTTTCAGGC
WB235_5:17629258-17629682 Satlength=425 Nr of Repeats=26 RepeatLength=16
seed=CCAGGGTTCC Num.seqs=25 Similarity=1.000000
2 TTCCAGGGTTCCAGGG
WB235_5:17629258-17630037 Satlength=780 Nr of Repeats=29 RepeatLength=16
seed=CCAGGGTTCC Num.seqs=27 Similarity=0.987654
2 TTCCAGGGTTCCAGGG

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Consensus:

TTcCAGGgTTcCAGGg

>WB235_Fam_105_11_3 Nr. of seq. 3 Alignment length(with gaps) = 12
Alignment score = 0.787037
WB235_3:8897677-8897798 Satlength=122 Nr of Repeats=11 RepeatLength=11
seed=ATT-TGGAATAT Num.seqs=11 Similarity=0.903030
0 ATT-TGGAATAT
WB235_4:10984356-10985109 Satlength=754 Nr of Repeats=4 RepeatLength=11
seed=TTTGAAATAT Num.seqs=3 Similarity=1.000000
1 ATT-TGAAATAT

Rev.of_WB235_4:6469806-6469955 Satlength=150 Nr of Repeats=10
RepeatLength=12 seed=CAGAAATATAT Num.seqs=7 Similarity=0.915344
6 ATTCTGGAATAT

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Consensus:

ATTTGgAATAT

>WB235_Fam_106_11_3 Nr. of seq. 3 Alignment length(with gaps) = 12
Alignment score = 0.722222

WB235_4:5690583-5690638 Satlength=56 Nr of Repeats=5 RepeatLength=11
seed=TCCACTGACC Num.seqs=5 Similarity=0.951515

0 TCCACTGACCA-

WB235_2:6296590-6296638 Satlength=49 Nr of Repeats=4 RepeatLength=12
seed=CCACTGACCA Num.seqs=4 Similarity=0.944444

1 CCCACTGACCAT

Rev.of_WB235_6:13775030-13775085 Satlength=56 Nr of Repeats=5
RepeatLength=11 seed=GTGCTTGGTC Num.seqs=5 Similarity=0.951515

5 AGCACTGACCA-

Consensus:

ncCACTGACCA

>WB235_Fam_107_10_3 Nr. of seq. 3 Alignment length(with gaps) = 10
Alignment score = 0.733333

WB235_2:7450879-7451382 Satlength=504 Nr of Repeats=27 RepeatLength=10
seed=TCCATCCCCGA Num.seqs=19 Similarity=0.831650

0 TCCATCCCCGA

Rev.of_WB235_6:16884509-16885875 Satlength=1367 Nr of Repeats=37
RepeatLength=10 seed=TGGATCGGGA Num.seqs=23 Similarity=0.908300

4 TCCATCCCCGA

WB235_6:15470071-15470810 Satlength=740 Nr of Repeats=22 RepeatLength=10
seed=TATCTAGATC Num.seqs=15 Similarity=0.964444

2 TCTATCTAGA

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Consensus:

TCcATCccGA

>WB235_Fam_108_177_2 Nr. of seq. 2 Alignment length(with gaps) = 177
Alignment score = 1.000000

WB235_5:2389657-2390366 Satlength=710 Nr of Repeats=4 RepeatLength=177
seed=GAGTCTCACG Num.seqs=3 Similarity=0.943196

0

GAGTCTCACGATGTGTCAACGTGTCTCAGTCGGCTTGATCTACGTAGATCTACAAAAAATGCGGGAGAAGAGA
CGCAGACTTATTCTCTGATTTTGCATGAGTAAGAGCGTGCTGGCGTCACATTTTTGTGCGCAAAAAATTCCCG
CATTTTTTTGTAGATCAAACCGTAATGGGACG

WB235_5:2497936-2498645 Satlength=710 Nr of Repeats=4 RepeatLength=177
seed=GAGTCTCACG Num.seqs=3 Similarity=0.943196

0

GCcacCcTTAAcCCTAAcCCAaGCAGAGCAGGaTGTAGGCCTGaaAcGcGGTaGcgAcaCaaTCAaGCCcAAc
AacCaGGGaTGAGGGCCGCAGGCCCGaaaaACTCTTaGAAACTgTaG

>WB235_Fam_111_110_2 Nr. of seq. 2 Alignment length(with gaps) = 110
Alignment score = 0.745455
WB235_6:11688529-11688958 Satlength=430 Nr of Repeats=4 RepeatLength=108
seed=TTTCACGTTT Num.seqs=3 Similarity=0.860082
0 TTTCACGTTTTTCAGGTGATTATCTAGGTCACGAACCTAATTTATTTTGAAAATTGACCT--
GTGGACCTATAACTTTGGAGATATGGGAAATTGAGTATGGGCTTTCAGAT
WB235_6:13242451-13244463 Satlength=2013 Nr of Repeats=18
RepeatLength=108 seed=TTTCAGATTT Num.seqs=17 Similarity=0.875000
100 TTTCACATTTTCACTTGATTATATAGGTCACGACCCAAATTATTTTGAAAATTGAGCTACACGG--
CTGTAACTTTGGAGCTATGGGTAATCAAGTATGAGCTTTCAGAT

Consensus:

TTTCACaTTTTCacgTGATTATaTAGGTCACGAaCcAAaTTATTTTGAAAATTGAcCTacacGGacCTaTAAC
TTTGAGaTaTGGGaATcaAGTATGaGCTTTCAGAT

>WB235_Fam_112_86_2 Nr. of seq. 2 Alignment length(with gaps) = 86
Alignment score = 0.689922
WB235_2:5073308-5077334 Satlength=4027 Nr of Repeats=52 RepeatLength=76
seed=TGTATTTTGA Num.seqs=36 Similarity=0.973545
0 TGTATTTTGAAAGGTCATCTCAATA--GAAAAGATGGAAGACTAC--AG--AA--A-AA-
CTATTGAGAGACCCCGAAATACTGGC
Rev.of_WB235_2:8975477-8977487 Satlength=2011 Nr of Repeats=24
RepeatLength=86 seed=AGCCAGTATT Num.seqs=23 Similarity=0.984619
1
TGTATTTTGAAAGGTCGTGGCAATAGGGAAAAGATGGAAGAGTTCGAAGTTAACGAGAAGCTATTGCCAGACC
CCGAAATACTGGC

Consensus:

TGTATTTTGAAAGGTCaTcgCAATAggGAAAAGATGGAAGAcTaCgaAGttAAcgAgAAgCTATTGacAGACC
CCGAAATACTGGC

>WB235_Fam_113_73_2 Nr. of seq. 2 Alignment length(with gaps) = 73
Alignment score = 0.945205
WB235_1:12192426-12192752 Satlength=327 Nr of Repeats=4 RepeatLength=73
seed=AATAAAATAT Num.seqs=3 Similarity=0.963470
0
AATAAAATATTGGAATCCCTATGACACACTTAAGCCTAAAGGCCCGAAAAACATACTAGGATGCCCAACTGG
Rev.of_WB235_5:15525755-15526135 Satlength=381 Nr of Repeats=5
RepeatLength=73 seed=TTAGGCTTAA Num.seqs=3 Similarity=0.939117
40
AATAAAATATTGGAATCCCTTATGACACACTTAAGCCTAAAGGCCCGAAAAAAACTAGGATGCCCAACTGG

Consensus:

AATAAAATATTGGAAATCCcTATGACACACTTAAGCCTAAAGGCCCGAAAAAaAaACTAGGATGCCCAACTGG

>WB235_Fam_114_44_2 Nr. of seq. 2 Alignment length(with gaps) = 44
Alignment score = 0.681818
WB235_2:9693772-9694139 Satlength=368 Nr of Repeats=4 RepeatLength=42
seed=CAGCCGACAG Num.seqs=3 Similarity=0.533769
0 -CAGCCGACAGCCGAAAAATT--GGAATTTTCGGCTGGTAGCAC
WB235_5:4029541-4030122 Satlength=582 Nr of Repeats=5 RepeatLength=42
seed=CCAGCCGACA Num.seqs=3 Similarity=0.684755
0 CCAGCCGACAGCCGAAATTTTCACG-ATTTTCGGCTGGTNGCG-

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Consensus:

cCAGCCGACAGCCGAAAAaTTcacGaATTTTCGGCTGGTaGCac

>WB235_Fam_115_44_2 Nr. of seq. 2 Alignment length(with gaps) = 44
Alignment score = 0.704545
WB235_1:11829562-11829989 Satlength=428 Nr of Repeats=5 RepeatLength=42
seed=TCGGCAAATC Num.seqs=3 Similarity=0.723514
0 TCGGCAAA-TCGGCAATTNCTGGTTTTTTTNAa-ATTTGCCGAGC
Rev.of_WB235_4:15776137-15776526 Satlength=390 Nr of Repeats=5
RepeatLength=42 seed=GCTCGGCAAA Num.seqs=3 Similarity=0.957672
0 ACGGCAAATTCGGCAAAT-CT-CTTTTTTCAATATTTGCCGAGC

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Consensus:

aCGGCAAAaTCGGCAAATnCTGcTTTTTTTcAaATTTGCCGAGC

>WB235_Fam_116_44_2 Nr. of seq. 2 Alignment length(with gaps) = 44
Alignment score = 0.969697
WB235_1:9636862-9637728 Satlength=867 Nr of Repeats=20 RepeatLength=44
seed=CTGTTTTCTG Num.seqs=18 Similarity=0.984749
0 CTGTTTTCTGAGCATTTTAGATTTTCGGATTGATGGCCGAAAGG
WB235_4:17128248-17129128 Satlength=881 Nr of Repeats=20 RepeatLength=44
seed=GATTGATGGC Num.seqs=20 Similarity=0.962360
27 CTGTTTTCTGAGCATTGTAGATTTTCGGATTGATGGCCGAAAGG

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

CTGTTTTCTGAGCATTgTAGATTTTCGGATTGATGGCCGAAAGG

>WB235_Fam_117_41_2 Nr. of seq. 2 Alignment length(with gaps) = 41
Alignment score = 0.711382
WB235_6:17125270-17125459 Satlength=190 Nr of Repeats=5 RepeatLength=38
seed=CCGTTTCGCC Num.seqs=4 Similarity=0.982456
0 CCGTTTCGCCCTTGAGCGATT-C--ACCCTTAAATGGGCCTC
WB235_6:7351473-7361391 Satlength=9919 Nr of Repeats=248 RepeatLength=40
seed=AATGGGCGCC Num.seqs=247 Similarity=0.954892
30 -GGTTTCGCTTTGAGCGATTTCCTTACCCTTAAATGGGCGCC

***** * ***** *

Consensus:

ccGTTTCGCcTTGAGCGATTcCttACCCTTAAATGGGCccC

>WB235_Fam_118_41_2 Nr. of seq. 2 Alignment length(with gaps) = 41
Alignment score = 1.000000

WB235_2:7379726-7379898 Satlength=173 Nr of Repeats=4 RepeatLength=41

seed=AAAACGGGAA Num.seqs=3 Similarity=0.978320

0 AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTTA

WB235_2:7379725-7380258 Satlength=534 Nr of Repeats=10 RepeatLength=41

seed=AAAAACGGGA Num.seqs=6 Similarity=0.956640

40 AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTTA

Consensus:

AAAACGGGAAAACGGGAATTCCCGTTCCCGTGAAAATTTTA

>WB235_Fam_119_40_2 Nr. of seq. 2 Alignment length(with gaps) = 40
Alignment score = 0.975000

WB235_3:1056939-1057667 Satlength=729 Nr of Repeats=14 RepeatLength=40

seed=AAAATCCACG Num.seqs=12 Similarity=0.883838

0 AAAATCCACGTAGATTATTGATTTTTTCATNGAATTTTGCA

WB235_3:1056932-1058332 Satlength=1401 Nr of Repeats=16 RepeatLength=40

seed=TTTTGCAAAA Num.seqs=11 Similarity=0.759596

33 AAAATCCACGTAGATTATTGATTTTTTCATGGAATTTTGCA

Consensus:

AAAATCCACGTAGATTATTGATTTTTTCATgGAATTTTGCA

>WB235_Fam_120_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.897436

WB235_4:11072392-11075919 Satlength=3528 Nr of Repeats=90 RepeatLength=39

seed=TTATGGAAAA Num.seqs=86 Similarity=0.949069

0 TTATGGAAAAGTGGCTCTAGAGCCACAAGAAATACCAGT

WB235_5:10605694-10612481 Satlength=6788 Nr of Repeats=174

RepeatLength=39 seed=GGCCACCAGA Num.seqs=173 Similarity=0.944141

20 TTATGAAAAAGTGGCTCTAGGGCCACCAGAAATACCAGT

Consensus:

TTATGaAAAAGTGGCTCTAGaGCCACaAGAAATACCAGT

>WB235_Fam_121_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.601852

WB235_4:3291067-3291207 Satlength=141 Nr of Repeats=5 RepeatLength=33

seed=CGGCATATGC Num.seqs=3 Similarity=0.946128

0 CGGCATA-TGCCGTGAATTTTAAAAT-CGGCATAA-

Rev.of_WB235_4:15517213-15517493 Satlength=281 Nr of Repeats=8
RepeatLength=35 seed=TTGCCGGATT Num.seqs=8 Similarity=0.983673
32 -GGCAAATTACCATAAATTTTCAAATCCGGCAAAAC

**** * * * * * ***** **** * *

Consensus:

cGGCAaAtTaCCaTaAATTTTaAAATcCGGCAaAAc

>WB235_Fam_122_34_2 Nr. of seq. 2 Alignment length(with gaps) = 34
Alignment score = 0.612745

WB235_4:1515989-1516221 Satlength=233 Nr of Repeats=8 RepeatLength=29
seed=CCACCCGGGA Num.seqs=8 Similarity=0.850575

0 CCACCCGGGAGGTGTCGGCTGCT---CTA-AAC

WB235_5:18577906-18578272 Satlength=367 Nr of Repeats=11 RepeatLength=33
seed=TGTCGGCTGC Num.seqs=10 Similarity=0.876094

11 -CTCCCGGCAGGTGTCGGCTGCTAAACTATAGC

* ***** ***** **** * *

Consensus:

cCaCCCGGcAGGTGTCGGCTGCTaaaaCTAtAaC

>WB235_Fam_123_32_2 Nr. of seq. 2 Alignment length(with gaps) = 32
Alignment score = 0.671875

WB235_3:255029-255455 Satlength=427 Nr of Repeats=12 RepeatLength=30
seed=TTTTTTGAGC Num.seqs=9 Similarity=0.761574

0 TTTTTTGAGCCAAAAATTC-AAAAAT-CTCG

WB235_3:244458-244613 Satlength=156 Nr of Repeats=4 RepeatLength=31
seed=AGCTCAAAAT Num.seqs=3 Similarity=0.711806

6 -TTTTTGAGCTCAAAATTCTGAAAAATGCTCA

***** ***** ***** ***

Consensus:

tTTTTTGAGCcAAAAATTCTaAAAAATgCTCa

>WB235_Fam_124_32_2 Nr. of seq. 2 Alignment length(with gaps) = 32
Alignment score = 1.000000

WB235_1:10945938-10952999 Satlength=7062 Nr of Repeats=238
RepeatLength=32 seed=GCACCAAATA Num.seqs=152 Similarity=0.889392

0 GCACCAAATAGCACCAATTTAGCACCGATGGA

Rev.of_WB235_6:12276852-12278772 Satlength=1921 Nr of Repeats=55
RepeatLength=32 seed=GGTGCTATTT Num.seqs=46 Similarity=0.867432

15 GCACCAAATAGCACCAATTTAGCACCGATGGA

Consensus:

GCACCAAATAGCACCAATTTAGCACCGATGGA

>WB235_Fam_125_31_2 Nr. of seq. 2 Alignment length(with gaps) = 31
Alignment score = 0.752688

WB235_1:1503613-1504297 Satlength=685 Nr of Repeats=18 RepeatLength=31
seed=GGT TACTGT A Num.seqs=11 Similarity=0.738025
0 GGT TACTGT AACTCAATTATAGGATACTTNG
WB235_2:3496033-3496764 Satlength=732 Nr of Repeats=18 RepeatLength=31
seed=GGT TACTGT A Num.seqs=11 Similarity=0.669318
0 GGT TACTGT AGATCGATCCTAGGATACTTTG

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

GGT TACTGT AaaTCaATcaTAGGATACTTtG

>WB235_Fam_126_31_2 Nr. of seq. 2 Alignment length(with gaps) = 31
Alignment score = 0.784946
WB235_2:2577037-2578087 Satlength=1051 Nr of Repeats=24 RepeatLength=31
seed=CTGAAATTCC Num.seqs=16 Similarity=0.855556
0 CTGAAATTCCAATTTTCCAGTGTA AAAATGT
WB235_5:18737977-18738195 Satlength=219 Nr of Repeats=6 RepeatLength=31
seed=TGTA AAAATG Num.seqs=5 Similarity=0.651613
20 CTGAAATTATGAATTTCCAATGT AAAATGT

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

CTGAAATTacaAaTTTCCAaTGTA AAAATGT

>WB235_Fam_127_31_2 Nr. of seq. 2 Alignment length(with gaps) = 31
Alignment score = 0.956989
WB235_4:15784879-15785128 Satlength=250 Nr of Repeats=6 RepeatLength=31
seed=TCGACAGAAG Num.seqs=4 Similarity=0.665825
0 TCGACAGAAGCTGTCTGGAAATCACACTTTCC
WB235_6:12606642-12606920 Satlength=279 Nr of Repeats=9 RepeatLength=31
seed=TCGACAGAAG Num.seqs=8 Similarity=0.729437
0 TCGACAGAAGCTGTCTGGACATCACACTTTCC

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

TCGACAGAAGCTGTCTGGAAATCACACTTTCC

>WB235_Fam_128_29_2 Nr. of seq. 2 Alignment length(with gaps) = 29
Alignment score = 1.000000
WB235_1:5152583-5153888 Satlength=1306 Nr of Repeats=45 RepeatLength=29
seed=AAGGATTTCC Num.seqs=45 Similarity=0.955138
0 AAGGATTTCCCACTATGTCAATACATTGT
Rev.of_WB235_5:7988900-7991510 Satlength=2611 Nr of Repeats=90
RepeatLength=29 seed=CATAGTGGA Num.seqs=90 Similarity=0.932705
17 AAGGATTTCCCACTATGTCAATACATTGT

Consensus:

AAGGATTTCCCACTATGTCAATACATTGT

>WB235_Fam_129_27_2 Nr. of seq. 2 Alignment length(with gaps) = 27
Alignment score = 0.901235
WB235_2:3102561-3102723 Satlength=163 Nr of Repeats=6 RepeatLength=27
seed=GCTGCTGGAG Num.seqs=6 Similarity=0.881481
0 GCTGCTGGAGGATCCACTGCATCAACT
WB235_2:3106228-3107119 Satlength=892 Nr of Repeats=33 RepeatLength=27
seed=GCTGCTGGAG Num.seqs=33 Similarity=0.919285
0 GCTGCTGGAGGATCAACTGCATCAACC

Consensus:

GCTGCTGGAGGATCaACTGCATCAACc

>WB235_Fam_130_26_2 Nr. of seq. 2 Alignment length(with gaps) = 26
Alignment score = 1.000000
WB235_1:1658366-1660394 Satlength=2029 Nr of Repeats=78 RepeatLength=26
seed=CAAAACCGGC Num.seqs=78 Similarity=0.926569
0 CAAAACCGGCAATTGCCGAAAATTCC
Rev.of_WB235_1:1807418-1807780 Satlength=363 Nr of Repeats=11
RepeatLength=26 seed=TTGCCGGTTT Num.seqs=8 Similarity=0.798535
12 CAAAACCGGCAATTGCCGAAAATTCC

Consensus:

CAAAACCGGCAATTGCCGAAAATTCC

>WB235_Fam_131_24_2 Nr. of seq. 2 Alignment length(with gaps) = 24
Alignment score = 0.722222
WB235_2:3753993-3754089 Satlength=97 Nr of Repeats=4 RepeatLength=24
seed=TGCATCTGCC Num.seqs=4 Similarity=0.750000
0 TGCATCTGCCGCTGGAGCTGGCGC
Rev.of_WB235_5:14320937-14321192 Satlength=256 Nr of Repeats=5
RepeatLength=24 seed=GCCGCTCCAG Num.seqs=3 Similarity=0.814815
3 GGCATCTGGTGCCGGAGCTGGAGC

***** **

Consensus:

gGCATCTGccGCcGGAGCTGGaGC

>WB235_Fam_132_24_2 Nr. of seq. 2 Alignment length(with gaps) = 24
Alignment score = 0.680556
WB235_2:11365554-11365650 Satlength=97 Nr of Repeats=5 RepeatLength=24
seed=GCTTAGGCTT Num.seqs=3 Similarity=0.648148
0 GCTTAGGCTTGGGCTTAGGCTNAA
Rev.of_WB235_5:18797535-18797724 Satlength=190 Nr of Repeats=5
RepeatLength=24 seed=GCCTAAGCCT Num.seqs=3 Similarity=0.666667
2 GCCTAGACTCAGGCTTAGGCTTAG

** *** ** ***** *

Consensus:

GCcTAGaCTcaGGCTTAGGCTtAa

>WB235_Fam_133_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
Alignment score = 0.630435
WB235_1:923168-925176 Satlength=2009 Nr of Repeats=89 RepeatLength=21
seed=AATTCTAGG Num.seqs=60 Similarity=0.911757
0 AATTCTAGGCCACGA-TTTGA-
Rev.of_WB235_1:1097742-1098271 Satlength=530 Nr of Repeats=23
RepeatLength=23 seed=GGCCTAGAAA Num.seqs=23 Similarity=0.818525
12 TATTCTAGGCCACCACGTTTCAG

***** * ** *
Consensus:

aAATTCTAGGCCACcAcgTTcAg

>WB235_Fam_134_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
Alignment score = 0.673913
WB235_5:19354949-19355211 Satlength=263 Nr of Repeats=11 RepeatLength=21
seed=TCTAATTAGA Num.seqs=10 Similarity=0.939330
0 TCTAATTAGAT-CACCTT-TTTT
WB235_5:19356787-19357065 Satlength=279 Nr of Repeats=13 RepeatLength=21
seed=TTCTAATTAG Num.seqs=10 Similarity=0.650000
20 -CTAATTAGATNCGCCNTCTTTT

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

tCTAATTAGATnCaCctTcTTTT

>WB235_Fam_135_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
Alignment score = 0.659420
WB235_5:19679307-19679396 Satlength=90 Nr of Repeats=4 RepeatLength=22
seed=ATTGGATTTT Num.seqs=3 Similarity=0.959596
0 ATTGGATTTTTTCAACCCAAAAA-
WB235_1:623235-624175 Satlength=941 Nr of Repeats=22 RepeatLength=23
seed=AAAAAAAATT Num.seqs=14 Similarity=0.950948
16 ATTAAATTTTTCAACAAAAAAA

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

ATTaaATTTTTTCaAcaAAAAa

>WB235_Fam_136_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.643939
WB235_3:1534930-1535260 Satlength=331 Nr of Repeats=16 RepeatLength=20
seed=CATAAAAATT Num.seqs=13 Similarity=0.947009
0 CATAAAAAT-TCAGAAAA-ATG
Rev.of_WB235_1:13960468-13960552 Satlength=85 Nr of Repeats=4
RepeatLength=21 seed=ATATTTGTG Num.seqs=4 Similarity=0.936508
0 AATAAAAATGTCACAAATAT-

***** *** **** **

Consensus:

aATAAAAAATgTCACAAAAAtATg

>WB235_Fam_137_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.681818
WB235_4:1949738-1952318 Satlength=2581 Nr of Repeats=113 RepeatLength=21
seed=GTAAATCTAC Num.seqs=78 Similarity=0.823929
0 GTAAATCTACAGTAAT-NCCCC
WB235_3:999373-999632 Satlength=260 Nr of Repeats=12 RepeatLength=22
seed=TAAATCTACA Num.seqs=10 Similarity=0.692929
1 GTAAATCTACACATAGCCCC

***** ** ****

Consensus:

GTAAATCTACAcAAATagCCCC

>WB235_Fam_138_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.621212
WB235_4:16491101-16491225 Satlength=125 Nr of Repeats=5 RepeatLength=21
seed=TTCAAGCCTT Num.seqs=3 Similarity=0.915344
0 TTCAAGCC-TTTTCAGACCAAT
Rev.of_WB235_1:13768184-13768352 Satlength=169 Nr of Repeats=7
RepeatLength=21 seed=CAAAATTTCGT Num.seqs=6 Similarity=0.814646
4 TTTGAGCNAATTTTCGGACGAAT

** *** ***** *** **

Consensus:

TTcaAGCcaTTTTCaGACcAAT

>WB235_Fam_139_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 1.000000
WB235_1:13085679-13085769 Satlength=91 Nr of Repeats=4 RepeatLength=22
seed=TCGAGAAAAA Num.seqs=3 Similarity=1.000000
0 TCGAGAAAAAATCTGAAAAAAT
Rev.of_WB235_1:13102088-13102201 Satlength=114 Nr of Repeats=5
RepeatLength=22 seed=TTTTTTCTCG Num.seqs=4 Similarity=1.000000
11 TCGAGAAAAAATCTGAAAAAAT

Consensus:

TCGAGAAAAAATCTGAAAAAAT

>WB235_Fam_140_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.954545
WB235_2:3301138-3301263 Satlength=126 Nr of Repeats=4 RepeatLength=22
seed=ATTCTGCGCA Num.seqs=3 Similarity=0.656566
0 ATTCTGCGCACCCCCTGCGCNG

Rev.of_WB235_5:19315501-19315626 Satlength=126 Nr of Repeats=4
RepeatLength=22 seed=GTGCGCAGAA Num.seqs=3 Similarity=0.676768
11 ATTCTGCGCACCCCCTGCGCAG

***** *

Consensus:

ATTCTGCGCACCCCCTGCGCaG

>WB235_Fam_141_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.933333
WB235_1:1755610-1758756 Satlength=3147 Nr of Repeats=154 RepeatLength=20
seed=CCACCAAAAA Num.seqs=145 Similarity=0.874815
0 CCACCAAAAAGGTTTCTAGG
WB235_1:1760846-1762239 Satlength=1394 Nr of Repeats=64 RepeatLength=20
seed=TTCTAGGCCA Num.seqs=51 Similarity=0.812235
13 CCACCAAAAATGTTTCTAGG

***** *

Consensus:

CCACCAAAAAGTTTCTAGG

>WB235_Fam_142_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.950000
WB235_1:2333731-2334442 Satlength=712 Nr of Repeats=8 RepeatLength=20
seed=GGACTAGTTT Num.seqs=6 Similarity=0.880000
0 GGACTAGTTTTCGAGTAGAG
WB235_1:2333731-2334603 Satlength=873 Nr of Repeats=11 RepeatLength=20
seed=GGACTAGTTT Num.seqs=7 Similarity=0.745276
0 GGACTAGTTTTNGAGTAGAG

***** *

Consensus:

GGACTAGTTTTcGAGTAGAG

>WB235_Fam_143_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.866667
WB235_5:2634833-2635037 Satlength=205 Nr of Repeats=7 RepeatLength=20
seed=CCCCGACGCT Num.seqs=5 Similarity=0.920000
0 CCCCgACGCTCGAGCTCAAA
WB235_5:2634964-2635164 Satlength=201 Nr of Repeats=10 RepeatLength=20
seed=GCTCGAGCTC Num.seqs=10 Similarity=0.928889
7 CCCCgAAGCTCGAGCTCAAG

***** *

Consensus:

CCCCGAaGCTCGAGCTCAAA

>WB235_Fam_144_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.800000

WB235_6:16050430-16050549 Satlength=120 Nr of Repeats=6 RepeatLength=20
seed=CCACCCTGTA Num.seqs=5 Similarity=0.706349
0 CCACCCTGTAATATCATGGA
Rev.of_WB235_6:16286380-16286520 Satlength=141 Nr of Repeats=7
RepeatLength=20 seed=TACAGGGTGG Num.seqs=5 Similarity=0.920000
10 CCACCCTGTATAATTATGGA

***** ** *****

Consensus:

CCACCCTGTAAaATcATGGA

>WB235_Fam_145_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19
Alignment score = 0.684211
WB235_2:14105236-14105489 Satlength=254 Nr of Repeats=11 RepeatLength=18
seed=CTAGGTGCCT Num.seqs=8 Similarity=0.804233
0 CTAGGTGCCTA-TCCATTC
Rev.of_WB235_4:2861147-2861589 Satlength=443 Nr of Repeats=12
RepeatLength=19 seed=ACCTAGGCAT Num.seqs=8 Similarity=0.751880
6 CTAGGTGCCTACTTTATGC

***** * ** *

Consensus:

CTAGGTGCCTAcTccATgC

>WB235_Fam_146_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19
Alignment score = 0.929825
WB235_4:2650676-2650942 Satlength=267 Nr of Repeats=11 RepeatLength=19
seed=CGCCAAGTAT Num.seqs=8 Similarity=0.694345
0 CGCCAAGTATCGAGAAAAG
Rev.of_WB235_5:19372325-19372591 Satlength=267 Nr of Repeats=11
RepeatLength=19 seed=GATCCTTGGC Num.seqs=9 Similarity=0.898636
11 CGCCAAGGATCGAGAAAAG

***** *****

Consensus:

CGCCAAGgATCGAGAAAAG

>WB235_Fam_147_17_2 Nr. of seq. 2 Alignment length(with gaps) = 17
Alignment score = 0.656863
WB235_2:14738853-14738949 Satlength=97 Nr of Repeats=6 RepeatLength=16
seed=GCAGTTTGCC Num.seqs=6 Similarity=0.794444
0 GCAGTTTGCC-GAATTG
Rev.of_WB235_6:16372783-16373033 Satlength=251 Nr of Repeats=11
RepeatLength=16 seed=TTCCGGCAAT Num.seqs=7 Similarity=0.976190
13 -CCGATTGCCGGAATTG

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Consensus:

gCaGaTTGCCgGAATTG

>WB235_Fam_148_17_2 Nr. of seq. 2 Alignment length(with gaps) = 17
Alignment score = 0.803922
WB235_6:6212839-6212968 Satlength=130 Nr of Repeats=8 RepeatLength=16
seed=GCACTGACAA Num.seqs=7 Similarity=0.876984
0 GCACTGA-CAATTTTTT
Rev.of_WB235_6:1334194-1334262 Satlength=69 Nr of Repeats=4
RepeatLength=17 seed=TGGTCAGTGC Num.seqs=4 Similarity=0.882353
10 GCACTGACCAACTTTTT

***** *** *****

Consensus:

GCACTGAcCAAcTTTTT

>WB235_Fam_149_16_2 Nr. of seq. 2 Alignment length(with gaps) = 16
Alignment score = 0.750000
WB235_5:18410594-18410720 Satlength=127 Nr of Repeats=9 RepeatLength=14
seed=GTCTGGGGTC Num.seqs=9 Similarity=0.978836
1 GGT-CTGGGGT-CTGG
WB235_5:20524563-20524679 Satlength=117 Nr of Repeats=5 RepeatLength=16
seed=GTACTAGGGT Num.seqs=3 Similarity=0.888889
1 GGTACTGGGGTACTGG

** ***** *****

Consensus:

GTaCTGGGGTaCTGGG

>WB235_Fam_150_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
Alignment score = 0.622222
WB235_1:11069544-11069616 Satlength=73 Nr of Repeats=6 RepeatLength=12
seed=CGATCTCCAC Num.seqs=6 Similarity=0.933333
0 CGAT-CTCCACCA--
WB235_1:11060982-11061207 Satlength=226 Nr of Repeats=15 RepeatLength=15
seed=CGATGCTCCA Num.seqs=15 Similarity=0.900106
0 CGATGCTCCACCCGA

**** *****

Consensus:

CGATgCTCCACCaga

>WB235_Fam_151_14_2 Nr. of seq. 2 Alignment length(with gaps) = 14
Alignment score = 0.761905
WB235_2:14190380-14191034 Satlength=655 Nr of Repeats=13 RepeatLength=13
seed=TATACAAAAA Num.seqs=9 Similarity=0.837607
0 TATACAAAAA-GTA
Rev.of_WB235_1:3712691-3712852 Satlength=162 Nr of Repeats=5
RepeatLength=14 seed=TTTTTGTAGA Num.seqs=3 Similarity=0.588235
10 TCTACAAAAANGTA

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Consensus:

TaTACAAAAAnGTA

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>WB235_Fam_152_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14
Alignment score = 0.666667
WB235_5:1718733-1718863 Satlength=131 Nr of Repeats=9 RepeatLength=13
seed=GCTCAAGCTA  Num.seqs=6 Similarity=0.815385
0      GCTCAAGC-TAGGA
WB235_6:1850672-1850839 Satlength=168 Nr of Repeats=11 RepeatLength=14
seed=TAGGCCCTCA  Num.seqs=8 Similarity=0.823129
9      CCTCAAGCGTAGGC
```

***** ****
Consensus:

cCTCAAGCgTAGGa

```
>WB235_Fam_153_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14
Alignment score = 0.619048
WB235_3:11221697-11221865 Satlength=169 Nr of Repeats=11 RepeatLength=14
seed=GATAATTGAA  Num.seqs=10 Similarity=0.980952
0      GATAATTGAAAATC
Rev.of_WB235_3:11399826-11400260 Satlength=435 Nr of Repeats=31
RepeatLength=14 seed=AATTATAAAT  Num.seqs=31 Similarity=0.976651
0      TATAATTTATAATT
```

***** * ***
Consensus:

gATAATTgAaAATc

```
>WB235_Fam_154_11_2  Nr. of seq. 2 Alignment length(with gaps) = 11
Alignment score = 0.878788
WB235_1:2650538-2650582 Satlength=45 Nr of Repeats=4 RepeatLength=11
seed=AAACTTGGGC  Num.seqs=4 Similarity=0.770833
0      AAACTTGGGCT
WB235_3:11027127-11027171 Satlength=45 Nr of Repeats=4 RepeatLength=11
seed=AAACTTGGGC  Num.seqs=4 Similarity=0.858586
0      AAACTTGGGCA
```

Consensus:

AAACTTGGGCa

```
>WB235_Fam_155_11_2  Nr. of seq. 2 Alignment length(with gaps) = 11
Alignment score = 0.636364
WB235_2:13372106-13372150 Satlength=45 Nr of Repeats=4 RepeatLength=11
seed=TGGAAAATTG  Num.seqs=4 Similarity=1.000000
0      TGGAAAATTGA
WB235_3:7593704-7593825 Satlength=122 Nr of Repeats=11 RepeatLength=11
seed=CGGATAATTA  Num.seqs=11 Similarity=1.000000
0      CGGATAATTAA
```

*** **** *

Consensus:

cGGAAaAATTaA

>WB235_Fam_156_11_2 Nr. of seq. 2 Alignment length(with gaps) = 11
Alignment score = 0.636364

WB235_6:404178-404266 Satlength=89 Nr of Repeats=7 RepeatLength=11
seed=CATAACTGAG Num.seqs=6 Similarity=1.000000

0 CATAACTGAGA

Rev.of_WB235_6:3365934-3366110 Satlength=177 Nr of Repeats=12
RepeatLength=11 seed=TAGCTCAGCT Num.seqs=8 Similarity=0.883117
2 TATAGCTGAGC

*** ****

Consensus:

cATAaCTGAGa

>WB235_Fam_157_255_1 Nr. of seq. 1 Alignment length(with gaps) = 255
Alignment score = 0.000000

WB235_5:17522891-17524718 Satlength=1828 Nr of Repeats=7 RepeatLength=255
seed=AACAAGTCGG Num.seqs=5 Similarity=0.720930

0

AACAAGTCGGGAACGTTTCGGAAGCTCTGAGGAAAACCTCCGACAATATCATGCTTAAGTACGCAATTGAGCTA
TCTTTATTAGATTTCGAAAAAGGACTCTTCAAAAATTGAAGCAATAACGAAGAAGCTTAAGTTGGAAGTGGCGA
AGCTTAAATTGGGANTTATGCAGTCTTTATCAGATTCAAAAAGACGATTCTTCGACCAATGAAGCAAGTCCGGA
GNACGATCTACCTTCGACTTCTGATGGCAGAACTCC

Consensus:

AACAAGTCGGGAACGTTTCGGAAGCTCTGAGGAAAACCTCCGACAATATCATGCTTAAGTACGCAATTGAGCTA
TCTTTATTAGATTTCGAAAAAGGACTCTTCAAAAATTGAAGCAATAACGAAGAAGCTTAAGTTGGAAGTGGCGA
AGCTTAAATTGGGANTTATGCAGTCTTTATCAGATTCAAAAAGACGATTCTTCGACCAATGAAGCAAGTCCGGA
GNACGATCTACCTTCGACTTCTGATGGCAGAACTCC

>WB235_Fam_158_230_1 Nr. of seq. 1 Alignment length(with gaps) = 230
Alignment score = 0.000000

WB235_1:10266294-10276924 Satlength=10631 Nr of Repeats=46
RepeatLength=231 seed=GCTGAATTCA Num.seqs=45 Similarity=0.806912

0

GCTGAATTCAAGTTGGGTANGATGTGACTTCATGGCTGAGTGGAATATCTTGAAGTTATCAGCACGATGTGTAG
AGTCGAGTGGTCCATCGTATTGTTTCAGAAATTGGATAATCAAGATGAGATGGAGATTTCTTGAACAATCCAGT
GATCTTCGATTTCAATGATGGCTCGTCCTTCTTCTGTCTCTTCAATCACAACCTGGGATGACATGCTCTGGC
AGCTTCTCATA

Consensus:

GCTGAATTCA GTTGGGTANGATGTGACTTCATGGCTGAGTGGAATATCTTGAAGTTATCAGCACGATGTGTAG
AGTCGAGTGGTCCATCGTATTGTTTCAGAAATTGGATAATCAAGATGAGATGGAGATTTCTTGAACAATCCAGT
GATCTTCGATTTCAATGATGGCTCGTCCTTCTTCTGTCTCTTCAATCACAACTGGGATGACATGCTCTGGC
AGCTTCTCATA

>WB235_Fam_159_228_1 Nr. of seq. 1 Alignment length(with gaps) = 228

Alignment score = 0.000000

WB235_3:5941097-5943578 Satlength=2482 Nr of Repeats=10 RepeatLength=228

seed=CCACCAGATC Num.seqs=6 Similarity=0.843765

0

CCACCAGATCAGCAACGTCTCATCTTCGCCGGAAGCAACTCGAGGACGGCCGCACCCTTTCGGACTACAACA
TCCAGAAGGAATCAACTCTTCATTTGGTTCTCCGTCTGAGAGGAGGTATGCAGATCTTCGTCAAGACATTGAC
CGGAAAGACCATCACCTCGAAGTCGAAGCCTCCGACACCATCGAAAATGTCAAGGCCAAGATCCAAGACAAG
GAAGGAATC

Consensus:

CCACCAGATCAGCAACGTCTCATCTTCGCCGGAAGCAACTCGAGGACGGCCGCACCCTTTCGGACTACAACA
TCCAGAAGGAATCAACTCTTCATTTGGTTCTCCGTCTGAGAGGAGGTATGCAGATCTTCGTCAAGACATTGAC
CGGAAAGACCATCACCTCGAAGTCGAAGCCTCCGACACCATCGAAAATGTCAAGGCCAAGATCCAAGACAAG
GAAGGAATC

>WB235_Fam_160_189_1 Nr. of seq. 1 Alignment length(with gaps) = 189

Alignment score = 0.000000

WB235_1:1593120-1594195 Satlength=1076 Nr of Repeats=5 RepeatLength=189

seed=TTTTTTTGA Num.seqs=3 Similarity=1.000000

0

TTTTTTTTTGA CTATGGAATTATAAAGAAAATCGAATTTCAAAAAAGCATGTATTAGCCAATGTAAACGCGCTC
CAATGATGATGTAGCCACGTGGTATCAGAGTGTCTCTTTACGGCTTGATTTAAATACGTAGATCTACAAATT
CACTTATCTGTTTTCTCACGGGTTTAGGATATTTTTTCTGTTA

Consensus:

TTTTTTTTTGA CTATGGAATTATAAAGAAAATCGAATTTCAAAAAAGCATGTATTAGCCAATGTAAACGCGCTC
CAATGATGATGTAGCCACGTGGTATCAGAGTGTCTCTTTACGGCTTGATTTAAATACGTAGATCTACAAATT
CACTTATCTGTTTTCTCACGGGTTTAGGATATTTTTTCTGTTA

>WB235_Fam_161_184_1 Nr. of seq. 1 Alignment length(with gaps) = 184

Alignment score = 0.000000

WB235_2:884525-885363 Satlength=839 Nr of Repeats=4 RepeatLength=184

seed=GTTCAAAAGA Num.seqs=3 Similarity=1.000000

0

GTTCAAAAGATACAAAATTTATCTACACATCTACAAGTTAAACTTGCAACTTAGTTAACCAAATTCAAAAGTT

ATGAGCCGGGGAAC TATAATAACCAACGTTTCACACTAAAAAGCCCAAAAAATTCGAAAATCATTTTTATC
TCATGACGCGGACAAGCTACAAATGTCTAGTTAGGCTT

Consensus:

GTTCAAAAGATACAAAATTTATCTACACATCTACAAGTTAAACTTGCAACTTAGTTAACCAAATTCAAAAGTT
ATGAGCCGGGGAAC TATAATAACCAACGTTTCACACTAAAAAGCCCAAAAAATTCGAAAATCATTTTTATC
TCATGACGCGGACAAGCTACAAATGTCTAGTTAGGCTT

>WB235_Fam_162_183_1 Nr. of seq. 1 Alignment length(with gaps) = 183
Alignment score = 0.000000
WB235_5:19498459-19499190 Satlength=732 Nr of Repeats=4 RepeatLength=183
seed=TTTCTCTGCG Num.seqs=3 Similarity=0.615789
0
TTTCTCTGCGTCTCGCCTCGCCTCACACTATTTTNCACACCAAACCTTGAGNCTATGTATCTCTGTAACGGGT
TGCGCTTTCTGAAAAATTCCAACTGACGGGATATATAAAATTTNGAATTCTTTCTACCGTTAAAAAACTAAA
CACCTAGGCAAGACGCAGACAGCGAGANACCCCAAT

Consensus:

TTTCTCTGCGTCTCGCCTCGCCTCACACTATTTTNCACACCAAACCTTGAGNCTATGTATCTCTGTAACGGGT
TGCGCTTTCTGAAAAATTCCAACTGACGGGATATATAAAATTTNGAATTCTTTCTACCGTTAAAAAACTAAA
CACCTAGGCAAGACGCAGACAGCGAGANACCCCAAT

>WB235_Fam_163_181_1 Nr. of seq. 1 Alignment length(with gaps) = 181
Alignment score = 0.000000
WB235_2:6073626-6077427 Satlength=3802 Nr of Repeats=21 RepeatLength=181
seed=TTTTTAACTT Num.seqs=21 Similarity=0.964606
0
TTTTTAACTTTTAAATCCACTAAAACTCGGAATGGTACAGAACATGCAAATTGTAATTTCAAGAACTGAATGT
GGTTTCGAATATTTATGGATTGCTTTATTCTAAAACTGACTCTGAAATATTTTGCATCCATTTGACTACTAAT
TGT CATATTATACCGAACACTACTA ACTTTAGTGG

Consensus:

TTTTTAACTTTTAAATCCACTAAAACTCGGAATGGTACAGAACATGCAAATTGTAATTTCAAGAACTGAATGT
GGTTTCGAATATTTATGGATTGCTTTATTCTAAAACTGACTCTGAAATATTTTGCATCCATTTGACTACTAAT
TGT CATATTATACCGAACACTACTA ACTTTAGTGG

>WB235_Fam_164_180_1 Nr. of seq. 1 Alignment length(with gaps) = 180
Alignment score = 0.000000
WB235_3:2977664-2978383 Satlength=720 Nr of Repeats=4 RepeatLength=180
seed=TGTCGGCCGC Num.seqs=3 Similarity=0.750153
0
TGTCGGCCGCTGTATCTTTTGCCTCAATTTTTTTTNAATTTTNAACATNCATATTCCAGTAGATAACATTAT

GAGCTACAGTTTGTAGTTAAAATTTTATTTCTAAAATTACTAGTTTCTGAGTTATACTCATTCCAACCCACC
CCAAGAGAAAATTCCTAAAAATGAACTCGCGAGG

Consensus:

TGTCGGCCGCTGTATCTTTTGCCTCAATTTTTTTTNAATTTTNAACATNCATATTCCAGTAGATAACATTAT
GAGCTACAGTTTGTAGTTAAAATTTTATTTCTAAAATTACTAGTTTCTGAGTTATACTCATTCCAACCCACC
CCAAGAGAAAATTCCTAAAAATGAACTCGCGAGG

>WB235_Fam_165_179_1 Nr. of seq. 1 Alignment length(with gaps) = 179

Alignment score = 0.000000

WB235_1:14024312-14025229 Satlength=918 Nr of Repeats=5 RepeatLength=179

seed=CTACCCAAAT Num.seqs=3 Similarity=0.995034

0

CTACCCAAATTTTTGAAATTTGGAAATTTTTCAAAAATTTCTCAAATTTTCAAATCCCATAATTCAGCCAATT
TTTGAGATTTTCAGATATTTTTTAATTGAAAATTTCTGTTTGTCTTATCCATTAACTATATCGCTGCATCTAC
ATTTTTCACAGTACCCCATGACTTTTCCCGATT

Consensus:

CTACCCAAATTTTTGAAATTTGGAAATTTTTCAAAAATTTCTCAAATTTTCAAATCCCATAATTCAGCCAATT
TTTGAGATTTTCAGATATTTTTTAATTGAAAATTTCTGTTTGTCTTATCCATTAACTATATCGCTGCATCTAC
ATTTTTCACAGTACCCCATGACTTTTCCCGATT

>WB235_Fam_166_177_1 Nr. of seq. 1 Alignment length(with gaps) = 177

Alignment score = 0.000000

WB235_1:14148103-14148989 Satlength=887 Nr of Repeats=5 RepeatLength=177

seed=CTAACAAAAT Num.seqs=4 Similarity=0.721286

0

CTAACAAAATAATCAGCGTAAATTTTCTACATTTTACTAGTTAACAATATTTTGATAACATCAGTGGTTTTT
GAGATACGCAAGTTTTAAGGTGGACGCCCAAAAATAGTTGTGAGCAGCTTTAATCAAAAACCGACATAACTTT
TTACTCACTAACGGTATCAAAAATGTTTTAA

Consensus:

CTAACAAAATAATCAGCGTAAATTTTCTACATTTTACTAGTTAACAATATTTTGATAACATCAGTGGTTTTT
GAGATACGCAAGTTTTAAGGTGGACGCCCAAAAATAGTTGTGAGCAGCTTTAATCAAAAACCGACATAACTTT
TTACTCACTAACGGTATCAAAAATGTTTTAA

>WB235_Fam_167_175_1 Nr. of seq. 1 Alignment length(with gaps) = 175

Alignment score = 0.000000

WB235_1:2430196-2431177 Satlength=982 Nr of Repeats=5 RepeatLength=175

seed=GATGCACCAT Num.seqs=3 Similarity=0.840552

0

GATGCACCATGTCTTTGACAGTCAATATCTCGGTTTATTTTGTAGCTATCAAAAATTTTCAACTACAAATCT

ATAGAAAAATTAAATGTTCAACATTTTCTCAGTTGACAGTTTTTTTGATAACTGCAATGACATCCGAGATATGAG
CTTTCAAAGTTGAGAGACCTCACTCGGTT

Consensus:

GATGCACCATGTCTTTGACAGTCAATATCTCGGTTTATTTTGTAGCTATCAAAAAATTTTCAACTACAAATCT
ATAGAAAAATTAAATGTTCAACATTTTCTCAGTTGACAGTTTTTTTGATAACTGCAATGACATCCGAGATATGAG
CTTTCAAAGTTGAGAGACCTCACTCGGTT

>WB235_Fam_168_175_1 Nr. of seq. 1 Alignment length(with gaps) = 175

Alignment score = 0.000000

WB235_4:2675283-2676104 Satlength=822 Nr of Repeats=4 RepeatLength=175

seed=AACTTGTGAC Num.seqs=3 Similarity=0.715980

0

AACTTGTGACGGTGGGTATGGATTTTATGCACATAATTTGTTTCGAAATAGTCTACCNAGTAACTGGTGAAGT
TTCAAAAACTTTGTGGATCTAGTTTTTGA AAAAAGTTCAAAATTTGTGCCAATTTTGACCAATTTTGGTGGTTT
TCTGAGCTAAAATTGAAAAGTTGGGAATG

Consensus:

AACTTGTGACGGTGGGTATGGATTTTATGCACATAATTTGTTTCGAAATAGTCTACCNAGTAACTGGTGAAGT
TTCAAAAACTTTGTGGATCTAGTTTTTGA AAAAAGTTCAAAATTTGTGCCAATTTTGACCAATTTTGGTGGTTT
TCTGAGCTAAAATTGAAAAGTTGGGAATG

>WB235_Fam_169_175_1 Nr. of seq. 1 Alignment length(with gaps) = 175

Alignment score = 0.000000

WB235_5:317369-318431 Satlength=1063 Nr of Repeats=6 RepeatLength=175

seed=AAATTTTGGG Num.seqs=4 Similarity=0.911111

0

AAATTTTGGGTTCACTCTTTTTACTAGACAGTGATTGTTGCATTGTAGGATTCGGTGGACTTGTCCAACAAC
TACTTTGGCATGAGTTTAATAAAAAGGTTTTACCATGAACTGAATCAATTCAAATAAAAACCTCGAGAATGA
AAACATCCTCAGTAATTTCAATCCTGTTC

Consensus:

AAATTTTGGGTTCACTCTTTTTACTAGACAGTGATTGTTGCATTGTAGGATTCGGTGGACTTGTCCAACAAC
TACTTTGGCATGAGTTTAATAAAAAGGTTTTACCATGAACTGAATCAATTCAAATAAAAACCTCGAGAATGA
AAACATCCTCAGTAATTTCAATCCTGTTC

>WB235_Fam_170_174_1 Nr. of seq. 1 Alignment length(with gaps) = 174

Alignment score = 0.000000

WB235_1:4338841-4339537 Satlength=697 Nr of Repeats=4 RepeatLength=174

seed=CTTCAAGAGC Num.seqs=4 Similarity=0.868455

0

CTTCAAGAGCTCAGTGTTATTTATGACATGCCAACCTCGACAATTGACCTGAACATGCTCCAAGGAATCGAAG

ACAACCTTGAACAGCCTTCCAGCTGAAGAATCTGATAAGATCCGAGAGAAGATTAACGATCTGAGAAGAAGGAA
ACAAGAAAAGCGATCAAGCTGAAGCTCTT

Consensus:

CTTCAAGAGCTCAGTGTTATTTATGACATGCCAACCTCGACAATTGACCTGAACATGCTCCAAGGAATCGAAG
ACAACCTTGAACAGCCTTCCAGCTGAAGAATCTGATAAGATCCGAGAGAAGATTAACGATCTGAGAAGAAGGAA
ACAAGAAAAGCGATCAAGCTGAAGCTCTT

>WB235_Fam_171_165_1 Nr. of seq. 1 Alignment length(with gaps) = 165
Alignment score = 0.000000
WB235_6:1718471-1719647 Satlength=1177 Nr of Repeats=4 RepeatLength=165
seed=CTTTTCCAAA Num.seqs=3 Similarity=1.000000
0
CTTTTCCAAAATGGCAATTTTTGATGAAAAAATCCGAATTTTCACAAATTTCAAAAAATTTTTAAACTTTA
TAATTTTAGCTTTGAATATTCCAAATGGAAGTGCATAACCTATCAATTTGATATATAAACTCGTGCCTACCT
TCAGGCATTCAGTTTTTCAC

Consensus:

CTTTTCCAAAATGGCAATTTTTGATGAAAAAATCCGAATTTTCACAAATTTCAAAAAATTTTTAAACTTTA
TAATTTTAGCTTTGAATATTCCAAATGGAAGTGCATAACCTATCAATTTGATATATAAACTCGTGCCTACCT
TCAGGCATTCAGTTTTTCAC

>WB235_Fam_172_155_1 Nr. of seq. 1 Alignment length(with gaps) = 155
Alignment score = 0.000000
WB235_2:2949876-2951271 Satlength=1396 Nr of Repeats=9 RepeatLength=155
seed=TCCCGCTGTG Num.seqs=6 Similarity=0.781691
0
TCCCGCTGTGGTTAAAAGTTTTTTCGCTGCTCAGTTCTGTACGGTAAATGTGTTAAAACTTCTGGAACTTG
AAATTCCAAGTTATTTCAGAAAATTGTTCAAATGGCGCAGTGGGAAATTCGATTTCTCAGACCCAAGAGGCCAC
GGGTTCAAT

Consensus:

TCCCGCTGTGGTTAAAAGTTTTTTCGCTGCTCAGTTCTGTACGGTAAATGTGTTAAAACTTCTGGAACTTG
AAATTCCAAGTTATTTCAGAAAATTGTTCAAATGGCGCAGTGGGAAATTCGATTTCTCAGACCCAAGAGGCCAC
GGGTTCAAT

>WB235_Fam_173_153_1 Nr. of seq. 1 Alignment length(with gaps) = 153
Alignment score = 0.000000
WB235_6:13923839-13924439 Satlength=601 Nr of Repeats=4 RepeatLength=153
seed=TGAGGTGCAG Num.seqs=3 Similarity=0.872186
0
TGAGGTGCAGGGCGTGATGAGCTTTGTTGAACTGGGAACTGTTGATTCCCGGAGCCGTGATTCATAGATGAGT

TGGAGGGACCTGCTGTGGAACCTGTTTCAACTTGAGCAATTCCATGAGCCATCAAGAAGCTTTCGGGCAGATT
GGGCAAC

Consensus:

TGAGGTGCAGGGCGTGATGAGCTTTGTTGAACTGGGAACTGTTGATTCCCGGAGCCGTGATTCATAGATGAGT
TGGAGGGACCTGCTGTGGAACCTGTTTCAACTTGAGCAATTCCATGAGCCATCAAGAAGCTTTCGGGCAGATT
GGGCAAC

>WB235_Fam_174_151_1 Nr. of seq. 1 Alignment length(with gaps) = 151
Alignment score = 0.000000
WB235_5:14053790-14054393 Satlength=604 Nr of Repeats=4 RepeatLength=151
seed=CATTTTCAGAT Num.seqs=3 Similarity=0.988227
0
CATTTTCAGATATTCATCACCACCAACACCTTCATCCACTTCTTCGCCTGGAACGACGGGATTTTCTACAAAA
ATCGGATTTTTTCTCTATGTCAGTTTAATTGATGTATAATTCCGAAAAGTCAGTCTTTCCTAGGTTTTTAAAT
TGAAA

Consensus:

CATTTTCAGATATTCATCACCACCAACACCTTCATCCACTTCTTCGCCTGGAACGACGGGATTTTCTACAAAA
ATCGGATTTTTTCTCTATGTCAGTTTAATTGATGTATAATTCCGAAAAGTCAGTCTTTCCTAGGTTTTTAAAT
TGAAA

>WB235_Fam_175_150_1 Nr. of seq. 1 Alignment length(with gaps) = 150
Alignment score = 0.000000
WB235_2:1496871-1497776 Satlength=906 Nr of Repeats=6 RepeatLength=150
seed=TTGCAACATG Num.seqs=4 Similarity=0.817145
0
TTGCAACATGCGGTCGGCGGAAAATTCTGAATTTTTTCAGTCCAAAACAGGTTTTTCGACCAATTTTTTCATATTT
TCAAGCGAAATTATGATAGAAAATTCAAATTTTCACTAAAAATCGCCAATTTTCCACATTTTCTCATTGGAGC
GCAC

Consensus:

TTGCAACATGCGGTCGGCGGAAAATTCTGAATTTTTTCAGTCCAAAACAGGTTTTTCGACCAATTTTTTCATATTT
TCAAGCGAAATTATGATAGAAAATTCAAATTTTCACTAAAAATCGCCAATTTTCCACATTTTCTCATTGGAGC
GCAC

>WB235_Fam_176_150_1 Nr. of seq. 1 Alignment length(with gaps) = 150
Alignment score = 0.000000
WB235_4:16681092-16681615 Satlength=524 Nr of Repeats=4 RepeatLength=150
seed=TTGAGGGCCG Num.seqs=3 Similarity=0.940741
0
TTGAGGGCCGCAGTCCCGAATACACGAAGAAGTGTGGAGATCCGTCAAGCCTATTCTAAGCATAATAATTCA

GTTTCGAGTGTTCGCAAGCCCAAATAGACGCAGAAGCGTTGGACAACTTTTAGGCCTATTCTGAGCCCAATAATT
CATG

Consensus:

TTGAGGGCCGCAGTCCCGAATACACGAAGAAGTGTGGAGATCCGTCAAGCCTATTCTAAGCATAATAATTCA
GTTTCGAGTGTTCGCAAGCCCAAATAGACGCAGAAGCGTTGGACAACTTTTAGGCCTATTCTGAGCCCAATAATT
CATG

>WB235_Fam_177_146_1 Nr. of seq. 1 Alignment length(with gaps) = 146
Alignment score = 0.000000
WB235_2:2811262-2812302 Satlength=1041 Nr of Repeats=6 RepeatLength=144
seed=TGGCCTAGAA Num.seqs=4 Similarity=0.634815
0
TGGCCTAGAAATCNCAAGTTTGCAAAAGTTAGGCCACCAACTTCAAATGCCTATAACTCAGCGGAAAATCAAT
ATTTTCCATTGATTTTAACTGCTAAGATGTAGCCAATTACGTAGCGCAACTTTTTGGCCTACTTAACAATTGG

Consensus:

TGGCCTAGAAATCNCAAGTTTGCAAAAGTTAGGCCACCAACTTCAAATGCCTATAACTCAGCGGAAAATCAAT
ATTTTCCATTGATTTTAACTGCTAAGATGTAGCCAATTACGTAGCGCAACTTTTTGGCCTACTTAACAATTGG

>WB235_Fam_178_144_1 Nr. of seq. 1 Alignment length(with gaps) = 144
Alignment score = 0.000000
WB235_4:2431055-2431771 Satlength=717 Nr of Repeats=5 RepeatLength=144
seed=TTCTAGGCCA Num.seqs=4 Similarity=0.915326
0
TTCTAGGCCACCAATTGGAAATCATCATAACTTGGCTTAAAATCCAGATTTTTGGAGTCTGGTAACTGCAACA
TGTTGCCCTGTAGTTTTTCTACAAGTTAGGATATATTAATTTTTGGTGGCCTAAAAGTCCAAATTATGGAT

Consensus:

TTCTAGGCCACCAATTGGAAATCATCATAACTTGGCTTAAAATCCAGATTTTTGGAGTCTGGTAACTGCAACA
TGTTGCCCTGTAGTTTTTCTACAAGTTAGGATATATTAATTTTTGGTGGCCTAAAAGTCCAAATTATGGAT

>WB235_Fam_179_143_1 Nr. of seq. 1 Alignment length(with gaps) = 143
Alignment score = 0.000000
WB235_5:17747299-17748649 Satlength=1351 Nr of Repeats=6 RepeatLength=143
seed=CAGTGGGATT Num.seqs=4 Similarity=0.759132
0
CAGTGGGATTTTCAATGTCTTCCAATCAAACGTCCGGGGTTCGAGTCCGCACAGGGGTATTTATTTTTTGCAA
GCTGTGATTAACAAGTTTATAGCTGCAAAAGTCATTTTAATCGAACTTTCAGGAAAATGTCCGAATGGCG

Consensus:

CAGTGGGATTTTCAATGTCTTCCAATCAAACGTCCGGGGTTCGAGTCCGCACAGGGGTATTTATTTTTTGCAA
GCTGTGATTAACAAGTTTATAGCTGCAAAAGTCATTTTAATCGAACTTTCAGGAAAATGTCCGAATGGCG

>WB235_Fam_180_122_1 Nr. of seq. 1 Alignment length(with gaps) = 122
Alignment score = 0.000000
WB235_2:13334193-13334831 Satlength=639 Nr of Repeats=5 RepeatLength=122
seed=GATCTACAAA Num.seqs=3 Similarity=0.927140
0

GATCTACAAAAATGCGGGAAAAGTGACACAGAGTTCTCAACTGATTTTGCATAAAAATTCCCGCATTTTTTGG
AGATCAAACCGTGATGGGACAGCCTGGCACCACTTGCTTGATCTACGTA

Consensus:

GATCTACAAAAATGCGGGAAAAGTGACACAGAGTTCTCAACTGATTTTGCATAAAAATTCCCGCATTTTTTGG
AGATCAAACCGTGATGGGACAGCCTGGCACCACTTGCTTGATCTACGTA

>WB235_Fam_181_121_1 Nr. of seq. 1 Alignment length(with gaps) = 121
Alignment score = 0.000000
WB235_5:16449792-16451728 Satlength=1937 Nr of Repeats=16
RepeatLength=121 seed=AAAAGATAGT Num.seqs=16 Similarity=0.955556
0

AAAAGATAGTTGCCCTAAGAGCAGAAGGTTGCAAACCGCAAGAGCAAACCTGCCAAATGACAAGCCACCCAAG
TACTCGTTGCACCTACCTATCATAAGCTCGTAGACTATAATTTCTCTG

Consensus:

AAAAGATAGTTGCCCTAAGAGCAGAAGGTTGCAAACCGCAAGAGCAAACCTGCCAAATGACAAGCCACCCAAG
TACTCGTTGCACCTACCTATCATAAGCTCGTAGACTATAATTTCTCTG

>WB235_Fam_182_117_1 Nr. of seq. 1 Alignment length(with gaps) = 117
Alignment score = 0.000000
WB235_5:6176242-6183220 Satlength=6979 Nr of Repeats=54 RepeatLength=117
seed=TGTTGGTTTCG Num.seqs=49 Similarity=0.881703
0

TGTTGGTTTCGACAGTAGGTGCACTAGTCTCTGGCACTGGAACATCCTTTTGCTCAACAATTTAGCTGGTTGT
ACTTCAGATGTTTCTTTTGATTCCACAGGTGCAAGTTTCTCAAC

Consensus:

TGTTGGTTTCGACAGTAGGTGCACTAGTCTCTGGCACTGGAACATCCTTTTGCTCAACAATTTAGCTGGTTGT
ACTTCAGATGTTTCTTTTGATTCCACAGGTGCAAGTTTCTCAAC

>WB235_Fam_183_114_1 Nr. of seq. 1 Alignment length(with gaps) = 114
Alignment score = 0.000000
WB235_5:8705331-8709788 Satlength=4458 Nr of Repeats=38 RepeatLength=114
seed=GTGTTTCAGA Num.seqs=36 Similarity=0.968737
0

GTGTTTCAGAATTACATGGAGTCTCACTACTTGCAGAATTTGTGGCTGTAGACGATGGGCCTGCTGTAGTTGA
ATCGTTTGGAACGTGCATAGTGGATGTTCCATCAGACGTTT

Consensus:

GTGTTTCAGAATTACATGGAGTCTCACTACTTGCAGAATTTGTGGCTGTAGACGATGGGCCTGCTGTAGTTGA
ATCGTTTGGAACGTGCATAGTGGATGTTCCATCAGACGTTT

>WB235_Fam_184_108_1 Nr. of seq. 1 Alignment length(with gaps) = 108

Alignment score = 0.000000

WB235_6:1549825-1550305 Satlength=481 Nr of Repeats=5 RepeatLength=108

seed=ATCCTCAACA Num.seqs=3 Similarity=0.732510

0

ATCCTCAACACCATCNGCGTCATCTAGTTCCTCCGGAACATATGTCGACAATTTTCAGGATCAACTGGTTCNACA
GTTACAGTTGTACCAGGATCNTCTAGCACATTTGG

Consensus:

ATCCTCAACACCATCNGCGTCATCTAGTTCCTCCGGAACATATGTCGACAATTTTCAGGATCAACTGGTTCNACA
GTTACAGTTGTACCAGGATCNTCTAGCACATTTGG

>WB235_Fam_185_108_1 Nr. of seq. 1 Alignment length(with gaps) = 108

Alignment score = 0.000000

WB235_6:13684248-13684998 Satlength=751 Nr of Repeats=7 RepeatLength=108

seed=TGGGTAATCA Num.seqs=6 Similarity=0.845267

0

TGGGTAATCAGGTACGGGCTTTCAGATTTTCAAGTTTTCACGTGAATATCTAGGTCACGAGCCAATTTTCAGCC
AGGAGTGGGACTAGAGATATGAAACTCTTGGGTTA

Consensus:

TGGGTAATCAGGTACGGGCTTTCAGATTTTCAAGTTTTCACGTGAATATCTAGGTCACGAGCCAATTTTCAGCC
AGGAGTGGGACTAGAGATATGAAACTCTTGGGTTA

>WB235_Fam_186_108_1 Nr. of seq. 1 Alignment length(with gaps) = 108

Alignment score = 0.000000

WB235_6:15226880-15229061 Satlength=2182 Nr of Repeats=20

RepeatLength=108 seed=AAGTCTTCTT Num.seqs=18 Similarity=0.959655

0

AAGTCTTCTTGATTCTGAGTTCTTGCTTCGAACTGTTGACCATCTCCTTGCAGGATCTTATTGTCAGATGGAA
CCTTCTTGGCATACCGTTCTCCACTGATGTGAGTG

Consensus:

AAGTCTTCTTGATTCTGAGTTCTTGCTTCGAACTGTTGACCATCTCCTTGCAGGATCTTATTGTCAGATGGAA
CCTTCTTGGCATACCGTTCTCCACTGATGTGAGTG

>WB235_Fam_187_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000
WB235_4:2397301-2398030 Satlength=730 Nr of Repeats=7 RepeatLength=104
seed=CCTGCGAAAG Num.seqs=6 Similarity=0.982906
0
CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGG
GTTATCGGTGAATTTTTGGGTCTGTCAGGGT

Consensus:

CCTGCGAAAGCGAATCTCTGGCCTGGCGGAGGGCCAACTAACTCTCTCCCTCAAGCCTTCGGGTGCTTCCTGG
GTTATCGGTGAATTTTTGGGTCTGTCAGGGT

>WB235_Fam_188_102_1 Nr. of seq. 1 Alignment length(with gaps) = 102
Alignment score = 0.000000
WB235_4:688812-698192 Satlength=9381 Nr of Repeats=92 RepeatLength=102
seed=TTGCTGCAGC Num.seqs=90 Similarity=0.947271
0
TTGCTGCAGCATATCTTTCTCCAGTACCACCTTGATATGTCTGAACGATTGATAGTTTGAGAATCAAGAGAATC
TGTTGGACGATCAATTCATCTTTGGGTC

Consensus:

TTGCTGCAGCATATCTTTCTCCAGTACCACCTTGATATGTCTGAACGATTGATAGTTTGAGAATCAAGAGAATC
TGTTGGACGATCAATTCATCTTTGGGTC

>WB235_Fam_189_102_1 Nr. of seq. 1 Alignment length(with gaps) = 102
Alignment score = 0.000000
WB235_6:1136184-1140765 Satlength=4582 Nr of Repeats=45 RepeatLength=102
seed=TGTACACTTC Num.seqs=30 Similarity=0.981008
0
TGTACACTTCTCCCAAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAAA
CTTCTCTCAAAAAGAAAATAGACTTCACA

Consensus:

TGTACACTTCTCCCAAATGACTGTAAGAATGGACTCCTTATATGATTTTAAACCCGACTCTGGACATACAAA
CTTCTCTCAAAAAGAAAATAGACTTCACA

>WB235_Fam_190_101_1 Nr. of seq. 1 Alignment length(with gaps) = 101
Alignment score = 0.000000
WB235_1:14329713-14330118 Satlength=406 Nr of Repeats=4 RepeatLength=101
seed=GCATTTGCAT Num.seqs=3 Similarity=0.826797
0
GCATTTGCATATNGAGATCAGATAAAAGTTAGAATTTTCCAGCCGTTGCAAGTGCGCTCTATTGAGAACATTT
TGAAAAATTGAATGTTTTACATTAGAGC

Consensus:

GCATTTGCATATNGAGATCAGATAAAAGTTAGAATTTTCCAGCCGTTGCAAGTGCCTCTATTGAGAACATTT
TGAAAATTGAATGTTTTACATTAGAGC

>WB235_Fam_191_101_1 Nr. of seq. 1 Alignment length(with gaps) = 101
Alignment score = 0.000000
WB235_3:267063-268369 Satlength=1307 Nr of Repeats=13 RepeatLength=101
seed=GGTTACTGTA Num.seqs=11 Similarity=0.942394

0
GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGC
AGAAAATCGCTAAAAATGACTTTACTGG

Consensus:

GGTTACTGTAGCTCCAGAAATACGCAAACACCGACTACGGTTCCTAATACATCAGATATTACGACAAAGTGC
AGAAAATCGCTAAAAATGACTTTACTGG

>WB235_Fam_192_101_1 Nr. of seq. 1 Alignment length(with gaps) = 101
Alignment score = 0.000000
WB235_4:1569894-1570719 Satlength=826 Nr of Repeats=7 RepeatLength=101
seed=TTGATTTTTC Num.seqs=5 Similarity=0.952475

0
TTGATTTTTCGTCTTATGAAGGAATATTGGTTTCGGGGTAGTGGGCGGATATGGTCGGGGTACTGTAGGTATA
CGGTAGGGTTACTGTAGTTTGGAAATT

Consensus:

TTGATTTTTCGTCTTATGAAGGAATATTGGTTTCGGGGTAGTGGGCGGATATGGTCGGGGTACTGTAGGTATA
CGGTAGGGTTACTGTAGTTTGGAAATT

>WB235_Fam_193_96_1 Nr. of seq. 1 Alignment length(with gaps) = 96
Alignment score = 0.000000
WB235_4:12314464-12315037 Satlength=574 Nr of Repeats=6 RepeatLength=96
seed=GGTTGATTTG Num.seqs=5 Similarity=0.991667

0
GGTTGATTTGCGGCACTCTACAGATAGTGGATCTGCTTCTTACCAATCTTCCCGTTACCGCCACGCACTTAAG
CTCCAAACTATTTTATTTTTTTG

Consensus:

GGTTGATTTGCGGCACTCTACAGATAGTGGATCTGCTTCTTACCAATCTTCCCGTTACCGCCACGCACTTAAG
CTCCAAACTATTTTATTTTTTTG

>WB235_Fam_194_96_1 Nr. of seq. 1 Alignment length(with gaps) = 96
Alignment score = 0.000000
WB235_4:12638029-12638605 Satlength=577 Nr of Repeats=6 RepeatLength=96
seed=CTTCTGGTAA Num.seqs=6 Similarity=0.952778
0
CTTCTGGTAATGTTCCCATAATTGGGTAAATACCACTCATAAGTAACTAGTATGGGACTGAAAAGATACTAA
ATGAGCTTATTCTAAGGGTGAAG

Consensus:

CTTCTGGTAATGTTCCCATAATTGGGTAAATACCACTCATAAGTAACTAGTATGGGACTGAAAAGATACTAA
ATGAGCTTATTCTAAGGGTGAAG

>WB235_Fam_195_93_1 Nr. of seq. 1 Alignment length(with gaps) = 93
Alignment score = 0.000000
WB235_4:6921936-6922772 Satlength=837 Nr of Repeats=9 RepeatLength=93
seed=TGCTTCTCGT Num.seqs=8 Similarity=0.966206
0
TGCTTCTCGTCGTCCACCACCACCACCGAAGGGAAGTGAACCCACCACCACCACCAACTGGAGAACCACAG
GATCTTTCTGGAGAAGGTAA

Consensus:

TGCTTCTCGTCGTCCACCACCACCACCGAAGGGAAGTGAACCCACCACCACCACCAACTGGAGAACCACAG
GATCTTTCTGGAGAAGGTAA

>WB235_Fam_196_93_1 Nr. of seq. 1 Alignment length(with gaps) = 93
Alignment score = 0.000000
WB235_5:1907825-1908395 Satlength=571 Nr of Repeats=7 RepeatLength=93
seed=CAGTACCCTC Num.seqs=5 Similarity=0.954122
0
CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCCGGTAACATAATGCCTTTGCCAGCACTTCCGATGCTC
CACAGTATCCAGGATCCTCC

Consensus:

CAGTACCCTCAAGGATCATCTGCTCCACGGTATCCCGGTAACATAATGCCTTTGCCAGCACTTCCGATGCTC
CACAGTATCCAGGATCCTCC

>WB235_Fam_197_87_1 Nr. of seq. 1 Alignment length(with gaps) = 87
Alignment score = 0.000000
WB235_4:2815904-2816246 Satlength=343 Nr of Repeats=4 RepeatLength=87
seed=TGAAGTCGTA Num.seqs=3 Similarity=0.685393
0
TGAAGTCGTAGGATTCTGTGTGGTGACTGGTGTGCTTGTANTCTGTGAAGGGGACGTGGCTTCTTCCGTTGTG
TCATGCTTCTNNGG

Consensus:

TGAAGTCGTAGGATTCTGTGTGGTGAAGTGGTGTGCGTTGTANTCTGTGAAGGGGACGTGGCTTCTTCCGTTGTG
TCATGCTTCTNNGG

>WB235_Fam_198_81_1 Nr. of seq. 1 Alignment length(with gaps) = 81

Alignment score = 0.000000

WB235_1:14443057-14443637 Satlength=581 Nr of Repeats=8 RepeatLength=73

seed=TGTCGGCCGC Num.seqs=6 Similarity=0.624829

0

TGTCGGCCGCTACCAAACATTTAGCANACACACCAAGCACTACGTTGCGCACACACACCAAACCTGCGGAACC
CCGAACAG

Consensus:

TGTCGGCCGCTACCAAACATTTAGCANACACACCAAGCACTACGTTGCGCACACACACCAAACCTGCGGAACC
CCGAACAG

>WB235_Fam_199_80_1 Nr. of seq. 1 Alignment length(with gaps) = 80

Alignment score = 0.000000

WB235_4:1965986-1967712 Satlength=1727 Nr of Repeats=15 RepeatLength=80

seed=AATTTCTCAA Num.seqs=14 Similarity=0.856227

0

AATTTCTCAATAGGGCGCGCTTGCAACATCTGAACGGCGCGAAATTTGAATTTTGGCCATAAAATAACGAAA
ACTAACT

Consensus:

AATTTCTCAATAGGGCGCGCTTGCAACATCTGAACGGCGCGAAATTTGAATTTTGGCCATAAAATAACGAAA
ACTAACT

>WB235_Fam_200_78_1 Nr. of seq. 1 Alignment length(with gaps) = 78

Alignment score = 0.000000

WB235_3:12985357-12986137 Satlength=781 Nr of Repeats=10 RepeatLength=78

seed=CGAAGTTGCT Num.seqs=10 Similarity=0.831974

0

CGAAGTTGCTGGACCAAAGATCACAACAGGCGGATTTGGCGGCATAACCGGAGCAACAGTAGTGTCATTTGGT
TCTTC

Consensus:

CGAAGTTGCTGGACCAAAGATCACAACAGGCGGATTTGGCGGCATAACCGGAGCAACAGTAGTGTCATTTGGT
TCTTC

>WB235_Fam_201_78_1 Nr. of seq. 1 Alignment length(with gaps) = 78
Alignment score = 0.000000
WB235_5:8714029-8714965 Satlength=937 Nr of Repeats=12 RepeatLength=78
seed=TGCAAGGCTC Num.seqs=12 Similarity=0.929325
0
TGCAAGGCTCCGATGATGATACCACTTCTAAAGTCGAGGTGTCACAATTTTCGGGTGTCGTAGAACTTGAATC
AGTAC

Consensus:

TGCAAGGCTCCGATGATGATACCACTTCTAAAGTCGAGGTGTCACAATTTTCGGGTGTCGTAGAACTTGAATC
AGTAC

>WB235_Fam_202_78_1 Nr. of seq. 1 Alignment length(with gaps) = 78
Alignment score = 0.000000
WB235_5:18173031-18173742 Satlength=712 Nr of Repeats=10 RepeatLength=78
seed=GAGCTTTGGG Num.seqs=7 Similarity=0.947904
0
GAGCTTTGGGGCTTTTGGCTTGATCTCAGTCGACTTGATGGATTCTGGCTTGGGTCTGCAGGCTTTTCGGGC
TCCTT

Consensus:

GAGCTTTGGGGCTTTTGGCTTGATCTCAGTCGACTTGATGGATTCTGGCTTGGGTCTGCAGGCTTTTCGGGC
TCCTT

>WB235_Fam_203_77_1 Nr. of seq. 1 Alignment length(with gaps) = 77
Alignment score = 0.000000
WB235_4:10540321-10540705 Satlength=385 Nr of Repeats=5 RepeatLength=77
seed=GGAAGCTTCA Num.seqs=4 Similarity=0.982684
0
GGAAGCTTCATCTTTTGAATTATAAAAAATAAATTTTCATTTCAAAATCAGTGTGTGCACTATCAAAAGTGTC
CACT

Consensus:

GGAAGCTTCATCTTTTGAATTATAAAAAATAAATTTTCATTTCAAAATCAGTGTGTGCACTATCAAAAGTGTC
CACT

>WB235_Fam_204_73_1 Nr. of seq. 1 Alignment length(with gaps) = 73
Alignment score = 0.000000
WB235_2:1319234-1319605 Satlength=372 Nr of Repeats=5 RepeatLength=73
seed=AGTTTGTAGT Num.seqs=3 Similarity=0.920852
0
ANTTTGTAGTTTGTAGTCTAGCAGACCAAAATTTATTAAAACTGCAGAAAATTGATGGGTCTGCTAATTAAG

Consensus:

ANNTTGTAGTTTGTAGTCTAGCAGACCAAAATTTATTA AAAA ACTGCAGAAAATTGATGGGTCTGCTAATTAAG

>WB235_Fam_205_72_1 Nr. of seq. 1 Alignment length(with gaps) = 72
Alignment score = 0.000000
WB235_2:863584-866193 Satlength=2610 Nr of Repeats=35 RepeatLength=72
seed=TCCATCCAGC Num.seqs=29 Similarity=0.928845
0
TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACTAGTAGTACCATTGGCTCCGTTTCG

Consensus:

TCCATCCAGCTGTGGTTGGTCTCTGGGTGAATCCTCGAGAAGTATCACTAGTAGTACCATTGGCTCCGTTTCG

>WB235_Fam_206_72_1 Nr. of seq. 1 Alignment length(with gaps) = 72
Alignment score = 0.000000
WB235_3:1608442-1609120 Satlength=679 Nr of Repeats=5 RepeatLength=72
seed=ATGAATTTTA Num.seqs=3 Similarity=0.975309
0
ATGAATTTTAATACAATTTTCCTGACGATGAAGTCATAAAAATTCATTTTTTGACCTTTCAACTTTAGTTTTT

Consensus:

ATGAATTTTAATACAATTTTCCTGACGATGAAGTCATAAAAATTCATTTTTTGACCTTTCAACTTTAGTTTTT

>WB235_Fam_207_72_1 Nr. of seq. 1 Alignment length(with gaps) = 72
Alignment score = 0.000000
WB235_6:15051665-15051975 Satlength=311 Nr of Repeats=5 RepeatLength=72
seed=TGGTTGTGTT Num.seqs=4 Similarity=0.990741
0
TGGTTGTGTTCCCAAAGTGAGAAAAGAGGGTACAGACCTCTGTACGAATATGTCTTATCAGCTTCAAAGA

Consensus:

TGGTTGTGTTCCCAAAGTGAGAAAAGAGGGTACAGACCTCTGTACGAATATGTCTTATCAGCTTCAAAGA

>WB235_Fam_208_71_1 Nr. of seq. 1 Alignment length(with gaps) = 71
Alignment score = 0.000000
WB235_1:1408704-1409384 Satlength=681 Nr of Repeats=8 RepeatLength=71
seed=ATTTATGTGA Num.seqs=6 Similarity=0.847840
0
ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAGGGAAATCTGAATTTTTCCGATTTTTCTGACGA

Consensus:

ATTTATGTGAAAATTCAGGTTTTTAGGGCATTTTTTGAGGGAAATCTGAATTTTTCCGATTTTTCTGACGA

>WB235_Fam_209_70_1 Nr. of seq. 1 Alignment length(with gaps) = 70
Alignment score = 0.000000

WB235_4:2393736-2396081 Satlength=2346 Nr of Repeats=23 RepeatLength=70
seed=AAAAATCGAT Num.seqs=14 Similarity=0.884668
0

AAAAATCGATTTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTCAACAGCGAAAAAATTGAATTTTCCGCC

Consensus:

AAAAATCGATTTTTTTGAAGTTTTTCTCAATAGAGCGCATTTTCAACAGCGAAAAAATTGAATTTTCCGCC

>WB235_Fam_210_69_1 Nr. of seq. 1 Alignment length(with gaps) = 69
Alignment score = 0.000000
WB235_2:12336337-12336616 Satlength=280 Nr of Repeats=4 RepeatLength=69
seed=AGGTAGGCCT Num.seqs=3 Similarity=0.747619
0

AGGTAGGCCTGTAGGCATTGACTGNCAGAAAAGCGTAGACAGGCAAGCAGGTAAAAAGATACATGAGGC

Consensus:

AGGTAGGCCTGTAGGCATTGACTGNCAGAAAAGCGTAGACAGGCAAGCAGGTAAAAAGATACATGAGGC

>WB235_Fam_211_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
WB235_1:13883897-13885190 Satlength=1294 Nr of Repeats=19 RepeatLength=68
seed=TTGGTTGAGG Num.seqs=14 Similarity=0.987503
0 TTGGTTGAGGCTAGAAAATGTTGTAGTTTGTAGTGTGTTAGCCTCAACCAAATTAATTTTTTTTTTAA

Consensus:

TTGGTTGAGGCTAGAAAATGTTGTAGTTTGTAGTGTGTTAGCCTCAACCAAATTAATTTTTTTTTTAA

>WB235_Fam_212_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
WB235_2:6296691-6297095 Satlength=405 Nr of Repeats=6 RepeatLength=68
seed=AATAGAGACG Num.seqs=4 Similarity=0.901961
0 AATAGAGACGAATAAAAATTTAAAATTTTTATTAGTGTCTCTATTTTATAAAGAAAATACATTTTCAA

Consensus:

AATAGAGACGAATAAAAATTTAAAATTTTTATTAGTGTCTCTATTTTATAAAGAAAATACATTTTCAA

>WB235_Fam_213_65_1 Nr. of seq. 1 Alignment length(with gaps) = 65
Alignment score = 0.000000
WB235_2:1858665-1858980 Satlength=316 Nr of Repeats=5 RepeatLength=65
seed=TATCGAGAGA Num.seqs=3 Similarity=0.658497
0 TATCGAGAGAATNTTCCACATTCACTTTGAATTCCNTTCCAATTTCAATAAGACTCTCAGTAAG

Consensus:

TATCGAGAGAATNTTCCACATTCACTTTGAATTCCNTTCCAATTTCAATAAGACTCTCAGTAAG

>WB235_Fam_214_62_1 Nr. of seq. 1 Alignment length(with gaps) = 62
Alignment score = 0.000000
WB235_1:14101896-14102785 Satlength=890 Nr of Repeats=4 RepeatLength=62
seed=GTAGTTTGTA Num.seqs=3 Similarity=0.928315
0 GTAGTTTGTAGCTTTAGCCTCAACCAAATTAGCTAAAGCTTGAGTGAGGCTATGGTGATTTT

Consensus:

GTAGTTTGTAGCTTTAGCCTCAACCAAATTAGCTAAAGCTTGAGTGAGGCTATGGTGATTTT

>WB235_Fam_215_62_1 Nr. of seq. 1 Alignment length(with gaps) = 62
Alignment score = 0.000000
WB235_2:13967824-13968381 Satlength=558 Nr of Repeats=7 RepeatLength=62
seed=TGCTAACTAG Num.seqs=6 Similarity=0.822222
0 TGCTAACTAGCTACGGCCAGCTTAGGTGCCGGCTGCACGAGCAGTCCTGGTTTAAATGTCGGC

Consensus:

TGCTAACTAGCTACGGCCAGCTTAGGTGCCGGCTGCACGAGCAGTCCTGGTTTAAATGTCGGC

>WB235_Fam_216_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
WB235_5:7259575-7259935 Satlength=361 Nr of Repeats=6 RepeatLength=60
seed=CTAGCTAGAT Num.seqs=6 Similarity=0.943704
0 CTAGCTAGATTAAACGCTCTCAAGAGACAGCATGTTGTTGTTGCCACAAGAAGAAGGCT

Consensus:

CTAGCTAGATTAAACGCTCTCAAGAGACAGCATGTTGTTGTTGCCACAAGAAGAAGGCT

>WB235_Fam_217_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
WB235_5:8699367-8702913 Satlength=3547 Nr of Repeats=59 RepeatLength=60
seed=ATTCAGTTGA Num.seqs=58 Similarity=0.926281
0 ATTCAGTTGAGCTCGTTATGTCGGTTGAAGACACAATTGGAGTGGTGCTTGAGGAGCTGG

Consensus:

ATTCAGTTGAGCTCGTTATGTCGGTTGAAGACACAATTGGAGTGGTGCTTGAGGAGCTGG

>WB235_Fam_218_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
WB235_5:14107921-14109961 Satlength=2041 Nr of Repeats=34 RepeatLength=60
seed=CTGCTGATTC Num.seqs=34 Similarity=0.924896
0 CTGCTGATTCGAGAAGAAGCCCCAGCCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

Consensus:

CTGCTGATTCCGAGAAGAAGGCCCCAGCCAAGAGAGAAGCTGATAAGCCAAAGACTGAAT

>WB235_Fam_219_59_1 Nr. of seq. 1 Alignment length(with gaps) = 59
Alignment score = 0.000000
WB235_2:1408410-1408750 Satlength=341 Nr of Repeats=5 RepeatLength=59
seed=CTACAAACTA Num.seqs=3 Similarity=0.969868
0 CTACAAACTACAAAAGCCTATTTAGCAGACCCACGCCAACTTCTGATGGGTCTGCTAGA

Consensus:

CTACAAACTACAAAAGCCTATTTAGCAGACCCACGCCAACTTCTGATGGGTCTGCTAGA

>WB235_Fam_220_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
WB235_5:14104614-14106168 Satlength=1555 Nr of Repeats=20 RepeatLength=57
seed=GAAGTCAACA Num.seqs=13 Similarity=0.959214
0 GAAGTCAACAAGCTGATCAAGAGCAACACCGTGGATCCCGAGCTGCCGGACAGAAGG

Consensus:

GAAGTCAACAAGCTGATCAAGAGCAACACCGTGGATCCCGAGCTGCCGGACAGAAGG

>WB235_Fam_221_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
WB235_2:1204743-1204963 Satlength=221 Nr of Repeats=4 RepeatLength=55
seed=GGGATTATTG Num.seqs=4 Similarity=0.903030
0 GGGATTATTGGAGTTTCTTTTTCTAGAATTTTTTGAAAATTTTGGACAGTTTTTTT

Consensus:

GGGATTATTGGAGTTTCTTTTTCTAGAATTTTTTGAAAATTTTGGACAGTTTTTTT

>WB235_Fam_222_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
WB235_4:6009084-6009409 Satlength=326 Nr of Repeats=6 RepeatLength=55
seed=AAGAGTCCCC Num.seqs=4 Similarity=1.000000
0 AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCCTAGGGTT

Consensus:

AAGAGTCCCCACACACTGAAAGGTTTTAAGGAATTTTTTGAGGATTCCTAGGGTT

>WB235_Fam_223_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
WB235_6:16837630-16838124 Satlength=495 Nr of Repeats=4 RepeatLength=52
seed=GCATGTCTTC Num.seqs=3 Similarity=0.626263
0 GCATGTCTTCCAAGCGTTTTGAGCCACGCNTGGGATTCCTATACACGGCTG

Consensus:

GCATGTCTTCCAAGCGTTTTGAGCCACGCNTGGGATTTCTTATACACGGCTG

>WB235_Fam_224_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
WB235_4:7727050-7727263 Satlength=214 Nr of Repeats=5 RepeatLength=51
seed=CCATCCGAAG Num.seqs=3 Similarity=0.912854
0 CCATCCGAAGATCCTCAACCATCTGGCCCACCATCTCCGGGACCAGTGGAC

Consensus:

CCATCCGAAGATCCTCAACCATCTGGCCCACCATCTCCGGGACCAGTGGAC

>WB235_Fam_225_50_1 Nr. of seq. 1 Alignment length(with gaps) = 50
Alignment score = 0.000000
WB235_1:12480947-12481197 Satlength=251 Nr of Repeats=5 RepeatLength=50
seed=ACACATGCTA Num.seqs=5 Similarity=0.952000
0 ACACATGCTATAACATTGTCTCCTTCCCCTAGTGACGAGAGCGGCCGTT

Consensus:

ACACATGCTATAACATTGTCTCCTTCCCCTAGTGACGAGAGCGGCCGTT

>WB235_Fam_226_50_1 Nr. of seq. 1 Alignment length(with gaps) = 50
Alignment score = 0.000000
WB235_4:16427870-16428521 Satlength=652 Nr of Repeats=13 RepeatLength=50
seed=GGGCGTGTTT Num.seqs=10 Similarity=0.897482
0 GGGCGTGTTTTACATGCCCCGCCACAAAATTGATGTTTCCACCAAAT

Consensus:

GGGCGTGTTTTACATGCCCCGCCACAAAATTGATGTTTCCACCAAAT

>WB235_Fam_227_49_1 Nr. of seq. 1 Alignment length(with gaps) = 49
Alignment score = 0.000000
WB235_1:1620047-1620586 Satlength=540 Nr of Repeats=9 RepeatLength=49
seed=CAATAATTTT Num.seqs=7 Similarity=0.909297
0 CAATAATTTTAAATTAAATTATCGATTTTTCTAAATTTTCCGAAAAAT

Consensus:

CAATAATTTTAAATTAAATTATCGATTTTTCTAAATTTTCCGAAAAAT

>WB235_Fam_228_49_1 Nr. of seq. 1 Alignment length(with gaps) = 49
Alignment score = 0.000000
WB235_5:14766633-14767947 Satlength=1315 Nr of Repeats=28 RepeatLength=49
seed=GCTACGATAT Num.seqs=20 Similarity=0.947870
0 GCTACGATATCGTAGCACTTTTTTATTTTCCATATCCACCAAAAAAC

Consensus:

GCTACGATATCGTAGCACTTTTTTATTTTCCATATTCCACCAAAAAAC

>WB235_Fam_229_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48

Alignment score = 0.000000

WB235_2:13284530-13285104 Satlength=575 Nr of Repeats=12 RepeatLength=48

seed=TGCTTACGTG Num.seqs=10 Similarity=0.812346

0 TGCCTACGTGCCTACAAAACAGGCGTAGGCAGCTTTAAAGGTGATGCA

Consensus:

TGCCTACGTGCCTACAAAACAGGCGTAGGCAGCTTTAAAGGTGATGCA

>WB235_Fam_230_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48

Alignment score = 0.000000

WB235_6:14262861-14263101 Satlength=241 Nr of Repeats=5 RepeatLength=48

seed=GGAGGTGGAG Num.seqs=5 Similarity=0.841667

0 GGAGGTGGAGAAAGTGTAGTTCCCGGTGGTCGNGGCTCTTCNGAGGGT

Consensus:

GGAGGTGGAGAAAGTGTAGTTCCCGGTGGTCGNGGCTCTTCNGAGGGT

>WB235_Fam_231_46_1 Nr. of seq. 1 Alignment length(with gaps) = 46

Alignment score = 0.000000

WB235_6:1980629-1980811 Satlength=183 Nr of Repeats=4 RepeatLength=46

seed=TTGTTAAATTG Num.seqs=3 Similarity=0.835749

0 TTGTTAAATTGCCTCCCGGANCACTTTTCTTATTCCCAACTA

Consensus:

TTGTTAAATTGCCTCCCGGANCACTTTTCTTATTCCCAACTA

>WB235_Fam_232_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45

Alignment score = 0.000000

WB235_4:7734990-7736070 Satlength=1081 Nr of Repeats=24 RepeatLength=45

seed=ACCATCAGGC Num.seqs=24 Similarity=0.963714

0 ACCATCAGGCGGACCACCAGGACCATTTGATCCATCAGGAGCACC

Consensus:

ACCATCAGGCGGACCACCAGGACCATTTGATCCATCAGGAGCACC

>WB235_Fam_233_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45

Alignment score = 0.000000

WB235_5:11273771-11274491 Satlength=721 Nr of Repeats=16 RepeatLength=45
seed=ACAACTGAAT Num.seqs=16 Similarity=0.992593
0 ACAACTGAATCAACTGCAGCACCAAGCACATCTACAGAGACACCT

Consensus:

ACAACTGAATCAACTGCAGCACCAAGCACATCTACAGAGACACCT

>WB235_Fam_234_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

WB235_6:17441768-17447783 Satlength=6016 Nr of Repeats=134
RepeatLength=45 seed=CCACCAGCAC Num.seqs=122 Similarity=0.923840
0 CCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGACTCCAT

Consensus:

CCACCAGCACTGCTTCGAGTACGACAGAAAGCACTTCGACTCCAT

>WB235_Fam_235_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000

WB235_2:2171107-2172182 Satlength=1076 Nr of Repeats=24 RepeatLength=43
seed=CGAGTTTGGC Num.seqs=23 Similarity=0.818978
0 CGAGTTTGGCCTACANCAAATTTGGCAAATTCGGCAAATTTGC

Consensus:

CGAGTTTGGCCTACANCAAATTTGGCAAATTCGGCAAATTTGC

>WB235_Fam_236_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000

WB235_2:14130915-14131087 Satlength=173 Nr of Repeats=4 RepeatLength=43
seed=GAAAACTAGG Num.seqs=4 Similarity=0.715762
0 GAAAACTAGGCCACAGAGTTCAAATTGATGGCCTAGAAATCTA

Consensus:

GAAAACTAGGCCACAGAGTTCAAATTGATGGCCTAGAAATCTA

>WB235_Fam_237_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000

WB235_3:1385873-1386532 Satlength=660 Nr of Repeats=5 RepeatLength=43
seed=GGCTCTCGGC Num.seqs=3 Similarity=0.627907
0 GGCTCTCGGCTCGCGCCGAGAGCCGAGNTCTACTNAAAGTTTC

Consensus:

GGCTCTCGGCTCGCGCCGAGAGCCGAGNTCTACTNAAAGTTTC

>WB235_Fam_238_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000
WB235_3:12305325-12305929 Satlength=605 Nr of Repeats=14 RepeatLength=43
seed=AGCAGCCGAC Num.seqs=11 Similarity=0.800423
0 AGCAGCCGACAGTTGCCGGTTGCCGAAAAATTGCAGTAATTTTC

Consensus:

AGCAGCCGACAGTTGCCGGTTGCCGAAAAATTGCAGTAATTTTC

>WB235_Fam_239_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
WB235_1:724780-724948 Satlength=169 Nr of Repeats=4 RepeatLength=42
seed=TTTGATCTAC Num.seqs=4 Similarity=0.968254
0 TTTGATCTACAAAAAATGCGGGAATTTTCCCAGCATTGCTCA

Consensus:

TTTGATCTACAAAAAATGCGGGAATTTTCCCAGCATTGCTCA

>WB235_Fam_240_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
WB235_5:6188375-6189068 Satlength=694 Nr of Repeats=15 RepeatLength=42
seed=AGGTGCTGCT Num.seqs=9 Similarity=0.859788
0 AGGTGCTGCTTCCTTTGGAACATCTGCTTGGGTTGGCTCCGA

Consensus:

AGGTGCTGCTTCCTTTGGAACATCTGCTTGGGTTGGCTCCGA

>WB235_Fam_241_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
WB235_4:3696437-3696683 Satlength=247 Nr of Repeats=6 RepeatLength=41
seed=AAATTTTAA Num.seqs=6 Similarity=0.947967
0 AAATTTTAAACGAGAAGTGGGCGAAAATCATTCAAAAATTC

Consensus:

AAATTTTAAACGAGAAGTGGGCGAAAATCATTCAAAAATTC

>WB235_Fam_242_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
WB235_5:20236849-20237152 Satlength=304 Nr of Repeats=5 RepeatLength=41
seed=GCATTTTTCG Num.seqs=3 Similarity=0.772358
0 GCATTTTTCGCCGATTTTNNATTAATTTTCAGTGAAAATTC

Consensus:

GCATTTTTCGCCGATTTTNNATTAATTTTCAGTGAAAATTC

>WB235_Fam_243_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
WB235_3:404417-405141 Satlength=725 Nr of Repeats=7 RepeatLength=40
seed=TCCACGTGGA Num.seqs=5 Similarity=0.650794
0 TCCACGTGGAATTTTCAGAATTTTCNCAGAAAATTGAAA

Consensus:

TCCACGTGGAATTTTCAGAATTTTCNCAGAAAATTGAAA

>WB235_Fam_244_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
WB235_5:18865200-18865555 Satlength=356 Nr of Repeats=7 RepeatLength=40
seed=GAATTTTTTG Num.seqs=6 Similarity=0.926667
0 GAATTTTTTGTCAATTCTACTGAATTTTCCAAATTTTCAGC

Consensus:

GAATTTTTTGTCAATTCTACTGAATTTTCCAAATTTTCAGC

>WB235_Fam_245_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
WB235_5:18879684-18879863 Satlength=180 Nr of Repeats=5 RepeatLength=40
seed=TTTTGCCGAA Num.seqs=3 Similarity=0.629630
0 TTTTGCCAAAAATNTGTCAATTTTGTGGAATTTCTNTCAT

Consensus:

TTTTTGCCAAAAATNTGTCAATTTTGTGGAATTTCTNTCAT

>WB235_Fam_246_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
WB235_2:3494517-3494748 Satlength=232 Nr of Repeats=5 RepeatLength=39
seed=AATTTCCCGC Num.seqs=3 Similarity=0.769444
0 AATTTCCCGCCAAAATTGAATTTTTTTAAAGAAAATTTA

Consensus:

AATTTCCCGCCAAAATTGAATTTTTTTAAAGAAAATTTA

>WB235_Fam_247_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
WB235_4:4996655-4997045 Satlength=391 Nr of Repeats=8 RepeatLength=39
seed=CCAACTGGAG Num.seqs=7 Similarity=0.784921
0 CCAACTGGAGCCAGCACNATGACCGCTGTTGGAGAGCA

Consensus:

CCAACTGGAGCCAGCACNATGACCGCTGTTGGAGGAGCA

>WB235_Fam_248_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
WB235_5:3694442-3694754 Satlength=313 Nr of Repeats=8 RepeatLength=39
seed=GATTTACGGG Num.seqs=6 Similarity=0.849573
0 GATTTACGGGCTTTAATCAGTTTCGAAAAAGCTTGTGTC

Consensus:

GATTTACGGGCTTTAATCAGTTTCGAAAAAGCTTGTGTC

>WB235_Fam_249_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
WB235_5:12633007-12633394 Satlength=388 Nr of Repeats=10 RepeatLength=39
seed=TGGTACGGTA Num.seqs=9 Similarity=0.880342
0 TGGTACGGTAGTTGTAGTGGTAGTGGAGGTTGTTGTTGG

Consensus:

TGGTACGGTAGTTGTAGTGGTAGTGGAGGTTGTTGTTGG

>WB235_Fam_250_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
WB235_5:18636764-18637321 Satlength=558 Nr of Repeats=15 RepeatLength=39
seed=GTAATTTATA Num.seqs=13 Similarity=0.917598
0 GTAATTTATAATTTTTTAAAGATGAGTAATATATTGCC

Consensus:

GTAATTTATAATTTTTTAAAGATGAGTAATATATTGCC

>WB235_Fam_251_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
WB235_6:17179152-17179971 Satlength=820 Nr of Repeats=21 RepeatLength=39
seed=ATTGATACTT Num.seqs=21 Similarity=0.932601
0 ATTGATACTTTGTTCGGGTTTAGACCATCGGCCGAGCTTC

Consensus:

ATTGATACTTTGTTCGGGTTTAGACCATCGGCCGAGCTTC

>WB235_Fam_252_38_1 Nr. of seq. 1 Alignment length(with gaps) = 38
Alignment score = 0.000000
WB235_1:1987299-1987635 Satlength=337 Nr of Repeats=5 RepeatLength=38
seed=AAAATCGATA Num.seqs=3 Similarity=1.000000
0 AAAATCGATAATTTTCAGTATGCAGTGAAATTCCTTGA

Consensus:

AAAAATCGATAATTTTCAGTATGCAGTGAAATTCTTGGA

>WB235_Fam_253_37_1 Nr. of seq. 1 Alignment length(with gaps) = 37
Alignment score = 0.000000
WB235_1:9925221-9925359 Satlength=139 Nr of Repeats=5 RepeatLength=37
seed=ATAATTTTTC Num.seqs=3 Similarity=1.000000
0 ATAATTTTTCCTTGAGTAATGAGAGACTTTTTCATAAT

Consensus:

ATAATTTTTCCTTGAGTAATGAGAGACTTTTTCATAAT

>WB235_Fam_254_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
WB235_3:12513645-12515229 Satlength=1585 Nr of Repeats=44 RepeatLength=36
seed=GATATTTTCA Num.seqs=44 Similarity=0.951257
0 GATATTTTCATGTTTCGGCAAAAGTACCGATTGCCA

Consensus:

GATATTTTCATGTTTCGGCAAAAGTACCGATTGCCA

>WB235_Fam_255_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
WB235_6:17674798-17675174 Satlength=377 Nr of Repeats=7 RepeatLength=36
seed=CCACCAACTC Num.seqs=6 Similarity=0.728395
0 CCACCAACTCCAAAATCAGCTGCTCCATCAGAAAGTC

Consensus:

CCACCAACTCCAAAATCAGCTGCTCCATCAGAAAGTC

>WB235_Fam_256_35_1 Nr. of seq. 1 Alignment length(with gaps) = 35
Alignment score = 0.000000
WB235_1:11201002-11201638 Satlength=637 Nr of Repeats=9 RepeatLength=35
seed=AATTGCCGAA Num.seqs=7 Similarity=0.793210
0 AATTGCCGAATTTCTCGTTTTTGGCAATTTACCAA

Consensus:

AATTGCCGAATTTCTCGTTTTTGGCAATTTACCAA

>WB235_Fam_257_35_1 Nr. of seq. 1 Alignment length(with gaps) = 35
Alignment score = 0.000000
WB235_2:12795532-12795808 Satlength=277 Nr of Repeats=8 RepeatLength=35
seed=TGTGTAATAA Num.seqs=5 Similarity=0.794286
0 TGTGTAATAAGAAAATTTCAAATTTTTTTCACGAA

Consensus:

TGTGTAATAAGAAAATTTCAAATTTTTTTCACGAA

>WB235_Fam_258_35_1 Nr. of seq. 1 Alignment length(with gaps) = 35
Alignment score = 0.000000
WB235_5:1015554-1016070 Satlength=517 Nr of Repeats=9 RepeatLength=35
seed=GCATTTGCCG Num.seqs=6 Similarity=0.817143
0 GCATTTGCCGATTTTTTAAAATTTCTGGCAATTCCA

Consensus:

GCATTTGCCGATTTTTTAAAATTTCTGGCAATTCCA

>WB235_Fam_259_34_1 Nr. of seq. 1 Alignment length(with gaps) = 34
Alignment score = 0.000000
WB235_2:14100395-14100701 Satlength=307 Nr of Repeats=8 RepeatLength=34
seed=CCGTGCCTAC Num.seqs=7 Similarity=0.828198
0 CCGTGCCTACTAACCTACCGACCTTGCTGCCTT

Consensus:

CCGTGCCTACTAACCTACCGACCTTGCTGCCTT

>WB235_Fam_260_34_1 Nr. of seq. 1 Alignment length(with gaps) = 34
Alignment score = 0.000000
WB235_3:11798467-11798684 Satlength=218 Nr of Repeats=6 RepeatLength=34
seed=TTGCCGAATT Num.seqs=5 Similarity=0.811765
0 TTGCCGAATTTGCCGTTTGCCGAGCTCGTCAAAT

Consensus:

TTGCCGAATTTGCCGTTTGCCGAGCTCGTCAAAT

>WB235_Fam_261_34_1 Nr. of seq. 1 Alignment length(with gaps) = 34
Alignment score = 0.000000
WB235_3:11864487-11864917 Satlength=431 Nr of Repeats=13 RepeatLength=34
seed=AAGTATTTTT Num.seqs=12 Similarity=0.954843
0 AAGTATTTTTTGCCGTTTTTTTTGCCGAAATTTCC

Consensus:

AAGTATTTTTTGCCGTTTTTTTTGCCGAAATTTCC

>WB235_Fam_262_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000

WB235_1:2251015-2251148 Satlength=134 Nr of Repeats=4 RepeatLength=33
seed=TAAGAAAAGT Num.seqs=3 Similarity=0.892256
0 TAAGAAAAGTTAGGCCACCAAACCTTTGGTGAAC

Consensus:

TAAGAAAAGTTAGGCCACCAAACCTTTGGTGAAC

>WB235_Fam_263_32_1 Nr. of seq. 1 Alignment length(with gaps) = 32
Alignment score = 0.000000
WB235_1:8484982-8485111 Satlength=130 Nr of Repeats=4 RepeatLength=32
seed=AAAATCGAAA Num.seqs=3 Similarity=1.000000
0 AAAATCGAAAAATTCTCGTTTTTCAATTTTTA

Consensus:

AAAATCGAAAAATTCTCGTTTTTCAATTTTTA

>WB235_Fam_264_32_1 Nr. of seq. 1 Alignment length(with gaps) = 32
Alignment score = 0.000000
WB235_1:11313617-11315164 Satlength=1548 Nr of Repeats=48 RepeatLength=32
seed=GCAATTTTTTA Num.seqs=37 Similarity=0.890140
0 GCAATTTTTTAGGCTAAAAATCACTAAAAAACT

Consensus:

GCAATTTTTTAGGCTAAAAATCACTAAAAAACT

>WB235_Fam_265_32_1 Nr. of seq. 1 Alignment length(with gaps) = 32
Alignment score = 0.000000
WB235_3:12072321-12073804 Satlength=1484 Nr of Repeats=45 RepeatLength=32
seed=AAATTTGTGA Num.seqs=34 Similarity=0.906566
0 AAATTTGTGAAAATTTAGGCCCATTTTGCTCA

Consensus:

AAATTTGTGAAAATTTAGGCCCATTTTGCTCA

>WB235_Fam_266_32_1 Nr. of seq. 1 Alignment length(with gaps) = 32
Alignment score = 0.000000
WB235_5:20705245-20705371 Satlength=127 Nr of Repeats=4 RepeatLength=32
seed=GTGCGTCCGG Num.seqs=3 Similarity=0.888889
0 GTGCGTCCGGCGTCCGGAAAAAGCGGACGCGT

Consensus:

GTGCGTCCGGCGTCCGGAAAAAGCGGACGCGT

>WB235_Fam_267_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_2:3070377-3070511 Satlength=135 Nr of Repeats=4 RepeatLength=31
seed=ATCGATTTTT Num.seqs=3 Similarity=0.700337
0 ATCGATTTTTTCGTTAAAAAATCAATAAAAT

Consensus:

ATCGATTTTTTCGTTAAAAAATCAATAAAAT

>WB235_Fam_268_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_2:3691112-3691360 Satlength=249 Nr of Repeats=8 RepeatLength=31
seed=GCTGATTGGT Num.seqs=8 Similarity=0.553571
0 GCTGATTGGTCGGCGNGGTTGCCCATCNTT

Consensus:

GCTGATTGGTCGGCGNGGTTGCCCATCNTT

>WB235_Fam_269_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_2:12455807-12455995 Satlength=189 Nr of Repeats=6 RepeatLength=31
seed=GACATCTCGC Num.seqs=4 Similarity=0.584229
0 GACATCTCGCAGGACATTATAAGAAGCGACC

Consensus:

GACATCTCGCAGGACATTATAAGAAGCGACC

>WB235_Fam_270_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_2:13281689-13282092 Satlength=404 Nr of Repeats=10 RepeatLength=31
seed=CACGCCTATT Num.seqs=7 Similarity=0.811572
0 CACGCCTATTTTATGGGCGGAGTCTACAAGC

Consensus:

CACGCCTATTTTATGGGCGGAGTCTACAAGC

>WB235_Fam_271_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_3:2009666-2010596 Satlength=931 Nr of Repeats=27 RepeatLength=31
seed=TGCGTCGGAA Num.seqs=23 Similarity=0.733775
0 TGCGTCGGAAATTNATTCCGATCATCGCCGG

Consensus:

TGCGTCGGAAATTNATTCCGATCATCGCCGG

>WB235_Fam_272_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_3:2011573-2012317 Satlength=745 Nr of Repeats=17 RepeatLength=31
seed=TCCGATGCAT Num.seqs=13 Similarity=0.625486
0 TCCGATGCATTGCCGATAATCGGAACCTGGT

Consensus:

TCCGATGCATTGCCGATAATCGGAACCTGGT

>WB235_Fam_273_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_3:11002899-11003053 Satlength=155 Nr of Repeats=5 RepeatLength=31
seed=GCAGCCGACG Num.seqs=4 Similarity=0.524411
0 GCAGCCGACGCTATACGGGTCTGATGGAGTA

Consensus:

GCAGCCGACGCTATACGGGTCTGATGGAGTA

>WB235_Fam_274_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_3:11189285-11189691 Satlength=407 Nr of Repeats=12 RepeatLength=31
seed=TCTGAGCTAC Num.seqs=11 Similarity=0.755258
0 TCTGAGCTACAGTACTCCTGTCAAGAACAAAT

Consensus:

TCTGAGCTACAGTACTCCTGTCAAGAACAAAT

>WB235_Fam_275_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_3:12817385-12817569 Satlength=185 Nr of Repeats=5 RepeatLength=31
seed=GATTTTTTCA Num.seqs=3 Similarity=0.659722
0 GATTTTTTCAGNGAAAANCNAAAAATTTTCG

Consensus:

GATTTTTTCAGNGAAAANCNAAAAATTTTCG

>WB235_Fam_276_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_3:13167617-13167762 Satlength=146 Nr of Repeats=5 RepeatLength=31
seed=CCAAAAATGA Num.seqs=4 Similarity=0.863799
0 CCAAAAATGACTGAAAATAGTCAAAAATTAG

Consensus:

CCAAAAATGACTGAAAATAGTCAAAAATTAG

>WB235_Fam_277_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_4:775288-775412 Satlength=125 Nr of Repeats=4 RepeatLength=31
seed=CAAAAATCGG Num.seqs=4 Similarity=0.949821
0 CAAAAATCGGGAAATTTTCACAAAAAATGC

Consensus:

CAAAAATCGGGAAATTTTCACAAAAAATGC

>WB235_Fam_278_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_5:18415750-18416287 Satlength=538 Nr of Repeats=16 RepeatLength=31
seed=TTGGCCCAGA Num.seqs=11 Similarity=0.885826
0 TTGGCCCAGAGCTCTCTTGACCCAAGCCCC

Consensus:

TTGGCCCAGAGCTCTCTTGACCCAAGCCCC

>WB235_Fam_279_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_5:18536998-18537693 Satlength=696 Nr of Repeats=5 RepeatLength=31
seed=AAAAATTTTGA Num.seqs=3 Similarity=0.971326
0 AAAAATTTTGACCCAGAAATCGAAAAATTCGC

Consensus:

AAAAATTTTGACCCAGAAATCGAAAAATTCGC

>WB235_Fam_280_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_5:18855835-18856039 Satlength=205 Nr of Repeats=6 RepeatLength=31
seed=TCGTTTTTTC Num.seqs=5 Similarity=0.819355
0 TCGTTTTTTCATGAAAAAATCAATTTTCGG

Consensus:

TCGTTTTTTCATGAAAAAATCAATTTTCGG

>WB235_Fam_281_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
WB235_5:20407384-20407602 Satlength=219 Nr of Repeats=4 RepeatLength=31
seed=GAAAAAGTGC Num.seqs=3 Similarity=0.784722
0 GAAAAAGTGCTGAAAATCACATTTTGAAT

Consensus:

GAAAAAGTGCTGAAAATCACATTTTGAAC

>WB235_Fam_282_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_1:1704545-1705424 Satlength=880 Nr of Repeats=24 RepeatLength=30
seed=AATTTGAATT Num.seqs=15 Similarity=0.732487
0 AATTTGAATTTTCCCGAATTTTNAACGAA

Consensus:

AATTTGAATTTTCCCGAATTTTNAACGAA

>WB235_Fam_283_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_1:6514283-6515118 Satlength=836 Nr of Repeats=13 RepeatLength=30
seed=TGGTGGAAC Num.seqs=11 Similarity=0.953131
0 TGGTGGAAC TGGATTCGGCAGTGGAATGC

Consensus:

TGGTGGAAC TGGATTCGGCAGTGGAATGC

>WB235_Fam_284_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_1:11404108-11404462 Satlength=355 Nr of Repeats=10 RepeatLength=30
seed=CCTTGGGCTC Num.seqs=7 Similarity=0.875132
0 CCTTGGGCTCCCTGAGCTCCAAATTGTGCT

Consensus:

CCTTGGGCTCCCTGAGCTCCAAATTGTGCT

>WB235_Fam_285_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_1:12109993-12110203 Satlength=211 Nr of Repeats=7 RepeatLength=30
seed=GTCATTATCA Num.seqs=7 Similarity=0.974603
0 GTCATTATCAGCTTCTGGTGTCTTAGAAGA

Consensus:

GTCATTATCAGCTTCTGGTGTCTTAGAAGA

>WB235_Fam_286_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_2:12171287-12172252 Satlength=966 Nr of Repeats=32 RepeatLength=30
seed=CAAACTACAG Num.seqs=27 Similarity=0.878569
0 CAAACTACAGTAGTACTGTAGTACCATAAC

Consensus:

CAAACCTACAGTAGTACTGTAGTACCATAAC

>WB235_Fam_287_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_2:12979640-12979790 Satlength=151 Nr of Repeats=4 RepeatLength=30
seed=TTCAGGCAGG Num.seqs=3 Similarity=0.644444
0 TTCAGGCAGGCATAGGTTACTTTGAAAATT

Consensus:

TTCAGGCAGGCATAGGTTACTTTGAAAATT

>WB235_Fam_288_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_3:3740014-3740583 Satlength=570 Nr of Repeats=9 RepeatLength=30
seed=CCTTGTCAGGC Num.seqs=6 Similarity=0.842963
0 CCTTGTCAGGCAAGGAGGTAGGCGTAGGTCA

Consensus:

CCTTGTCAGGCAAGGAGGTAGGCGTAGGTCA

>WB235_Fam_289_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_3:13268025-13268308 Satlength=284 Nr of Repeats=8 RepeatLength=30
seed=TTTCAGGCCA Num.seqs=5 Similarity=0.822222
0 TTTCAGGCCAATTCNGTCATTTTTGGACA

Consensus:

TTTCAGGCCAATTCNGTCATTTTTGGACA

>WB235_Fam_290_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_4:16649049-16649496 Satlength=448 Nr of Repeats=15 RepeatLength=30
seed=AAAAATCAAAA Num.seqs=12 Similarity=0.938721
0 AAAATCAAAAATTAGATGAATTTTCGATTA

Consensus:

AAAAATCAAAAATTAGATGAATTTTCGATTA

>WB235_Fam_291_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000

WB235_5:20246749-20247078 Satlength=330 Nr of Repeats=11 RepeatLength=30
seed=CTCAAATTTG Num.seqs=10 Similarity=0.911111
0 CTCAAATTTGCACTAAAAATTCCAATTTTT

Consensus:

CTCAAATTTGCACTAAAAATTCCAATTTTT

>WB235_Fam_292_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
WB235_6:1548656-1549346 Satlength=691 Nr of Repeats=19 RepeatLength=30
seed=ACTACCCAAC Num.seqs=18 Similarity=0.923021
0 ACTACCCAACCGGCTCCGGCAACCAGTCCA

Consensus:

ACTACCCAACCGGCTCCGGCAACCAGTCCA

>WB235_Fam_293_29_1 Nr. of seq. 1 Alignment length(with gaps) = 29
Alignment score = 0.000000
WB235_3:10636973-10637342 Satlength=370 Nr of Repeats=11 RepeatLength=29
seed=GGCCTAGAAA Num.seqs=7 Similarity=0.700055
0 GGCCTAGAAANTTCTATTTGAAAGTTGAT

Consensus:

GGCCTAGAAANTTCTATTTGAAAGTTGAT

>WB235_Fam_294_29_1 Nr. of seq. 1 Alignment length(with gaps) = 29
Alignment score = 0.000000
WB235_4:13964027-13964143 Satlength=117 Nr of Repeats=4 RepeatLength=29
seed=TACATTGCAA Num.seqs=4 Similarity=0.946360
0 TACATTGCAAGATCTTCTTACTATGTAGG

Consensus:

TACATTGCAAGATCTTCTTACTATGTAGG

>WB235_Fam_295_29_1 Nr. of seq. 1 Alignment length(with gaps) = 29
Alignment score = 0.000000
WB235_5:19278568-19278735 Satlength=168 Nr of Repeats=5 RepeatLength=29
seed=CTCGTCAGTG Num.seqs=4 Similarity=0.954023
0 CTCGTCAGTGGGTGGACGAGGAATGAGCG

Consensus:

CTCGTCAGTGGGTGGACGAGGAATGAGCG

>WB235_Fam_296_28_1 Nr. of seq. 1 Alignment length(with gaps) = 28
Alignment score = 0.000000
WB235_2:2980111-2980251 Satlength=141 Nr of Repeats=5 RepeatLength=28
seed=AATGTCGGCT Num.seqs=5 Similarity=0.847619
0 AATGTCGGCTGCTTCTAGAAACCAGGCA

Consensus:

AATGTCGGCTGCTTCTAGAAACCAGGCA

>WB235_Fam_297_28_1 Nr. of seq. 1 Alignment length(with gaps) = 28
Alignment score = 0.000000
WB235_2:3415307-3415447 Satlength=141 Nr of Repeats=4 RepeatLength=28
seed=TGCCTCGCCT Num.seqs=3 Similarity=0.968254
0 TGCCTCGCCTACGTGCTTATTTTCAGGCA

Consensus:

TGCCTCGCCTACGTGCTTATTTTCAGGCA

>WB235_Fam_298_28_1 Nr. of seq. 1 Alignment length(with gaps) = 28
Alignment score = 0.000000
WB235_5:18447331-18447583 Satlength=253 Nr of Repeats=9 RepeatLength=28
seed=CCAAGAGAAT Num.seqs=9 Similarity=0.915344
0 CCAAGAGAATTTCAACCACCTGGAAATT

Consensus:

CCAAGAGAATTTCAACCACCTGGAAATT

>WB235_Fam_299_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
WB235_2:13668387-13668731 Satlength=345 Nr of Repeats=12 RepeatLength=27
seed=TTCCGGCAAA Num.seqs=8 Similarity=0.904762
0 TTCCGGCAAATCGGCAAATTGCAAAAT

Consensus:

TTCCGGCAAATCGGCAAATTGCAAAAT

>WB235_Fam_300_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
WB235_4:12500507-12500642 Satlength=136 Nr of Repeats=5 RepeatLength=27
seed=ACAATAAAGT Num.seqs=5 Similarity=1.000000
0 ACAATAAAGTACTATGTATTACCGTAT

Consensus:

ACAATAAAGTACTATGTATTACCGTAT

>WB235_Fam_301_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
WB235_6:10973510-10974510 Satlength=1001 Nr of Repeats=30 RepeatLength=27
seed=CACTGACCAA Num.seqs=21 Similarity=0.803410
0 CACTGACCAAAGAAAATATTANACGTG

Consensus:

CACTGACCAAAGAAAATATTANACGTG

>WB235_Fam_302_26_1 Nr. of seq. 1 Alignment length(with gaps) = 26
Alignment score = 0.000000
WB235_1:3117070-3117200 Satlength=131 Nr of Repeats=4 RepeatLength=26
seed=GGCAGGCGTC Num.seqs=3 Similarity=0.931624
0 GGCAGGCGTCAAGCAGGCAGGTTTCA

Consensus:

GGCAGGCGTCAAGCAGGCAGGTTTCA

>WB235_Fam_303_26_1 Nr. of seq. 1 Alignment length(with gaps) = 26
Alignment score = 0.000000
WB235_1:11312599-11313143 Satlength=545 Nr of Repeats=18 RepeatLength=26
seed=ACCTACAGTA Num.seqs=12 Similarity=0.881896
0 ACCTACAGTACCCCTGTCCTAGAATG

Consensus:

ACCTACAGTACCCCTGTCCTAGAATG

>WB235_Fam_304_26_1 Nr. of seq. 1 Alignment length(with gaps) = 26
Alignment score = 0.000000
WB235_2:1178522-1178806 Satlength=285 Nr of Repeats=8 RepeatLength=26
seed=TACTGTAGTT Num.seqs=5 Similarity=0.621429
0 TACTGTAGTTTGACCTACTTANGGAT

Consensus:

TACTGTAGTTTGACCTACTTANGGAT

>WB235_Fam_305_26_1 Nr. of seq. 1 Alignment length(with gaps) = 26
Alignment score = 0.000000
WB235_2:1892810-1893486 Satlength=677 Nr of Repeats=26 RepeatLength=26
seed=ATTTACGGAG Num.seqs=22 Similarity=0.829282
0 ATTTACGGAGCTTCAAGCTTGTGTCG

Consensus:

ATTTACGGAGCTTCAAGCTTGTGTCG

>WB235_Fam_306_26_1 Nr. of seq. 1 Alignment length(with gaps) = 26
Alignment score = 0.000000
WB235_5:19065856-19066708 Satlength=853 Nr of Repeats=32 RepeatLength=26
seed=TGAAATTTCA Num.seqs=23 Similarity=0.906760
0 TGAAATTTCACAAAATATCGATTTTC

Consensus:

TGAAATTTCACAAAATATCGATTTTC

>WB235_Fam_307_26_1 Nr. of seq. 1 Alignment length(with gaps) = 26
Alignment score = 0.000000
WB235_6:11260441-11260545 Satlength=105 Nr of Repeats=4 RepeatLength=26
seed=AAATTAATCT Num.seqs=4 Similarity=0.803419
0 AAATTAATCTGTCACTCTAACTTTTT

Consensus:

AAATTAATCTGTCACTCTAACTTTTT

>WB235_Fam_308_25_1 Nr. of seq. 1 Alignment length(with gaps) = 25
Alignment score = 0.000000
WB235_2:1089504-1089883 Satlength=380 Nr of Repeats=5 RepeatLength=26
seed=GTCGGCTGCT Num.seqs=3 Similarity=0.339869
0 GTCGGCTGCTTNCAAACCCTGAGTT

Consensus:

GTCGGCTGCTTNCAAACCCTGAGTT

>WB235_Fam_309_25_1 Nr. of seq. 1 Alignment length(with gaps) = 25
Alignment score = 0.000000
WB235_5:19420419-19420546 Satlength=128 Nr of Repeats=5 RepeatLength=25
seed=AAAAATCTGT Num.seqs=3 Similarity=0.822222
0 AAAAATCTGTTCTNNGAGGTCCCTG

Consensus:

AAAAATCTGTTCTNNGAGGTCCCTG

>WB235_Fam_310_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
WB235_2:4205778-4205946 Satlength=169 Nr of Repeats=5 RepeatLength=24
seed=GTGAGGTACG Num.seqs=3 Similarity=0.611111
0 GTGAGGTACGAGGTGAGGTANGAG

Consensus:

GTGAGGTACGAGGTGAGGTANGAG

>WB235_Fam_311_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
WB235_3:12397168-12397264 Satlength=97 Nr of Repeats=4 RepeatLength=24
seed=AAGCACCACC Num.seqs=4 Similarity=0.972222
0 AAGCACCACCTCCTCCAACACTACAA

Consensus:

AAGCACCACCTCCTCCAACACTACAA

>WB235_Fam_312_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
WB235_3:13583331-13583502 Satlength=172 Nr of Repeats=7 RepeatLength=24
seed=AAGAAGGATG Num.seqs=6 Similarity=0.825926
0 AAGAAGGATGCTGAAGAGAAGAAG

Consensus:

AAGAAGGATGCTGAAGAGAAGAAG

>WB235_Fam_313_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
WB235_4:2855122-2855338 Satlength=217 Nr of Repeats=5 RepeatLength=24
seed=GCTTCTGGAG Num.seqs=3 Similarity=0.777778
0 GCTTCTGGAGCTACAGGTTATCCA

Consensus:

GCTTCTGGAGCTACAGGTTATCCA

>WB235_Fam_314_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
WB235_4:17323162-17323330 Satlength=169 Nr of Repeats=7 RepeatLength=24
seed=TCAACAACAA Num.seqs=7 Similarity=1.000000
0 TCAACAACAACAGGAGAAGCTTCT

Consensus:

TCAACAACAACAGGAGAAGCTTCT

>WB235_Fam_315_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
WB235_5:6171700-6176164 Satlength=4465 Nr of Repeats=182 RepeatLength=24
seed=TTTCAGTTTA Num.seqs=178 Similarity=0.769398
0 TTTCAGTTTATCATCTCTCTG

Consensus:

TTTCAGTTTATCATCATTCTCCTG

>WB235_Fam_316_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
WB235_6:7879877-7880045 Satlength=169 Nr of Repeats=7 RepeatLength=24
seed=GGTGGCTGGT Num.seqs=7 Similarity=1.000000
0 GGTGGCTGGTCACAAAAGTAAGTT

Consensus:

GGTGGCTGGTCACAAAAGTAAGTT

>WB235_Fam_317_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
WB235_1:14332472-14332641 Satlength=170 Nr of Repeats=5 RepeatLength=23
seed=GCACCATAAG Num.seqs=3 Similarity=0.726852
0 GCATCATAAGGATCATAGTTGAT

Consensus:

GCATCATAAGGATCATAGTTGAT

>WB235_Fam_318_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
WB235_2:1578528-1579311 Satlength=784 Nr of Repeats=24 RepeatLength=23
seed=CGCTGTAAGA Num.seqs=16 Similarity=0.806763
0 CGCTGTAAGACCCTTCGCTGTAC

Consensus:

CGCTGTAAGACCCTTCGCTGTAC

>WB235_Fam_319_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
WB235_2:15278603-15278843 Satlength=241 Nr of Repeats=12 RepeatLength=23
seed=GCTACAGTAC Num.seqs=8 Similarity=0.821946
0 GCTACAGTACCCAGCTTGACTT

Consensus:

GCTACAGTACCCAGCTTGACTT

>WB235_Fam_320_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000

WB235_5:19487887-19488024 Satlength=138 Nr of Repeats=6 RepeatLength=23
seed=TTTTCAGAAA Num.seqs=5 Similarity=0.631944
0 TTTTCAGAAATAGGTATTTTCAGA

Consensus:

TTTTCAGAAATAGGTATTTTCAGA

>WB235_Fam_321_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000

WB235_1:808432-808756 Satlength=325 Nr of Repeats=8 RepeatLength=22
seed=TTAAAATTTT Num.seqs=6 Similarity=0.886869
0 TTAAAATTTTGTTCAGTTTGACC

Consensus:

TTAAAATTTTGTTCAGTTTGACC

>WB235_Fam_322_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000

WB235_1:14267336-14267775 Satlength=440 Nr of Repeats=17 RepeatLength=22
seed=GCACGGCCTG Num.seqs=13 Similarity=0.701226
0 GCACGGCCTGGCGGTCCTGAGG

Consensus:

GCACGGCCTGGCGGTCCTGAGG

>WB235_Fam_323_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000

WB235_2:14114648-14115030 Satlength=383 Nr of Repeats=12 RepeatLength=22
seed=CTACAGTAAC Num.seqs=8 Similarity=0.798395
0 CTACAGTAACCCTAGTATTGAA

Consensus:

CTACAGTAACCCTAGTATTGAA

>WB235_Fam_324_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000

WB235_4:6599056-6599139 Satlength=84 Nr of Repeats=4 RepeatLength=22
seed=AAGCGGTAAC Num.seqs=3 Similarity=1.000000
0 AAGCGGTAACGTCGTCTATATA

Consensus:

AAGCGGTAACGTCGTCTATATA

>WB235_Fam_325_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
WB235_5:16945467-16945572 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=TGCTAATTAG Num.seqs=3 Similarity=0.545455
0 TGCTAATTAGCGCGGNTGCGTN

Consensus:

TGCTAATTAGCGCGGNTGCGTN

>WB235_Fam_326_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
WB235_5:19427400-19427634 Satlength=235 Nr of Repeats=7 RepeatLength=22
seed=ACGTATACAG Num.seqs=5 Similarity=0.915152
0 ACGTATACAGGCATATACACAT

Consensus:

ACGTATACAGGCATATACACAT

>WB235_Fam_327_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
WB235_6:1916196-1916614 Satlength=419 Nr of Repeats=14 RepeatLength=22
seed=CCGGCGTG TGT Num.seqs=9 Similarity=0.677134
0 CCGGCGTG TGTNTTGAAGCGGTC

Consensus:

CCGGCGTG TGTNTTGAAGCGGTC

>WB235_Fam_328_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
WB235_6:14638909-14639063 Satlength=155 Nr of Repeats=5 RepeatLength=22
seed=TTTGTGGGAG Num.seqs=3 Similarity=0.757576
0 TTTGTGGGAGGCGACATATACC

Consensus:

TTTGTGGGAGGCGACATATACC

>WB235_Fam_329_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_1:823801-824454 Satlength=654 Nr of Repeats=29 RepeatLength=21
seed=TGGCCTAGAT Num.seqs=21 Similarity=0.658586
0 TGGCCTAGATTTNTTTACAGGG

Consensus:

TGGCCTAGATTTNTTTACAGGG

>WB235_Fam_330_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_1:1652306-1652642 Satlength=337 Nr of Repeats=16 RepeatLength=21
seed=TCTCCTGGTA Num.seqs=16 Similarity=0.963492
0 TCTCCTGGTAAATTTAAAAAT

Consensus:

TCTCCTGGTAAATTTAAAAAT

>WB235_Fam_331_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_1:12585721-12585826 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=ACCACCCCTA Num.seqs=5 Similarity=0.815873
0 ACCACCCCTACAACNACCACC

Consensus:

ACCACCCCTACAACNACCACC

>WB235_Fam_332_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_1:15025277-15025549 Satlength=273 Nr of Repeats=10 RepeatLength=21
seed=AACTTTTGG Num.seqs=6 Similarity=0.791919
0 AACTTTTGGCAATTTTCCAA

Consensus:

AACTTTTGGCAATTTTCCAA

>WB235_Fam_333_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_2:2273842-2274055 Satlength=214 Nr of Repeats=8 RepeatLength=21
seed=TGTGCCCTGG Num.seqs=6 Similarity=0.936508
0 TGTGCCCTGGAAAGCTGGCAG

Consensus:

TGTGCCCTGGAAAGCTGGCAG

>WB235_Fam_334_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_2:4054458-4054819 Satlength=362 Nr of Repeats=4 RepeatLength=21
seed=CTACGTAAGA Num.seqs=3 Similarity=0.830688
0 CTACGTAAGAGTAGCGCAGGA

Consensus:

CTACGTAAGAGTAGCGCAGGA

>WB235_Fam_335_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_2:13184130-13184277 Satlength=148 Nr of Repeats=7 RepeatLength=21
seed=AATCTAGCCA Num.seqs=7 Similarity=0.930461
0 AATCTAGCCAGACGCACACCT

Consensus:

AATCTAGCCAGACGCACACCT

>WB235_Fam_336_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_2:14212202-14212432 Satlength=231 Nr of Repeats=10 RepeatLength=21
seed=CAATTTTCTG Num.seqs=8 Similarity=0.841270
0 CAATTTTCTGTTNAACTTTGA

Consensus:

CAATTTTCTGTTNAACTTTGA

>WB235_Fam_337_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_3:8254497-8254602 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=AAGTTTACT Num.seqs=5 Similarity=0.974603
0 AAGTTTACTTTGATTTTTTT

Consensus:

AAGTTTACTTTGATTTTTTT

>WB235_Fam_338_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_3:11242813-11243253 Satlength=441 Nr of Repeats=21 RepeatLength=21
seed=GGCAATTTTC Num.seqs=20 Similarity=0.903425
0 GGCAATTTTCCAGTGCAATTC

Consensus:

GGCAATTTTCCAGTGCAATTC

>WB235_Fam_339_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_4:1565274-1565421 Satlength=148 Nr of Repeats=7 RepeatLength=21
seed=CCATAGGTGG Num.seqs=7 Similarity=0.794407
0 CCATAGGTGGAAGATCTNATA

Consensus:

CCATAGGTGGAAGATCTNATA

>WB235_Fam_340_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_4:2156341-2157203 Satlength=863 Nr of Repeats=38 RepeatLength=21
seed=GATTTACGGG Num.seqs=31 Similarity=0.686520
0 GATTTACGGGGTGAACATGTG

Consensus:

GATTTACGGGGTGAACATGTG

>WB235_Fam_341_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_5:6392866-6392950 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=TTGGTGACAA Num.seqs=4 Similarity=1.000000
0 TTGGTGACAATGTGGAAACAA

Consensus:

TTGGTGACAATGTGGAAACAA

>WB235_Fam_342_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_5:9933015-9933120 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=TTCTAATTCG Num.seqs=5 Similarity=0.726984
0 TTCTAATTCGACGCGCATNGT

Consensus:

TTCTAATTCGACGCGCATNGT

>WB235_Fam_343_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_5:16941584-16941761 Satlength=178 Nr of Repeats=5 RepeatLength=21
seed=CTAATTAGCG Num.seqs=3 Similarity=0.640212
0 CTAATTAGCGTCGCTTCCNTT

Consensus:

CTAATTAGCGTCGCTTCCNTT

>WB235_Fam_344_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_5:18644347-18644921 Satlength=575 Nr of Repeats=24 RepeatLength=21
seed=AAAAATCGAT Num.seqs=18 Similarity=0.739602
0 AAAAATCGATAAAATTTGGAN

Consensus:

AAAAATCGATAAAATTTGGAN

>WB235_Fam_345_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_5:19261027-19261174 Satlength=148 Nr of Repeats=7 RepeatLength=21
seed=CACACGAGCT Num.seqs=7 Similarity=0.727891
0 CACACGAGCTTGAGAGCCCGG

Consensus:

CACACGAGCTTGAGAGCCCGG

>WB235_Fam_346_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_5:19427290-19427806 Satlength=517 Nr of Repeats=5 RepeatLength=21
seed=TATTTTCAAA Num.seqs=3 Similarity=0.957672
0 TATTTTCAAAAAAATTTAAAA

Consensus:

TATTTTCAAAAAAATTTAAAA

>WB235_Fam_347_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_5:19645096-19645264 Satlength=169 Nr of Repeats=6 RepeatLength=21
seed=ACCCCGATTT Num.seqs=5 Similarity=0.911111
0 ACCCCGATTTTCACCCAAAAA

Consensus:

ACCCCGATTTTCACCCAAAAA

>WB235_Fam_348_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_5:19963720-19963804 Satlength=85 Nr of Repeats=4 RepeatLength=21
seed=CTCAATTCAA Num.seqs=4 Similarity=0.883598
0 CTCAATTCAATCAAGGAAATC

Consensus:

CTCAATTCAATCAAGGAAATC

>WB235_Fam_349_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000

WB235_6:3713912-3714032 Satlength=121 Nr of Repeats=5 RepeatLength=20
seed=CCATGTAGCT Num.seqs=4 Similarity=0.561869
0 CCATGTAGCTTCAAAATTNCT

Consensus:

CCATGTAGCTTCAAAATTNCT

>WB235_Fam_350_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_6:15507328-15507477 Satlength=150 Nr of Repeats=4 RepeatLength=21
seed=TGTCCGTGAT Num.seqs=3 Similarity=0.666667
0 TGTCCGTGATGATCATGNGCA

Consensus:

TGTCCGTGATGATCATGNGCA

>WB235_Fam_351_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
WB235_6:17087637-17087742 Satlength=106 Nr of Repeats=5 RepeatLength=21
seed=GGTGGACCCA Num.seqs=5 Similarity=0.822222
0 GGTGGACCCANGGGTTCCTAG

Consensus:

GGTGGACCCANGGGTTCCTAG

>WB235_Fam_352_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
WB235_2:3641762-3641852 Satlength=91 Nr of Repeats=5 RepeatLength=20
seed=CTATCGCCTG Num.seqs=4 Similarity=0.833333
0 CTATCGCCTGCTATCGCCTA

Consensus:

CTATCGCCTGCTATCGCCTA

>WB235_Fam_353_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
WB235_5:17780829-17781140 Satlength=312 Nr of Repeats=5 RepeatLength=20
seed=ATTGACCTA Num.seqs=4 Similarity=0.900000
0 ATTGACCTACTTTTTAAAA

Consensus:

ATTGACCTACTTTTTAAAA

>WB235_Fam_354_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
WB235_1:359078-359230 Satlength=153 Nr of Repeats=8 RepeatLength=19
seed=GTACTACCTT Num.seqs=8 Similarity=0.982456
0 GTACTACCTTTTAATGTAT

Consensus:

GTACTACCTTTTAATGTAT

>WB235_Fam_355_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
WB235_1:14137893-14138026 Satlength=134 Nr of Repeats=7 RepeatLength=19
seed=CCCTGATACC Num.seqs=7 Similarity=0.788889
0 CCCTGATACCCCCTAGTCC

Consensus:

CCCTGATACCCCCTAGTCC

>WB235_Fam_356_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
WB235_2:13007141-13007285 Satlength=145 Nr of Repeats=6 RepeatLength=19
seed=TATGGTGCAT Num.seqs=4 Similarity=0.707602
0 TATGGTGCATCTAACTAGT

Consensus:

TATGGTGCATCTAACTAGT

>WB235_Fam_357_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
WB235_4:3206393-3209585 Satlength=3193 Nr of Repeats=168 RepeatLength=19
seed=GCCTCACTCA Num.seqs=132 Similarity=0.897464
0 GCCTCACTCAAAATCCTCA

Consensus:

GCCTCACTCAAAATCCTCA

>WB235_Fam_358_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_1:10650908-10650980 Satlength=73 Nr of Repeats=4 RepeatLength=18
seed=AAAAGTTACA Num.seqs=4 Similarity=1.000000
0 AAAAGTTACAGTGTCTT

Consensus:

AAAAGTTACAGTGTCTT

>WB235_Fam_359_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_1:14338207-14338743 Satlength=537 Nr of Repeats=26 RepeatLength=18
seed=TTGTAGATCA Num.seqs=22 Similarity=0.869489
0 TTGTAGATCAACGGGGTC

Consensus:

TTGTAGATCAACGGGGTC

>WB235_Fam_360_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_2:1467853-1467943 Satlength=91 Nr of Repeats=5 RepeatLength=18
seed=GGAGGTCCAG Num.seqs=5 Similarity=0.859259
0 GGAGGTCCAGGTACCCCG

Consensus:

GGAGGTCCAGGTACCCCG

>WB235_Fam_361_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_2:10466292-10466385 Satlength=94 Nr of Repeats=5 RepeatLength=18
seed=TAAATAAGTG Num.seqs=3 Similarity=0.950617
0 TAAATAAGTGGCTATAAT

Consensus:

TAAATAAGTGGCTATAAT

>WB235_Fam_362_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_2:12889260-12889656 Satlength=397 Nr of Repeats=21 RepeatLength=18
seed=ACTACTGTAT Num.seqs=18 Similarity=0.797628
0 ACTACTGTATCNCAGGAG

Consensus:

ACTACTGTATCNCAGGAG

>WB235_Fam_363_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_4:3195411-3195573 Satlength=163 Nr of Repeats=6 RepeatLength=18
seed=CCTTCGCCTA Num.seqs=4 Similarity=0.765432
0 CCTTCGCCTACCTACGTG

Consensus:

CCTTCGCCTACCTACGTG

>WB235_Fam_364_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_4:4335057-4335129 Satlength=73 Nr of Repeats=4 RepeatLength=18
seed=TTTTTTGATA Num.seqs=4 Similarity=0.962963
0 TTTTTTGATAATTCTTGA

Consensus:

TTTTTTGATAATTCTTGA

>WB235_Fam_365_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_5:4268549-4268631 Satlength=83 Nr of Repeats=4 RepeatLength=18
seed=AAATATTCTT Num.seqs=3 Similarity=0.851852
0 AAATATTCTTATTTTCAG

Consensus:

AAATATTCTTATTTTCAG

>WB235_Fam_366_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_5:4653023-4653224 Satlength=202 Nr of Repeats=8 RepeatLength=18
seed=CCTGGCTGTC Num.seqs=5 Similarity=0.607407
0 CCTGGTTGTCCNTCTNNT

Consensus:

CCTGGTTGTCCNTCTNNT

>WB235_Fam_367_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_5:7337779-7337924 Satlength=146 Nr of Repeats=8 RepeatLength=18
seed=TTTCATAAGA Num.seqs=7 Similarity=0.943563
0 TTTCATAAGAAGTAAATN

Consensus:

TTTCATAAGAAGTAAATN

>WB235_Fam_368_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_5:20210955-20211513 Satlength=559 Nr of Repeats=29 RepeatLength=18
seed=CATTGTCACT Num.seqs=27 Similarity=0.884774
0 CATTGTCACTTTCTTCTC

Consensus:

CATTGTCACTTTCTTCTC

>WB235_Fam_369_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
WB235_6:1836329-1837109 Satlength=781 Nr of Repeats=39 RepeatLength=18
seed=AAGCCTATGC Num.seqs=28 Similarity=0.765628
0 AAGCCTATGCCTTTCCCA

Consensus:

AAGCCTATGCCTTTCCCA

>WB235_Fam_370_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
WB235_2:12575393-12575478 Satlength=86 Nr of Repeats=5 RepeatLength=17
seed=ACTTGGTACA Num.seqs=5 Similarity=0.890196
0 ACTTGGTACATAGGCCA

Consensus:

ACTTGGTACATAGGCCA

>WB235_Fam_371_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
WB235_3:12389240-12389685 Satlength=446 Nr of Repeats=15 RepeatLength=17
seed=ATTTTTTCCG Num.seqs=10 Similarity=0.687449
0 ATTTTTTCCGCAAGTAG

Consensus:

ATTTTTTCCGCAAGTAG

>WB235_Fam_372_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
WB235_4:11615692-11615955 Satlength=264 Nr of Repeats=13 RepeatLength=17
seed=AAAATCAAAC Num.seqs=10 Similarity=0.809259
0 AAAATCAAACCGCGGA

Consensus:

AAAATCAAACCGCGGA

>WB235_Fam_373_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
WB235_5:4866206-4866377 Satlength=172 Nr of Repeats=5 RepeatLength=17
seed=AAATGCCAAA Num.seqs=3 Similarity=0.641975
0 AAATGCCAAAANTGCCA

Consensus:

AAATGCCAAAANTGCCA

>WB235_Fam_374_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
WB235_5:16672548-16672735 Satlength=188 Nr of Repeats=11 RepeatLength=17
seed=TAACCTGACT Num.seqs=11 Similarity=0.957219
0 TAACCTGACTGCTACAG

Consensus:

TAACCTGACTGCTACAG

>WB235_Fam_375_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
WB235_5:19402253-19402490 Satlength=238 Nr of Repeats=14 RepeatLength=17
seed=GAATTAGAAA Num.seqs=13 Similarity=0.554584
0 GAATTAGAAAAATTTGA

Consensus:

GAATTAGAAAAATTTGA

>WB235_Fam_376_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
WB235_5:19488506-19489530 Satlength=1025 Nr of Repeats=58 RepeatLength=17
seed=TTGCAAGAAA Num.seqs=55 Similarity=0.923312
0 TTGCAAGAAAATCTGCA

Consensus:

TTGCAAGAAAATCTGCA

>WB235_Fam_377_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
WB235_6:3347373-3347577 Satlength=205 Nr of Repeats=10 RepeatLength=17
seed=TTTTAACGTG Num.seqs=8 Similarity=0.901961
0 TTTTAACGTGACCTAGT

Consensus:

TTTTAACGTGACCTAGT

>WB235_Fam_378_16_1 Nr. of seq. 1 Alignment length(with gaps) = 16
Alignment score = 0.000000

WB235_1:12562161-12562497 Satlength=337 Nr of Repeats=20 RepeatLength=16
seed=TGATCTGATG Num.seqs=18 Similarity=0.831699
0 TGATCTGATGATCTGA

Consensus:

TGATCTGATGATCTGA

>WB235_Fam_379_16_1 Nr. of seq. 1 Alignment length(with gaps) = 16
Alignment score = 0.000000
WB235_1:13093190-13093270 Satlength=81 Nr of Repeats=5 RepeatLength=16
seed=AATACGGGAA Num.seqs=5 Similarity=1.000000
0 AATACGGGAATACGGG

Consensus:

AATACGGGAATACGGG

>WB235_Fam_380_16_1 Nr. of seq. 1 Alignment length(with gaps) = 16
Alignment score = 0.000000
WB235_3:1011046-1011124 Satlength=79 Nr of Repeats=5 RepeatLength=16
seed=TTATAGTGTT Num.seqs=3 Similarity=0.888889
0 TTATAGTGTTATAGTG

Consensus:

TTATAGTGTTATAGTG

>WB235_Fam_381_16_1 Nr. of seq. 1 Alignment length(with gaps) = 16
Alignment score = 0.000000
WB235_3:3018177-3018907 Satlength=731 Nr of Repeats=5 RepeatLength=16
seed=TGTATATATA Num.seqs=3 Similarity=1.000000
0 TGTATATATATATATA

Consensus:

TGTATATATATATATA

>WB235_Fam_382_16_1 Nr. of seq. 1 Alignment length(with gaps) = 16
Alignment score = 0.000000
WB235_5:12077837-12077917 Satlength=81 Nr of Repeats=5 RepeatLength=16
seed=AAAAATTATT Num.seqs=5 Similarity=1.000000
0 AAAAATTATTGAATAC

Consensus:

AAAAATTATTGAATAC

>WB235_Fam_383_16_1 Nr. of seq. 1 Alignment length(with gaps) = 16
Alignment score = 0.000000
WB235_5:17653226-17653322 Satlength=97 Nr of Repeats=6 RepeatLength=16
seed=GAATAATATT Num.seqs=6 Similarity=0.972222
0 GAATAATATTGGAGAA

Consensus:

GAATAATATTGGAGAA

>WB235_Fam_384_16_1 Nr. of seq. 1 Alignment length(with gaps) = 16
Alignment score = 0.000000
WB235_5:19753320-19753624 Satlength=305 Nr of Repeats=19 RepeatLength=16
seed=CTTAGATCTC Num.seqs=19 Similarity=0.931287
0 CTTAGATCTCAATTCC

Consensus:

CTTAGATCTCAATTCC

>WB235_Fam_385_16_1 Nr. of seq. 1 Alignment length(with gaps) = 16
Alignment score = 0.000000
WB235_6:2989994-2990074 Satlength=81 Nr of Repeats=5 RepeatLength=16
seed=AGAGAGTATA Num.seqs=5 Similarity=1.000000
0 AGAGAGTATAGATTAG

Consensus:

AGAGAGTATAGATTAG

>WB235_Fam_386_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
WB235_3:12239290-12239399 Satlength=110 Nr of Repeats=5 RepeatLength=15
seed=CGACCTGCGA Num.seqs=3 Similarity=0.940741
0 CGACCTGCGACCTAG

Consensus:

CGACCTGCGACCTAG

>WB235_Fam_387_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
WB235_4:13431343-13431418 Satlength=76 Nr of Repeats=5 RepeatLength=15
seed=CACAGGAGGC Num.seqs=5 Similarity=1.000000
0 CACAGGAGGCTGGGA

Consensus:

CACAGGAGGCTGGGA

>WB235_Fam_388_14_1 Nr. of seq. 1 Alignment length(with gaps) = 14
Alignment score = 0.000000
WB235_1:11084941-11085053 Satlength=113 Nr of Repeats=7 RepeatLength=14
seed=AGCTTGAAGC Num.seqs=5 Similarity=0.800000
0 AGCTTGAAGCTTGG

Consensus:

AGCTTGAAGCTTGG

>WB235_Fam_389_14_1 Nr. of seq. 1 Alignment length(with gaps) = 14
Alignment score = 0.000000
WB235_2:7446830-7448192 Satlength=1363 Nr of Repeats=34 RepeatLength=14
seed=GAAGGATCGG Num.seqs=26 Similarity=0.910916
0 GAAGGATCGGGCCG

Consensus:

GAAGGATCGGGCCG

>WB235_Fam_390_14_1 Nr. of seq. 1 Alignment length(with gaps) = 14
Alignment score = 0.000000
WB235_6:7918015-7918071 Satlength=57 Nr of Repeats=4 RepeatLength=14
seed=TTACCAAAAT Num.seqs=4 Similarity=0.888889
0 TTACCAAAATCTAA

Consensus:

TTACCAAAATCTAA

>WB235_Fam_391_13_1 Nr. of seq. 1 Alignment length(with gaps) = 13
Alignment score = 0.000000
WB235_5:19495335-19495400 Satlength=66 Nr of Repeats=5 RepeatLength=13
seed=TTGGGGTGGG Num.seqs=5 Similarity=1.000000
0 TTGGGGTGGGCCT

Consensus:

TTGGGGTGGGCCT

>WB235_Fam_392_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
WB235_2:13522160-13522220 Satlength=61 Nr of Repeats=5 RepeatLength=12
seed=AATACCAACC Num.seqs=5 Similarity=0.933333
0 AATACCAACCAC

Consensus:

AATACCAACCAC

>WB235_Fam_393_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
WB235_3:13129352-13129936 Satlength=585 Nr of Repeats=45 RepeatLength=12
seed=AGTTATATAG Num.seqs=41 Similarity=0.931707
0 AGTTATATAGTA

Consensus:

AGTTATATAGTA

>WB235_Fam_394_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
WB235_5:16530645-16530908 Satlength=264 Nr of Repeats=16 RepeatLength=12
seed=CATTGACTTG Num.seqs=13 Similarity=0.842209
0 CATTGACTTGAG

Consensus:

CATTGACTTGAG

>WB235_Fam_395_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
WB235_4:2896505-2896560 Satlength=56 Nr of Repeats=5 RepeatLength=11
seed=TTGTTTACAA Num.seqs=5 Similarity=1.000000
0 TTGTTTACAAG

Consensus:

TTGTTTACAAG

>WB235_Fam_396_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
WB235_5:1249610-1249931 Satlength=322 Nr of Repeats=10 RepeatLength=11
seed=TACCTACTAG Num.seqs=6 Similarity=0.789899
0 TACCTACTAGA

Consensus:

TACCTACTAGA

>WB235_Fam_397_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
WB235_5:10450709-10450922 Satlength=214 Nr of Repeats=19 RepeatLength=11
seed=AGATACACTT Num.seqs=15 Similarity=0.983838
0 AGATACACTTC

Consensus:

AGATACACTTC

>WB235_Fam_398_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
WB235_5:18641364-18641663 Satlength=300 Nr of Repeats=5 RepeatLength=11
seed=TTTCAGGCCT Num.seqs=3 Similarity=0.796296
0 TTTCAGGCCTA

Consensus:

TTTCAGGCCTA

>WB235_Fam_399_10_1 Nr. of seq. 1 Alignment length(with gaps) = 10
Alignment score = 0.000000
WB235_1:13968489-13968559 Satlength=71 Nr of Repeats=6 RepeatLength=10
seed=GATTTTCATA Num.seqs=5 Similarity=1.000000
0 GATTTTCATA

Consensus:

GATTTTCATA

>WB235_Fam_400_10_1 Nr. of seq. 1 Alignment length(with gaps) = 10
Alignment score = 0.000000
WB235_2:2279378-2279438 Satlength=61 Nr of Repeats=4 RepeatLength=10
seed=CAGCAGAGTG Num.seqs=3 Similarity=1.000000
0 CAGCAGAGTG

Consensus:

CAGCAGAGTG

>WB235_Fam_401_10_1 Nr. of seq. 1 Alignment length(with gaps) = 10
Alignment score = 0.000000
WB235_2:3145088-3145138 Satlength=51 Nr of Repeats=4 RepeatLength=10
seed=AACTTTCGAA Num.seqs=3 Similarity=1.000000
0 AACTTTCGAA

Consensus:

AACTTTCGAA

>WB235_Fam_402_10_1 Nr. of seq. 1 Alignment length(with gaps) = 10
Alignment score = 0.000000
WB235_5:19495245-19495315 Satlength=71 Nr of Repeats=5 RepeatLength=10
seed=TGGCGAAAGC Num.seqs=3 Similarity=1.000000
12 GCTGGCGAAA

Consensus:

TGGCGAAAGC