

The program is running under the following parameters:

Output:

Prefix of the family name Bacillus

Circular permutations are allowed

Reverse sequences are considered.

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

Number of sequences=8058

There are 1967 alignments:

>Bacillus_Fam_1_60_41 Nr. of seq. 41 Alignment length(with gaps) = 64

Alignment score = 0.721735

Bacillus_murimartini_Bacillusgenomic.fna_7:140667-140967 Satlength=301 Nr

of Repeats=5 RepeatLength=60 seed=TCCGCCCTTT Num.seqs=5

Similarity=0.815556

0 TCCGCC-TTTTTNG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTT-GCTAGTGGCTTC

Rev.of_GCF_000245335.1_ASM24533v1_genomic.fna_8:299494-299734

Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=AAAGGCGGAG Num.seqs=4

Similarity=0.790984

TCCGCC-TTTTTCG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTT-GCTAGTGGCTTC

Rev.of_GCF_001517115.1_ASM151711v1_genomic.fna_21:315882-316122

Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=AAAGGCGGAG Num.seqs=4

Similarity=0.816485

TCCGCC-TTTTTCG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTT-GCTAGTGGCTTC

Rev.of_GCF_000009045.1_ASM904v1_genomic.fna_1:494545-494845 Satlength=301

Nr of Repeats=5 RepeatLength=60 seed=AAAAGGCGGA Num.seqs=5

Similarity=0.800546

TCCGCC-TTTTTCA-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTT-GCTAGTGGCTTC

Rev.of_GCF_001719185.1_ASM171918v1_genomic.fna_1:3366512-3366812

Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=AAAAGGCGGA Num.seqs=5

Similarity=0.800546

TCCGCC-TTTTTCA-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTT-GCTAGTGGCTTC

GCF_001517135.1_ASM151713v1_genomic.fna_12:117121-117361 Satlength=241 Nr

of Repeats=4 RepeatLength=60 seed=TTCTCCGCCT Num.seqs=4

Similarity=0.837037

TCCGCC-TTTTTCG-CCGATTTCTTGATAGAATTCTTTATCATGGTT-TTT-GCTAGTGGCTTC

GCF_000245315.1_ASM24531v1_genomic.fna_74:144784-145024 Satlength=241 Nr

of Repeats=4 RepeatLength=60 seed=TCTCCGCCTT Num.seqs=4

Similarity=0.833333

58 TCCGCC-TTTTTCG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTC-GCTAGTGGCTTC

GCF_000507145.1_KCTC_13622_01_genomic.fna_31:58182-58422 Satlength=241 Nr

of Repeats=4 RepeatLength=60 seed=TTCTCCGCCT Num.seqs=4

Similarity=0.803704

TCCGCC-TTTTTCG-CCAATTTCTTGATAGAATTCTTTGTCATGGTT-TTC-GCTAGTGGCTTC

Rev.of_GCF_000769555.1_ASM76955v1_genomic.fna_1:447703-447943

Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=AAAAAGGCGG Num.seqs=4

Similarity=0.840741 11
 TCCGCC-TTTTTGG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTT-GCTTGTGGCTTC
 Rev.of_GCF_000742675.1_ASM74267v1_genomic.fna_1:4062283-4062583
 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=AAAAGGCGGA Num.seqs=5
 Similarity=0.886667 10
 TCCGCC-TTTTTCG-CCAATCTCTTGATAGAATTCTTTGTCGTGGTT-TTT-GCTAGTGGCTTC
 Rev.of_GCF_000196735.1_ASM19673v1_genomic.fna_1:456884-457124
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=AAAAAGGCGG Num.seqs=4
 Similarity=0.881481 11
 TCCGCC-TTTTTGA-CCGATTTCTTGATAGAATTCTTTGTCGTGATT-TTT-GCTTGTGGCTTC
 Rev.of_GCF_000204275.1_ASM20427v1_genomic.fna_1:438961-439261
 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=AAAAAGGCGG Num.seqs=5
 Similarity=0.893333 11
 TCCGCC-TTTTTCA-CCGATTTCTTGATAGAATTCTTTGTCATGATT-TTT-GCTTGTGGCTTC
 GCF_000262045.1_KCTC_13613_01_genomic.fna_37:124118-124418 Satlength=301
 Nr of Repeats=5 RepeatLength=60 seed=TCCGCCTTTT Num.seqs=5
 Similarity=0.866667 60
 TCCGCC-TTTTTGA-CCGATTTCTTGATAGAATTCTTTGTCATGATT-TTT-GCTTGTGGCTTC
 Rev.of_GCF_000008425.1_ASM842v1_genomic.fna_1:540638-540938 Satlength=301
 Nr of Repeats=5 RepeatLength=60 seed=AAAAAGGCGG Num.seqs=5
 Similarity=0.844444 11
 TCCGCC-TTTTTCG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-GCG-GCTTGTGGCTTC
 GCF_000186125.1_Bacillus_BT1B_CT2_V1_genomic.fna_3:99314-99614
 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=CCGCCTTTTT Num.seqs=5
 Similarity=0.840000 61
 TCCGCC-TTTTTCG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTG-GCTTGTGGCTTC
 Rev.of_GCF_000408885.1_ASM40888v1_genomic.fna_1:560702-560942
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=AAAGAATTCT Num.seqs=4
 Similarity=0.881481 96
 TCCGCC-TTTTTCG-CCGATTTCTTGATAGAATTCTTTGTCATGATT-TTG-GCTTGTGGCTTC
 Rev.of_GCF_000009825.1_ASM982v1_genomic.fna_1:3644328-3644568
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=AAAGAATTCT Num.seqs=4
 Similarity=0.859259 36
 TCCGCC-TTTTTCG-CCAATTTCTTGATAGAATTCTTTGTCGTGGTT-GTG-GCTAGTAGCTTC
 Rev.of_GCF_900142675.1_IMG-
 taxon_2654588196_annotated_assembly_genomic.fna_7:422068-422308
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=AAAGAATTCT Num.seqs=4
 Similarity=0.862963 36 TCCGCC-TTTTTCG-
 CCAATTTCTTGATAGAATTCTTTGTCGTGGTT-GTG-GCTAGTAGCTTC
 Rev.of_GCF_900093775.1_EVONIK_BGLY_genomic.fna_1:580499-580799
 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=ACAAGCAAAA Num.seqs=5
 Similarity=0.807650 54
 TCCGCC-TTTTTCA-CCGATCTCCTGATAGAATTCTTTATCGTGGTT-TTT-GCTTGTGGCTTC
 Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:2718394-2718694
 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=AAAGGCGGAG Num.seqs=5
 Similarity=0.811111 9
 TCCGCC-TTTTTTG-CCGATTTCTTGATAGAATTCTTTATCATGNTT-TTCNGC-AGTAGNTTC
 Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:1791266-1791506
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=GAATTCTATC Num.seqs=4
 Similarity=0.788889 33
 TCCGCC-TTTTTTG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTCAGC-AGTGGCTTC
 GCF_001700275.1_ASM170027v1_genomic.fna_26:46937-47426 Satlength=490 Nr
 of Repeats=4 RepeatLength=60 seed=GCTTCGCCGC Num.seqs=3

Similarity=0.940741
 55 GCGGCC-TTTTTTG-CCGATTTCTTGATAGAAGTCTTTGTCGTGGTT-TTCAGC-AGTGGCTTC
 Rev.of_GCF_000812025.2_ASM81202v2_genomic.fna_65:14068-14964
 Satlength=897 Nr of Repeats=6 RepeatLength=60 seed=GGAGAAGCTA Num.seqs=4
 Similarity=0.707650 63
 TCCGCC-TTTNTGG-CCGATTTCTTGGTAGAATTCTTTATCGTGGTT-TTCGGC-GGTAGCTTC
 Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_32:2694-2934 Satlength=241
 Nr of Repeats=4 RepeatLength=60 seed=AAAGGCGGAG Num.seqs=4
 Similarity=0.740741 9
 TCCGCC-TTTTTTG-CCGATTTCTTGATAGAATTCTTTGTCATGTTT-GTCAGC-TGTCGTTTC
 GCF_000430765.1_ASM43076v1_genomic.fna_12:86711-87701 Satlength=991 Nr of
 Repeats=11 RepeatLength=60 seed=GCTTCTCCGC Num.seqs=9
 Similarity=0.760494
 55 TCCGCC-TTTTTTG-CCAATTTCTTGGTAGAATTCTTTGTCATGATT-CTCNGA-AGTAGCTTC
 GCF_001591545.1_ASM159154v1_genomic.fna_1:1026037-1026277 Satlength=241
 Nr of Repeats=4 RepeatLength=60 seed=GTAGCTTCTC Num.seqs=4
 Similarity=0.829630 112
 TCCACC-TTTTTTG-CCGATTTCTTCATAAAAGTCTTTGTCATGATT-TTCGGA-AGTAGCTTC
 Rev.of_GCF_001587375.1_ASM158737v1_genomic.fna_44:3736-4036 Satlength=301
 Nr of Repeats=5 RepeatLength=60 seed=GGAGAAGCTA Num.seqs=5
 Similarity=0.793333 64
 TCCACC-TT-TTTGACCAATTTCTTGATAGAATTCTTTGTCATGGTT-TTTNGC-GGTAGCTTC
 Rev.of_GCF_001645705.1_ASM164570v1_genomic.fna_56:31150-31450
 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=CATGATAAAG Num.seqs=5
 Similarity=0.911111 103
 TCCACC-TT-TTTGTCCGATTTCTTGATAGAATTCTTTATCATGATT-CTTGGC-AGTAGCTTC
 GCF_000181495.1_ASM18149v1_genomic.fna_185:150083-150323 Satlength=241 Nr
 of Repeats=4 RepeatLength=60 seed=TGATAGAATT Num.seqs=4
 Similarity=0.844444 22
 TCCGCC-TTTTTCA-CCAATCTCCTGATAGAATTCTTTATCATGGTT-ATTAGA-CGTTGCTTC
 GCF_000473245.1_ASM47324v1_genomic.fna_1:4494162-4494402 Satlength=241 Nr
 of Repeats=4 RepeatLength=60 seed=GCTTCTCCGC Num.seqs=4
 Similarity=0.763441 55
 TCCGCC-TTTTTGA-CCGATCTCCTGATAGAATTCCTTGTCATGGTT-TTCAGA-AGTAGCTTC
 Rev.of_GCF_000153365.1_ASM15336v1_genomic.fna_17:33525-33765
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=GGCGGAGAAG Num.seqs=4
 Similarity=0.749559 66
 TCCGCCNTTTTTTG-CCGATTTCTTGATAGAATTCTTTGTCATGGTT-TTCAGA-AGTTGCTTC
 Rev.of_GCF_001636425.1_ASM163642v1_genomic.fna_1:2982966-2983206
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=AAAGGCGGAG Num.seqs=4
 Similarity=0.751852 69
 TCCGCC-TTTTTGT-CCAATTTCTTGATAGAATTCTTTGTCATGGCT-TTTAGA-AGTTGCTTC
 Rev.of_GCF_002019635.1_ASM201963v1_genomic.fna_3:166192-166432
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=TTCTATCAAG Num.seqs=4
 Similarity=0.900000 90
 TCCGCC-TTTTTGT-CCTATTTCTTGATAGAATTCCTTATCATGATT-TTCAGA-AGTCGCTTC
 GCF_001243895.1_Bacillus_testis_genomic.fna_9:994577-995012 Satlength=436
 Nr of Repeats=7 RepeatLength=60 seed=GCTTCTCCGC Num.seqs=6
 Similarity=0.824408 55
 TCCGCC-TTTTTCG-CCGATTTCTTGATAGAATTCTTTGCCATGGCT-ATCAGA-AGTAGCTTC
 Rev.of_GCF_001375535.1_Bacillus_niamensis_genomic.fna_6:3621472-3621832
 Satlength=361 Nr of Repeats=6 RepeatLength=60 seed=GGTGGAGAAG Num.seqs=6
 Similarity=0.833333 66 TCCACC-
 CTTTTGA-CCGATCTCTTGATAGAATTCCTTATCATGATT-CTCAGC-CGTTGCTTC

GCF_001578185.1_ASM157818v1_genomic.fna_1:4250078-4250593 Satlength=516
 Nr of Repeats=5 RepeatLength=60 seed=CTCCGCCCTTT Num.seqs=4
 Similarity=0.918519 119
 TCCGCC-TTTTTGG-CCAATCTCTTGATAAAATTCCTTATCATGATT-TTCGGA-TGTTGCTTC
 Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:3918880-3919180
 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=CATGATAAAG Num.seqs=5
 Similarity=0.915556 162
 TCCGCC-TTTCGT-CCAATCTCTTGATAAAATCTTTATCATGATT-CTCGGC-TGTTGCTTC
 Rev.of_GCF_900098925.1_PRJEB15625_genomic.fna_19:237981-238620
 Satlength=640 Nr of Repeats=6 RepeatLength=60 seed=GGCGGCGAAG Num.seqs=4
 Similarity=0.739982 66
 GCCGCC-TTTTGT-CCGATTCCTGGTAAAATCTTTATCATGATT-TTTGGA-AGTTGCTTC
 GCF_900111815.1_PRJEB17078_genomic.fna_1:2949352-2949652 Satlength=301 Nr
 of Repeats=5 RepeatLength=60 seed=GCTTCGCCGC Num.seqs=5
 Similarity=0.815301 115
 GCCGCC-TTTTTTA-CCGATCTCCTGGTAGAATTCTTTGTCATGATT-TTCNGC-TGTTGCTTC
 GCF_001654695.1_ASM165469v1_genomic.fna_22:26665-26893 Satlength=229 Nr
 of Repeats=4 RepeatLength=60 seed=TTTTTCTCCA Num.seqs=3
 Similarity=0.866667
 54 TCCACC-TTTTCGA-CCAATCTCTTGGTAAAATCTTTATCATGTTC-CTCAGC-TGTTTTTTC
 Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:1762840-1763080
 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=ACAGCAAGAG Num.seqs=4
 Similarity=0.840741 54
 TCCGCC-CTTTTGG-CCAATCTCTTGATAGAATTCCTTATCATGCTCTCT-TGC-TGTTTTTTC

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 Consensus:

TCCGCCTTTTTngCCgAtTtCtTGaTAGAATTCTTTgTCATGgTtTnnGcaGTnGCTTC

>Bacillus_Fam_2_52_36 Nr. of seq. 36 Alignment length(with gaps) = 57
 Alignment score = 0.678177
 GCF_000169195.2_ASM16919v2_genomic.fna_1:114628-114888 Satlength=261 Nr
 of Repeats=4 RepeatLength=52 seed=CTTAACGTAG Num.seqs=3
 Similarity=0.760684
 0 CTTAACGTAGACGGGCTCTAGGTGAAGGAAG-GACTTTGTTTTTN-CN--CGCTTC
 Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:485819-486339
 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=ACATAGAGCC
 Num.seqs=10 Similarity=0.791475
 23 CTTAACGTAGACGGGCTCTATGTAAAGGAAG-GTCTTCGTTTTTC-CG--CGCTTT
 GCF_000169195.2_ASM16919v2_genomic.fna_1:1467180-1467492 Satlength=313 Nr
 of Repeats=6 RepeatLength=52 seed=CTTAACGTAG Num.seqs=6
 Similarity=0.707692 52
 CTTAACGTAGACGGGCTCTATGTGAAGAAAG-GCCTTCGTTTTTC-CT--CGCTTC
 Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:328870-329234
 Satlength=365 Nr of Repeats=6 RepeatLength=52 seed=TTAAGGAAGC Num.seqs=5
 Similarity=0.800000 57
 CTTAACGTAGACGGGTTCTATGTGAAGAAAG-GCCGTCTTTTTTC-CG--CGCTTC
 Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:2663853-2664582
 Satlength=730 Nr of Repeats=14 RepeatLength=52 seed=GTCTACGTTA
 Num.seqs=13 Similarity=0.703596
 64 CTTAACGTAGACGCGCTCTATGTNAAGAAAG-GCCNTCGTTTTTC-CG--TGCTTC
 Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:2467497-2467705
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GTTAAGGAAG Num.seqs=4

Similarity=0.829060 58
CTTAACGTAGACGGGGTCTATGTGAAGGAAG-GCCTTCGTTTTTC-CA---TGCTTC
GCF_000217835.1_ASM21783v1_genomic.fna_1:1961170-1961482 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=CTCTATGTTA Num.seqs=6
Similarity=0.823932 67
CTTAACCTAGACGGGGTCTATGTGAAGGAAG-GCCTTCGTTTTTC-CA---TGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:261360-261828
Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=CTTCACATAG Num.seqs=9
Similarity=0.817664 27
CTTAACGTAGACGNGCTCTATGTGAAGGAAG-GCCNTCATTTTTTG-CN---CGCTTT
GCF_000169195.2_ASM16919v2_genomic.fna_1:2075586-2075846 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GCTTCCTTAA Num.seqs=5
Similarity=0.841026 47
CTTAACGTAGACGGGGTCTATGTGAAGGAAG-GCCNTCATTTTTTG-CA---CGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:1126423-1126942
Satlength=520 Nr of Repeats=10 RepeatLength=52 seed=CTACGTAAAG
Num.seqs=9 Similarity=0.768519
62 CTTAACGTAGCCGGGGTCTATGTGAAGGAAG-GCCGTCATTTTTTN-CA---TGCTTT
GCF_000217835.1_ASM21783v1_genomic.fna_1:231429-232210 Satlength=782 Nr
of Repeats=15 RepeatLength=52 seed=GTGAAGGAAG Num.seqs=14
Similarity=0.859115 73
CTTAACGTAGCCGGGGTCTATGTGAAGGAAG-GCCGTCATTTTTG-CA---AGCTTT
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:1080639-1081263
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=CGTCTACGTT
Num.seqs=12 Similarity=0.785548
65 CTTAACGTAGACGGGGTCTATGTGAAGGAAG-GCCNTCNTTTTTT-CG---TGCTTT
GCF_000217835.1_ASM21783v1_genomic.fna_1:935120-935692 Satlength=573 Nr
of Repeats=10 RepeatLength=52 seed=CTTAACGTAG Num.seqs=9
Similarity=0.777428
104 CTTAACGTAGACGNGCTCTATGTGAAGNAAG-GCCNTCATTTTTTT-CG---TGCTTT
GCF_000217835.1_ASM21783v1_genomic.fna_1:261415-261675 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CTTAACGTAG Num.seqs=5
Similarity=0.803774
104 CTTAACGTAGACGGGGTCTATGTGAAGGAAG-ACCNTCAATTTTTT-CG---TGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:305183-306170
Satlength=988 Nr of Repeats=13 RepeatLength=52 seed=CCTTCCTTAA
Num.seqs=9 Similarity=0.810541
32 CTTAACATAGACGAGCTCTAAGTTAAGGAAG-GCCTTCATTTTTT-CG---TGCTTT
GCF_000169195.2_ASM16919v2_genomic.fna_1:1990467-1990883 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=GCTTCTTAA Num.seqs=8
Similarity=0.800366 47
CTTAACATAGACGCGCTCTATGTGAAGGAAG-GCCGTCATTTTTT-CG---TGCTTT
GCF_000169195.2_ASM16919v2_genomic.fna_1:2001242-2001502 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CTATGTGAAG Num.seqs=5
Similarity=0.742138 69
CTTAACGTAGNCGTGCNCTATGTGAAGGAAG-GCCTTCANTTTTC-CG---TGCTTC
GCF_000169195.2_ASM16919v2_genomic.fna_1:266768-267444 Satlength=677 Nr
of Repeats=13 RepeatLength=52 seed=CTTCCTTAAAC Num.seqs=13
Similarity=0.710351 48
CTTAACATAGACGCCCTCTACGTGAAGGAAG-ACCNTCNTTTTTT-CN---TGCTTC
GCF_000217835.1_ASM21783v1_genomic.fna_1:1959525-1959733 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=AAGAAAGACC Num.seqs=4
Similarity=0.794872 76
CTTAACGTAGACGGCCTCTACGTGAAGGAAG-ACCTTCGTTTTTC-CG---TGCTTC

GCF_000169195.2_ASM16919v2_genomic.fna_1:988693-989005 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GCTTCCTTAA Num.seqs=6 Similarity=0.777778

99 CTTAACATAGACGCACTCTAGGTGAAGGAAG-GCCGTCTTTTTTC-CA---CGCTTC
GCF_000169195.2_ASM16919v2_genomic.fna_1:1031511-1032032 Satlength=522 Nr of Repeats=9 RepeatLength=52 seed=AAGACCTCCT Num.seqs=7 Similarity=0.848596 132

CTTAACNTAGACGGGCTCTATGTGAAGGAAG-ACCTCCTTTTTTC-CG---CGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:2791625-2792093 Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=GTTAAGGAAG Num.seqs=9 Similarity=0.647498 162

CTTAACATAGACGCGCTCTATGTGAAGGAAG-ACNGACTTTTTTC-CN---CGCTTC
GCF_000169195.2_ASM16919v2_genomic.fna_1:1374642-1375162 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=GCTTCCTTAA Num.seqs=10 Similarity=0.751166 151

CTTAACGTAGACGCGCTCTATGTGAAGGAAG-ACCTTCGTTTTTG-CTT---GCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:1690005-1690680 Satlength=676 Nr of Repeats=12 RepeatLength=52 seed=TTAAGGAAGC Num.seqs=10 Similarity=0.748987

162 CTTAACNTAGACGCNCTCTATGTGAAGGAAG-ACCTTCATTTTTTC-CG---CGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:2018548-2019171 Satlength=624 Nr of Repeats=12 RepeatLength=52 seed=GTTAAGGAAG Num.seqs=11 Similarity=0.690572

163 CTTAACGTAGACGCGCTCTATGTGAAGGAAG-GCCTTCATTTTTTC-CN---TGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:2631291-2631603 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TCTACGTTAA Num.seqs=6 Similarity=0.791195 168

CTTAACGTAGACGCTCTCTATGTGAAGGAAGNGCCTTCGTTTTTC-CG---CGCTTC
GCF_000169195.2_ASM16919v2_genomic.fna_1:1043778-1044356 Satlength=579 Nr of Repeats=10 RepeatLength=52 seed=CCTTAACGTA Num.seqs=8 Similarity=0.815043 51

CTTAACGTAGACGCCCTCTAGGTGAAGGAAG-AGCCTCGTTTTTTT-CA---CGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:2627959-2628323 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TTAAGGAAGC Num.seqs=7 Similarity=0.775336 57

CTTAACGTAGACGCGCCCTATGTGAAGGAAC-ANCTTCTTTTTTTT-CA---CGCTTC
GCF_000217835.1_ASM21783v1_genomic.fna_1:2106488-2106748 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CGCTTCCTTA Num.seqs=5 Similarity=0.789937 98

CTTAACGTAGACGCGCCCTATGTGAAGGAAC-ATCTTCTTTTTTTT-CA---CGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:867678-868249 Satlength=572 Nr of Repeats=11 RepeatLength=52 seed=GTTAAGAAAG Num.seqs=10 Similarity=0.750997

6 CTTAACGTAGGCGTGCTCTATGTAAAGGAAG-GNCGCCGAATTTT-CT---TGCTTT
GCF_000217835.1_ASM21783v1_genomic.fna_1:429182-429858 Satlength=677 Nr of Repeats=13 RepeatLength=52 seed=CTTCTTAAC Num.seqs=9 Similarity=0.751747

48 CTTAACGTAGACGTGCTCTATGTAAAGGAAG-GACGCCGATTTTTT-CT---NNCTTT
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:1607690-1608264 Satlength=575 Nr of Repeats=9 RepeatLength=52 seed=TCTACGTTAA Num.seqs=6 Similarity=0.834188 11

CTTAACGTAGACGCGCTCTATGTGAAGAAAC-AAGCTC-ATTTTC-CT--TCGCTTC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:1815223-1815483 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AAGGAAGCGA Num.seqs=5

Similarity=0.746154 55
 CTTAACGTAGACGCCTTCTATGTTAAGATAG-ANCCGCAATTTTT-C---TCGCTTC
 GCF_000169195.2_ASM16919v2_genomic.fna_1:3359605-3359865 Satlength=261 Nr
 of Repeats=4 RepeatLength=52 seed=TACGTTAAGA Num.seqs=3
 Similarity=0.692308 18
 CTTAACNTAGACGCACTCTACGTTAAGAAAC-A--TCGATTTTTNCN-CNCGCTTC
 GCF_000169195.2_ASM16919v2_genomic.fna_1:1835633-1836413 Satlength=781 Nr
 of Repeats=15 RepeatLength=52 seed=CTTAACGTAG Num.seqs=15
 Similarity=0.802198 0
 CTTAACGTAGACANCCCTCTATGTGAAGGAAC-AAGGCCAATTTTN-CA---TGCTTT
 Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:2666582-2667102
 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=TCTACGTTAA
 Num.seqs=8 Similarity=0.784799
 11 CTTAACGTAGACAGCCTCTATGTAAAGGAAC-AAGGCCATTTTTG-CA---TGCTTC

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 Consensus:

CTTAACgTAGACGngCTCTATGTgAAGgAAGgcCnTCntTTTTnCnnGCTTc

>Bacillus_Fam_3_50_31 Nr. of seq. 31 Alignment length(with gaps) = 64
 Alignment score = 0.605623
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:120942-121911 Satlength=970 Nr of
 Repeats=18 RepeatLength=51 seed=GAATCGCGGG Num.seqs=16
 Similarity=0.881866 0
 GAATCGCGGGGTTGCGAGT--CGA-A--AAA-GGAG--G--A--GAAACCCCGAGCAAAGGCG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:41923-42331 Satlength=409 Nr of
 Repeats=8 RepeatLength=51 seed=CCCGAGCAAA Num.seqs=8 Similarity=0.830065
 37 GAATCGCGGGGTTACGAGC--GGA-A--AAA-GGAG--G--A--GAAACCCCGAGCAAAGCG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:467020-467377 Satlength=358 Nr of
 Repeats=7 RepeatLength=51 seed=GGAATCGCGG Num.seqs=7 Similarity=0.855587
 50 GAATCGCGGGGTTGCGAGC--GGA-A--AAA-GCTG--G--A--GAAAGCCCGAGCAAACGTG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_10:87072-87479 Satlength=408 Nr of
 Repeats=8 RepeatLength=51 seed=GAATCGCGGG Num.seqs=7 Similarity=0.809524
 51 GAATCGCGGGGTTGCGAGC--GGA-A--AAA-GCGG--G--A--GAAACCCCGAGTAAACGNG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_10:200782-200986 Satlength=205 Nr
 of Repeats=4 RepeatLength=51 seed=CCCGAGCAAA Num.seqs=4
 Similarity=0.869281 88
 GAATCGCGGGGTTGCGAGC--TGG-A--AAA-GCGG--G--A--GTAACCCCGAGCAAACGCG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:163285-163591 Satlength=307 Nr of
 Repeats=6 RepeatLength=51 seed=CCCGAGCAAA Num.seqs=6 Similarity=0.874510
 37 GAATCTCGGGGTTGCGAGC--GAA-A--AAA-GTAG--G--A--GAAAGCCCGAGCAAAGCG-
 Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:546985-547648
 Satlength=664 Nr of Repeats=13 RepeatLength=51 seed=TTTGCTCGGG
 Num.seqs=13 Similarity=0.861440
 47 GAATCGCGGGGTTGCGGGC--TGA-A--AAA-GTAG--G--A--GAAAGCCCGAGCAAAGCG-
 Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:198906-199161
 Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=CGGGCTTTCT Num.seqs=5
 Similarity=0.761635 41
 GAATCACGGGGTTGCGNGC--GGA-A--AAA-GNAG--G--A--GAAAGCCCGAGCAAAGCC-
 Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:236716-237058
 Satlength=343 Nr of Repeats=7 RepeatLength=51 seed=CAACCCCGAG Num.seqs=6
 Similarity=0.833333 65
 GAATCTCGGGGTTGTGGC--TGA-AN-AAA-GNAG--G--A--GAAAGCCCGAGCAAAGCG-

Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:531203-531509
 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=GCAACCCCGC Num.seqs=6
 Similarity=0.824145 15
 GAATCGCGGGTTGCGATG--GGA-A-AAAA-AGAG--G--A--GAAAGCCCCGAGCAAACGCG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:440937-442057 Satlength=1121 Nr
 of Repeats=22 RepeatLength=51 seed=AAGCCCGAGC Num.seqs=20
 Similarity=0.839835 34
 GAATCACGGGGTTGCGAGC--TGA-A--AAA-G-GA--G--A-AGAAAGCCCCGAGCAAAAGCT-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:490720-491158 Satlength=439 Nr of
 Repeats=8 RepeatLength=51 seed=GAAGAAAGCC Num.seqs=6 Similarity=0.879739
 80 GAATCGCGGGGTGCGAGC--TGA-A--AAA-A-CG--G--A-AGAAAGCCCCGAGCAAAAGCT-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:415567-415873 Satlength=307 Nr of
 Repeats=6 RepeatLength=51 seed=GAATCACGGG Num.seqs=6 Similarity=0.853595
 51 GAATCACGGGGTTGCGGGC--TGA-A--AAA-G-CG--G--A-AGAAAGCCCCGAGCAAACGCT-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_3:325147-325506 Satlength=360 Nr of
 Repeats=7 RepeatLength=51 seed=AAAGCCCGAG Num.seqs=6 Similarity=0.835470
 84 GAATCACGGGGTTACGAGC--AGA-A--AAA-G-AA--G--A-AGAAAGCCCCGAGCAAACGCT-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:683344-683599 Satlength=256 Nr of
 Repeats=5 RepeatLength=51 seed=AACGCCGAAT Num.seqs=5 Similarity=0.963399
 45 GAATCGCGGGGTGCGAGC--TGA-A--AAA-G-AG--G--T-AGAAAGCCCCGAGCAAACGCC-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:519811-520121 Satlength=311 Nr of
 Repeats=6 RepeatLength=51 seed=GAATCACGGG Num.seqs=4 Similarity=0.947712
 50 GAATCACGGGGTTGCGAGC--TGA-A--AAAGG-AA--G--A-GGA-AGCCCCGAGCAAACGCC-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_12:22376-22706 Satlength=331 Nr of
 Repeats=7 RepeatLength=51 seed=GAGGAGAAAAG Num.seqs=6 Similarity=0.855338
 77 GAATCACGGGGTTACGAGC--TGA-A--AAAAG-AG--G--A-GAA-AGCCCCGAGCAAACGCG-
 Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:68984-69392 Satlength=409
 Nr of Repeats=8 RepeatLength=51 seed=AACCCCGAGA Num.seqs=8
 Similarity=0.815018 64
 GAATCTCGGGTTGCGAGC--NGA-A--AAA-G-AGA-G--A-AGTAAGCCCCGAGCAAAAGCC-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_3:181573-181930 Satlength=358 Nr of
 Repeats=7 RepeatLength=51 seed=GAATCACGGG Num.seqs=7 Similarity=0.905384
 50 GAATCACGGGGTTGCGAGC--AGA-A--AAA-G-CG-AA--A-GGA-AGCCCCGAGCAAACGTG-
 Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:167904-168436
 Satlength=533 Nr of Repeats=9 RepeatLength=51 seed=TCTCTTTTTC Num.seqs=6
 Similarity=0.823965 80
 GAATCGCGGGTTGCGAGC--AGA-A--AAA-G-AG-AG--A-GGA-AGCCCCGAGCAAACGCG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:180186-180593 Satlength=408 Nr of
 Repeats=7 RepeatLength=51 seed=CGGAATCACG Num.seqs=6 Similarity=0.786325
 100 GAATCACGGGGTTGCGNGCT-TGA-A--AAA-G-AG-AG--A-GGA-AGCCCCGAGCAAAAGCG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:932806-933113 Satlength=308 Nr of
 Repeats=6 RepeatLength=51 seed=GAGCAAACGC Num.seqs=5 Similarity=0.734591
 40 GAATCACGGGGTTGC-AGC--TGG-A--AAA-G-NN--G--AGAGAAAGCCCCGAGCAAACGCT-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:160131-160593 Satlength=463 Nr of
 Repeats=8 RepeatLength=51 seed=CGGGGTGCG Num.seqs=6 Similarity=0.805983
 5 -AATCACGGGGTTGCGAGC--GG--A--AAA-A-NG-AGT-A--GAAACCCCGAGCAAACGTGCG
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:550534-551044 Satlength=511 Nr of
 Repeats=10 RepeatLength=51 seed=AATCTCGGGG Num.seqs=10
 Similarity=0.822934 51
 -AATCTCGGGGTGCGGGC--TG--A--AAA-G-TG-AGG-A--GAAACCCCGAGCAAACGTGCG
 Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:186956-187518
 Satlength=563 Nr of Repeats=11 RepeatLength=51 seed=AACCCCGAGA
 Num.seqs=10 Similarity=0.780627
 12 -AATCTCGGGGTGCGAGC--GGA-A--AAA-G-GG-CG--A--GGAACCCCGAGCAAACGCCG

Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:188762-189169
 Satlength=408 Nr of Repeats=8 RepeatLength=51 seed=AACCCCGAGA Num.seqs=7
 Similarity=0.795788 12 -
 AATCTCGGGGTTGCGAGC--GGA-A--AAA-G-NG-NG--A--GGAACCCCGTGCAAACGCNG
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:312159-312465 Satlength=307 Nr of
 Repeats=6 RepeatLength=51 seed=GAGAAAGCCC Num.seqs=6 Similarity=0.919826
 29 -AATCTCGGGATTGCGGGC--GGA-A--AAA-G-CG-AG--A--GAAAGCCCGAGCAAACGGTG
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_16:40561-41234 Satlength=674 Nr of
 Repeats=12 RepeatLength=51 seed=GAGAAAGCCC Num.seqs=10
 Similarity=0.811184 29
 -AATCTCGGGGTTGCGAGC--GGA-A--AAA-G-AG-AG--A--GAAAGCCCGAGTAAACGNGG
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_16:49541-49796 Satlength=256 Nr of
 Repeats=5 RepeatLength=51 seed=CCCGAGCAAA Num.seqs=5 Similarity=0.789744
 36 -AATCTCGGGGTTGCGAGC--GGA-A--AAA-G-CG-AG--A--GAAAGCCCGAGCAAACGCCG
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_10:308612-309476 Satlength=865 Nr
 of Repeats=17 RepeatLength=51 seed=CCCGAGCAAA Num.seqs=13
 Similarity=0.762619 36
 -AATCACGGGGTTGCGGGC--GAGA--AAA-G-AG--G-NA--GAAAGCCCGAGCAAAAGTCG
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:175088-175495 Satlength=408 Nr of
 Repeats=8 RepeatLength=51 seed=AAGCCCGAGC Num.seqs=7 Similarity=0.757113
 34 GAATCGCGGGTTACATGC-CGGA-A--AAT-G-AG----A-AGAAAGCCCGAGCAAAAGCG-

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Consensus:

gAATCnCGGGGTTGCGaGcNAAAAAGaGGAGAAAgCCCGAGCAAACGcn

>Bacillus_Fam_4_52_27 Nr. of seq. 27 Alignment length(with gaps) = 53
 Alignment score = 0.745847
 GCF_002019645.1_ASM201964v1_genomic.fna_1:953299-954474 Satlength=1176 Nr
 of Repeats=23 RepeatLength=51 seed=AAGGGAATCA Num.seqs=21
 Similarity=0.949953 0
 AAGGGAATCAGACA-GCGTCTTTCGTTCCCTTTCTTCGACTTTTGGCATCAA-
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:542786-543150
 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=AGGGAACGAA Num.seqs=7
 Similarity=0.881563 30
 AAAGGAATCTGACA-GCACCTTTCGTTCCCTTTCTTCGACTTTTAGCACCAGT
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:991762-991970
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AGGGAATCAA Num.seqs=4
 Similarity=0.897436 30
 AAAGGAATCAGACACAC-TCTTTGATTCCCTTTCTCAGGCTTTTGGCATCAGA
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:2696032-2696338
 Satlength=307 Nr of Repeats=6 RepeatLength=52 seed=CCAAGAAAGG Num.seqs=4
 Similarity=0.944444 37
 AAGGGAATCAGACA-ACGCCTTTGATTCCCTTTCTTGGGCTTTTGACAACAGT
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:3491116-3491372
 Satlength=257 Nr of Repeats=5 RepeatLength=52 seed=TGTCTGATTC Num.seqs=3
 Similarity=0.752137 66
 AAGGGAATCAGACA-ACCNCTTTGATTCCCTTTGTTGGGCTTTTGGCATCAGA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:2379685-2379997 Satlength=313
 Nr of Repeats=6 RepeatLength=52 seed=TCAGACAACC Num.seqs=6
 Similarity=0.938462 7
 AAGGGAATCAGACA-ACCACTTCGTTCCCTTTCTCGCGCTCTTGGCACCAGA

Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:341445-341964
 Satlength=520 Nr of Repeats=10 RepeatLength=52 seed=TGTTTGATTC
 Num.seqs=9 Similarity=0.982906
 14 AAGGGAATCAAACA-ATGCCTTTCATTCCCTTTGTTGGGCTTTTGGCATGAGA
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:4262761-4263071
 Satlength=311 Nr of Repeats=6 RepeatLength=52 seed=AAAGGGAATG Num.seqs=5
 Similarity=0.912821 32
 AAGGGAATCAAACA-ATGCCTTTCATTCCCTTTGTTGGGCTTTTGGCATGAGA
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:1336769-1336977
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TGTTTGATTC Num.seqs=4
 Similarity=0.957265 14
 AAGGGAATCAAACA-GTGCCTTTCATTCCCTTTGTTGGGCTTTTGGGCATGAGA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:1412262-1412728 Satlength=467
 Nr of Repeats=9 RepeatLength=52 seed=TTTGGCATGA Num.seqs=7
 Similarity=0.890110 40
 AAGGGAATCAGACA-ACTCCTTTCATTCCCTTTGTTGGGCTTTTGGCATGAGA
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:2792762-2793074
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=AAAGGGAATG Num.seqs=6
 Similarity=0.897436 84
 AAGGGAATCAAACA-ACTCTTTTCATTCCCTTTGTTGGGCTTTTGGGCATGAGA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:4144195-4144455 Satlength=261
 Nr of Repeats=5 RepeatLength=52 seed=TTCATTCCT Num.seqs=5
 Similarity=0.882051 124
 AAGGGAATCAAACA-ACTCTTTTCATTCCCTTTGTTGGGCTTTTGGGCATGAGA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:4292959-4293477 Satlength=519
 Nr of Repeats=9 RepeatLength=52 seed=AAACAACTCT Num.seqs=7
 Similarity=0.899878 113
 AAGGGAATCAAACA-ACTCTTTTCATTCCCTTTGTTGGGCTTTTGGCATGAGA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:3630624-3630935 Satlength=312
 Nr of Repeats=6 RepeatLength=52 seed=ATCAAACAAC Num.seqs=5
 Similarity=0.948718 110
 AAGGGAATCAAACA-ACTCTTTTCATTCCCTTTGTTGGGCTTATGGCATGAGA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:5084517-5084881 Satlength=365
 Nr of Repeats=7 RepeatLength=52 seed=GGAATCAAAC Num.seqs=7
 Similarity=0.941392 107
 AAAGGAATCAAACA-ACTCTTTTCATTCCCTTTGTTGGGCTTTAGGCATGAGA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:3924084-3924292 Satlength=209
 Nr of Repeats=4 RepeatLength=52 seed=TTGGCATGAG Num.seqs=4
 Similarity=0.901709 41
 AAGGGAATGAAACA-ACGCTTTTCATTCCCTTTGTTGAGCTTTTGGCATGAGA
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:3983763-3984127
 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GGAATGAAAA Num.seqs=7
 Similarity=0.899878 80
 AAGGGAATGAAACA-ACGCTTTTCATTCCCTTTGTTGGGCTTTTGGGCATGAGA
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:1400861-1401069
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CAAAGGGAAT Num.seqs=4
 Similarity=0.872642 33
 AAAGGAATGAAACA-ATGCTTTTCATTCCCTTTGGATAGCTTTTGGCATGAGA
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:4004918-4005178
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTTCTCATGC Num.seqs=5
 Similarity=0.892308 54
 AAAGGAATGAAACA-ATGCTTTTCATTCCCTTTGGATAGCTTTTGGCATGAGA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:2268253-2268461 Satlength=209
 Nr of Repeats=4 RepeatLength=52 seed=GCATGAGAAA Num.seqs=4

Similarity=0.841880 44
AAAGGAATGAAACA-ACGCTTTTCATTCCCTTTGGAGAGCTTTGGGCATGAGA
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:2767735-2768306
Satlength=572 Nr of Repeats=11 RepeatLength=52 seed=CAAAGGGAAT
Num.seqs=10 Similarity=0.903424
33 AAGGGAATCAAACA-ACGCTTTTCATTCCCTTTGGATGGCTTTTGGCCTGAGA
GCF_002019645.1_ASM201964v1_genomic.fna_1:3095308-3095622 Satlength=315
Nr of Repeats=6 RepeatLength=52 seed=TTTCATTCCC Num.seqs=5
Similarity=0.893082 71
AAGGGAATCAAACA-ATGCTTTTCATTCCCTTTGGATGGCTTTTGGCATGAGA
GCF_002019645.1_ASM201964v1_genomic.fna_1:4272434-4272694 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=TTTCATTCCC Num.seqs=5
Similarity=0.897436 71
AAGGGAATCAAACA-ACGCTTTTCATTCCCTTTGTAGGGCTTTTGGCATGAGA
GCF_002019645.1_ASM201964v1_genomic.fna_1:908246-908556 Satlength=311 Nr
of Repeats=6 RepeatLength=52 seed=GAAAGGGAAT Num.seqs=4
Similarity=0.804527
50 AAGGGAATCAGACA-ACACCTTTCAATCCCTTTCTTGGACTTTTTGCGTGAGA
GCF_002019645.1_ASM201964v1_genomic.fna_1:1747684-1748098 Satlength=415
Nr of Repeats=8 RepeatLength=52 seed=GAGAAAGGGA Num.seqs=6
Similarity=0.873504 48
AAGGGAATCAAACA-GCGCCTTTTCGTTCCCTTGCACCGGCTTTTGGCGAGAGA
GCF_002019645.1_ASM201964v1_genomic.fna_1:1602707-1604007 Satlength=1301
Nr of Repeats=25 RepeatLength=52 seed=TTTCGTTCCC Num.seqs=25
Similarity=0.865470 19
AAGGGAATCAGAGA-ACATCTTTTCGTTCCCTTTTCATGGGCTATTGGTGTGGGA
GCF_002019645.1_ASM201964v1_genomic.fna_1:4783299-4783558 Satlength=260
Nr of Repeats=5 RepeatLength=52 seed=CTTTCGTTCC Num.seqs=4
Similarity=0.833333 70
AAGGGAACCTGAGA-ACACCTTTTCGTTCCCTTTCTCGAGCTTTTGGTGTGAAGA

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Consensus:

AAgGGAATCAaACAACgCtTTTCaTTCCCTTTgttggGCTTTtGGCATgAGA

>Bacillus_Fam_5_52_25 Nr. of seq. 25 Alignment length(with gaps) = 56
Alignment score = 0.706369
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:47214-47630 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=GTTAATGTGA Num.seqs=8 Similarity=0.884615
0 GTTAATGTGAAGATAACGAGACCAAACCTTGGAGT---ATCTGCACAAAGAGAG-G
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:348032-348606 Satlength=575 Nr of
Repeats=11 RepeatLength=52 seed=GGTTAATGTG Num.seqs=10
Similarity=0.814186 51
GTTAATGTGCAGATAAGGAGNCCAAACCATGGAGT---ATCTGCACAAAGAGGT-G
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:223083-223654 Satlength=572 Nr of
Repeats=11 RepeatLength=52 seed=CTGCACAAAG Num.seqs=10
Similarity=0.874074 37
GTTAATGTGAAGATACAGAGTCCAAACCTTGGAGT---AACTGCACAAAGAGGC-G
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:413864-414427 Satlength=564 Nr of
Repeats=11 RepeatLength=52 seed=GGTTAATGTG Num.seqs=10
Similarity=0.883476 51
GTTAATGTGAAGATACAGAGGCCAAACCTTGGAGT---AACTGCACAAAGAGAG-G

Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_9:0-207 Satlength=208 Nr of
 Repeats=4 RepeatLength=52 seed=CAGTATCTGC Num.seqs=4 Similarity=0.901709
 70 GTTAATGTGCAGATACTGAGGCCAAACCTTGGAGT---AACTGCACAAAGAGGG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_10:340482-340690 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=CTGCACAAAG Num.seqs=4
 Similarity=0.871795 37
 GTTAATGTGCAGATACAGAGGCCAAACCTTGAAGT---ATCTGCACAAAGAGGC-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:905229-906112 Satlength=884 Nr of
 Repeats=17 RepeatLength=52 seed=CGGAGTAACT Num.seqs=15
 Similarity=0.876923 81
 GTTAATGTGAAGATACGGAGGCCAAACTTCGGAGT---AACTGCACAAAGAGGN-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:525442-526534 Satlength=1093 Nr
 of Repeats=21 RepeatLength=52 seed=GGTTAATGTG Num.seqs=21
 Similarity=0.801385 51
 GTTAATGTGAAGATACGGAAGCCAAACCTTGGAGT---ATCTGCACAAAGAAGG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:1292643-1292851 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=GTATCTGCAC Num.seqs=4
 Similarity=0.876068 85
 GTTAATGTGTAGATACTGAGGCCAAACCTTGGAGT---ATCTGCACAAAGAAGG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:791934-792403 Satlength=470 Nr of
 Repeats=9 RepeatLength=52 seed=TGTGAAGATA Num.seqs=8 Similarity=0.939560
 57 GTTAATGTGAAGATACGGACGCCAAACCTTAGAGT---ATCTGCACAAAGAGCG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:112951-113306 Satlength=356 Nr of
 Repeats=7 RepeatLength=52 seed=TGTGCAGATA Num.seqs=6 Similarity=0.875052
 5 GTTAATGTGCAGATACGGAGGCCAAACACCGAGT---ATCTGCACAAAGAGAG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:269767-270183 Satlength=417 Nr of
 Repeats=8 RepeatLength=52 seed=AATGTGAAGA Num.seqs=8 Similarity=0.903846
 55 GTTAATGTGAAGATACGGAGGCCAAACCTCGGAGT---ATCTGCACAAAGAGAG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_10:253447-254227 Satlength=781 Nr
 of Repeats=15 RepeatLength=52 seed=TGTGAAGATA Num.seqs=13
 Similarity=0.965812 57
 GTTAATGTGAAGATACGGAGGCCAAACCTCGGAGT---ATCTGAACAAAGAGAG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_3:374971-375234 Satlength=264 Nr of
 Repeats=5 RepeatLength=52 seed=AAGATACGGA Num.seqs=4 Similarity=0.893162
 9 GTTAATGTAAAGATACGGAGGCCAAACCTTGGAGT---AACTGCACAAAGAGAG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:285662-285974 Satlength=313 Nr of
 Repeats=6 RepeatLength=52 seed=TGAAGATACT Num.seqs=6 Similarity=0.852991
 7 GTTAATGTGAAGATACTAAGGCCAAACCATGGAGT---ATCTGCACAAAGAGCG-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:210419-210887 Satlength=469 Nr of
 Repeats=8 RepeatLength=52 seed=GGAGTAACTG Num.seqs=7 Similarity=0.887668
 30 GTTAATGTTCAGATAAGGAGGCCAAACCTTGGAGT---AACTGCACAAAAGGC-G
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:443820-444288 Satlength=469 Nr of
 Repeats=9 RepeatLength=52 seed=AGTATCTGCA Num.seqs=9 Similarity=0.915954
 31 -TTAATGTGAAGATACTGAGGTCAAACGATGAAGT---ATCTGCACAAAGAGGGTG
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_3:62621-62933 Satlength=313 Nr of
 Repeats=6 RepeatLength=52 seed=CAAACCAAGT Num.seqs=6 Similarity=0.960684
 73 -TTAATGTGCAGATACGGAGGTCAAACCAAGTAGT---ATCTGCACAAAGAGGGTG
 Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:515438-515906
 Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=ATCTGCACAT Num.seqs=9
 Similarity=0.891738 65 -
 TTAATGTGCAGATACGGAAGCTAAACCANGTAGT---AACTGCACAAAGAGGGGG
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:201723-201931 Satlength=209 Nr of
 Repeats=4 RepeatLength=52 seed=GTTTATGTGA Num.seqs=4 Similarity=0.927350
 0 GTTTATGTGAAGATGCTGGGTCCAAACCTTGGAGT---ATCTGCACAAAAGAC-A

BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:501746-502107 Satlength=362 Nr of Repeats=7 RepeatLength=52 seed=AGTTTATGTG Num.seqs=6 Similarity=0.892308
51 GTTTATGTGAAGATACGGAGGCCAAACCTTGAGT---ATCTGCACAAAAGAC-A
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:486162-486682 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=AGTATCTGCA Num.seqs=10
Similarity=0.835150 32
TTTTATGTGCAGATACTGATGNCAAACCTTGAGT---ATCTGCACAAAAGAGNC-G
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:503624-503988 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=AATGTGAAGA Num.seqs=7 Similarity=0.714002
3 GTTAATGTGAAGATACGAGAG-CAAAAG--CGAGTGGTATCTGCACAAAAGAG-A
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:511772-512978 Satlength=1207 Nr of Repeats=13 RepeatLength=52 seed=GTTAATGTGA Num.seqs=12
Similarity=0.891997 52
GTTAATGTGAAGATAAGAAAGCCAAAAGGACGATT---ATCTGCACAAAAGAGGC-A
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:363633-363841 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=ATGTGAAGAT Num.seqs=4 Similarity=0.935897
56 GTTTATGTGAAGATACGGGAGCCGAGAGAGCGACT---ATCTTCACAAAAGAGGC-G

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

GTTAATGTGaAGATACgGAgGcAAACcttGgAGTAtCTGCACAAAGAGggG

>Bacillus_Fam_6_20_21 Nr. of seq. 21 Alignment length(with gaps) = 22
Alignment score = 0.672366
GCF_000153365.1_ASM15336v1_genomic.fna_13:128542-128642 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TTGCTAATAA Num.seqs=5
Similarity=0.693651
0 TTGCTAATAAAC--NGAAAAGN
Rev.of_GCF_000153365.1_ASM15336v1_genomic.fna_16:86330-86410 Satlength=81
Nr of Repeats=4 RepeatLength=20 seed=TTTATTAGCA Num.seqs=4
Similarity=0.593915 11
TTGCTAATAAAA--TGAAAAAC
Rev.of_GCF_000153365.1_ASM15336v1_genomic.fna_18:319407-319507
Satlength=101 Nr of Repeats=4 RepeatLength=20 seed=TTATTAGCAA Num.seqs=3
Similarity=0.730159 30
TTGCTAATAAAA--TGAAAAAC
GCF_000473245.1_ASM47324v1_genomic.fna_1:632989-633089 Satlength=101 Nr of Repeats=4 RepeatLength=20 seed=TTGCTAATAA Num.seqs=3
Similarity=0.735450
20 TTGCTAATAAAA--TGAAAAAN
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:3206997-3207097
Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TTTATTAGCA Num.seqs=5
Similarity=0.707937 11
TTGCTAATAAAC--TGAAAAAN
GCF_000153365.1_ASM15336v1_genomic.fna_16:171173-171253 Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=AAAAGTTGCT Num.seqs=4
Similarity=0.731481
14 -TGCTAATAAAA-CAAAAAAGT
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:3892181-3892261
Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=TTTATTAGCA Num.seqs=4
Similarity=0.661376 30 -
TGCTAATAAAATCACAAAAGT

GCF_000153365.1_ASM15336v1_genomic.fna_17:76317-76417 Satlength=101 Nr of
 Repeats=5 RepeatLength=20 seed=AGTTGCTAAT Num.seqs=5 Similarity=0.646970
 17 -TGCTAATAAAN-CGGAAAAGT
 GCF_000473245.1_ASM47324v1_genomic.fna_1:662499-662693 Satlength=195 Nr
 of Repeats=5 RepeatLength=20 seed=TGCTAATAAA Num.seqs=4
 Similarity=0.722222
 20 -TGCTAATAAAA-CGGAAAAGT
 Rev.of_GCF_000153365.1_ASM15336v1_genomic.fna_18:289784-289884
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TTATTAGCAA Num.seqs=5
 Similarity=0.740000 29 -
 TGCTAATAAAA-CNGAAAAGT
 Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:4451397-4451497
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TATTAGCAAC Num.seqs=5
 Similarity=0.700000 28 -
 TGCTAATAAAN-NGGAAAAGT
 Rev.of_GCF_000153365.1_ASM15336v1_genomic.fna_18:63090-63190
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TTTATTAGCA Num.seqs=5
 Similarity=0.666667 30
 -TGCTAATAAAA-NGNAAAAGT
 GCF_000473245.1_ASM47324v1_genomic.fna_1:889265-889365 Satlength=101 Nr
 of Repeats=5 RepeatLength=20 seed=AGTTGCTAAT Num.seqs=3
 Similarity=0.688889
 37 -TGCTAATAAAA-NGNAAAAGT
 GCF_000153365.1_ASM15336v1_genomic.fna_18:304350-304945 Satlength=596 Nr
 of Repeats=11 RepeatLength=20 seed=AGTTGCTAAT Num.seqs=9
 Similarity=0.716667 17
 -TGCTAATATAA-CGNAAAAGT
 GCF_000153365.1_ASM15336v1_genomic.fna_18:620027-620127 Satlength=101 Nr
 of Repeats=5 RepeatLength=20 seed=AGTTGCTAAT Num.seqs=5
 Similarity=0.642857
 17 -TGCTAATAAAN-TNGAAAAGT
 GCF_000153365.1_ASM15336v1_genomic.fna_17:566797-566897 Satlength=101 Nr
 of Repeats=5 RepeatLength=20 seed=AGTTGCTAAT Num.seqs=5
 Similarity=0.713333
 17 -TGCTAATAAAN-NNNAAAAGT
 Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:3960943-3961043
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TATTAGCAAC Num.seqs=5
 Similarity=0.713333 28 -
 TGCTAATAAAN-NNNAAAAGT
 Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2638864-2638944
 Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=TAGCAACTTT Num.seqs=4
 Similarity=0.711640 25 -
 TGCTAGTAAAA-GTGAAAAGT
 GCF_000153365.1_ASM15336v1_genomic.fna_17:471750-471850 Satlength=101 Nr
 of Repeats=5 RepeatLength=20 seed=AGTTGCTAAT Num.seqs=5
 Similarity=0.733333
 17 -TGCTAATATAT-GGGGAAAGT
 Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:4055915-4056015
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TATTAGCAAC Num.seqs=5
 Similarity=0.733333 28 -
 TGCTAATATAT-GGGGAAAGT
 Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:647550-648145
 Satlength=596 Nr of Repeats=11 RepeatLength=20 seed=TATTAGCAAC

Num.seqs=9 Similarity=0.652357
28 -TGCTAATATAA-ANGAAAAGT

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Consensus:

TGCTAATAAAanngAAAAGt

>Bacillus_Fam_7_52_18 Nr. of seq. 18 Alignment length(with gaps) = 60
Alignment score = 0.620516
GCF_000708755.2_ASM70875v2_genomic.fna_1:271081-271444 Satlength=364 Nr
of Repeats=7 RepeatLength=52 seed=AATCGTACCC Num.seqs=6
Similarity=0.800000
0 AATCGTACCCTATAAACTGAGAAACGAATTTAT--AGGGTAAGCAAA--CG--CC-GG-
GCF_000709935.2_ASM70993v2_genomic.fna_1:283764-284023 Satlength=260 Nr
of Repeats=5 RepeatLength=52 seed=AATCGTACCC Num.seqs=4
Similarity=0.760684
0 AATCGTACCCTATAAAACCGAAAAACAAATTTAT--AGGGTAAGCAAA--AG--CC-GG-
GCF_000708755.2_ASM70875v2_genomic.fna_1:448824-449084 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CGTACCCTCG Num.seqs=5
Similarity=0.953846
2 -AACGTACCCTCGAAAACCGTAAAACG-ATTTGC-GAGGGTAAGCAAAC-AG---G-AGA
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:874968-875332
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TTGCTTACCC Num.seqs=7
Similarity=0.824199 44 -
ATCGTACCCTCGCAAACCGAAAAACG-ATGTGG-GAGGGTAAGCAAG--GC--CG-CGA
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:926049-926309
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTGCTTACCC Num.seqs=5
Similarity=0.825926 44 -
ATCGTACCCTCGGAAACCGAGAAACG-ATTTGG-GAGGGTAAGCAAG--NG--CG-CGA
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_4:181059-181318
Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=TTGCTTACCC Num.seqs=4
Similarity=0.856394 44 -
ATCGTACCCTCGGAAACCGAGAAACG-ATTTGG-GAGGGTAAGCAAG--CG--CG-CGA
GCF_000709935.2_ASM70993v2_genomic.fna_24:175334-175594 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TACCCTCGGA Num.seqs=5
Similarity=0.877987
56 -ATCGTACCCTCGGAAACCGAGAAACG-ATCTGG-GAGGGTAAGCAAA--AG--CG-TGA
GCF_000709935.2_ASM70993v2_genomic.fna_13:142596-142908 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=GGAATCGTAC Num.seqs=6
Similarity=0.841026
49 -ATCGTACCCTGCCAAACCGAAAAACG-ATATGG-GAGGGTAAGCAAG--CG--CC-GGA
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:1045503-1045815
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TTGCTTACCC Num.seqs=6
Similarity=0.761934 44 -
ATCGTACCCTCGTAAACTGTAAAACG-ATCTGG-GAGGGTAAGCAA---AG-NCA-TGA
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_4:300377-300585
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TTGCTTACCC Num.seqs=4
Similarity=0.755241 44 -
ATCGTACCCTCGTAAACTGTAAAACG-ATCTGG-GAGGGTAAGCAA---AG-TCA-TGA
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:1167641-1168164
Satlength=524 Nr of Repeats=8 RepeatLength=52 seed=TTTGCTTACC Num.seqs=5
Similarity=0.969231 45 -
ATCGTACCCTCGGAAACTGAGAAACG-ATGTGG-GAGGGTAAGCAA---AG-TGG-TGA

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Consensus:

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>Bacillus_Fam_8_52_17 Nr. of seq. 17 Alignment length(with gaps) = 56
Alignment score = 0.680278
GCF_000751775.1_A1A_genomic.fna_10:40891-41880 Satlength=990 Nr of
Repeats=19 RepeatLength=52 seed=GACGACGAGA Num.seqs=18
Similarity=0.730730
25 AAAAGT-GAGTTTCCGCC--AAAAAAN-GACGACGAGAACGGGTCTCGTCGCCAA
GCF_000751775.1_A1A_genomic.fna_20:26659-27491 Satlength=833 Nr of
Repeats=16 RepeatLength=52 seed=TCGTCGCCAA Num.seqs=16
Similarity=0.651343
41 AAAAGG-GGGTTTCCCGTG--CAAAAATG-ACGACGAGAAAGGGTCTCGTCGCCAA
GCF_000751775.1_A1A_genomic.fna_30:19681-20513 Satlength=833 Nr of
Repeats=16 RepeatLength=52 seed=GTCTCGTCGC Num.seqs=14
Similarity=0.737114
90 AAAANG-GAGTTTCCCGCC--CAAAAACG-ACGACGAGAAAGGGTCTCGTCGCCAA
Rev.of_GCF_000751775.1_A1A_genomic.fna_86:16-431 Satlength=416 Nr of
Repeats=8 RepeatLength=52 seed=TTTGGCGACG Num.seqs=7 Similarity=0.832723
52 AAAATG-GAGTTTCCCGCN--CAAAAGTG-ACGACGAGAAGNGGTCTCGTCGCCAA
Rev.of_GCF_000751775.1_A1A_genomic.fna_88:33038-34338 Satlength=1301 Nr
of Repeats=26 RepeatLength=52 seed=TTTTTGGCGA Num.seqs=24
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Similarity=0.695501 54
 AAAGTG-GAGTTTTCCGCC--CAAAAATG-ACGACGAGAANGAGTNTCGTCGCCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_85:17849-18108 Satlength=260 Nr of
 Repeats=5 RepeatLength=52 seed=TTTTGGCGAC Num.seqs=4 Similarity=0.727778
 106 AAAGTG-GAGTTTTCCGNCT-CAAAAATG-ACGACGAGAAGTGGTCTCGTCGCCAA
 GCF_000751775.1_A1A_genomic.fna_10:73198-73666 Satlength=469 Nr of
 Repeats=9 RepeatLength=52 seed=ACGACGAGAA Num.seqs=9 Similarity=0.774217
 26 AAAATG-AGGTTTTNCGGC-NCAAAAC--GACGACGAGAAGTGGTCTCGTCGCCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_22:78517-79089 Satlength=573 Nr of
 Repeats=11 RepeatLength=52 seed=TTTTTTGGCG Num.seqs=11
 Similarity=0.773223
 56 AAAAGG-GAGTTTCTCGGC-TCAAAAT--GACGACGAGAANAGGTCTCGTCGCCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_35:49719-50032 Satlength=314 Nr of
 Repeats=5 RepeatLength=52 seed=CCATTTCTCG Num.seqs=3 Similarity=0.859539
 92 AAAAAG-GAGTTTCTCGGC-TCAAAAT--GACGACGAGAAATGGCCTCGTCGCCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_101:14447-15227 Satlength=781 Nr
 of Repeats=15 RepeatLength=52 seed=TTTTTGCGCA Num.seqs=15
 Similarity=0.743563 107
 AAAANG-GAGTTTTTCGCC-TCAAAAT--GNCGACGAGAANGGGTCTCGTCGCCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_26:642-1369 Satlength=728 Nr of
 Repeats=14 RepeatLength=52 seed=TCTCGTCACC Num.seqs=13
 Similarity=0.674451
 87 AAAATN-GAGTTTCTCGCC-TCAAAAT--GGTGACGAGATCAGGNCTCGTCGCCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_65:14846-15626 Satlength=781 Nr of
 Repeats=15 RepeatLength=52 seed=TTCTCGTCAC Num.seqs=15
 Similarity=0.727883
 88 AAAAGA-GNGTTTTNCGGC-TCAAAAT--GGTGACGAGAANGGGTCTCGTCGTCAA
 GCF_000751775.1_A1A_genomic.fna_77:13214-13941 Satlength=728 Nr of
 Repeats=13 RepeatLength=52 seed=AAAATGGTGA Num.seqs=12
 Similarity=0.764371
 124 AAAATG-GGGTTTTCCGGC-TCAAAAT--GGTGACGAGAATAGGTTTCGTGTCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_83:74740-75571 Satlength=832 Nr of
 Repeats=16 RepeatLength=52 seed=CATTCTCGTC Num.seqs=15
 Similarity=0.748847
 142 AAAATG-GGGTTTTCCGGC-TCAAAAT--GGTGACGAGAATGGGTTTCGTGCCAA
 GCF_000751775.1_A1A_genomic.fna_65:50685-51777 Satlength=1093 Nr of
 Repeats=21 RepeatLength=52 seed=GTCGCCAAAA Num.seqs=21
 Similarity=0.668548
 96 AAAANG-GNGTTTTTCGAC-TCAAAAC--GGTGACGAGAATTGGTCTCGTCGCCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_47:1465-1879 Satlength=415 Nr of
 Repeats=8 RepeatLength=52 seed=TTTTGGCGAC Num.seqs=6 Similarity=0.677183
 54 AAAAGC-AAGTTTTTCGGC-TTAAAT--GGCGACGAGAACGGGGTTCGTGCCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_27:14100-14724 Satlength=625 Nr of
 Repeats=12 RepeatLength=52 seed=TTTTGGCGAC Num.seqs=12
 Similarity=0.702525
 53 AATATGAGANTTTT-CGAC--CAAAAACG-GTGACGAGAACAGGTTTCGTGCCAA

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 Consensus:

gacGACGAGAAnnGGTcTCGTGCCAAAAAngGaGTTTtnCGnCcAAAAAn

>Bacillus_Fam_9_52_16 Nr. of seq. 16 Alignment length(with gaps) = 60
 Alignment score = 0.601759

GCF_000292245.2_ASM29224v2_genomic.fna_7:40548-40756 Satlength=209 Nr of
 Repeats=4 RepeatLength=52 seed=CTTTGATTCC Num.seqs=4 Similarity=0.764403
 0 ---CTTTGATTCCCTTT-ACGGCTCTTATTCAATCGCTTTTGAAATCATT--GAC-AGG-
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_82:9184-9652 Satlength=469
 Nr of Repeats=9 RepeatLength=52 seed=AATCAAAGGC Num.seqs=9
 Similarity=0.915954 8
 ---CTTTGATTCCCTTT-CTGGCTCTGATTGATGGCTTCTGGCTTCATT--GAC-AGC-
 GCF_000292245.2_ASM29224v2_genomic.fna_91:13346-13554 Satlength=209 Nr of
 Repeats=4 RepeatLength=52 seed=TGATTCCCTT Num.seqs=4 Similarity=0.751048
 3 ---CTTTGATTCCCTTT-CCGACTTTTATTCAATGGCTTTCGGACTCATT--GAC--GCT
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_38:13764-14076
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=AAAGGGAATC Num.seqs=6
 Similarity=0.713939 14
 C---TTTGATTCCCTTT-NCGGCTTTGATTTGATGGCTTTTGGTTTCATTG-G-C-TGG-
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_38:24849-25109
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CAATGAATCC Num.seqs=5
 Similarity=0.753086 47
 CT-CTTTGATTCCCTTT-GAGGCTTTTATTTGATGGCTTTCGGATTCATT--G---GGG-
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_38:34016-34224
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CAAAGGGAAT Num.seqs=4
 Similarity=0.901709 67
 C--CTTTGATTCCCTTT-GCGGCTTTTATTTGCTGGCTTTTGGCTTCATT--G-C-GGG-
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_38:38220-38584
 Satlength=365 Nr of Repeats=8 RepeatLength=52 seed=GAATCAAAGG Num.seqs=6
 Similarity=0.846541 113
 C--CTTTGATTCCCTTT-GCGGCTTTTATTTGATGGCTTTCGGCTTCATT--G-C-TGG-
 GCF_000292245.2_ASM29224v2_genomic.fna_41:5487-5747 Satlength=261 Nr of
 Repeats=5 RepeatLength=52 seed=CTTTGATTCC Num.seqs=5 Similarity=0.666667
 104 C--CTTTGATTCCCTTT-CCGGCTTTTATTGATGGCTTCGGGCTTCATT--G-C-GGG-
 GCF_000292245.2_ASM29224v2_genomic.fna_84:3892-4206 Satlength=315 Nr of
 Repeats=6 RepeatLength=52 seed=TTTGATTCCC Num.seqs=4 Similarity=0.746399
 53 C--CTTTGATTCCCTTT-CCGGCTTTGATTCAACGGCTTCCGGATTCATT--G-C-GGG-
 GCF_000292245.2_ASM29224v2_genomic.fna_10:69101-69413 Satlength=313 Nr of
 Repeats=6 RepeatLength=52 seed=TATGATTCCC Num.seqs=6 Similarity=0.775354
 1 C---TATGATTCCCTTT-GCAGCTCTGATTGATGCTTTTGACATCATT-CG-AGCT--
 GCF_000292245.2_ASM29224v2_genomic.fna_126:27-495 Satlength=469 Nr of
 Repeats=9 RepeatLength=52 seed=CTCTGATTCA Num.seqs=9 Similarity=0.782492
 18 C-CCTATGATTCCCTTTGGCA-CTCTGATTGATGCTTTTGGCATCATT--G-A-CT--
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_31:24471-25040
 Satlength=570 Nr of Repeats=11 RepeatLength=52 seed=AAGGGAATCA
 Num.seqs=9 Similarity=0.793447
 13 C-CCTTTGATTCCCTTT-GCGGCTTTTATTCATATGCTTTAGGAATCATT--G-G-CG--
 GCF_000292245.2_ASM29224v2_genomic.fna_77:841-1153 Satlength=313 Nr of
 Repeats=7 RepeatLength=52 seed=TGATTCCCTT Num.seqs=5 Similarity=0.841026
 55 C-CCTATGATTCCCTTT-GCGGCTCTTATTCATATGCTTTTGGCATCATT--G-A-CG--
 GCF_000292245.2_ASM29224v2_genomic.fna_92:15221-15533 Satlength=313 Nr of
 Repeats=6 RepeatLength=52 seed=CTCTATGATT Num.seqs=6 Similarity=0.863248
 50 C-TCTATGATTCCCTTT-CTGGCTTTGATTCACCGGCTTTTGACATCATT--G-C-GG--
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_171:47-724 Satlength=678 Nr
 of Repeats=13 RepeatLength=52 seed=AAAGGGAATC Num.seqs=12
 Similarity=0.761673 66
 C-TCTATGATTCCCTTT-CTGGCTTTGATTCACCGGCTTTTGACATCATT--G-C-GG--
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_106:11691-12195
 Satlength=505 Nr of Repeats=8 RepeatLength=52 seed=GAAAGGGAAT Num.seqs=7

Similarity=0.843965

67

C-TCTATGATTCCTTTT-CCGGCTTTAATTCACTGGCTTTTGACATCATT--G-C-NG--

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

Consensus:

CCTtTGATTCCTTTTncGGCTtTtATTcaatgGCTTTtGgcaTCATTGcnGn

>Bacillus_Fam_10_20_16 Nr. of seq. 16 Alignment length(with gaps) = 22

Alignment score = 0.662626

GCF_000934845.1_ASM93484v1_genomic.fna_170:34797-34878 Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TCGCCAATAA Num.seqs=3 Similarity=0.528889

0 TCGCCAATAAAA-NAAATT-T-

Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_41:14151-14232

Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3 Similarity=0.514493 11

TCGCCAATAAAA-TCATTT-T-

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_75:42581-42683

Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=TTATTGGCGA Num.seqs=3 Similarity=0.733333 10

TCGCCAATAAAAATTATATT-T-

GCF_001315165.1_ASM131516v1_genomic.fna_6:81809-81911 Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=CGCCAATAAA Num.seqs=3 Similarity=0.688889

21 TCGCCAATAAAAATTAAATT-T-

Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_207:5245-5347 Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3 Similarity=0.688889 11

TCGCCAATAAAAATTTATT-T-

GCF_001315165.1_ASM131516v1_genomic.fna_3:16512-16593 Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TCGCCAATAA Num.seqs=3 Similarity=0.711111

20 TCGCCAATAAAAATTTNATT-T-

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_100:28725-28826

Satlength=102 Nr of Repeats=5 RepeatLength=20 seed=TTATTGGCGA Num.seqs=4 Similarity=0.788889 10

TCGCCAATAAAAATTGGATT-T-

Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_140:1784-1886 Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=TTATTGGCGA Num.seqs=3 Similarity=0.714286 10

TCGCCAATAAAAATAAATT-T-

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_129:61647-61728

Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3 Similarity=0.711111 11

TCGCCAATAAAAANNANATT-T-

Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_68:88019-88120

Satlength=102 Nr of Repeats=4 RepeatLength=20 seed=TATTGGCGAA Num.seqs=3 Similarity=0.714286 29

TCGCCAATANAATTTTNTT-T-

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_100:19594-19675

Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3 Similarity=0.688889 10

-CGCCAATAAATCATAATAT-

GCF_001315165.1_ASM131516v1_genomic.fna_22:40668-40770 Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=CGCCAATAAA Num.seqs=3

Similarity=0.711111
 20 -CGCCAATAAAAANATATTAT-
 GCF_001315165.1_ASM131516v1_genomic.fna_3:41031-41132 Satlength=102 Nr of
 Repeats=5 RepeatLength=20 seed=CGCCAATAAA Num.seqs=4 Similarity=0.722222
 20 -CGCCAATAAAATGAAATTAT-
 Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_16:12683-12764
 Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3
 Similarity=0.656566 30
 -CGCCAATAAANTNAAANTAT-
 Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_98:38828-38909 Satlength=82
 Nr of Repeats=4 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3
 Similarity=0.777778 11
 TCGCCAATAAAAATCGA-T-TA
 GCF_000813125.1_ASM81312v1_genomic.fna_51:14452-14553 Satlength=102 Nr of
 Repeats=5 RepeatLength=20 seed=TCGCCAATAA Num.seqs=4 Similarity=0.487778
 21 TCGCCAATAAAAATCGATT-TN

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Consensus:

tCGCCAATAAAAAttanATTT

>Bacillus_Fam_11_51_15 Nr. of seq. 15 Alignment length(with gaps) = 56
 Alignment score = 0.625454
 GCF_000292245.2_ASM29224v2_genomic.fna_2:54137-54392 Satlength=256 Nr of
 Repeats=5 RepeatLength=51 seed=TTTTTCATTAC Num.seqs=5 Similarity=0.691667
 0 TTTTCATTACCTATT-ANC--ATTTATTCGCACCCTAAT-TCCTCACACCCGNN-
 GCF_000292245.2_ASM29224v2_genomic.fna_8:10287-10542 Satlength=256 Nr of
 Repeats=5 RepeatLength=51 seed=TTTTTCATTAC Num.seqs=5 Similarity=0.717284
 0 TTTTCATTACCTATT-AAC--NGTGATTTCGCACCGTAAT-CNCTCACAGCACGGG-
 GCF_000292245.2_ASM29224v2_genomic.fna_2:95942-96554 Satlength=613 Nr of
 Repeats=12 RepeatLength=51 seed=TTTCATTACC Num.seqs=12
 Similarity=0.821747
 1 TTTTCATTACCTATT-ACC--GTTTATTCGCACCGTAAT-TCCGA-CAACNCGGCT
 GCF_000292245.2_ASM29224v2_genomic.fna_84:12497-12803 Satlength=307 Nr of
 Repeats=6 RepeatLength=51 seed=CTTTTCATT Num.seqs=6 Similarity=0.706080
 49 TTTTCATTACCTATT-ACC--AATTTTTCGCACCCTAAT-CCGGC-CAACTCNGCT
 GCF_000292245.2_ASM29224v2_genomic.fna_105:6378-7343 Satlength=966 Nr of
 Repeats=18 RepeatLength=51 seed=TTTCATTACC Num.seqs=14
 Similarity=0.681019
 1 TTTTCATTACCTATT-CANC--ATTATTCGCACCTTAATCTCCG--CAACTCGGCT
 GCF_000292245.2_ASM29224v2_genomic.fna_3:26666-27023 Satlength=358 Nr of
 Repeats=7 RepeatLength=51 seed=TCATTACCTA Num.seqs=7 Similarity=0.625037
 3 TTTTCATTACCTATT--CC-NGTTTTTTCGCACCCAAATC-CGNCACAGCTCGGC-
 GCF_000292245.2_ASM29224v2_genomic.fna_133:14-269 Satlength=256 Nr of
 Repeats=5 RepeatLength=51 seed=TTTTTCATTAC Num.seqs=5 Similarity=0.639766
 51 TTTTCATTACCTATT--CC-TGTTTATTCGCACCCTAATCTCTT-ACAGCACGGC-
 GCF_000292245.2_ASM29224v2_genomic.fna_43:36326-36680 Satlength=355 Nr of
 Repeats=7 RepeatLength=51 seed=TTTTTCATTAC Num.seqs=6 Similarity=0.790598
 51 TTTTCATTACCTATT--CC-TGNTTATTCGCACCCTAATNTCTTCACAGCACGGC-
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_59:24274-24682
 Satlength=409 Nr of Repeats=8 RepeatLength=51 seed=GGTTCGAAAA Num.seqs=8
 Similarity=0.909430 31
 TTTTCATTACCTATT--CA-AGTTTTTTTCGAACCCTAAT-TCTTAACACCTCGGC-

GCF_000292245.2_ASM29224v2_genomic.fna_5:34399-34863 Satlength=465 Nr of Repeats=9 RepeatLength=51 seed=TTTCGACCCCT Num.seqs=7 Similarity=0.833639
 23 TTTTCATTACTTATC--CC-GCTTTATTTCGCACCCTAAT-TTGACTCAGCTCGGC-
 GCF_000292245.2_ASM29224v2_genomic.fna_20:40449-40806 Satlength=358 Nr of Repeats=7 RepeatLength=51 seed=ATTTCGACCC Num.seqs=7 Similarity=0.788260
 73 TTTTCATTACCTATC--CC-GCTCAATTTCGCACCCTAAT-TTGACTCAGCACCGC-
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_26:8-518 Satlength=511 Nr of Repeats=10 RepeatLength=51 seed=GTAATGAAAA Num.seqs=10
 Similarity=0.770940 61
 TTTTCATTACTTATT--CC-AGTTTATTTCGCACCCTAAT-TTGGCACTGCTCGGC-
 Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_139:4619-4975 Satlength=357
 Nr of Repeats=7 RepeatLength=51 seed=GTAATGAAAA Num.seqs=6
 Similarity=0.788889 61
 TTTTCATTACTTATC--CC-AGTTTATTTCGCACTCTAAT-TTGGCACTGCACAGC-
 GCF_000292245.2_ASM29224v2_genomic.fna_42:17059-17365 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=TTTTTCGCAC Num.seqs=6 Similarity=0.814675
 70 TTTTCATTACTTATT--CCAGCTTTT-TCGCACCGTAAT-CTGACTCAGCACGGT-
 GCF_000292245.2_ASM29224v2_genomic.fna_8:67209-67464 Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=TTTTCATTAC Num.seqs=5 Similarity=0.824837
 51 TTTTCATTACCAATT--CC-CTTTTATTTCGCACCNATAAT-TTCTCGCAGCACCGC-

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Consensus:

TTTTCATTACcTATtcCnntTTaTTCGCACCcTAATtcnncaCAgCnCcGc

>Bacillus_Fam_12_52_15 Nr. of seq. 15 Alignment length(with gaps) = 54
 Alignment score = 0.703939
 GCF_000751775.1_A1A_genomic.fna_10:11861-12903 Satlength=1043 Nr of Repeats=20 RepeatLength=52 seed=TTTTGACGAC Num.seqs=18
 Similarity=0.678447
 0 TTTTGACGACGAAA-CGCATTCTCGTCACCATTTTGAGGTGAAAAACGC-TCAA
 GCF_000751775.1_A1A_genomic.fna_21:16757-17329 Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=TCTCGTCACC Num.seqs=11
 Similarity=0.696398
 19 TTTTGACGACGAGA-TCTAATCTCGTCACCATTTTGAGGTGGGAAATGC-TCAA
 GCF_000751775.1_A1A_genomic.fna_10:2556-2815 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=TCTCGTCACC Num.seqs=4 Similarity=0.633230
 20 TTTTGACGACGAAATCCTATTCTCGTCACCAATTTGAGGCGAGAAACAC-CCAA
 GCF_000751775.1_A1A_genomic.fna_35:77020-77852 Satlength=833 Nr of Repeats=16 RepeatLength=52 seed=TTTTGGCGAC Num.seqs=14
 Similarity=0.698921
 0 TTTTGGCGACGAGC-CCCGTTCTCGTCGTCATTTTGAGGTGAGAAATGC-TCAA
 Rev.of_GCF_000751775.1_A1A_genomic.fna_42:1584-2449 Satlength=866 Nr of Repeats=17 RepeatLength=52 seed=GTGACGAGAA Num.seqs=13
 Similarity=0.799803
 28 TTTTGGCGACGAGA-CCCGTTCTCGTCACCATTTTGAGGTGAAAAATNC-TCGT
 Rev.of_GCF_000751775.1_A1A_genomic.fna_42:28877-29449 Satlength=573 Nr of Repeats=10 RepeatLength=52 seed=AAAATGGTGA Num.seqs=9
 Similarity=0.760631
 34 TTTTGGCGACGAGA-CCNNTTCTCGTCACCATTTTGAGGCGNGAAATGC-TCTT
 GCF_000751775.1_A1A_genomic.fna_70:5639-6159 Satlength=521 Nr of Repeats=9 RepeatLength=52 seed=CTCGTCACCA Num.seqs=8 Similarity=0.803792
 72 TTTTGGCGACGAGA-CCCTTTCTCGTCACCATTTTGGGGCGAAAATGC-TCGA

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Consensus:

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>Bacillus_Fam_13_21_15 Nr. of seq. 15 Alignment length(with gaps) = 24
Alignment score = 0.642196
GCF_900111815.1_PRJEB17078_genomic.fna_1:83842-84237 Satlength=396 Nr of
Repeats=7 RepeatLength=21 seed=TTACCGTAGA Num.seqs=6 Similarity=0.679798
0 TTACCGTAGATA-AAAGGCNG--T
GCF_900111815.1_PRJEB17078_genomic.fna_9:3907-4741 Satlength=835 Nr of
Repeats=11 RepeatLength=21 seed=TTACCGTAGA Num.seqs=9
Similarity=0.742504
0 TTACCGTAGATA-AATGGTGG--T
Rev.of_GCF_900111815.1_PRJEB17078_genomic.fna_1:368287-368371
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TATCTACGGT Num.seqs=4
Similarity=0.642677 12
TTACCGTAGATA-AATNGACG--T
GCF_900111815.1_PRJEB17078_genomic.fna_1:2689763-2690346 Satlength=584 Nr
of Repeats=5 RepeatLength=21 seed=TTTACCGTAG Num.seqs=3
Similarity=0.873016 20
TTACCGTAGATA-AATTGCCG--T
Rev.of_GCF_900111815.1_PRJEB17078_genomic.fna_1:2705984-2706732
Satlength=749 Nr of Repeats=12 RepeatLength=21 seed=TATCTACGGT

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Num.seqs=10 Similarity=0.714654
33 TTACCGTAGATA-AATTGCCG--T
GCF_900111815.1_PRJEB17078_genomic.fna_1:541624-541708 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTACCGTAGA Num.seqs=4 Similarity=0.642361
21 TTACCGTAGATA-AATTGCAG--N
GCF_900111815.1_PRJEB17078_genomic.fna_1:397204-397592 Satlength=389 Nr
of Repeats=7 RepeatLength=21 seed=TTACCGTAGA Num.seqs=6
Similarity=0.716162
0 TTACCGTAGATA-AANTGNCGA-T
Rev.of_GCF_900111815.1_PRJEB17078_genomic.fna_1:2954420-2954813
Satlength=394 Nr of Repeats=7 RepeatLength=21 seed=TATCTACGGT Num.seqs=6
Similarity=0.708081 11 -
TACCGTAGATA-AATGGAGN-AT
Rev.of_GCF_900111815.1_PRJEB17078_genomic.fna_1:136654-137062
Satlength=409 Nr of Repeats=8 RepeatLength=21 seed=TATCAACGGT Num.seqs=7
Similarity=0.645503 12
TTACCGTTGATA-AATCGCNG--T
Rev.of_GCF_900111815.1_PRJEB17078_genomic.fna_1:2902508-2902991
Satlength=484 Nr of Repeats=7 RepeatLength=21 seed=TATCAACGGT Num.seqs=6
Similarity=0.631313 12
TTACCGTTGATA-AATGGCNA--T
Rev.of_GCF_900111815.1_PRJEB17078_genomic.fna_1:2906204-2907642
Satlength=1439 Nr of Repeats=21 RepeatLength=21 seed=TATCTACGGT
Num.seqs=13 Similarity=0.791616
12 TTACCGTAGATA-AATCGCNA--T
GCF_900111815.1_PRJEB17078_genomic.fna_1:2936585-2937431 Satlength=847 Nr
of Repeats=11 RepeatLength=21 seed=TTACCGTTGA Num.seqs=8
Similarity=0.767587 21
TTACCGTAGATA-AATCGTGA--T
GCF_900111815.1_PRJEB17078_genomic.fna_1:80313-80667 Satlength=355 Nr of
Repeats=5 RepeatLength=21 seed=TTACCGTTGA Num.seqs=4 Similarity=0.664251
22 TTACCGTTGATAAAATGGCTG--A
GCF_900111815.1_PRJEB17078_genomic.fna_1:2407942-2408247 Satlength=306 Nr
of Repeats=4 RepeatLength=21 seed=TTACCGTTGA Num.seqs=3
Similarity=0.666667 21
TTACCGTTGATA-AATGNNCA--N
GCF_900111815.1_PRJEB17078_genomic.fna_11:38238-39212 Satlength=975 Nr of
Repeats=13 RepeatLength=21 seed=TTACCGTTGA Num.seqs=10
Similarity=0.709428
21 TTACCGTTGATA-AATGNNGA--N

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Consensus:

TTACCGTaGATAAAATnGcngt

>Bacillus_Fam_14_21_15 Nr. of seq. 15 Alignment length(with gaps) = 23
Alignment score = 0.651484
GCF_001889165.1_ASM188916v1_genomic.fna_1:21005-21172 Satlength=168 Nr of
Repeats=8 RepeatLength=21 seed=AATCGCGGAT Num.seqs=7 Similarity=0.782828
0 AATCGCGGAT-A-GAGCCCGGAA
GCF_001889165.1_ASM188916v1_genomic.fna_1:25511-25700 Satlength=190 Nr of
Repeats=9 RepeatLength=21 seed=CGGATAGAGC Num.seqs=9 Similarity=0.873016
5 AATCGCGGAT-A-GAGCACTGAA

Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:3155990-3156777
 Satlength=788 Nr of Repeats=15 RepeatLength=21 seed=TCCGCGATTT
 Num.seqs=10 Similarity=0.732323
 9 AATCGCGGAT-A-GAGCGCCGAA
 GCF_001889165.1_ASM188916v1_genomic.fna_1:497918-498023 Satlength=106 Nr
 of Repeats=5 RepeatLength=21 seed=AATCGCGGAT Num.seqs=5
 Similarity=0.875758
 0 AATCGCGGAT-A-GAGGGCTGAA
 Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:2579124-2579418
 Satlength=295 Nr of Repeats=14 RepeatLength=21 seed=TATCCGCGAT
 Num.seqs=14 Similarity=0.806035
 11 AATCGCGGAT-A-GAGCGCTCAG
 Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:3277057-3277141
 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TATCCGCGAT Num.seqs=4
 Similarity=0.666667 11
 AATCGCGGATAA-GAGCGGTGAT
 Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:790108-790234
 Satlength=127 Nr of Repeats=6 RepeatLength=21 seed=TATCCGCGAT Num.seqs=6
 Similarity=0.817989 11
 AATCGCGGAT-A-CAGCACCTAT
 Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:2862732-2862858
 Satlength=127 Nr of Repeats=6 RepeatLength=21 seed=CTATCCGCGA Num.seqs=6
 Similarity=0.713636 11
 AATCGCGGAT-AGCAGCATGTAT
 GCF_001889165.1_ASM188916v1_genomic.fna_1:29979-30084 Satlength=106 Nr of
 Repeats=5 RepeatLength=21 seed=AATCGCGGAT Num.seqs=5 Similarity=0.701515
 0 AATCGCGGAT-A-GACGNACCAG
 GCF_001889165.1_ASM188916v1_genomic.fna_1:757325-757823 Satlength=499 Nr
 of Repeats=14 RepeatLength=21 seed=AATCGCGGAT Num.seqs=13
 Similarity=0.655147 0
 AATCGCGGAT-A-GAAGCCCCAA
 GCF_001889165.1_ASM188916v1_genomic.fna_1:3362340-3362445 Satlength=106
 Nr of Repeats=5 RepeatLength=21 seed=ATCGCGGATA Num.seqs=5
 Similarity=0.847619 1
 AATCGCGGAT-A-GAACCCCAT
 GCF_001889165.1_ASM188916v1_genomic.fna_1:4295617-4296096 Satlength=480
 Nr of Repeats=10 RepeatLength=21 seed=AATCGCGGAT Num.seqs=8
 Similarity=0.577877 0
 AATCGCGGAT-A-GAGGNCCNAT
 GCF_001889165.1_ASM188916v1_genomic.fna_1:802803-802887 Satlength=85 Nr
 of Repeats=4 RepeatLength=21 seed=AATCGCGGAT Num.seqs=4
 Similarity=0.767196
 0 AATCGCGGAT-A-GAGCATCCAA
 GCF_001889165.1_ASM188916v1_genomic.fna_1:3702467-3702782 Satlength=316
 Nr of Repeats=15 RepeatLength=21 seed=ATCGCGGATA Num.seqs=15
 Similarity=0.860922 1
 AATCGCGGAT-A-GAGCACCCAC
 GCF_001889165.1_ASM188916v1_genomic.fna_1:2986923-2987175 Satlength=253
 Nr of Repeats=12 RepeatLength=21 seed=ATCGCGGATA Num.seqs=12
 Similarity=0.785474 1
 AATCGCGGAT-A-GAGCNCCCTT

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Consensus:

AATCGCGGATAGAgcncnAn

>Bacillus_Fam_15_52_14 Nr. of seq. 14 Alignment length(with gaps) = 54
Alignment score = 0.680301
GCF_000374345.1_ASM37434v1_genomic.fna_44:21064-21532 Satlength=469 Nr of
Repeats=9 RepeatLength=52 seed=ATGAACGCC Num.seqs=9 Similarity=0.580460
0 ATGAACGCCCGCAGCACGGATTTT-NTNCCGGCACGGTCTTTCATACC-CNT-
GCF_000374345.1_ASM37434v1_genomic.fna_5:37937-38145 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=GGCTTTCATT Num.seqs=4 Similarity=0.803419
36 ATGAACGACCACGGGCACGGGTTTT-CCACGGGAACGGGCTTTCATTCCCCTT-
GCF_000374345.1_ASM37434v1_genomic.fna_22:25197-25509 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=ATGAACGACC Num.seqs=6 Similarity=0.724109
52 ATGAACGACCATGGGCGCGGCTTTT-TCTTGGGAACGGGCATTCATTCGCCGT-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_9:32790-34036
Satlength=1247 Nr of Repeats=24 RepeatLength=52 seed=GGTCGTTCAT
Num.seqs=20 Similarity=0.767414
62 ATGAACGACCGNGCGCGGGTTTTCT-CCGGCACGGGCTTTCATTCTCTCT-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_42:4571-4935 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=GAATGAAAGC Num.seqs=7
Similarity=0.738240 99
ATGAACGACCGGAAGCGCGGGTTTTACT-CCGGCNTGGGCTTTCATTCCACTT-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_13:64454-65078
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=CACGGTCGTT
Num.seqs=12 Similarity=0.837995
65 ATGAACGACCGTGGGCGCGGATTTT-CTTCCGGCACGGGCTTTCATTTCCCTT-
GCF_000374345.1_ASM37434v1_genomic.fna_29:21895-22466 Satlength=572 Nr of
Repeats=11 RepeatLength=52 seed=GGGCTTTCAT Num.seqs=10
Similarity=0.851852
87 ATGAACGACCGTGGGCGGGGATTTT-CTCCGGCGCGGGCTTTCATTCCCCTT-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_57:9268-10100 Satlength=833
Nr of Repeats=16 RepeatLength=52 seed=AATGAAAGCC Num.seqs=16
Similarity=0.831838 98
ATGAACGACCGCGGGCACGAATTTT-CTTCCGACGCGGGCTTTCATTTCTCTCT-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_43:29468-30092
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=GTCGTTCATA
Num.seqs=12 Similarity=0.758353
113 ATGAACGACCGCATCATGGTTTTT-CTTCCAGCGCGGGCTTTCATTCCCCTT-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_53:47-463 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=GGTCGTTCAT Num.seqs=8
Similarity=0.782051
114 ATGAACGACCGCGCACGTGGGTTTT-CTTCCGCCGCGGGCTTTCATTCCCCTT-
GCF_000374345.1_ASM37434v1_genomic.fna_99:27-339 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=CTTATGAACG Num.seqs=6 Similarity=0.769231
153 ATGAACGACCGCGCACACGGGTTTT-CTCCGCCGCGGGCTTTCATTCCCCTT-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_47:7566-7826 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=GGTCGTTCAT Num.seqs=5
Similarity=0.691358 62
ATGAACGACCNCGAACNCAGATTTT-CCTCCGTCACGGGCTTTCATTCCACTT-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_8:71582-72050 Satlength=469
Nr of Repeats=9 RepeatLength=52 seed=ATGAAAGCCC Num.seqs=9
Similarity=0.760117 45
ATGAACGACCGGGTGCTGTTTTT-CTTCCGGTGCGGGCTTTCAT-CGCCTTG

Similarity=0.514423 36
 ATGAGAACCGNAA-NAGGACCAG-NGNTAGGAGGAANCGGTCTTCATAAAGGAG
 GCF_900156875.1_PRJEB18969_genomic.fna_11:540121-540433 Satlength=313 Nr
 of Repeats=6 RepeatLength=52 seed=CGGTCTTCAT Num.seqs=6
 Similarity=0.841026
 87 ATGAGAACCGAAA-CAGGATCAG-CGGTAGAAGGAAACGGTCTTCATAAAGGAA
 GCF_900156875.1_PRJEB18969_genomic.fna_11:512429-513105 Satlength=677 Nr
 of Repeats=13 RepeatLength=52 seed=CGGTCTTCAT Num.seqs=11
 Similarity=0.790744 87
 ATGAGAACCGATC-CAGGATCAG-TGGAAGCAAGAACCGGTCTTCATAAAGGAG
 GCF_900156875.1_PRJEB18969_genomic.fna_11:443658-443970 Satlength=313 Nr
 of Repeats=6 RepeatLength=52 seed=GACCGAAAGA Num.seqs=6
 Similarity=0.928205
 5 ATGAGGACCGAAA-GATGATCAG-GGGAAGCAGAAACCGTCATCATCAAGGGA

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 Consensus:

ATGAGAACCGAAAgAGgtccAGcGnaAgcaGgaAaCGGTCTTCATaAagGgg

>Bacillus_Fam_17_12_14 Nr. of seq. 14 Alignment length(with gaps) = 14
 Alignment score = 0.607535
 GCF_000292245.2_ASM29224v2_genomic.fna_17:22115-22158 Satlength=44 Nr of
 Repeats=4 RepeatLength=11 seed=TTTTTACTTT Num.seqs=3 Similarity=1.000000
 0 -TTTTTACTTTC--
 Rev.of_GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_1:1238234-
 1238324 Satlength=91 Nr of Repeats=7 RepeatLength=12 seed=AAAGGAAAAG
 Num.seqs=6 Similarity=1.000000 4 CTTT-T-
 CCTTTTC
 Rev.of_GCF_000305495.1_BacPsy2.0_genomic.fna_263:11580-11634 Satlength=55
 Nr of Repeats=4 RepeatLength=12 seed=GAAAAAGAAA Num.seqs=3
 Similarity=0.925926 12
 CTTT-T-CTTTTTC
 GCF_000299035.1_ASM29903v1_genomic.fna_3:203147-203195 Satlength=49 Nr of
 Repeats=4 RepeatLength=12 seed=TTTCTTTTTC Num.seqs=4 Similarity=0.888889
 15 CTTTTT-CTTTTT-
 GCF_000712615.1_ASM71261v1_genomic.fna_1:55537-55585 Satlength=49 Nr of
 Repeats=4 RepeatLength=12 seed=TTCTTTTCT Num.seqs=4 Similarity=0.944444
 16 CTTTTT-CTTTTT-
 GCF_000775975.1_ASM77597v1_genomic.fna_1:5340410-5341236 Satlength=827 Nr
 of Repeats=6 RepeatLength=12 seed=CTTTTCTTT Num.seqs=4
 Similarity=0.833333 18
 CTTTTT-CTTTTT-
 Rev.of_GCF_001439965.1_ASM143996v1_genomic.fna_122:196979-197027
 Satlength=49 Nr of Repeats=4 RepeatLength=12 seed=AAGAAAAAGA Num.seqs=4
 Similarity=0.925926 15
 CTTTTT-CTTTTT-
 GCF_000380245.2_ASM38024v2_genomic.fna_8:153502-153556 Satlength=55 Nr of
 Repeats=4 RepeatLength=12 seed=TTCTTTTCT Num.seqs=3 Similarity=0.925926
 16 CTTTTT-CTTCTT-
 Rev.of_GCF_001654695.1_ASM165469v1_genomic.fna_2:100746-101358
 Satlength=613 Nr of Repeats=4 RepeatLength=12 seed=TGAAAAAGAA Num.seqs=3
 Similarity=1.000000 20
 CTTTTT-CATATT-

GCF_900109925.1_IMG-
 taxon_2651870116_annotated_assembly_genomic.fna_21:131911-131965
 Satlength=55 Nr of Repeats=4 RepeatLength=12 seed=TTTTCTTTTT Num.seqs=3
 Similarity=0.925926 20 CTTTTT-CATTTT-
 GCF_000430765.1_ASM43076v1_genomic.fna_20:41962-42022 Satlength=61 Nr of
 Repeats=5 RepeatLength=12 seed=ATCTTTATCT Num.seqs=5 Similarity=1.000000
 4 CTTTAT-CTTTAT-
 GCF_000621445.1_ASM62144v1_genomic.fna_4:61862-61916 Satlength=55 Nr of
 Repeats=4 RepeatLength=12 seed=TCTTTGTCTT Num.seqs=3 Similarity=0.925926
 5 CTTTGT-CTTTGT-
 Rev.of_GCF_001315065.1_ASM131506v1_genomic.fna_4:107347-107395
 Satlength=49 Nr of Repeats=4 RepeatLength=12 seed=AAGGATAAAG Num.seqs=4
 Similarity=0.925926 4
 CCTTGT-CTTTAT-
 GCF_001591585.1_ASM159158v1_genomic.fna_33:29459-29615 Satlength=157 Nr
 of Repeats=13 RepeatLength=12 seed=TTCTTTATCT Num.seqs=13
 Similarity=1.000000 4
 CTATTT-CTTTAT-

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Consensus:

CTTTtTcTtTtT

>Bacillus_Fam_18_52_13 Nr. of seq. 13 Alignment length(with gaps) = 57
 Alignment score = 0.612086
 GCF_001712755.1_ASM171275v1_genomic.fna_1:340959-341167 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=GTTTCATGAGT Num.seqs=4
 Similarity=0.827044
 0 -GTTTCATGAGTAAGTAAAAAGGAGAA-AAAT-TG--ATTTATAGTAACTCATAGAGA
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_34:211464-211828
 Satlength=365 Nr of Repeats=6 RepeatLength=52 seed=TTTTACTTAC Num.seqs=5
 Similarity=0.800000 18 -
 GTTCATGAGTAAGTAAAAAAGTGAA-AATG-AG--AAATTTAGTAACTCATAGAGG
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_34:282789-283049
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CTTACTCATG Num.seqs=5
 Similarity=0.953846 65 -
 GTTCATGAGTAAGTAAAAAAG-GAA-AAAGAAG--AAATATAGTAACTCATAAAGG
 GCF_001712755.1_ASM171275v1_genomic.fna_2:181356-181770 Satlength=415 Nr
 of Repeats=8 RepeatLength=52 seed=GGTTCATGAG Num.seqs=7
 Similarity=0.877900
 0 GGTTCATGAGTAAGTAAAAATG-NAAGAAAT-CG--CGATTTAGTGACTCATA-ATA
 GCF_001712755.1_ASM171275v1_genomic.fna_2:298439-299011 Satlength=573 Nr
 of Repeats=11 RepeatLength=52 seed=TACTCATAAG Num.seqs=11
 Similarity=0.876457 40
 -GTTTCATGAGTAAGTAAAATAG-CAA-AAANATG-AAAA-ATGGTTACTCATAAGGA
 GCF_001712755.1_ASM171275v1_genomic.fna_33:281199-281458 Satlength=260 Nr
 of Repeats=5 RepeatLength=52 seed=TTGGTTACTC Num.seqs=4
 Similarity=0.829060 87
 -CTTCATGAGTATGTACAAAAG-CAA-AAACATG-ATAA-TTGGTTACTCATAAGGG
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_9:99562-99924
 Satlength=363 Nr of Repeats=7 RepeatLength=52 seed=GTAAGTTATT Num.seqs=5
 Similarity=0.958974 43
 -GTTTCATGAGTAAGTAAAAAAG-CAA-AAAGATG-AAAA-TAACTTACTCATAGGAG

Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_9:90464-91454
 Satlength=991 Nr of Repeats=5 RepeatLength=52 seed=TTTGCTGTTT Num.seqs=3
 Similarity=0.888889 77
 -GTTTCATGAGTAAGTAAAACAG-CAA-AAATAAG-AAAA-AAGGTNCCGCATGAAGG
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_33:181107-181419
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=ACTTACTCAT Num.seqs=6
 Similarity=0.941880 118 -
 GTTCATGAGTAAGTAAAACAG-CAA-AAAGAAG-CAAA-TAGGTTACTCATGAGTG
 GCF_001712755.1_ASM171275v1_genomic.fna_5:85395-85810 Satlength=416 Nr of
 Repeats=8 RepeatLength=52 seed=TAATCATAA Num.seqs=7 Similarity=0.934066
 91 -GTTTCATGAGTAAGTAAAACAG-CGA-GAATCTG--AAACTTAGTAACTCATAAGAG
 GCF_001712755.1_ASM171275v1_genomic.fna_11:53806-54274 Satlength=469 Nr
 of Repeats=9 RepeatLength=52 seed=ATGAGTAAAGT Num.seqs=9
 Similarity=0.906695
 108 -GTTTCATGAGTAAGTAAAAGAG-CAN-GAATCCG--AAATATAGTTCCTCATAAAGG
 GCF_001712755.1_ASM171275v1_genomic.fna_13:154313-154676 Satlength=364 Nr
 of Repeats=7 RepeatLength=52 seed=TACTTACTCA Num.seqs=6
 Similarity=0.928205 140
 -GCTCATGAGTAAGTAAAACAG-CAA-AAATCAGAGAAA--TACTTACTCATAACAG
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_35:106552-106864
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=ACTTACTCAT Num.seqs=6
 Similarity=0.886792 170 -
 GTTCATGAGTAAGTAAAACAG-TAA-AAAGAAG-GAAA-GTACTTACTCATAAAGG

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Consensus:

GTTCATGAGTAAGTAAAAnAGcAAAAAnanGnAAAntagTtACTCATAaagg

>Bacillus_Fam_19_53_13 Nr. of seq. 13 Alignment length(with gaps) = 57
 Alignment score = 0.601589
 GCF_000708755.2_ASM70875v2_genomic.fna_1:435766-436081 Satlength=316 Nr
 of Repeats=6 RepeatLength=53 seed=TGCTGCCACT Num.seqs=5
 Similarity=0.904402
 0 TGCTGCCACTTTTCATCGGAAG--AGGAACCTCATTTGTGGCGTTATTC--GAGGTAG
 GCF_000709935.2_ASM70993v2_genomic.fna_1:450592-450857 Satlength=266 Nr
 of Repeats=5 RepeatLength=53 seed=TTGTGGCGT Num.seqs=5
 Similarity=0.924528
 31 TGCTGCCACTTTTCATCGGAAG--AGGAACCTCATTTGTGGCGTTATTC--GAGGTAG
 Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:1471847-1472112
 Satlength=266 Nr of Repeats=5 RepeatLength=53 seed=ACCACTCTGG Num.seqs=5
 Similarity=0.869182 4
 TGGTACCACTTTTATCGGAAG--TTGATCCACATTAGTGGCGTCATTC--GCCAGAG
 Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_5:422395-422607
 Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=GAATGACGCC Num.seqs=4
 Similarity=0.882600 46
 TGGTGCCACTTTAATCGGAAG--TTGATCCACATTGTGGCGTCATTC--TCCAGAG
 GCF_000709935.2_ASM70993v2_genomic.fna_15:156751-157015 Satlength=265 Nr
 of Repeats=5 RepeatLength=53 seed=CTCATTTGTG Num.seqs=4
 Similarity=0.899371
 27 TGCTGCCACTTTTATCTGAGG--TGAATCCTCATTTGTGGCGCCATTC--GCCCCGAG
 Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_6:281885-282097
 Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=CGCCACAAAC Num.seqs=4

Similarity=0.890985 40
 TGCTGCCACTTTT-CATGT-GAAAGCATCCATGTTTGTGGCGTCATTC-CCC-GTAG
 Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_15:188408-188619
 Satlength=212 Nr of Repeats=4 RepeatLength=53 seed=CGCCACAAAC Num.seqs=3
 Similarity=0.899371 40
 TGCCGCCACTTTT-CATGT-GAAAGCATCCATGTTTGTGGCGTCATTC-CCC-GTAG
 GCF_000708755.2_ASM70875v2_genomic.fna_22:121820-122085 Satlength=266 Nr
 of Repeats=5 RepeatLength=53 seed=TGGCGTCATT Num.seqs=5
 Similarity=0.899371
 88 TGCTGCCACTTTTGCCGGA-G-AAGGGTCTTGTGTTGTGGCGTCATTC-CGC-GAAG
 GCF_000709935.2_ASM70993v2_genomic.fna_24:232406-232777 Satlength=372 Nr
 of Repeats=7 RepeatLength=53 seed=TGGCGTCATT Num.seqs=7
 Similarity=0.901767
 88 TGCTGCCACTTTTGCCAGA-G-AAGGGTCTNGTTTGTGGCGTCATTC-CGC-GTAG
 GCF_000709935.2_ASM70993v2_genomic.fna_1:491832-492044 Satlength=213 Nr
 of Repeats=4 RepeatLength=53 seed=ATCCTAGTTT Num.seqs=4
 Similarity=0.809671
 77 TGGTGCCACTTTTATCGTA-G-TTGGATCCTAGTTTGTGGCGTCATTC--GCTGTAG
 Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_5:571905-572276
 Satlength=372 Nr of Repeats=7 RepeatLength=53 seed=ACGAATGACG Num.seqs=7
 Similarity=0.841869 101
 TGCCGCCACTTTTACCAGA-G-ATGGATGATGGTTAGTGGCGTCATTC--GTTGTAG
 GCF_000709935.2_ASM70993v2_genomic.fna_4:195544-195756 Satlength=213 Nr
 of Repeats=4 RepeatLength=53 seed=CCACTTTTTC Num.seqs=4
 Similarity=0.895178
 111 TGACGCCACTTTTTCCAGT-G-ATGGATCCTCATTTGTGGCGTCATTCA-GC-TTAG
 Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_15:32457-32775
 Satlength=319 Nr of Repeats=5 RepeatLength=53 seed=CACTACCGCG Num.seqs=4
 Similarity=0.756813 161
 TGGCGCCACTTTTGCCTTT-G-ATGAATGCTCATTTGTGGCGTCATTC--GCGGTAG

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 Consensus:

TGctGCCACTTTtacCnGaGatGgATcCtcaTTTGTGGCGTCATTCgcngtAG

>Bacillus_Fam_20_52_13 Nr. of seq. 13 Alignment length(with gaps) = 53
 Alignment score = 0.740364
 GCF_000175075.1_ASM17507v1_genomic.fna_7:33338-33546 Satlength=209 Nr of
 Repeats=4 RepeatLength=52 seed=ATGAAGACCT Num.seqs=4 Similarity=0.867521
 0 ATGAAGACCTGAGTGACCAGGAAAAAGGAGAAGAGATGTCCTCATC-GCCGTG
 GCF_000175075.1_ASM17507v1_genomic.fna_34:118251-118459 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=AGTCCTCATA Num.seqs=4
 Similarity=0.910256
 36 ATGAAGACCTGAGTGACGAGGAAAAAGGAGAGAGAAGTCCTCATA-GCGGTG
 GCF_000175075.1_ASM17507v1_genomic.fna_36:211307-211515 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=TCAGTGACGA Num.seqs=4
 Similarity=0.854701
 9 ATGAAGACCTCAGTGACGAGGAAAAAGGACGAGAGACGTCCTCATC-GCCGTG
 GCF_000175075.1_ASM17507v1_genomic.fna_36:173392-173704 Satlength=313 Nr
 of Repeats=6 RepeatLength=52 seed=GGTATGAAGA Num.seqs=6
 Similarity=0.865199
 48 -TGAAGACCTGAGTGACAAGGAAAACGGAGAAGAGAAGTCCTCATCGGCGGTA

Rev.of_GCF_000175075.1_ASM17507v1_genomic.fna_29:100527-100736
 Satlength=210 Nr of Repeats=4 RepeatLength=52 seed=GGTCTTCATA Num.seqs=3
 Similarity=0.880342 9
 ATGAAGACCTCAGTGGCAAAGAAAAAGGAGAAGAGAGGTTCTCATC-GCCGTT
 GCF_000175075.1_ASM17507v1_genomic.fna_39:32383-32643 Satlength=261 Nr of
 Repeats=5 RepeatLength=52 seed=GTTATGAAGA Num.seqs=5 Similarity=0.902564
 49 ATGAAGACNCCAGTGACAAGGAAAAAGGAGGAGAGAAGTCTTCATC-GCTGTT
 GCF_000175075.1_ASM17507v1_genomic.fna_42:230894-231206 Satlength=313 Nr
 of Repeats=5 RepeatLength=52 seed=GTGATGAAGA Num.seqs=4
 Similarity=0.860587
 49 ATGAAGACATGAGTGACGAGGAAAAAGGAATAGAGGAGTCCTCATG-GTTGTG
 Rev.of_GCF_000175075.1_ASM17507v1_genomic.fna_31:61128-61440
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TCACTGATGT Num.seqs=6
 Similarity=0.900855 16
 ATGAAGACATCAGTGACGGGAAATTAGGAGGAGAGAGGTCCTCATC-GGTGTT
 GCF_000175075.1_ASM17507v1_genomic.fna_32:122785-122993 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=CGTTATGAAG Num.seqs=4
 Similarity=0.841880
 48 ATGAAGACATCAGTGACGAGAAATTAGGAGGAGAGAAGTCCTCATT-AGCGTT
 GCF_000175075.1_ASM17507v1_genomic.fna_32:237136-237500 Satlength=365 Nr
 of Repeats=7 RepeatLength=52 seed=CCGTTATGAA Num.seqs=7
 Similarity=0.931624
 99 ATGAAGACATCAGTGACGAGAAATCAGGAGGAGAGATGTCCTCATC-ACCGTT
 GCF_000175075.1_ASM17507v1_genomic.fna_34:65970-66178 Satlength=209 Nr of
 Repeats=4 RepeatLength=52 seed=GTTATGAAGA Num.seqs=4 Similarity=0.876068
 49 ATGAAGACTTCAGTGACGAAGAATTAGGAGGAGAAAAGGTCCTCATC-GCCGTT
 GCF_000175075.1_ASM17507v1_genomic.fna_39:143077-143336 Satlength=260 Nr
 of Repeats=5 RepeatLength=52 seed=GTCCTCATCG Num.seqs=4
 Similarity=0.910256
 37 ATGAAGACCTCAGTGACGAAAAATCAGGAGGAGAGAAGTCCTCATC-GCCCGT
 GCF_000175075.1_ASM17507v1_genomic.fna_42:276011-276219 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=GAGAGAAGTC Num.seqs=4
 Similarity=0.846154
 82 ATGAAGACATCAGTGACGAGAAATCAGGAGGAGAGAAGTCCTCATC-GGCCGT

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Consensus:

ATGAAGACnTcAGTGACgAggAAaaAGGAGgAGAGAAgTCCTCATcGccGTt

>Bacillus_Fam_21_36_13 Nr. of seq. 13 Alignment length(with gaps) = 36
 Alignment score = 0.755935
 GCF_000007825.1_ASM782v1_genomic.fna_1:4360738-4360990 Satlength=253 Nr
 of Repeats=7 RepeatLength=36 seed=TGTTATCCAT Num.seqs=7
 Similarity=0.827160
 0 TGTTATCCATAATCGGCATTATATTCGGCGGTTGGT
 Rev.of_GCF_000299035.1_ASM29903v1_genomic.fna_1:106604-107612
 Satlength=1009 Nr of Repeats=28 RepeatLength=36 seed=ATGATGGATA
 Num.seqs=28 Similarity=0.959436
 13 TATTATCCATCATTGGCATCATATTCGGCATTTGGT
 GCF_000712615.1_ASM71261v1_genomic.fna_1:665208-666336 Satlength=1129 Nr
 of Repeats=27 RepeatLength=36 seed=TTATCCATCA Num.seqs=26
 Similarity=0.882051 38
 TATTATCCATCATTGGCATTATGTTTGGCATTTGGT

GCF_000496285.1_ASM49628v1_genomic.fna_1:1627516-1628017 Satlength=502 Nr of Repeats=11 RepeatLength=36 seed=GGCATCATAT Num.seqs=10
 Similarity=0.912757 14
 TGTTATCCATAATCGGCATCATATTCGGCATTTGAT
 GCF_000831065.1_ASM83106v1_genomic.fna_1:4140717-4141077 Satlength=361 Nr of Repeats=10 RepeatLength=36 seed=TTGTTATCCA Num.seqs=10
 Similarity=0.897942 35
 TGTTATCCATAATTCGGCATCATATTCGGCATTTGAT
 Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:459960-460176
 Satlength=217 Nr of Repeats=6 RepeatLength=36 seed=ATAATGGATA Num.seqs=6
 Similarity=0.935802 49
 TGTTATCCATTATTGGCATCATGTTTGGCATTTGGT
 Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:1527851-1528355
 Satlength=505 Nr of Repeats=14 RepeatLength=36 seed=ATAATGGATA
 Num.seqs=14 Similarity=0.853073
 49 TGTTATCCATTATCGGCATCATGTTTGGCATTTGAT
 Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_1:182266-182692
 Satlength=427 Nr of Repeats=8 RepeatLength=36 seed=AATATGATGC Num.seqs=6
 Similarity=0.859259 61
 TGTTATCCATTATCGGCATCATATTTGGCATTTGAT
 GCF_000007845.1_ASM784v1_genomic.fna_1:4233572-4233860 Satlength=289 Nr of Repeats=5 RepeatLength=36 seed=GGTGGTTGAT Num.seqs=4
 Similarity=0.981481
 26 TGTTATCCATGATTGGCATAATGTTTGGTGGTTGAT
 GCF_000008505.1_ASM850v1_genomic.fna_1:4223082-4223442 Satlength=361 Nr of Repeats=6 RepeatLength=36 seed=GGTGGTTGAT Num.seqs=4
 Similarity=0.888889
 26 TATTATCCATGATCGGCATAATGTTTGGTGGTTGAT
 Rev.of_GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_2:421558-421882 Satlength=325 Nr of Repeats=9 RepeatLength=36 seed=TGGATAACAA
 Num.seqs=9 Similarity=0.842593 45
 TGTTATCCATAATTCGGCATGATGTTTGGTGGTTGAT
 GCF_000017425.1_ASM1742v1_genomic.fna_1:3190001-3190505 Satlength=505 Nr of Repeats=14 RepeatLength=36 seed=GATTATTTTC Num.seqs=14
 Similarity=0.928775 33
 TATTTTCCGTCATCGGCATAATGTTTGGCATTTGGAT
 Rev.of_GCF_000712595.1_ASM71259v1_genomic.fna_7:58-238 Satlength=181 Nr of Repeats=5 RepeatLength=36 seed=CCGATGCCAA Num.seqs=5
 Similarity=0.933333
 34 TATCCCCATCATTTGGCATTACATTTGGCATCGGGT

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Consensus:

TgTTATCCATnATtGGCATnATgTTtGGcatTTGaT

>Bacillus_Fam_22_53_12 Nr. of seq. 12 Alignment length(with gaps) = 56

Alignment score = 0.655032

GCF_002019665.1_ASM201966v1_genomic.fna_1:26343-26811 Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=GTTCCCTCTA Num.seqs=9 Similarity=0.864672

0 GTTCCCTCTATTT-TCGTTTTTC-AC-GATTTTCAGGGCACGAT-TACCCCTTGATC

Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:250907-251218

Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=GATCAAGGCG Num.seqs=5

Similarity=0.911950 0
 GTTCCCTCTATTC-TCTTTTTTCGAA-G-TTTCAGGGCACGAT-GACGCCTTGATC
 GCF_002019665.1_ASM201966v1_genomic.fna_1:2689409-2689721 Satlength=313
 Nr of Repeats=6 RepeatLength=52 seed=TTGATCGTTA Num.seqs=6
 Similarity=0.943590 46
 GTTACCTCTATTT-TCACTTTCC-CC-AATTTGAGGGCACGAT-TAGACCTTGATC
 Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:1816049-1816621
 Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=AAAAGAGAGG
 Num.seqs=11 Similarity=0.875991
 14 GTTCCCTCTCTTT-TNGTTTTTG-GC-AATTTGAGGGCACGATCGGCGCC-TCATC
 Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:422515-422775
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=ATCGTGCCCT Num.seqs=5
 Similarity=0.969231 40
 GTTCCCTCTTTTTCTCGTTTTTC-GG--TTTTGAGGGCACGAT-TACGCTCTGATC
 Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:584690-585472
 Satlength=783 Nr of Repeats=15 RepeatLength=52 seed=CCCTCAAAAA
 Num.seqs=11 Similarity=0.894639
 86 GTTCCCTCTTTTTCTCTTTTTTC-GT--TTTTGAGGGCACGAT-CACGCGCTGATC
 Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:1391349-1391817
 Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=GGGAACGATC Num.seqs=9
 Similarity=0.933048 58
 GTTCCCCCTTTTTCTCGTTTTTC-GT--TTTTGAGGGAACGAT-TATGCTCTGATC
 Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:1774595-1775572
 Satlength=978 Nr of Repeats=11 RepeatLength=52 seed=AAAAGAGGGA
 Num.seqs=9 Similarity=0.883191
 64 GTTCCCTCTTTTTCTCATTTTTTC-AT--TTTTGAGGGCACGAT-CACGCTCCGATC
 Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:1834884-1835195
 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=GAACGATTAG Num.seqs=5
 Similarity=0.894872 56
 GTTCCACCTATTTCTCTTTTTTC-GT--TTTTGAGGGCACGAT-CACGCGCTAATC
 GCF_002019665.1_ASM201966v1_genomic.fna_1:3150058-3150578 Satlength=521
 Nr of Repeats=10 RepeatLength=52 seed=GTTTTGAGGG Num.seqs=10
 Similarity=0.849573 76
 GTTCCCTCTATTTCTGGTTTTTC-GG--TTTTGAGGGCACGAT-CACGCTNCGATC
 Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:1307617-1308294
 Satlength=678 Nr of Repeats=13 RepeatLength=52 seed=AAGAAAATAG
 Num.seqs=12 Similarity=0.815371
 69 GTTCCCTCTATTT-TC-TTTTTG-GGNGTTTTGAGGGCACGAT-TGCGCTCTGATC
 GCF_002019665.1_ASM201966v1_genomic.fna_1:3411347-3411970 Satlength=624
 Nr of Repeats=11 RepeatLength=52 seed=TTTGCTTTTT Num.seqs=9
 Similarity=0.841880 114
 GTTCCCTCTATTT-GC-TTTTTTC-GGCTTTTTGAGGGNACGAT-TACGCCCTGATC

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Consensus:

GTTCCCTCTaTTTcTCnTTTTTCgnntTTTgAGGGCACGATtACGCncTGATC

>Bacillus_Fam_23_52_12 Nr. of seq. 12 Alignment length(with gaps) = 55
 Alignment score = 0.736639
 GCF_000169195.2_ASM16919v2_genomic.fna_1:334744-335940 Satlength=1197 Nr
 of Repeats=21 RepeatLength=52 seed=TTTTGTCCCTT Num.seqs=19
 Similarity=0.483296 0
 T---TTTGTCCTTTTGACNNNNTNAAAAAGACATTTTCGAGCCCNNGNGCATC-CG

GCF_000169195.2_ASM16919v2_genomic.fna_1:137480-138203 Satlength=724 Nr of Repeats=13 RepeatLength=52 seed=TTTGTCCCTTT Num.seqs=11
Similarity=0.651623 1
T---TTTGTCCCTTTTGACAGCTTCAAAAGGACATTTTCGNGCCCAGATACAGCTTG
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:2466680-2467304
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=CAAAAGGACA
Num.seqs=12 Similarity=0.709783
13 T---TTTGTCCCTTTTGACAGCTTCAAAAGGACATTTTCGGGCCCGGATGCAGCTCC
GCF_000217835.1_ASM21783v1_genomic.fna_1:2234859-2235431 Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=TTTGTCCCTTT Num.seqs=11
Similarity=0.715600 53
T---TTTGTCCCTTTTGACAGCTTCAAAAGGACATTTTCGAGCCCGGATGCAGCTCN
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:979431-979847
Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=TGTCCTTTTG Num.seqs=8
Similarity=0.771062 30
T---TTTGTCCCTTTTGACAGGTTCAAAAGGACATTTTCGTTCCTCCGGATGCNGCTCG
GCF_000217835.1_ASM21783v1_genomic.fna_1:335197-336033 Satlength=837 Nr of Repeats=14 RepeatLength=52 seed=TTGTCCCTTT Num.seqs=9
Similarity=0.777778
54 T---TTTGTCCCTTTTGACAGGATCAAAAGGACATTTTCGTTCCTCCGGATGCNGCAGC
GCF_000832905.1_ASM83290v1_genomic.fna_1:2697159-2697888 Satlength=730 Nr of Repeats=14 RepeatLength=52 seed=TCAAAAGGAC Num.seqs=13
Similarity=0.784309 71
T---TTTGTCCCTTTTGACAGGATCAAAAGGACATTTTCGTTCCTCCGGATGCNGCAGC
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:320698-321219
Satlength=522 Nr of Repeats=10 RepeatLength=52 seed=CAAAAGGACA
Num.seqs=9 Similarity=0.800570
13 T---TTTGTCCCTTTTGACGGNTTCAAAAAGACATTTTCGGGCCCGGATGCANCGTG
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:1299605-1300125
Satlength=521 Nr of Repeats=9 RepeatLength=52 seed=ATGTCTTTTT Num.seqs=8
Similarity=0.791217 31 T--
-TTTGTCTTTTTGACGGCTTCAAAAGGACATTTTCGGGCCCGGATGCAACGTG
GCF_000169195.2_ASM16919v2_genomic.fna_1:2593824-2594862 Satlength=1039
Nr of Repeats=20 RepeatLength=52 seed=AAAAAGACAT Num.seqs=18
Similarity=0.816323 21
T---TTTGTCTTTTTGGCAGGTTCAAAAAGACATTTTCGGGCCCGGATGCAGCGTG
GCF_000217835.1_ASM21783v1_genomic.fna_1:921872-922184 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TGTTTTGTCC Num.seqs=6
Similarity=0.866667
50 T---TTTGTCCCTTTGTGCGCTTCAAAAAGACATTTTCGAGCCCGGATGCAACATG
Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:908745-908953
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TCAAAAGGAC Num.seqs=4
Similarity=0.655136 14
TCCTTTTGTCCCTTTTGACGGCTTCAAAAAGACATTTTCGGGCC--AAGCGNCA-G

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Consensus:

TTTTGTCCCTTTTGACaGctTCAAAAgGACATTTTCGngCCCGATGCagCncG

>Bacillus_Fam_24_21_12 Nr. of seq. 12 Alignment length(with gaps) = 23
Alignment score = 0.627141

GCF_000307875.1_BABA1.0_genomic.fna_58:10690-10774 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=CGCTCATTGA Num.seqs=4 Similarity=0.638889
0 CGCTCATTG-ACAGC-TTAAATT
Rev.of_GCF_000307875.1_BABA1.0_genomic.fna_137:4596-4680 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATGAGCGAAT Num.seqs=4
Similarity=0.703704
7 CGCTCATTGAACA-T-CGAAATT
GCF_000508325.1_BAVI_1_genomic.fna_122:15786-15870 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=AATTCGCCCA Num.seqs=4 Similarity=0.642677
17 CGCCCATAGAACA-C-TGAAATT
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_72:12480-12564 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATGGGCGAAT Num.seqs=4
Similarity=0.613636 28
CGCCCATTTGAAC-T-TGAAATT
GCF_001591445.1_ASM159144v1_genomic.fna_17:116034-116118 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCTGAT Num.seqs=4
Similarity=0.820106
18 CGCTGATAGAACC-T-GGAAATT
GCF_000508325.1_BAVI_1_genomic.fna_85:26959-27124 Satlength=166 Nr of Repeats=4 RepeatLength=21 seed=GAAAATTCGC Num.seqs=3 Similarity=0.830688
14 CGCCCATTTGAACC-C-GAAAATT
GCF_000508325.1_BAVI_1_genomic.fna_92:110555-110639 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCCCAT Num.seqs=4 Similarity=0.512731
18 CGCCCATTTGAANG-C-TAAAATT
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_58:4850-4934 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=AATGGGCGAA Num.seqs=4
Similarity=0.625604 29
CGCCCATTTGAACG-T-CAAAATT
GCF_000508325.1_BAVI_1_genomic.fna_87:23723-23807 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=AATTCGCCCA Num.seqs=4 Similarity=0.717172
39 CGCCCATTTGAACC-TGCAAAATT
Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_105:66812-66896 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATGGGCGAAT Num.seqs=4
Similarity=0.589372 27
CGCCCATTTGAAAC-CC-GAAATT
Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_180:2145-2229 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATGGGCGAAT Num.seqs=4
Similarity=0.671958
27 CGCCCATTTGAACA-CC-NAAATT
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_60:47968-48052 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATGGGCGAAT Num.seqs=4
Similarity=0.664141 27
CGCCCATTTGAATA-CC-AAAATT

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Consensus:

CGCcATTGAACncnnAAATT

>Bacillus_Fam_25_20_12 Nr. of seq. 12 Alignment length(with gaps) = 21
Alignment score = 0.723545
GCF_000813125.1_ASM81312v1_genomic.fna_20:18031-18110 Satlength=80 Nr of Repeats=4 RepeatLength=20 seed=TTTTTATAGC Num.seqs=3 Similarity=0.656566
0 TTTTTAT-AGCGANAATTTCT

Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_16:40325-40425
Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=CGCTATAAAA Num.seqs=5
Similarity=0.563636 11
NTTTTAT-AGCGAAAATTTNA
GCF_001315165.1_ASM131516v1_genomic.fna_27:5637-5717 Satlength=81 Nr of
Repeats=4 RepeatLength=20 seed=TTTTATAGCG Num.seqs=4 Similarity=0.666667
21 TTTTAT-AGCGAAAATTTCA
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_79:1018-1119 Satlength=102
Nr of Repeats=5 RepeatLength=20 seed=GCTATAAAAA Num.seqs=4
Similarity=0.711640 30
TTTTTAT-AGCGAAAAGTTTA
GCF_000813125.1_ASM81312v1_genomic.fna_39:13920-14020 Satlength=101 Nr of
Repeats=4 RepeatLength=20 seed=TTTTTATAGC Num.seqs=3 Similarity=0.611111
0 TTTTTAT-AGCGAAAATTCAN
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_53:15227-15327
Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TCGCTATAAA Num.seqs=5
Similarity=0.621739 12
TTTTTAT-AGCGAAATTTTAN
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_73:60683-60763 Satlength=81
Nr of Repeats=4 RepeatLength=20 seed=TTTCGCTATAA Num.seqs=4
Similarity=0.578283 13
TTTTTAT-AGCGAAAATCTAG
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_10:70726-70826
Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TCGCTATAAA Num.seqs=5
Similarity=0.593333 32
TTTTTAT-AGCGAAAATCTNG
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_15:43524-43604
Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=TTTCGCTATA Num.seqs=4
Similarity=0.667989 14
TTTTTAT-AGCGAAAATCTAA
Rev.of_GCF_001591465.1_ASM159146v1_genomic.fna_6:87823-87925
Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=TCGCTCATAA Num.seqs=3
Similarity=0.606061 12
-TTTTATGAGCGAAAATTTAN
GCF_000813125.1_ASM81312v1_genomic.fna_65:30212-30291 Satlength=80 Nr of
Repeats=4 RepeatLength=20 seed=TTATAGCGAA Num.seqs=3 Similarity=0.644444
3 ATATTAT-AGCGAAAATNTAN
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_16:47524-47624
Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TTTTCGCTAT Num.seqs=5
Similarity=0.544000 15
TTTNTAT-AGCGAAAANAAAN

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Consensus:

tTTTTATAGCGAAAATtTan

>Bacillus_Fam_26_53_11 Nr. of seq. 11 Alignment length(with gaps) = 58
Alignment score = 0.666458
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:484476-484813 Satlength=338 Nr of
Repeats=7 RepeatLength=53 seed=GGTTAGTCGA Num.seqs=5 Similarity=0.869182
0 GGTTAGTCGACATGATCATGGGCAAAAAAGGTCGAGAACCTGTCGATGAGG---AC--

BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:427050-427315 Satlength=266 Nr of Repeats=5 RepeatLength=53 seed=CATGTCGATG Num.seqs=5 Similarity=0.854088
 38 GGTGTCGACATGATCTTGGGCCAAAAAGGACGAGAACATGTCGATGAAG---GC--
 Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:417351-418025
 Satlength=675 Nr of Repeats=12 RepeatLength=53 seed=CTCGACCTTT
 Num.seqs=10 Similarity=0.911111
 89 AGTTGGTCGACATGATCATGGGTAAAAAAGGTCGAGATCATGTCGATGAAG---GC--
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:150308-150520 Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=CGATGAAGGA Num.seqs=4 Similarity=0.861635
 42 -GTTGGTCGACATGATCAAGAGCAAAAAAGGTCAAGAACCTGTCGATGAAG---GAG-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:327893-328213 Satlength=321 Nr of Repeats=6 RepeatLength=53 seed=TGTCGATGAA Num.seqs=4 Similarity=0.928721
 92 -GCTGGTCGACATGAACATGAGTAAAAAAGGCCAAGAACCTGTCGATGAAG---GAA-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:528815-529185 Satlength=371 Nr of Repeats=7 RepeatLength=53 seed=CTGTCGATGA Num.seqs=6 Similarity=0.921174
 144 -GCTGGTCGACATGATCATGAGTAAAAAAGGTCAAGAACCTGTCGATGAAG---GAA-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_16:65979-66245 Satlength=267 Nr of Repeats=5 RepeatLength=53 seed=GACATGATCA Num.seqs=4 Similarity=0.928721
 60 -GCTGGTCGACATGATCATGGGCCAAAAAAGCTGAAGAACCTGTCGATGAAG---GAA-
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:496997-497526 Satlength=530 Nr of Repeats=10 RepeatLength=53 seed=GACATGATCA Num.seqs=9
 Similarity=0.889588 8
 GGTAGTCGACATGATCACGAGAAAAAAGGGTAAGAACCTGTCGATAAAGA--G---
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_10:92314-92960 Satlength=647 Nr of Repeats=12 RepeatLength=53 seed=GTGGTCGACA Num.seqs=11
 Similarity=0.828931 1
 AG-TGGTCGACATGATCAGGANGAAAAAAGGCNGAGAACCTGTCGATGAAG--GGC--
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:157629-157946 Satlength=318 Nr of Repeats=6 RepeatLength=53 seed=AGAACATGTC Num.seqs=5 Similarity=0.904402
 32 --ATGGACGACATGATCATGGGCCAAAAAAGTCAAGAACATGTCGATGA-G--TGAGT
 BACILLUS_PSEUDALCALIPHILUS_genomic.fna_4:6835-7366 Satlength=532 Nr of Repeats=10 RepeatLength=53 seed=TGGTCGACAT Num.seqs=9
 Similarity=0.831962
 3 CGTTGGTCGACATGATGTAGGTTGAAAAAGGGCCGGATCATGTCGATGA-G-AAG---

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Consensus:

nGtTGGTCGACATGATCAtGgGnAAAAAAGGncaAGAACcTGTTCGATGAaGGn

>Bacillus_Fam_27_39_11 Nr. of seq. 11 Alignment length(with gaps) = 40
 Alignment score = 0.799394
 GCF_000007825.1_ASM782v1_genomic.fna_1:4361056-4361329 Satlength=274 Nr of Repeats=7 RepeatLength=39 seed=CTACATTTTC Num.seqs=7
 Similarity=0.810298
 0 CTACATTTTCTTTCTTCACTTGCGGCGATACTATATT-TC
 GCF_000007845.1_ASM784v1_genomic.fna_1:4233977-4234409 Satlength=433 Nr of Repeats=7 RepeatLength=39 seed=TTTTCTTTCT Num.seqs=6
 Similarity=0.920228
 5 CTACATTTTCTTTCTTCACTTGCGGTGATACTATATT-TC
 GCF_000008505.1_ASM850v1_genomic.fna_1:4223515-4223749 Satlength=235 Nr of Repeats=6 RepeatLength=39 seed=CTACATTTTC Num.seqs=6
 Similarity=0.872365
 0 CTACATTTTCTTTCTTTACTTGCGGTGATACTATATT-TC

GCF_000496285.1_ASM49628v1_genomic.fna_1:1628212-1628485 Satlength=274 Nr of Repeats=7 RepeatLength=39 seed=ACATTTTCTT Num.seqs=7
 Similarity=0.863248 2
 CTACATTTTCTTTCTTTACTTGCGGCGATACTATGTT-TC
 Rev.of_GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_2:421236-421470 Satlength=235 Nr of Repeats=6 RepeatLength=39 seed=ATAGTGTCAC
 Num.seqs=6 Similarity=0.872365 34
 CTACATTTTCTTTCTTTACTTGTTGGTGACACTATGTT-TC
 Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_1:181927-182083
 Satlength=157 Nr of Repeats=4 RepeatLength=39 seed=ATAGTATCAC Num.seqs=4
 Similarity=0.914530 34
 CTACATTTTCTTTCTTTACTTGTTGGTGATACTATGTT-TC
 Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:459197-459950
 Satlength=754 Nr of Repeats=13 RepeatLength=39 seed=GCAAGTGAAG
 Num.seqs=12 Similarity=1.000000
 23 CTACATTCTCTTTCTTCACTTGCGGCGACACTATATT-CC
 Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:1527503-1527698
 Satlength=196 Nr of Repeats=5 RepeatLength=39 seed=CCGCAAGTGA Num.seqs=5
 Similarity=0.945299 25
 CTACATTNTCTTTCTTCACTTGCGGCGACACTATATT-CC
 GCF_000831065.1_ASM83106v1_genomic.fna_1:4141206-4141440 Satlength=235 Nr of Repeats=6 RepeatLength=39 seed=GACACTATAT Num.seqs=6
 Similarity=0.906553 26
 CTACATTTTCTTTTTTCACTTGCGGCGACACTATATT-TC
 GCF_000161455.1_ASM16145v1_genomic.fna_1:3733849-3734302 Satlength=454 Nr of Repeats=5 RepeatLength=39 seed=TTTTCTTTTT Num.seqs=3
 Similarity=0.749288 5
 TTACATTTTCTTTTTTCATTTGCGGCGCAACTATATT-AC
 GCF_000017425.1_ASM1742v1_genomic.fna_1:3190635-3191025 Satlength=391 Nr of Repeats=10 RepeatLength=39 seed=ATTTTCTTTT Num.seqs=10
 Similarity=0.900475 3
 -TATATTTTCTTTTTTCACTTGTTGGTGCTGCGATATTCTC

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Consensus:

CTACATTTTCTTTcTTcACTTGcGGcGAtACTATaTTtC

>Bacillus_Fam_28_21_11 Nr. of seq. 11 Alignment length(with gaps) = 25
 Alignment score = 0.604364
 GCF_001645685.2_ASM164568v2_genomic.fna_1:3317387-3317534 Satlength=148
 Nr of Repeats=7 RepeatLength=21 seed=TTTACTCGCC Num.seqs=7
 Similarity=0.848828 0
 TTTACTCGCCAATT--CGCG-GGC-
 GCF_001645685.2_ASM164568v2_genomic.fna_1:3318620-3318745 Satlength=126
 Nr of Repeats=6 RepeatLength=21 seed=TTTACTCGCC Num.seqs=5
 Similarity=0.815873 0
 TTTACTCGCCAATT--CGCA-NGC-
 GCF_001645685.2_ASM164568v2_genomic.fna_1:3443422-3443693 Satlength=272
 Nr of Repeats=12 RepeatLength=21 seed=CTTTACTCGC Num.seqs=11
 Similarity=0.826446 20
 TTTACTCGCCAATT--CGAG-TGC-
 GCF_001645685.2_ASM164568v2_genomic.fna_1:3920495-3920579 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=CTCGCCAATT Num.seqs=4

Similarity=0.851852 25
 TTTACTCGCCAATT--CGAG-CAC-
 GCF_001645685.2_ASM164568v2_genomic.fna_1:3972827-3973253 Satlength=427
 Nr of Repeats=9 RepeatLength=21 seed=TTTACTCGCC Num.seqs=6
 Similarity=0.729101 0
 TTTACTCGCCAATT--CG-G-GGNT
 GCF_001645685.2_ASM164568v2_genomic.fna_1:3656001-3656127 Satlength=127
 Nr of Repeats=6 RepeatLength=21 seed=CTCGCCAATT Num.seqs=6
 Similarity=0.856085 4
 TTTACTCGCCAATT-CCG-G-TCG-
 GCF_001645685.2_ASM164568v2_genomic.fna_1:4110462-4110546 Satlength=85 Nr
 of Repeats=4 RepeatLength=21 seed=TTTACTCGCC Num.seqs=4
 Similarity=0.683081 21
 TTTACTCGCCAATT-TCG-G-CGT-
 Rev.of GCF_001645685.2_ASM164568v2_genomic.fna_1:180575-180782
 Satlength=208 Nr of Repeats=6 RepeatLength=21 seed=TGGCGAGTAA Num.seqs=5
 Similarity=0.660606 32
 TTTACTCGCCAATTNTTCG-G-TGN-
 GCF_001645685.2_ASM164568v2_genomic.fna_1:4286180-4286302 Satlength=123
 Nr of Repeats=4 RepeatLength=21 seed=TTTACTCGCC Num.seqs=3
 Similarity=0.647343 0
 TTTACTCGCCAATT--TGNA-CGA-
 GCF_001645685.2_ASM164568v2_genomic.fna_1:4375763-4376192 Satlength=430
 Nr of Repeats=11 RepeatLength=21 seed=TTTACTCGCC Num.seqs=7
 Similarity=0.788600 0
 TTTACTCGCCAATT--TGAG-CNG-
 GCF_001645685.2_ASM164568v2_genomic.fna_1:4377725-4378156 Satlength=432
 Nr of Repeats=11 RepeatLength=21 seed=TTTACTCGCC Num.seqs=7
 Similarity=0.753968 0
 TTTACTCGCCAATT--TNAGNCT--

Consensus:

TTTACTCGCCAATTcGnGngn

>Bacillus_Fam_29_20_11 Nr. of seq. 11 Alignment length(with gaps) = 22
 Alignment score = 0.720386
 GCF_000813125.1_ASM81312v1_genomic.fna_10:26480-26581 Satlength=102 Nr of
 Repeats=4 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3 Similarity=0.676768
 10 ATNTT--CAAATTTTATTGGCG
 GCF_000813125.1_ASM81312v1_genomic.fna_92:129270-129372 Satlength=103 Nr
 of Repeats=5 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3
 Similarity=0.622222
 10 ATTTT--NAAATTTTATTGGCG
 GCF_000813125.1_ASM81312v1_genomic.fna_26:19181-19302 Satlength=122 Nr of
 Repeats=6 RepeatLength=20 seed=TTTATTGGCG Num.seqs=5 Similarity=0.771429
 10 ATATT--CTAATTTTATTGGCG
 GCF_000813125.1_ASM81312v1_genomic.fna_128:14716-14818 Satlength=103 Nr
 of Repeats=5 RepeatLength=20 seed=TTTATTGGCG Num.seqs=3
 Similarity=0.671958
 10 ATATT--TTAATTTTATTGGCG

GCF_000813125.1_ASM81312v1_genomic.fna_40:39070-39170 Satlength=101 Nr of Repeats=4 RepeatLength=20 seed=TTATTGGCGA Num.seqs=3 Similarity=0.688889
 11 ATTTT--CTAATTTTATTGGCG
 Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_54:20708-20789
 Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TCGCCAATAA Num.seqs=3
 Similarity=0.622222 21
 ATTTT--CNAATTTTATTGGCG
 GCF_000813125.1_ASM81312v1_genomic.fna_69:8482-8584 Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=TTATTGGCGA Num.seqs=3 Similarity=0.560606
 11 ANTTT--CANATTTTATTGGCG
 GCF_000813125.1_ASM81312v1_genomic.fna_144:11821-11921 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TTTTATTGGC Num.seqs=5
 Similarity=0.723810
 29 ATTTT--CAGTTTTTATTGGCG
 Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_189:8715-8817 Satlength=103
 Nr of Repeats=5 RepeatLength=20 seed=CGCCAATAAA Num.seqs=3
 Similarity=0.755556 20
 ATAAT--CANATTTTATTGGCG
 GCF_000813125.1_ASM81312v1_genomic.fna_40:72461-72583 Satlength=123 Nr of Repeats=6 RepeatLength=20 seed=TTATTGGCGA Num.seqs=4 Similarity=0.633102
 32 ATAATC--CAAATTTTATTGGCG
 Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_68:108728-108809
 Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=CGCCAATAAA Num.seqs=3
 Similarity=0.666667 19
 ATTTT-TTNCAT-TTATTGGCG

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Consensus:

TTTATTGGCGATtTTcaaAT

>Bacillus_Fam_30_18_11 Nr. of seq. 11 Alignment length(with gaps) = 19
 Alignment score = 0.651675
 GCF_000007825.1_ASM782v1_genomic.fna_1:2602019-2602271 Satlength=253 Nr of Repeats=13 RepeatLength=18 seed=CCTGTTACTC Num.seqs=12
 Similarity=0.975309 0
 CCTGTTACTCCAGTTGGA-
 Rev.of_GCF_000712595.1_ASM71259v1_genomic.fna_10:146400-146544
 Satlength=145 Nr of Repeats=8 RepeatLength=18 seed=GGTCCAACCTG Num.seqs=8
 Similarity=0.928571 2
 CCTGTTGCTCCAGTTGGA-
 GCF_000775975.1_ASM77597v1_genomic.fna_1:2396734-2396859 Satlength=126 Nr of Repeats=7 RepeatLength=18 seed=GGACCCGTTA Num.seqs=6
 Similarity=0.906173 15
 CCGGTTACTCCCGTTGGA-
 GCF_000832605.1_ASM83260v1_genomic.fna_1:3447183-3447381 Satlength=199 Nr of Repeats=11 RepeatLength=18 seed=GTGGACCCG Num.seqs=11
 Similarity=0.935354 30
 CCGGTTACTCCTGTTGGA-
 Rev.of_GCF_001307105.1_ASM130710v1_genomic.fna_16:4592-4880 Satlength=289
 Nr of Repeats=14 RepeatLength=18 seed=CCAACGGGAG Num.seqs=10
 Similarity=0.840329 17
 CCGGTTACTCCCGTTGGG-

Rev.of_GCF_001584325.1_ASM158432v1_genomic.fna_5:37432-37900
 Satlength=469 Nr of Repeats=19 RepeatLength=18 seed=ACCGGAGTAA
 Num.seqs=12 Similarity=0.787347
 14 CCTGTTACTCCGGTT-GAC
 Rev.of_GCF_000305495.1_BacPsy2.0_genomic.fna_162:38-785 Satlength=748 Nr
 of Repeats=21 RepeatLength=18 seed=CAGGAGCAAC Num.seqs=13
 Similarity=0.711651 4
 CCTGTTACTCCTGTTGCT-
 GCF_900096965.1_IMG-
 taxon_2671180223_annotated_assembly_genomic.fna_5:141837-142206
 Satlength=370 Nr of Repeats=20 RepeatLength=18 seed=CCTGTCACTC
 Num.seqs=19 Similarity=0.843621 18
 CCTGTCACTCCNGTTGCT-
 Rev.of_GCF_000831065.1_ASM83106v1_genomic.fna_1:2131967-2132240
 Satlength=274 Nr of Repeats=13 RepeatLength=18 seed=GGAGCAACAG
 Num.seqs=10 Similarity=0.856790
 20 CCTGTAAACCTGTTGCT-
 Rev.of_GCF_000380245.2_ASM38024v2_genomic.fna_12:1413968-1414058
 Satlength=91 Nr of Repeats=5 RepeatLength=18 seed=ACAGGAGTAA Num.seqs=5
 Similarity=0.770000 14
 CCAGTTACTCCTGTCTCA-
 GCF_001307105.1_ASM130710v1_genomic.fna_2:66844-66916 Satlength=73 Nr of
 Repeats=4 RepeatLength=18 seed=TCCTGTGGCA Num.seqs=4 Similarity=0.802469
 26 CCCGTAACCTCCTGTGGCA-

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 Consensus:

CCTGTTACTCCnGTTGga

>Bacillus_Fam_31_51_10 Nr. of seq. 10 Alignment length(with gaps) = 56
 Alignment score = 0.632407
 GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:206605-207962
 Satlength=1358 Nr of Repeats=18 RepeatLength=51 seed=GTTGTCCATT
 Num.seqs=17 Similarity=0.781297 0
 GTTGTCCATTAGAA-GCGNGCTATTGGACANGAATCTGG---CGAATAGTGAAAA-
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:595095-595401
 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=GACAACTTTT Num.seqs=6
 Similarity=0.752621 6
 GTTGTCCAATAGAA-GCGGTCTAATGGACAAGAAACTGG---CGGAAAGCGAAAA-
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_12:6507-6864
 Satlength=358 Nr of Repeats=7 RepeatLength=51 seed=TGTCCATTAG Num.seqs=7
 Similarity=0.750649 29
 GTTGTCCAATAGAA-GCGGTCTAATGGACAAGAATCCGG---TGAAAAGGGAAAA-
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_16:36137-37771
 Satlength=1635 Nr of Repeats=32 RepeatLength=51 seed=GACAACTTTT
 Num.seqs=30 Similarity=0.860404 6
 GTTGTCCAATAGAA-GCGGTCTAATGGACAAGAAT-TCGA--GAAAANGCGAAAA-
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_30:179952-181023
 Satlength=1072 Nr of Repeats=21 RepeatLength=51 seed=TTGTCCATTA
 Num.seqs=21 Similarity=0.886905 30
 GATGTCCAATAGAA-GCAGTCTAATGGACAAGAATCTCG---TAAAAAGCGAAAA-
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_33:32726-35276
 Satlength=2551 Nr of Repeats=50 RepeatLength=51 seed=TTGGACAGCT

Num.seqs=50 Similarity=0.848494 60
 GCTGTCCAATAGAA-GCGGTCTAATGGACAAGAATNTGG---TAAAAAGCGAAAA-
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:535628-535985
 Satlength=358 Nr of Repeats=6 RepeatLength=51 seed=CCAATAGACC Num.seqs=5
 Similarity=0.921569 25 -
 TTGTCCAATAGAA-GAGGTCTATTGGACAAAAATTCGG---TAAAATCCAGAAAG
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_12:28322-28577
 Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=CACCTTCTAT Num.seqs=5
 Similarity=0.932026 68 -
 CTGTCCAATAGAA-GGTGTCTATTGGACAAAAACAGAG---AGAAACGCGAAAAAG
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:525341-525954
 Satlength=614 Nr of Repeats=12 RepeatLength=51 seed=TGTCATTAG
 Num.seqs=11 Similarity=0.773310 29
 GTTGTCCAATAGGAGGCG-TCTAATGGACAAGAATCTAG-TTTTTCAA--GAAAA-
 Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:608592-608898
 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=CAACTTTTCT Num.seqs=6
 Similarity=0.925054 55
 GTTGTCCGATAGGA-GCGTTCTAATGGACAAGAACTGG-ATTTTTAA--GAAAA-

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Consensus:

gtTGTCCAATAGaAGcggTCTAaTGGACAaGAAAtctgGtnaaAagcGAAAA

>Bacillus_Fam_32_52_10 Nr. of seq. 10 Alignment length(with gaps) = 56
 Alignment score = 0.659061
 GCF_001439965.1_ASM143996v1_genomic.fna_95:88322-88842 Satlength=521 Nr
 of Repeats=10 RepeatLength=52 seed=TTTCGTTACC Num.seqs=10
 Similarity=0.717710 0
 TTTCGTTACCCCTGGACACNCGTTTTTCCTCCTTCTCGGTAACCAA--ACGCTCCC--
 GCF_001887185.1_ASM188718v1_genomic.fna_43:14953-15212 Satlength=260 Nr
 of Repeats=5 RepeatLength=52 seed=TTTCGTTACC Num.seqs=4
 Similarity=0.759259
 0 TTTCGTTACCCCTGCACAACCATTTTCCTCCTTCTCGGTAACCAATCACGCTTCC--
 Rev.of_GCF_001439965.1_ASM143996v1_genomic.fna_97:186923-187395
 Satlength=473 Nr of Repeats=8 RepeatLength=52 seed=AAAAAGCGTG Num.seqs=6
 Similarity=0.810256 25
 TTTAGTTACCCCTGCACACGCTTTTTTCTCCTTCTCGGTAATCATT--CGCTCAC--
 GCF_001887185.1_ASM188718v1_genomic.fna_124:9302-9509 Satlength=208 Nr of
 Repeats=4 RepeatLength=52 seed=TTTTCTCCT Num.seqs=3 Similarity=0.871795
 21 TTTTGTTACCGACACACATATTTTCCTCCTTCTCGGTAACCAAT--CACTCTC--
 Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_447:7-267 Satlength=261 Nr
 of Repeats=5 RepeatLength=52 seed=ACCGAGAAGG Num.seqs=5
 Similarity=0.887179 38
 TTTTGTTACCCGACACACATATTTTCCTCCTTCTCGGTAACCAAT--CACTCTC--
 GCF_002009555.1_ASM200955v1_genomic.fna_401:30074-30282 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=CTCCTTCTCG Num.seqs=4
 Similarity=0.897436
 26 TTTTGTTACCAGACACACATATTTTCCTCCTTCTCGGTAACCAAT--CGCTCTC--
 GCF_002009555.1_ASM200955v1_genomic.fna_259:2631-2838 Satlength=208 Nr of
 Repeats=4 RepeatLength=52 seed=CTCCTTCTCG Num.seqs=3 Similarity=0.709402
 26 TTTCGTTACCCGACACACACATTTTCCTCCTTCTCGGTCACCAAT--CGCTCTC--
 Rev.of_GCF_001439965.1_ASM143996v1_genomic.fna_122:142659-143596
 Satlength=938 Nr of Repeats=18 RepeatLength=52 seed=AGAGTTTGAT

Num.seqs=17 Similarity=0.797323
 49 TTTCGTTACCGGGCTCGCGCTATTTCTCCTTCANGGTAATCAAA--CTCT-TC-C
 Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_552:2070-2278
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GGTAACGAAA Num.seqs=4
 Similarity=0.820513 63
 TTTCGTTACCGTGCTCGCGCAATTTTCTCCTTCAAGGTAATCAAT--CGC--TCTC
 Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_138:2615-3236
 Satlength=622 Nr of Repeats=10 RepeatLength=52 seed=GAGAGTTTGA
 Num.seqs=8 Similarity=0.873626
 49 TTGGTTACCGTGCACGCTCATTTTCTCCTTCAAAGGAATCAAA--CTCTCTC--

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Consensus:

TTTcGTTACcggCaCaCncatTTTcCTCCTTctcGGTAAcCAAtCgCTctC

>Bacillus_Fam_33_52_10 Nr. of seq. 10 Alignment length(with gaps) = 55
 Alignment score = 0.634747
 GCF_000177235.2_ASM17723v2_genomic.fna_1:18432-18848 Satlength=417 Nr of
 Repeats=8 RepeatLength=52 seed=GTGTATCATA Num.seqs=8 Similarity=0.638889
 0 GTGTATCATACGAGG-CCAATGACACGCGAGAAAGTA-G-TAGGAACGAAATAAA
 GCF_000177235.2_ASM17723v2_genomic.fna_1:43977-44445 Satlength=469 Nr of
 Repeats=9 RepeatLength=52 seed=AATAAAGTGT Num.seqs=7 Similarity=0.689594
 46 GTGTATCATACGAAG-GCAATGACACGNGAGAAAGTA-G-TGGGAACGNAATAAA
 GCF_000177235.2_ASM17723v2_genomic.fna_1:112827-113243 Satlength=417 Nr
 of Repeats=8 RepeatLength=52 seed=AATAAAGTGT Num.seqs=6
 Similarity=0.628283
 47 GTGTATCATACGAAG-GCAATGACACATAAGAAAGTAGG-GAGGAACGGAATAAA
 Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:2556156-2556519
 Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=ACACTTTATT Num.seqs=6
 Similarity=0.648148 4
 GTGTGTCATAGAAGT-GCAATGACACGTGAGAAAGTANG-TGGAAACG-AATAAA
 Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:2731003-2731368
 Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=ACACTTTATT Num.seqs=5
 Similarity=0.677987 4
 GTGTATCATACGAGN-GCAATGACACGTGAGAAAGTANG-TGGAAACG-AATAAA
 Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:3973488-3975773
 Satlength=2286 Nr of Repeats=37 RepeatLength=52 seed=TTTATTTGCT
 Num.seqs=27 Similarity=0.882460
 0 GTGTTTCATACGNAG-TCAATGACACATGAGAATGAA-GAAAGAAGCA-AATAAA
 Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:4069392-4069808
 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=CTTCGTATGA Num.seqs=6
 Similarity=0.780247 15
 GTGTATCATACGAAG-TCAATGACACGTGAAAAAGCC-G-AAGAGCCAGAATAAT
 Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:2719945-2720257
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GCGTGTTCATT Num.seqs=6
 Similarity=0.817094 27
 ATGTGTCATACGGGG-TCAATGACACGCGAGAAAGCT-G-AAGAATTGAAATAAG
 Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:2784025-2784389
 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TCGTGTGTCA Num.seqs=7
 Similarity=0.880204 29
 ATGTATCATACAAAG-GCAATGACACACGAGAAAGAA-G-AAGAATGAAAATAAG
 GCF_000177235.2_ASM17723v2_genomic.fna_1:275907-276426 Satlength=520 Nr
 of Repeats=9 RepeatLength=52 seed=ATAAGATGTG Num.seqs=8

Similarity=0.823302

47 ATGTGTCATACGAGGAGCAATGCCACGCGAAAAAGTC-G-AGTCGTCAAATAAG

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Consensus:

gTGTaTCATACgaaggCAATGACACgtGAgAAAGtaGaaGaaacgnAATAAa

>Bacillus_Fam_34_52_10 Nr. of seq. 10 Alignment length(with gaps) = 54

Alignment score = 0.660905

GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_2:429780-430040

Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TGTCCGAAGT Num.seqs=5

Similarity=0.928205 0

TGTCCGAAGTGGCGCTAAGTTCGGACTCACTCTCCCTGTTTTCTG-CT-TCTTC

GCF_000294775.2_ASM29477v2_genomic.fna_1:5091581-5091934 Satlength=354 Nr

of Repeats=5 RepeatLength=52 seed=TCCCTGTTTT Num.seqs=3

Similarity=0.931624 32

TGTCCGAAGTAGCGCTAAGTTCGGACTCACTCTCCCTGTTTTCCG-CT-TCTTC

GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_2:563975-564288

Satlength=314 Nr of Repeats=6 RepeatLength=52 seed=GATTTCTGCT Num.seqs=5

Similarity=0.864103 37

TGTCCGAAGTGGCTTCAGGTTTCGGACTCTTTCTCCCCGATTTCTG-CT-TCTCC

Rev.of_GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_5:65621-

65881 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AAGCGAAAAA

Num.seqs=5 Similarity=0.906289 48

TGTCCGAAGTTCGCACCAACTTCGGACTCCTTCTCTCCCTTTTTTCG-CTTT-TCC

GCF_000294775.2_ASM29477v2_genomic.fna_1:2845024-2845284 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=GCACCAACTT Num.seqs=5

Similarity=0.907692 64

TGTCCGAAGTTCGCACCAACTTCGGACTCTTTCTCTCCCTTTTTTCG-CT-TCTTC

GCF_000294775.2_ASM29477v2_genomic.fna_1:5362631-5363411 Satlength=781 Nr

of Repeats=15 RepeatLength=52 seed=CTGTCCGAAG Num.seqs=15

Similarity=0.870574 51

TGTCCGAAGTTACACCAAGTTCGGACTCTATCTCTCGGTTTTCCGNCT--CTCC

GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_2:825884-826248

Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=CTGTCCGAAT Num.seqs=7

Similarity=0.768010 51

TGTCCGAATCNGCGCCAACTTCGGACTCATTNCNCTCGGATTTCTC-CT-CCTCC

GCF_000294775.2_ASM29477v2_genomic.fna_1:5435232-5435596 Satlength=365 Nr

of Repeats=7 RepeatLength=52 seed=CTGTCCGAAT Num.seqs=7

Similarity=0.768010 51

TGTCCGAATCNGCGCCAACTTCGGACTCATTNCNCTCGGATTTCTC-CT-CCTCC

GCF_000294775.2_ASM29477v2_genomic.fna_1:3419345-3419761 Satlength=417 Nr

of Repeats=8 RepeatLength=52 seed=TTCGGACTCA Num.seqs=6

Similarity=0.837607 71

TGTCCGAAGGTGCGCCGACTTCGGACTCATTCCCTCGGATTCTTG-CT-TCTTC

GCF_000294775.2_ASM29477v2_genomic.fna_1:5335150-5335462 Satlength=313 Nr

of Repeats=6 RepeatLength=52 seed=ACTTCGGACT Num.seqs=6

Similarity=0.593487 69

TGTCCGAATAACTGCCAACTTCGGACTCAACCTCTCCGATTTCTA-CT-CCTAC

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Consensus:

TGTCCGAAGtngCgCcAAcTTCGGACTCatTcTcCngaTTTctgCTtCTcC

>Bacillus_Fam_35_52_10 Nr. of seq. 10 Alignment length(with gaps) = 53
Alignment score = 0.701887
GCF_000708755.2_ASM70875v2_genomic.fna_1:11198-11612 Satlength=415 Nr of
Repeats=8 RepeatLength=52 seed=TTGATGGTTC Num.seqs=7 Similarity=0.831502
0 TTGATGGTTCGATCACGGAGATAAGTGCCATCAAAACAGAAAATCCTCNGT-
GCF_000708755.2_ASM70875v2_genomic.fna_6:420022-420334 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=TTGATGGTTC Num.seqs=6
Similarity=0.788034
0 TTGATGGTTCCTATCCCGAGATAAGTGCCACCAAAAANGGAAAATCCACCGC-
GCF_000709935.2_ASM70993v2_genomic.fna_5:627734-628098 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=TTGATGGTTC Num.seqs=7
Similarity=0.785104
0 TTGATGGTTCCTATCTCCGAGATAAGTGCCACCAAGATGGAAAATCCACCGC-
GCF_000708755.2_ASM70875v2_genomic.fna_6:153329-153693 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=GATAAGTGCC Num.seqs=7
Similarity=0.846154
20 TTGATGGTTCGAACTCAGAGATAAGTGCCACCAAAAAGGATATTCCTCCGT-
GCF_000709935.2_ASM70993v2_genomic.fna_15:70593-70957 Satlength=365 Nr of
Repeats=7 RepeatLength=52 seed=TTGATGGTTC Num.seqs=7 Similarity=0.829060
52 TTGATGGTTCGAACTCAGAGATAAGTGCCACCAAAAATGATATTCCTCCGT-
GCF_000708755.2_ASM70875v2_genomic.fna_22:240402-240610 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GCTTGATGGT Num.seqs=4
Similarity=0.773504
50 TTGATGGTACCGAACTCGGAGATAAGTGCCATCAAACCGGAAAA-CCGCTGGC
GCF_000709935.2_ASM70993v2_genomic.fna_24:351132-351644 Satlength=513 Nr
of Repeats=10 RepeatLength=52 seed=GAGATAAGTG Num.seqs=8
Similarity=0.879605 70
TTGATGGTTCGAACTCGGAGATAAGTGCCATCAAACGGGAGAA-ACGCTGGC
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_1:387582-387842
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GGAACCATCA Num.seqs=5
Similarity=0.838462 11
TTGATGGTTCCTATCTCACCAGATAAGTGCCATCAAATCAGATTTCCTCCGCGT-
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_1:408489-408848
Satlength=360 Nr of Repeats=7 RepeatLength=52 seed=GGAACCATCA Num.seqs=6
Similarity=0.882051 11
TTGATGGTTCGATCTCACCAGATAAGTGCCATCAAATCAGATTCTCCGCGC-
GCF_000709935.2_ASM70993v2_genomic.fna_1:824423-824735 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=ATAAGTGCCA Num.seqs=6
Similarity=0.840042
21 TTGATGGTACCGAACGCACCGATAAGTGCCATCAAACAGAAATCCAACCGC-

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Consensus:

TTGATGGTtCCgAaCtCagaGATAAGTGCCAtCAAaAcgGAaaatCCnCcGn

>Bacillus_Fam_36_20_10 Nr. of seq. 10 Alignment length(with gaps) = 26
Alignment score = 0.611966
GCF_001591805.1_ASM159180v1_genomic.fna_23:9242-9347 Satlength=106 Nr of
Repeats=5 RepeatLength=21 seed=GTTTTGGCTA Num.seqs=5 Similarity=0.668056
7 TTCAA---G-G-GTTTTGGCTATTT-

Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_27:63705-63986
 Satlength=282 Nr of Repeats=8 RepeatLength=21 seed=TAGCCAAAAC Num.seqs=5
 Similarity=0.568056 17
 TTCNA---G-G-GTTTTGGCTATTT-
 Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_15:39118-39285 Satlength=168 Nr
 of Repeats=8 RepeatLength=21 seed=TAGCCAAAAC Num.seqs=7
 Similarity=0.753247 17
 TTCAA---GAG-GTTTTGGCTATTT-
 Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_27:93496-93601
 Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TAGCCAAAAC Num.seqs=5
 Similarity=0.651515 17
 TTCGAN--G-G-GTTTTGGCTATTT-
 GCF_001591805.1_ASM159180v1_genomic.fna_40:28416-28500 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=TTTTGGCTAT Num.seqs=4 Similarity=0.765700
 8 TCCAA---G-G-GTTTTGGCTATTTTC
 GCF_000508325.1_BAVI_1_genomic.fna_48:11356-11461 Satlength=106 Nr of
 Repeats=5 RepeatLength=21 seed=GTTTTGGCTA Num.seqs=5 Similarity=0.647826
 7 TTCAA---G-GAGTTTTGGCTACTT-
 GCF_001591805.1_ASM159180v1_genomic.fna_5:147425-147508 Satlength=84 Nr
 of Repeats=4 RepeatLength=21 seed=GTTTTGGCTA Num.seqs=3
 Similarity=0.661616
 7 TTCGA---N-GAGTTTTGGCTANTT-
 GCF_001591805.1_ASM159180v1_genomic.fna_7:49374-49506 Satlength=133 Nr of
 Repeats=5 RepeatLength=21 seed=TTTGTCTATT Num.seqs=4 Similarity=0.788360
 9 TCCAA--AG-G-GTTTTGTCTATTT-
 GCF_000508325.1_BAVI_1_genomic.fna_43:5059-5143 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=TTGGCTATTT Num.seqs=4 Similarity=0.714286
 10 TTCNA-CCT---GTTTTGGCTATTT-
 GCF_000508325.1_BAVI_1_genomic.fna_87:25255-25339 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=GTTTTGGCTA Num.seqs=4 Similarity=0.724868
 28 TCTGA-CCG---GTTTTGGCTATTT-

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Consensus:

GTTTTGGCTAtTTTtCaAgg

>Bacillus_Fam_37_21_10 Nr. of seq. 10 Alignment length(with gaps) = 24
 Alignment score = 0.601389
 GCF_001636345.1_ASM163634v1_genomic.fna_1:1542440-1542856 Satlength=417
 Nr of Repeats=20 RepeatLength=21 seed=TTTGATAGGA Num.seqs=18
 Similarity=0.543615 0
 TTTGATAGGAAACCCAGG-AA--
 GCF_001636345.1_ASM163634v1_genomic.fna_1:847129-847687 Satlength=559 Nr
 of Repeats=16 RepeatLength=21 seed=TTTGATAGGA Num.seqs=14
 Similarity=0.627456 0
 TTTGATAGGAAACNCAGA-AAT--
 GCF_001636345.1_ASM163634v1_genomic.fna_1:967178-968025 Satlength=848 Nr
 of Repeats=23 RepeatLength=21 seed=TTGATAGGAA Num.seqs=20
 Similarity=0.549379 1
 TTTGATAGGAAACANNGA-AAT--
 Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:3423391-3423622
 Satlength=232 Nr of Repeats=11 RepeatLength=21 seed=TTTCCTATCA

```

Num.seqs=11 Similarity=0.678237
12      TTTGATAGGAAACTGAAA-AAT--
Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:3846604-3846688
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TCCTATCAA Num.seqs=4
Similarity=0.661376 32
TTTGATAGGAAAAGTNAAA-AAN--
Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:3810945-3811113
Satlength=169 Nr of Repeats=8 RepeatLength=21 seed=TCCTATCAA Num.seqs=8
Similarity=0.608383 10
TTTGATAGGAAAAGNCAGANAAG--
GCF_001636345.1_ASM163634v1_genomic.fna_1:481918-482023 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=TTTGATAGGA Num.seqs=5
Similarity=0.630303
0      TTTGATAGGAAAANCGAA-AAN--
GCF_001636345.1_ASM163634v1_genomic.fna_1:1838104-1838250 Satlength=147
Nr of Repeats=7 RepeatLength=21 seed=TTTGATAGGA Num.seqs=6
Similarity=0.705556 0
TTTGATAGGAAAA-CGAA-AATTN
Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:3259418-3259523
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TCCTATCAA Num.seqs=5
Similarity=0.533333 10
TTTGATAGGAAAAGCNNT-AAN--
Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:4039943-4040090
Satlength=148 Nr of Repeats=7 RepeatLength=21 seed=TCCTATCAA Num.seqs=7
Similarity=0.639061 11
TTTGATAGGAAAANCGAT-TAA--

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Consensus:

TTTGATAGGAAAnncaaaAAn

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>Bacillus_Fam_38_15_10 Nr. of seq. 10 Alignment length(with gaps) = 15
Alignment score = 0.786667
GCF_000007825.1_ASM782v1_genomic.fna_1:428801-429311 Satlength=511 Nr of
Repeats=27 RepeatLength=15 seed=CCAGAACCGT Num.seqs=22
Similarity=0.802982
0      CCAGAACCGTTACCA
GCF_000496285.1_ASM49628v1_genomic.fna_1:3052985-3053600 Satlength=616 Nr
of Repeats=34 RepeatLength=15 seed=CACCAGAACC Num.seqs=27
Similarity=0.816651 13
CCAGAACCGTTGCCA
GCF_000007845.1_ASM784v1_genomic.fna_1:416172-416412 Satlength=241 Nr of
Repeats=11 RepeatLength=15 seed=CCAGAACCGT Num.seqs=7
Similarity=0.881481
0      CCAGAACCGTTGCCG
Rev.of_GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_5:83347-
83542 Satlength=196 Nr of Repeats=8 RepeatLength=15 seed=TGGTTCTGGT
Num.seqs=5 Similarity=0.893333 9
CCAGAACCATTGCCA
GCF_000775975.1_ASM77597v1_genomic.fna_1:4964492-4964898 Satlength=407 Nr
of Repeats=25 RepeatLength=15 seed=TGCCACCAGA Num.seqs=23
Similarity=0.846113 10
CCAGAACCATTGCCA

```

Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:71948-72608 Satlength=661
 Nr of Repeats=38 RepeatLength=15 seed=TCTGGTGGCA Num.seqs=32
 Similarity=0.872043 20
 CCAGAACCATTGCCA
 GCF_000831065.1_ASM83106v1_genomic.fna_1:282158-282248 Satlength=91 Nr of
 Repeats=6 RepeatLength=15 seed=TGCCACCAGA Num.seqs=6 Similarity=0.733333
 10 CCAGAGCCGTTGCCA
 Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_5:1617-1782 Satlength=166
 Nr of Repeats=8 RepeatLength=15 seed=TCTGGTGGCA Num.seqs=6
 Similarity=0.845926 5
 CCAGAACCCTGCCA
 GCF_000831065.1_ASM83106v1_genomic.fna_1:282271-282451 Satlength=181 Nr
 of Repeats=8 RepeatLength=15 seed=GAACCGTTAC Num.seqs=5
 Similarity=1.000000
 3 CCGGAACCGTTACCG
 GCF_001439635.1_ASM143963v1_genomic.fna_175:41594-41820 Satlength=227 Nr
 of Repeats=15 RepeatLength=15 seed=ATTGCCAGCT Num.seqs=14
 Similarity=0.948230 8
 GCTGACCCATTGCCA

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Consensus:

CCaGAaCCgTTgCCa

>Bacillus_Fam_39_81_9 Nr. of seq. 9 Alignment length(with gaps) = 83
 Alignment score = 0.715640
 GCF_000196735.1_ASM19673v1_genomic.fna_1:1355402-1356375 Satlength=974 Nr
 of Repeats=13 RepeatLength=81 seed=AGCAAAATTCATTCATGGGGAAAGTGGACGAAATCG
 Similarity=0.779313 0
 AGCAAA-
 TTCAGCCCGAAACGATATTAACAGAACTGGATAAGTTCACAACCTCATTTCATGGGGAAAGTGGACGAAATCG
 -CA
 GCF_000769555.1_ASM76955v1_genomic.fna_1:1225964-1227098 Satlength=1135
 Nr of Repeats=13 RepeatLength=81 seed=GCAAAATTCAG Num.seqs=12
 Similarity=0.748152 1
 AGCAAA-
 TTCAGCCCGAAACGATATTAGCAGAACTGGATAAGTTCACAACNTCATTTCATGGGAAAAGTAGACGAAATCG
 -CN
 GCF_000204275.1_ASM20427v1_genomic.fna_1:1272554-1273283 Satlength=730 Nr
 of Repeats=9 RepeatLength=81 seed=AAATTCAGTC Num.seqs=9
 Similarity=0.677599 3
 AGCAAA-
 TTCAGTCCNGAAACGATATTAACAGAGCTGGATAAATTCACGACCTCATTTCATGGGGAAAGTNGACGANATCG
 -CN
 Rev.of_GCF_000262045.1_KCTC_13613_01_genomic.fna_13:664127-664856
 Satlength=730 Nr of Repeats=9 RepeatLength=81 seed=GGACTGAATT Num.seqs=7
 Similarity=0.675630 14
 AGCAAA-
 TTCAGTCCGAAACNATTTTAACCGAGCTGGATAAGTTCACGACNTCATTTATGGGAAAAGTGGACGANATCG
 -CN
 GCF_001584325.1_ASM158432v1_genomic.fna_36:27-513 Satlength=487 Nr of
 Repeats=5 RepeatLength=81 seed=GCAAAATTCAG Num.seqs=4 Similarity=0.690041
 0 -GCAAA-

TTCAGCCCGGAATCAATATTAAAAGAACTGGACAAATTTACGGCTTCATTTATGAAAAAATAGACGACATCG
TCA

CAAAGTTCAGTCCGGAAACNATTCTNAAACAGCTGGATAAGTTCACAACATCATTTATGAGAAAAGTGGATGC
AATCG-CA

33 A-
CAAAGTTCAGTCCAGANACGATTTTGACAGAGCTGGATAAGTTTACAACATCGTTTATGAGTAAGGTGGATGC
AATTG-CG

112 A-
CGAAGTTCAGTCCAGAAACGATTTTGTGCGAGCTGGATAAATTTACAACATCGTTCATGAGTAAAGTGGACGC
AATTG-CN

169
AGCAAANTTCAGTCCAGAAACGATTTTGNCGCAGCTGGATAAGTTTACAACATCGTTCATGAGTAAAGTGGAC
GCAATCG-CA

Consensus :

```
>Bacillus Fam 40 52 9   Nr. of seq. 9 Alignment length(with gaps) = 58
```

GCF_000169195.2_ASM16919v2_genomic.fna 1:960957-961477 Satlength=521 Nr

Similarity=0.839316

TCTTTTGTCTTTTGTAGCCCTCC-A-AAAGGACAATTCGCCC-CT-GAT-C-CGGCTC

Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=TCAAAAAGAC

16 TCTTTTGTCTTTTGTGAGCTCTCC-A-AAAGGACAATTTGCTC-CT-GGT-C-CGGCTT

Satlength=989 Nr of Repeats=19 RepeatLength=52 seed=AAAAGACAAA

65 TCTTTTGTCTTTTGTGAGCCCTCC-A-AAAAGACAATTTGCTC-CT-GGT-C-CGGCTC

SatLength=625 Nr of Repeats=12 RepeatLength=52 seed=AAAGACAAAA

12 TCTTTTGTCTTTTGANACCCCC-A-AAAGGACAATTTG-CC-CG-GGTNC-CAGCTT

GC1_000105195.2_ASM105195v2_genomic.tla_1:585575-590455 Sat
of Repeats=10 RepeatLength=53 seed=CTTTTGTCTT Num segs=10

Similarity=0.599686 54
TCTTTTGTCTTTTGAACCTCC-A-AAAGGACAATTTGCCC-CG-GATNC-CAGCTC
Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:88046-88410 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=AAAAGGACAA Num.seqs=5
Similarity=0.769811 13
-CTTTTGTCTTTTGAATACTCC-A-AAAGGACANTTTGCTC-CG-GTT-CATGGCTC
Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:2689393-2690174
Satlength=782 Nr of Repeats=15 RepeatLength=52 seed=AAAGACAAAA
Num.seqs=14 Similarity=0.488918
12 TCTTTTGTCTTTTGTATACCTCCGATGAAGGACANTTTGCNN-CGNGGT-C-CGNCCTC
Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:298642-299112
Satlength=471 Nr of Repeats=9 RepeatLength=52 seed=AAATGTCCTT Num.seqs=7
Similarity=0.657848 35
GCTTTTGTCTTTTGAANCCTCC-A-AAAGGACATTTTCGANCACT--AC-C-CGGGCC
Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:2653134-2654217
Satlength=1084 Nr of Repeats=20 RepeatLength=52 seed=AAATGTCCTT
Num.seqs=18 Similarity=0.450699
35 CCTTTTGTCTTTTGAACCCTCC-A-AAAGGACATTTTCGATCACT--GN-C-CGGGTC

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Consensus:

tCTTTTGTCTTTTGAAnnCCTCCAAAGGACAaTTtGcnCCtggtCCgGcTc

>Bacillus_Fam_41_51_9 Nr. of seq. 9 Alignment length(with gaps) = 57
Alignment score = 0.622157
GCF_000292245.2_ASM29224v2_genomic.fna_34:46830-47085 Satlength=256 Nr of
Repeats=5 RepeatLength=51 seed=TTTTTTATTA Num.seqs=5 Similarity=0.853595
0 TTTTTTATTACTTATTACT-GGTTTTTCGCACCGTAATTTT---NACT-GGCT-GGC
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_38:11355-11712
Satlength=358 Nr of Repeats=7 RepeatLength=51 seed=GTAATGAAAA Num.seqs=7
Similarity=0.776580 11
TTTTTCATTACTTATTACG-GGTTTTTCGCNCCTTAATTTG---GACT-GGCT-GGC
GCF_000292245.2_ASM29224v2_genomic.fna_52:29439-29796 Satlength=358 Nr of
Repeats=7 RepeatLength=51 seed=TTTTTCATTA Num.seqs=7 Similarity=0.895425
0 TTTTTCATTAACCTA-TCCTCACTTTTTTCGCACCGTAATTTT---GCCT--GCTCGGC
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_57:27020-27280
Satlength=261 Nr of Repeats=5 RepeatLength=51 seed=GTAATGAAAA Num.seqs=4
Similarity=0.610063 11
TTTTTCATTACCTATTCTCA-TTTTTTCGCACCGTAATTTT---GCCTCAGCATGGC
GCF_000292245.2_ASM29224v2_genomic.fna_61:1751-1955 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=TTTTCATTA Num.seqs=4 Similarity=0.656061
1 TTTTTCATTAACCTA-TCCGCCCTTTTTTCGCACCTAATTTG---GCCC--ACTCTCC
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_66:18-323 Satlength=306 Nr
of Repeats=6 RepeatLength=51 seed=GTAATGAAAA Num.seqs=5
Similarity=0.724359
11 TTTTTCATTAACCTATTACACTNTTTTTCGCACCTAATTTG---GCCN--GCTCNCC
GCF_000292245.2_ASM29224v2_genomic.fna_80:17413-17718 Satlength=306 Nr of
Repeats=6 RepeatLength=51 seed=TTTCATTACC Num.seqs=5 Similarity=0.869281
2 TTTTTCATTAACCTA-TTACCCTTTTTTCGCACCTAATTTG---GCAT--TCACCGC
GCF_000292245.2_ASM29224v2_genomic.fna_53:28960-29215 Satlength=256 Nr of
Repeats=4 RepeatLength=51 seed=CGGCTTTTTT Num.seqs=3 Similarity=0.912854
47 TTTTTCATTAACCTA-TCTCAAGTTTTTCGCACTCTAATTTG---ACCT--GCTCGGC

GCF_000292245.2_ASM29224v2_genomic.fna_5:9-315 Satlength=307 Nr of
Repeats=6 RepeatLength=51 seed=TTTTTCATTAC Num.seqs=6 Similarity=0.673939
52 TTTTTCATTACCTA-TCCCAAGTTTTTCGCACTCTAATTTGCNCACCT--GCTCGAC

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Consensus:

TTTTTCATTACcTATcCncnnTTTTTCGCACcnTAATTTggcCtgCtcggC

>Bacillus_Fam_42_53_9 Nr. of seq. 9 Alignment length(with gaps) = 56
Alignment score = 0.615245
GCF_000181495.1_ASM18149v1_genomic.fna_69:3432-3803 Satlength=372 Nr of
Repeats=6 RepeatLength=53 seed=CGACCCAACA Num.seqs=5 Similarity=0.749383
0 CGACCCAACAACCATTCAATA-ATC-CATTCTCCTTGGCCCGATTACNCCCT-TTT
GCF_000181495.1_ASM18149v1_genomic.fna_112:1323-1747 Satlength=425 Nr of
Repeats=8 RepeatLength=53 seed=CGCCCTATTC Num.seqs=6 Similarity=0.775262
44 CGACCCAACATCCCCTCTATA-AGC-CAATCTCCTTGGATTGATTACGCCCT-ATT
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_151:10383-10754
Satlength=372 Nr of Repeats=7 RepeatLength=53 seed=ACCAGTGAGA Num.seqs=7
Similarity=0.857442 37
CANACCAACATCCCCTTCCATA-ATC-CGTTCTCACTGGTCTGTTTACTCTCT-TTT
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_170:36099-36417
Satlength=319 Nr of Repeats=6 RepeatLength=53 seed=GATGTTGGTC Num.seqs=6
Similarity=0.847379 65
CAGACCAACATCCCCTTCCATC-ATC-CGTTCTCATTGGTTTATTTACTNCCT-TTT
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_186:370855-371491
Satlength=637 Nr of Repeats=9 RepeatLength=53 seed=TGAAAAGGGA Num.seqs=6
Similarity=0.812159 55
CAAACCAACATCCCCTCACATA-ATC-CATTCTCATTGGTCTGATTACTCCCT-TTT
GCF_000181495.1_ASM18149v1_genomic.fna_143:4307-4677 Satlength=371 Nr of
Repeats=7 RepeatLength=53 seed=CGTTTACTCC Num.seqs=6 Similarity=0.931237
38 CGCACCAACACCCCTC-CAAA-ATTTTCATTCTCATTGGGCCGTTTACTCCCT-TTT
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_185:152078-153191
Satlength=1114 Nr of Repeats=21 RepeatLength=53 seed=GAGTAAACGA
Num.seqs=21 Similarity=0.835626
47 CGACCCAACATCTCTC-CAAA-ATTTCAATCTCATTGGGTCGTTTACTCCCT-TTT
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_186:315613-316090
Satlength=478 Nr of Repeats=9 RepeatLength=53 seed=CAATGAGATT Num.seqs=7
Similarity=0.858613 88
CACACCAACATC-CTCACAAAGATT-CAATCTCATTGGGCTGATTAGTCCGT-TTT
GCF_000181495.1_ASM18149v1_genomic.fna_185:82017-82493 Satlength=477 Nr
of Repeats=9 RepeatLength=53 seed=TTTCACACCA Num.seqs=8
Similarity=0.806878
104 CACACCAACTTC-CTCACAAA-ATTCCATTCTCATCGGGGTGATTAGTCCGTCTTT

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Consensus:

CanaCCAACAtCcCTcncAtAATcCatTCTCaTTGGnctGaTTActCCcTTTT

>Bacillus_Fam_43_53_9 Nr. of seq. 9 Alignment length(with gaps) = 56
Alignment score = 0.632275
GCF_000813125.1_ASM81312v1_genomic.fna_101:16844-17056 Satlength=213 Nr
of Repeats=4 RepeatLength=53 seed=GGGCTGCATA Num.seqs=4

GCF_000331575.1_ASM33157v1_genomic.fna_1:244438-244999 Satlength=562 Nr of Repeats=11 RepeatLength=51 seed=TTTTGCTGAT Num.seqs=11
 Similarity=0.932501 1
 GTTTTGCTGATAGTAAATCCTT-TTTATCGTCAGCAAATTGAGGA-TCGCGAC-
 Rev.of_GCF_000331575.1_ASM33157v1_genomic.fna_2:526077-526485
 Satlength=409 Nr of Repeats=8 RepeatLength=51 seed=ATCAGCAAAA Num.seqs=8
 Similarity=0.831158 11
 GTTTTGCTGATAGTAAATCCGT-TTTATCGTCAGCAAATTGAGGA-TCGCTCC-
 GCF_000331575.1_ASM33157v1_genomic.fna_1:651421-651726 Satlength=306 Nr of Repeats=6 RepeatLength=51 seed=GTTTTGCTGA Num.seqs=5
 Similarity=0.853595
 51 GTTTTGCTGATCGTAAATCCTT-TTTATCGTCAGCAAATCCAGTC-TCACGCC-
 Rev.of_GCF_000331575.1_ASM33157v1_genomic.fna_2:25217-25727 Satlength=511
 Nr of Repeats=10 RepeatLength=51 seed=AAAAGGATTT Num.seqs=10
 Similarity=0.957008 75
 GTTTTGCTGATAGTAAATCCTT-TTTATCGTCAGCAAATCCAGTC-TCACGCC-
 Rev.of_GCF_000331575.1_ASM33157v1_genomic.fna_2:599172-599835
 Satlength=664 Nr of Repeats=13 RepeatLength=51 seed=TATCAGCAAA
 Num.seqs=13 Similarity=0.884699
 12 ATTTTGCTGATAATAAATCCAT-TTTATCGTCAGCAAATCGAGCA-TCACACC-
 Rev.of_GCF_000331575.1_ASM33157v1_genomic.fna_2:632825-633284
 Satlength=460 Nr of Repeats=9 RepeatLength=51 seed=ATTTGGTGAC Num.seqs=9
 Similarity=0.936093 38
 GTTTTGCTGATAGTAAATCCGT-TTTATCGTCACCAAATCGAAAATTCA-ATC-

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 Consensus:

GTTTTGCTGATAGTAAAtCCtTTTTATCGTCAGCAAAAtcgAGnaTcaCgnC

>Bacillus_Fam_45_52_9 Nr. of seq. 9 Alignment length(with gaps) = 53
 Alignment score = 0.615129
 GCF_000169195.2_ASM16919v2_genomic.fna_1:320228-320592 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GATGAAGGAC Num.seqs=5
 Similarity=0.739623
 0 GATGAAGGACAATTNGGCTTTNCCAGNCCNGTGTTTTGTCCTTCATCACCTC-
 Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:922243-922973
 Satlength=731 Nr of Repeats=14 RepeatLength=52 seed=TGTCCTTCAT
 Num.seqs=10 Similarity=0.774144
 11 GATGAAGGACAATTTGGCTTTGCCAGGCCTGTGTTTTGTCCTTCATCACC-CN
 Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:2537506-2537922
 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=GTCCTTCATA Num.seqs=8
 Similarity=0.715939 10
 TATGAAGGACAGTTCGTCGTTTCCTGGCCGGTGTTTTGTCTTCATCGGC-CC
 GCF_000169195.2_ASM16919v2_genomic.fna_1:2655058-2655318 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=ATGAAGGACA Num.seqs=5
 Similarity=0.637107 53
 TATGAAGGACATTTGCCGTTTGCCGGCACNTGTTTTGTCTTCATCATN-CT
 GCF_001591485.1_ASM159148v1_genomic.fna_63:10648-10908 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTTCCTTTT Num.seqs=5
 Similarity=0.820513
 12 AATGAAGGACAATTTCTTTTTTCAANCCCCGGATTTGTCCTTCATCGCC-CC
 GCF_000169195.2_ASM16919v2_genomic.fna_1:990416-990781 Satlength=366 Nr of Repeats=6 RepeatLength=52 seed=ATGAAAGACA Num.seqs=4

Similarity=0.790598
 1 GATGAAAGACATTTGCTGCCCCGACACCTCTCTTTTGTCTTCATCACC-CC
 Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:327095-327408
 Satlength=314 Nr of Repeats=5 RepeatLength=52 seed=GTCTTTTCAT Num.seqs=3
 Similarity=0.760684 11
 GATGAAAGACATTTGCTGCTGCGGACCTCNCCTTTTGTCTTCATCACC-CC
 Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:2689111-2689632
 Satlength=522 Nr of Repeats=10 RepeatLength=52 seed=AATGTCCTTC
 Num.seqs=9 Similarity=0.772792
 13 GATGAAGGACATTTGCGCCCGGACGCCCCCTCTTTTGTCTTCATCACC-CC
 GCF_000169195.2_ASM16919v2_genomic.fna_1:2031833-2032093 Satlength=261 Nr
 of Repeats=5 RepeatLength=52 seed=GTCTTCAT Num.seqs=5
 Similarity=0.874359 36
 GATGAAGGACATTTGCTTGCAAGGGAGCCGGTGATTTGTCTTCATAACC-GT

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 Consensus:

gATGAAGGACATTTGCTGCGGACGCCCCCTCTTTTGTCTTCATCACC

>Bacillus_Fam_46_36_9 Nr. of seq. 9 Alignment length(with gaps) = 36
 Alignment score = 0.777263
 GCF_000715205.1_SOAPdenovo_v1.05_genomic.fna_90:66-390 Satlength=325 Nr
 of Repeats=8 RepeatLength=36 seed=ATCTCCGGTA Num.seqs=6
 Similarity=0.822222
 0 ATCTCCGGTAACACCTGTAGCGCCAGTAGAACCAGT
 GCF_001038845.1_ASM103884v1_genomic.fna_31:5-185 Satlength=181 Nr of
 Repeats=4 RepeatLength=36 seed=CCAGTTACAC Num.seqs=3 Similarity=0.834835
 4 ATCACCAGTTACACAGTGGCNCCTAGGACCGGT
 GCF_001457015.1_ASM145701v1_genomic.fna_2:17-395 Satlength=379 Nr of
 Repeats=10 RepeatLength=36 seed=GTATCTCCAG Num.seqs=8
 Similarity=0.850529
 25 TACACCAGTGGCACCAGTAGGNCCAGTATCTCCAGT
 GCF_001896335.1_ASM189633v1_genomic.fna_5:59-1301 Satlength=1243 Nr of
 Repeats=31 RepeatLength=36 seed=GTATCTCCAG Num.seqs=19
 Similarity=0.797488
 25 TACACCAGTGGCACCAGTAGGTCCNGTATCTCCAGT
 GCF_001896335.1_ASM189633v1_genomic.fna_49:56-272 Satlength=217 Nr of
 Repeats=6 RepeatLength=36 seed=GTATCTCCAG Num.seqs=6 Similarity=0.834568
 25 TACACCAGTGGCACCAGTAGGTCCAGTATCTCCAGT
 GCF_001896335.1_ASM189633v1_genomic.fna_54:44-188 Satlength=145 Nr of
 Repeats=4 RepeatLength=36 seed=GTATCTCCAG Num.seqs=4 Similarity=0.839506
 25 TACACCAGTGGCACCAGTAGGTCCAGTATCTCCAGT
 Rev.of_GCF_001896335.1_ASM189633v1_genomic.fna_52:35-170 Satlength=136 Nr
 of Repeats=4 RepeatLength=36 seed=ACTGGAGATA Num.seqs=3
 Similarity=0.876543 36
 TACACCAGTGGCACCAGTAGGTCCGGTATCTCCAGT
 GCF_001457015.1_ASM145701v1_genomic.fna_5:226551-227512 Satlength=962 Nr
 of Repeats=13 RepeatLength=36 seed=GTATCTCCAG Num.seqs=8
 Similarity=0.828042 25
 TACACCAGTNGCACCAGTAGGTCCAGTATCACCAGT
 Rev.of_GCF_001896335.1_ASM189633v1_genomic.fna_8:50-437 Satlength=388 Nr
 of Repeats=10 RepeatLength=36 seed=CCTACCGGTG Num.seqs=6

Similarity=0.832099
AACACCAGTNGCACCGGTAGGTCCAGTATCTCCAGT

57

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Consensus:

taCACCACTggCACCGGTAGgtCCaGTAtctCCAGT

>Bacillus_Fam_47_21_9 Nr. of seq. 9 Alignment length(with gaps) = 24
Alignment score = 0.626157
GCF_001578185.1_ASM157818v1_genomic.fna_1:1878234-1879214 Satlength=981
Nr of Repeats=38 RepeatLength=21 seed=CACGAGTAAA Num.seqs=27
Similarity=0.615271 0
-CACGAGTAAA--TAGC-CAAAAT
Rev.of_GCF_001273755.1_ASM127375v1_genomic.fna_17:4099551-4099980
Satlength=430 Nr of Repeats=21 RepeatLength=21 seed=TTTACTCGTG
Num.seqs=13 Similarity=0.817405
10 -CACGAGTAAA-GCAGC-CAAACT
Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:3721377-3721608
Satlength=232 Nr of Repeats=11 RepeatLength=21 seed=TTTACTCGTG
Num.seqs=11 Similarity=0.805785
30 -CACGAGTAAA-GCGCC-CAAACT
GCF_001273755.1_ASM127375v1_genomic.fna_17:4304916-4305337 Satlength=422
Nr of Repeats=20 RepeatLength=21 seed=TCACGAGTAA Num.seqs=15
Similarity=0.793507 0
TCACGAGTAAA--TTGCTCAAAC-
GCF_001578185.1_ASM157818v1_genomic.fna_1:4390176-4390628 Satlength=453
Nr of Repeats=15 RepeatLength=21 seed=TCACGAGTAA Num.seqs=12
Similarity=0.732553 0
TCACGAGTAAA--CTGCTNAAAC-
GCF_001578185.1_ASM157818v1_genomic.fna_1:4868615-4868909 Satlength=295
Nr of Repeats=14 RepeatLength=21 seed=CGAGTAAACA Num.seqs=14
Similarity=0.891156 3
TCACGAGTAAA--CAGCTCAAAC-
GCF_001578185.1_ASM157818v1_genomic.fna_1:1732763-1732929 Satlength=167
Nr of Repeats=7 RepeatLength=21 seed=CACGAGTAAA Num.seqs=5
Similarity=0.746032 1
TCACGAGTAAA--GTGCNCAAAT-
Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:4121151-4122285
Satlength=1135 Nr of Repeats=50 RepeatLength=21 seed=TTTACTCGTG
Num.seqs=41 Similarity=0.780101
11 TCACGAGTAAA--AGGCTCAAAT-
Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:4151346-4151430
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTTACTCGTG Num.seqs=4
Similarity=0.681159 11
TCACGAGTAAACTAGGCTGAAAT-

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Consensus:

tCACGAGTAAAnnGCTcAAAc

>Bacillus_Fam_48_21_9 Nr. of seq. 9 Alignment length(with gaps) = 23
Alignment score = 0.644525

GCF_000508325.1_BAVI_1_genomic.fna_68:3560-3643 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCTAAT Num.seqs=3 Similarity=0.537778
 0 ATTCGCTAAT-AAACCCTCN-A-
 Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_103:18741-18824 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTATTAGCGA Num.seqs=3
 Similarity=0.640212 12
 ATTCGCTAAT-AAACNNTCN-AG
 Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_12:67671-67793
 Satlength=123 Nr of Repeats=5 RepeatLength=21 seed=TATTAGCGAA Num.seqs=3
 Similarity=0.597884 32
 ATTCGCTAAT-AAACNNNCN-AG
 GCF_000508325.1_BAVI_1_genomic.fna_94:20272-20356 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCTGAT Num.seqs=4 Similarity=0.557971
 0 ATTCGCTGATAAAACCCTCG-A-
 GCF_000508325.1_BAVI_1_genomic.fna_98:31365-31448 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCTAAT Num.seqs=3 Similarity=0.671498
 0 ATTCGCTAAT-AAACTNGCA-A-
 Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_119:10301-10384 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTTATTAGCG Num.seqs=3
 Similarity=0.661616 13
 ATTCGCTAAT-AAACATGGA-AG
 Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_1:35221-35304 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTTATTAGCG Num.seqs=3
 Similarity=0.661616 13
 ATTCGCTAAT-AAACTTGGA-AG
 Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_12:66529-66612
 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTTATTAGCG Num.seqs=3
 Similarity=0.626263 13
 ATTCGCTAAT-AAATNTGGA-AG
 GCF_001591665.1_ASM159166v1_genomic.fna_53:46428-46511 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCTAAT Num.seqs=3 Similarity=0.545455
 0 ATTCGCTAAT-AAACTNNNAGA-

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Consensus:

ATTCGCTAATAAACnnncaAg

>Bacillus_Fam_49_21_9 Nr. of seq. 9 Alignment length(with gaps) = 22
 Alignment score = 0.671296
 GCF_001273755.1_ASM127375v1_genomic.fna_17:3993724-3993858 Satlength=135
 Nr of Repeats=5 RepeatLength=21 seed=TTACTCGTGA Num.seqs=4
 Similarity=0.746032 12
 AATTC-CGAGCATTTACTCGTG
 Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:724068-724640
 Satlength=573 Nr of Repeats=21 RepeatLength=21 seed=AATTCACGAG
 Num.seqs=13 Similarity=0.733683
 25 AATTT-NGAGCAAATACTCGTG
 Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:4101854-4102160
 Satlength=307 Nr of Repeats=15 RepeatLength=21 seed=TCACGAGTAT
 Num.seqs=10 Similarity=0.964727
 43 AGTTT-GGAGCAAATACTCGTG
 GCF_001578185.1_ASM157818v1_genomic.fna_1:2283060-2283368 Satlength=309
 Nr of Repeats=9 RepeatLength=21 seed=TACTCGTGAA Num.seqs=7

Similarity=0.696248 13
 ANATT-NGTGCATTTACTCGTG
 GCF_001578185.1_ASM157818v1_genomic.fna_1:4201354-4201438 Satlength=85 Nr
 of Repeats=4 RepeatLength=21 seed=ATTTACTCGT Num.seqs=4
 Similarity=0.737374 32
 AATTTNAGTGCATTTACTCGTG
 GCF_001578185.1_ASM157818v1_genomic.fna_1:4254210-4254294 Satlength=85 Nr
 of Repeats=4 RepeatLength=21 seed=TTTACTCGTG Num.seqs=4
 Similarity=0.737374 33
 AATTTTGAAGCATTTACTCGTG
 Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:4716658-4716888
 Satlength=231 Nr of Repeats=11 RepeatLength=21 seed=CTCACGAGTA
 Num.seqs=8 Similarity=0.770975
 23 AGTTT-GGTTTCGTTTACTCGTG
 GCF_001578185.1_ASM157818v1_genomic.fna_1:5100829-5100974 Satlength=146
 Nr of Repeats=7 RepeatLength=21 seed=TTTACTCGTG Num.seqs=6
 Similarity=0.655556 32
 AATTT-NGTGCATTTACTCGTG
 GCF_001273755.1_ASM127375v1_genomic.fna_17:4575317-4575422 Satlength=106
 Nr of Repeats=5 RepeatLength=21 seed=TTTACTCGTG Num.seqs=5
 Similarity=0.726984 32
 AATTA-GATGGATTTACTCGTG

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Consensus:

tTACTCGTGAAaTTtngtGCat

>Bacillus_Fam_50_18_9 Nr. of seq. 9 Alignment length(with gaps) = 21
 Alignment score = 0.615520
 GCF_000007825.1_ASM782v1_genomic.fna_1:1257786-1258002 Satlength=217 Nr
 of Repeats=11 RepeatLength=18 seed=CAAAAGAAAG Num.seqs=10
 Similarity=0.878189 0
 CAAAAGAAAG--CAGAAGAA-
 GCF_000496285.1_ASM49628v1_genomic.fna_1:3845536-3845770 Satlength=235 Nr
 of Repeats=13 RepeatLength=18 seed=AGAAGAACAG Num.seqs=13
 Similarity=0.914530 11
 CAGAAGAAAG--TAGAAGAA-
 GCF_000831065.1_ASM83106v1_genomic.fna_1:1083186-1083312 Satlength=127 Nr
 of Repeats=7 RepeatLength=18 seed=GAAGAACAGA Num.seqs=7
 Similarity=0.915344 12
 CAGAAGAAAG--TAGAAGAA-
 Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_49:95444-95588
 Satlength=145 Nr of Repeats=8 RepeatLength=18 seed=TCTTCTACTT Num.seqs=6
 Similarity=0.950617 17
 CAGAAGAAAG--TAGAAGAA-
 GCF_000007825.1_ASM782v1_genomic.fna_1:2224259-2224349 Satlength=91 Nr of
 Repeats=4 RepeatLength=18 seed=CAAGAAGAAC Num.seqs=3 Similarity=0.728395
 9 CTNAAGAAAC--AAGAAGAA-
 Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:2528886-2528958
 Satlength=73 Nr of Repeats=4 RepeatLength=18 seed=TCTTGTTTCT Num.seqs=4
 Similarity=0.814815 14
 CAAAAGAAAC--AAGAAGAG-

Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_12:477954-478062
 Satlength=109 Nr of Repeats=5 RepeatLength=18 seed=TTGTTTCTTT Num.seqs=4
 Similarity=0.864198 30
 GAAAAGAAAC--AAGAAGAG-
 GCF_000008505.1_ASM850v1_genomic.fna_1:1260925-1260997 Satlength=73 Nr of
 Repeats=4 RepeatLength=18 seed=CAAGCGGAAG Num.seqs=4 Similarity=0.901235
 6 CAGAAACAAG--CGGAAGAA-
 Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_10:16518-16623
 Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TCTTTCTTAT Num.seqs=3
 Similarity=0.746032 11
 NATAAGAAAGACAAGAAGAAAN

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Consensus:

cAnAAGAAAGnAGAAGAA

>Bacillus_Fam_51_21_9 Nr. of seq. 9 Alignment length(with gaps) = 21
 Alignment score = 0.772046
 GCF_001273755.1_ASM127375v1_genomic.fna_17:3615490-3615885 Satlength=396
 Nr of Repeats=19 RepeatLength=21 seed=ACTCGTGAGT Num.seqs=15
 Similarity=0.766667 27
 ACNNTTACTCGTGAGTTTCAG
 GCF_001273755.1_ASM127375v1_genomic.fna_17:3619849-3620172 Satlength=324
 Nr of Repeats=15 RepeatLength=21 seed=TTTACTCGTG Num.seqs=11
 Similarity=0.831457 45
 CCTTTTACTCGTGAGTTTCAN
 GCF_001273755.1_ASM127375v1_genomic.fna_17:4533871-4534039 Satlength=169
 Nr of Repeats=8 RepeatLength=21 seed=TTTACTCGTG Num.seqs=8
 Similarity=0.759637 45
 TCATTTACTCGTGAGTTTCAC
 GCF_001578185.1_ASM157818v1_genomic.fna_1:4693833-4694085 Satlength=253
 Nr of Repeats=12 RepeatLength=21 seed=TTTACTCGTG Num.seqs=12
 Similarity=0.904762 45
 CCATTTACTCGTGAGTTTCGG
 Rev.of_GCF_001273755.1_ASM127375v1_genomic.fna_17:4054385-4054658
 Satlength=274 Nr of Repeats=13 RepeatLength=21 seed=TCACGAGTAA
 Num.seqs=13 Similarity=0.759870
 35 ACTTTTACTCGTGAGTTTGGC
 GCF_001578185.1_ASM157818v1_genomic.fna_1:4048935-4049535 Satlength=601
 Nr of Repeats=25 RepeatLength=21 seed=TTTACTCGTG Num.seqs=20
 Similarity=0.749482 45
 ACGTTTACTCGTGAGTTTCGC
 GCF_001578185.1_ASM157818v1_genomic.fna_1:4644456-4644561 Satlength=106
 Nr of Repeats=5 RepeatLength=21 seed=TTTACTCGTG Num.seqs=5
 Similarity=0.873016 45
 GCTTTTACTCGTGAGTTTTCG
 GCF_001578185.1_ASM157818v1_genomic.fna_1:5224710-5224918 Satlength=209
 Nr of Repeats=9 RepeatLength=21 seed=TTTACTCGTG Num.seqs=8
 Similarity=0.709627 45
 GCTTTTACTCGTGAATTTTCGC
 GCF_001578185.1_ASM157818v1_genomic.fna_1:3591601-3592013 Satlength=413
 Nr of Repeats=12 RepeatLength=21 seed=TTTACTCGTG Num.seqs=10

Similarity=0.673302
ACNTTTACTCGTGAATTTTGC

45

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Consensus:

ACTCGTGAgTTTcgcnCnTTT

>Bacillus_Fam_52_18_9 Nr. of seq. 9 Alignment length(with gaps) = 18
Alignment score = 0.911008
GCF_000007825.1_ASM782v1_genomic.fna_1:797166-797535 Satlength=370 Nr of
Repeats=18 RepeatLength=18 seed=GAGCTTTAGC Num.seqs=16
Similarity=0.733951
0 GAGCTTTAGCTGCTTCTT
GCF_000007845.1_ASM784v1_genomic.fna_1:811902-812082 Satlength=181 Nr of
Repeats=10 RepeatLength=18 seed=GAGCTTTAGC Num.seqs=10
Similarity=0.759671
0 GAGCTTTAGCTGCTTCTT
GCF_000008505.1_ASM850v1_genomic.fna_1:810171-810495 Satlength=325 Nr of
Repeats=18 RepeatLength=18 seed=GAGCTTTAGC Num.seqs=16
Similarity=0.764198
0 GAGCTTTAGCTGCTTCTT
GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_9:66816-67098
Satlength=283 Nr of Repeats=15 RepeatLength=18 seed=GAGCTTTAGC
Num.seqs=14 Similarity=0.766382 0
GAGCTTTAGCTGCTTCTT
Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:3984486-3984747
Satlength=262 Nr of Repeats=14 RepeatLength=18 seed=GCTAAAGCTC
Num.seqs=13 Similarity=0.771130
10 GAGCTTTAGCTGCTTCTT
GCF_001645555.1_ASM164555v1_genomic.fna_48:62690-62960 Satlength=271 Nr
of Repeats=13 RepeatLength=18 seed=GAGCTTTAGC Num.seqs=8
Similarity=0.788360
0 GAGCTTTAGCTGCTTCTT
GCF_000496285.1_ASM49628v1_genomic.fna_1:3419837-3420107 Satlength=271 Nr
of Repeats=13 RepeatLength=18 seed=GAGCTTTAGC Num.seqs=11
Similarity=0.714478 0
GAGCTTTAGCTGCTTCNT
Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:4931692-4932007
Satlength=316 Nr of Repeats=17 RepeatLength=18 seed=GCTAAAGCTC
Num.seqs=16 Similarity=0.683626
10 GAGCTTTAGCTGCTTCNC
GCF_000299035.1_ASM29903v1_genomic.fna_2:1062701-1063439 Satlength=739 Nr
of Repeats=41 RepeatLength=18 seed=CTTCTTGCGC Num.seqs=41
Similarity=0.916474 12
GCGCTTTCGCTACTTCTT

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Consensus:

GAGCTTTAGCTGCTTctT

>Bacillus_Fam_53_18_9 Nr. of seq. 9 Alignment length(with gaps) = 18
Alignment score = 0.913580

GCF_000007825.1_ASM782v1_genomic.fna_1:4490484-4491069 Satlength=586 Nr of Repeats=9 RepeatLength=18 seed=CCTTGGTTGT Num.seqs=6
 Similarity=0.930864
 0 CCTTGGTTGTGTTTCCA
 Rev.of_GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_2:317567-318278 Satlength=712 Nr of Repeats=13 RepeatLength=18 seed=ACAACCAAGG
 Num.seqs=11 Similarity=0.849158 10
 CCTTGGTTGTCGTTTCCA
 Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_1:82827-83484
 Satlength=658 Nr of Repeats=14 RepeatLength=18 seed=ACAACCAAGG
 Num.seqs=13 Similarity=0.827160
 10 CCTTGGTTGTCGTTTCCA
 GCF_000712615.1_ASM71261v1_genomic.fna_1:773424-773550 Satlength=127 Nr of Repeats=7 RepeatLength=18 seed=TTGTCTCCAC Num.seqs=7
 Similarity=0.844797
 9 CCTTGGTTGTGTCTCCA
 GCF_000008505.1_ASM850v1_genomic.fna_1:4343825-4344464 Satlength=640 Nr of Repeats=9 RepeatLength=18 seed=CCTTGGTTGT Num.seqs=7
 Similarity=0.823633
 0 CCTTGGTTGTCGTTTCCG
 GCF_000496285.1_ASM49628v1_genomic.fna_1:1747374-1748121 Satlength=748 Nr of Repeats=18 RepeatLength=18 seed=TTTCCGCCTT Num.seqs=17
 Similarity=0.909586 12
 CCTTGGTTGTCGTTTCCG
 Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:319755-320394
 Satlength=640 Nr of Repeats=13 RepeatLength=18 seed=ACAACCAAGG
 Num.seqs=12 Similarity=0.849607
 10 CCTTGGTTGTCGTTTCCG
 GCF_000831065.1_ASM83106v1_genomic.fna_1:4247332-4247404 Satlength=73 Nr of Repeats=4 RepeatLength=18 seed=CCTTGGTTGT Num.seqs=4
 Similarity=0.962963
 0 CCTTGGTTGTCGTTTCCG
 Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:1427286-1427889
 Satlength=604 Nr of Repeats=11 RepeatLength=18 seed=ACAACCAAGG
 Num.seqs=10 Similarity=0.889712
 10 CCTTGGTTGTCGTTTCCG

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Consensus:

CCTTGGTTGTcGTTTCCg

>Bacillus_Fam_54_114_8 Nr. of seq. 8 Alignment length(with gaps) = 115
 Alignment score = 0.790890
 GCF_000242895.2_ASM24289v3_genomic.fna_1:2821534-2822245 Satlength=712 Nr of Repeats=5 RepeatLength=114 seed=CCGCTTACAT Num.seqs=4
 Similarity=0.752437 0
 CCGCTTACATCGCATTGGCCATACTTATTATAACCCACAGCCGCCACCGTGCCGTCAGATTTAAGGCCGACGG
 TATGANTGC-AACCCGCCGCTACCGCCACAATACACGCCAG
 GCF_001278705.1_ASM127870v1_genomic.fna_1:2862067-2862637 Satlength=571
 Nr of Repeats=4 RepeatLength=114 seed=CGCGCCAGTC Num.seqs=3
 Similarity=0.641762 106
 TCGCTTACATCGCATTGACCATACTCATTNTCAACCCACAGCAACCACCGTNCCATCAGATTTAAGGCCGATGG
 TATGANNAC-AACCCGCCGCAACCGCCACAATACCGCGCCAG

Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_152:2346-2916 Satlength=571
Nr of Repeats=4 RepeatLength=114 seed=CTTAAATCGG Num.seqs=3
Similarity=0.610136 65

TCGTTTACATTGCATTGGCCATNCTTATTNCNACCCACAGCTGCCACCGTACCGTCCGATTTAAGCCCAATGG
TATGACANT-AACCCGCCGCAACCGCCACAATATCGCGCCAG

Rev.of_GCF_001591625.1_ASM159162v1_genomic.fna_135:4361-5072
Satlength=712 Nr of Repeats=6 RepeatLength=114 seed=GGGCTTAAAT
Num.segs=5 Similarity=0.608832

68
TCGCTTACATTGCATTGGCCATACTTATTNCNACCCACAGCCACCACCGTACCGTCCGATTTTAAGNCCAATNG
TATGNAGNC - AACCCGCCGCNACCGCCACAATATCGTGCCAG

Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_6:40523-41234
Satlength=712 Nr of Repeats=6 RepeatLength=114 seed=CTTAAATCGG
Num.segs=5 Similarity=0.636182

TCGCTTACATTGCATTGGCCATNCTTATTCCANCCACAGCCATCACCGTTCCGTCCGATTTAAGNCCGATGG
TATGANNNC-AACCCGCCGCNACCGCCACAATATCGCGCCAG

Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_74:3413-4124 Satlength=712
Nr.of.Repeats=6 RepeatLength=114 seed=GGGCTTAAAT Num.seqs=5
Similarity=0.632749 68

TCGCTTACATTCGATTGGCCATNCTTATTNNNACCCACAGCNGCCACNGTACCGTCCGATTTAAGNCCGATNG
TATGNNNAC-AACCCGCCGCAACCGCCACAATATCGNNCCAG

GCF_000307875.1_BABA1.0_genomic.fna_35:121244-121841 Satlength=598 Nr of Repeats=4 RepeatLength=114 seed=CGCCACAATA Num.seqs=3 Similarity=0.648309

96
TCATTACATTGCATTGGCCATACTNATTCAACCTACAGCCATCACNGTACCGTCCGATTTAAGNCCGATNG
TATGANNANTAGCCCCGCCGCTATCGCCACAATATCGCGCCAG

GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-14515_genome_genomic.fna_1:606481-607078 Satlength=598 Nr_of Repeats=4 RepeatLength=114 seed=CGCCACAATA Num.seqs=3 Similarity=0.686957 96 TCGCTTACATTGCATTGGCGATACTNATTCAACCCACAGCCGACACTGTACCGTCCGATTTAAGACCGATGG TATGANNANTCNCCAGCCGCGATCGCCACAATATCGCGCCAG

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Consensus:

TCGCTTACATtGCATTGGCCATaCTtATTnnaACCCACAGCcacCACcGTaCCGTcGATTTAAGnCCgATgG
TATGannacAaCCCGCCGcNacCGCCACAATAtCGcGCCAG

>Bacillus_Fam_55_52_8 Nr. of seq. 8 Alignment length(with gaps) = 59
Alignment score = 0.632062

GCF_000311725.1_ASM31172v1_genomic.fna_4:214050-214934 Satlength=885 Nr
of Repeats=17 RepeatLength=52 seed=TCATGAGGAC Num.seqs=13
Similarity=0.774714

TCATGAGGACA-AAGTC-GGGC-GAAA-ATCAGGAAAGTTTGTCTCAT--AGAGG-GT

Rev.of_GCF_000311725.1_ASM31172v1_genomic.fna_4:573981-574346
Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=ACTTTGTCCT Num.seqs=6
Similarity=0.777778 15

TCATGAGGACA-AAGTC-GGAC-GAAA-ACCAGGAAAGTTTGTCTCAT--AGAGG-GT

Rev_of_GCF_000311725.1_ASM31172v1_genomic.fna_4:290049-290519
Satlength=471 Nr of Repeats=9 RepeatLength=52 seed=TATGAGGACA Num.seqs=7

Similarity=0.867026 46
 TCATGAGGACA-AAGTC-GAAC-GAAA-AGGAAGAAAGTTTGTCTCAT--AGAGN-GT
 GCF_000311725.1_ASM31172v1_genomic.fna_11:254-826 Satlength=573 Nr of
 Repeats=11 RepeatLength=52 seed=GTTCATGAGG Num.seqs=11
 Similarity=0.792453
 50 TCATGAGGACA-AAGTC-GAAC-GAAA-TCCAAGAAAGANTGTCTCAT--AGAGG-GT
 Rev.of_GCF_000311725.1_ASM31172v1_genomic.fna_12:53034-53294
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GACTTTGTCC Num.seqs=5
 Similarity=0.763030 16
 TCATGAGGACA-AAGTC-AGAC-GAAA-ATCAAGAAAGTTTGTCTCAT--A-AGGNGT
 Rev.of_GCF_000311725.1_ASM31172v1_genomic.fna_4:326412-326730
 Satlength=319 Nr of Repeats=6 RepeatLength=53 seed=TGTGGACAAA Num.seqs=6
 Similarity=0.906080 44 -
 CATGAGGACA-AACTCTGGAA-GAAA-AGCGGTGAAGTTTGTCCACATA-AGAGG-TT
 GCF_001591665.1_ASM159166v1_genomic.fna_17:30304-30511 Satlength=208 Nr
 of Repeats=4 RepeatLength=52 seed=GGGCTCATGA Num.seqs=3
 Similarity=0.897436
 48 TCATGAGGACAGAAAT--GGCGAGAAA-ACCAAGAAA-ATTGTCTCAT-GA-AGG-GC
 GCF_001636315.1_ASM163631v1_genomic.fna_1:3657440-3657908 Satlength=469
 Nr of Repeats=9 RepeatLength=52 seed=ATGAGGACAA Num.seqs=9
 Similarity=0.884615 54
 TCATGAGGACA-AAATC-GGAG-GAAACCCCCAGGAA-TCTGTCTCAT-GA-AAG-GC

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 Consensus:

TCATGAGGACAAAgTCGgacGAAAacCaaGaAAgttTGTCTCATAgAGGGt

>Bacillus_Fam_56_52_8 Nr. of seq. 8 Alignment length(with gaps) = 58
 Alignment score = 0.632389
 GCF_000621445.1_ASM62144v1_genomic.fna_1:29213-29577 Satlength=365 Nr of
 Repeats=7 RepeatLength=52 seed=GAGTTTTGTC Num.seqs=7 Similarity=0.892183
 117 T-CTC--TTTTC-CCTCGAGTTT-TGTCCTTCATCTCTCTTATGAAGGACACTTC-TC
 GCF_000621445.1_ASM62144v1_genomic.fna_4:243825-244085 Satlength=261 Nr
 of Repeats=5 RepeatLength=52 seed=GGACACTTCT Num.seqs=5
 Similarity=0.837736
 145 T-CNC--TTTTT-CTTC-TCTTTCTGTCCTTCATCGCTCTTATGAAGGACACTTC-TC
 Rev.of_GCF_000621445.1_ASM62144v1_genomic.fna_17:35462-35826
 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GATGAAGGAC Num.seqs=7
 Similarity=0.907204 134
 A-CTC--TTTCC-TCTCCTCTTT-TGTCCTTCATCAAGCTTATGAAGGACACTTC-TC
 Rev.of_GCF_000621445.1_ASM62144v1_genomic.fna_2:192691-193107
 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=8
 Similarity=0.905678 150
 TGCT---TTTTC-AC-CTAGTTT-TGTCCTTCATCACCTTATGAAGGACACTTCTTT
 GCF_000621445.1_ASM62144v1_genomic.fna_3:29111-29423 Satlength=313 Nr of
 Repeats=7 RepeatLength=52 seed=GTTTTGTCTT Num.seqs=5 Similarity=0.941026
 171 T-CTA--TTTTC-AC-CTCGTTT-TGTCCTTCATCAACCTTATGAAGGACACTTCCTC
 GCF_000621445.1_ASM62144v1_genomic.fna_22:34839-35099 Satlength=261 Nr of
 Repeats=5 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=5 Similarity=0.815385
 122 --CTC-ATTTTCCACTC-CATTT-TGTCCTTCATCNGCCTTATGAAGGACACTTC-TC
 GCF_001591805.1_ASM159180v1_genomic.fna_52:18377-18636 Satlength=260 Nr
 of Repeats=5 RepeatLength=52 seed=TGTCTTCAT Num.seqs=4

Similarity=0.841880

122 --CTCGATTTCCAAGT-AGTTT-TGTCCTTCATCAGCTTTATGAAGGACACTTC--C
GCF_000621445.1_ASM62144v1_genomic.fna_12:17218-17686 Satlength=469 Nr of
Repeats=9 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=9 Similarity=0.821803
122 A-CCG-TTTTTC-GCTC-ACTTT-TGTCCTTCATCAGCTTATGAAGGACACTTT-AC

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Consensus:

nagTTTGTCTTCATCaccCTTATGAAGGACACTTCTCtCtCtCtTTtCaCtC

>Bacillus_Fam_57_52_8 Nr. of seq. 8 Alignment length(with gaps) = 57

Alignment score = 0.671261

GCF_000751775.1_A1A_genomic.fna_13:16-692 Satlength=677 Nr of Repeats=13

RepeatLength=52 seed=GGACAAAATG Num.seqs=13 Similarity=0.818930

0 GGACAAAA--TGGAGNC-TCAATCAGGAAA--AACTGTCCAATAGAACGGTTCTCAT

Rev.of_GCF_000751775.1_A1A_genomic.fna_98:24731-25094 Satlength=364 Nr of

Repeats=7 RepeatLength=52 seed=CTATTGGACA Num.seqs=6 Similarity=0.760684

40 GGACAAAA--TGGGGG-TCAATCAGGAAA--AACTGTCCAATAGAACGGCTCTCGT

Rev.of_GCF_000751775.1_A1A_genomic.fna_98:28702-29324 Satlength=623 Nr of

Repeats=12 RepeatLength=52 seed=TCTATTGGAC Num.seqs=8

Similarity=0.787062

41 GGACAAAA--TGAGGAG-TCAATCAGGAAA--AACTGTCCAATAGAACGGTTCTCGT

GCF_000751775.1_A1A_genomic.fna_94:14879-15191 Satlength=313 Nr of

Repeats=6 RepeatLength=52 seed=TCCAATAGAA Num.seqs=6 Similarity=0.834188

32 GGACAAAA--TGGAGCC-TCAACCAGGTGA--AACTGTCCAATAGAACGACTCTCGT

GCF_000751775.1_A1A_genomic.fna_93:1659-2387 Satlength=729 Nr of

Repeats=14 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=14

Similarity=0.827631

30 GGACAAAA--TGAGGAG-GCAATCTGCAAA--AAATGTCCAATAGAACGGCTCTCAT

Rev.of_GCF_000751775.1_A1A_genomic.fna_100:11954-12735 Satlength=782 Nr

of Repeats=15 RepeatLength=52 seed=TTGTCCATGA Num.seqs=14

Similarity=0.800055

58

GGACAAAA--AAGNGTCCAATCAGNAAA--AATTGTCCAATAGAACGGCTTTCAT

Rev.of_GCF_000751775.1_A1A_genomic.fna_81:7055-7471 Satlength=417 Nr of

Repeats=8 RepeatLength=52 seed=TTTTGTCCAT Num.seqs=8 Similarity=0.750433

8 GGACAAAACCTGAAG--TCAACCAGCAAA--AACTGTCCAATAGAACGGCTCTAAT

GCF_000751775.1_A1A_genomic.fna_12:34323-34582 Satlength=260 Nr of

Repeats=5 RepeatLength=52 seed=AACTGTCCAA Num.seqs=4 Similarity=0.528283

28 GGACAAAA--TTGAG-N-TAAAAAAGAAAGGAACGTCCAAGAGAACGGTTCTCAT

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Consensus:

GGACAAAATgaaGngtCAAtCAGgAAAAAcTGTCCAATAGAACGGcTCTCaT

>Bacillus_Fam_58_52_8 Nr. of seq. 8 Alignment length(with gaps) = 57

Alignment score = 0.619779

GCF_000813125.1_ASM81312v1_genomic.fna_49:14856-15064 Satlength=209 Nr of

Repeats=4 RepeatLength=52 seed=TTTCTTGACA Num.seqs=4 Similarity=0.884615

2 G-TTTTCTTGACAAC-TTGGCGCTCT-GA-AC-CCTGAAACCTGTCACAATAACGGC

GCF_000813125.1_ASM81312v1_genomic.fna_50:13-221 Satlength=209 Nr of

Repeats=4 RepeatLength=52 seed=AAACCTGTCA Num.seqs=4 Similarity=0.777778

32 T-TTTTCTTGACAGC-TTGGGCTCC-AC-TA-CCTGAAACCTGTCACAATAACGGC

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_136:11-271 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CTGTCAAGAA Num.seqs=5
Similarity=0.761538 65
T-TTTTCTTGACAGC-TTTGGGCTCC-GC-AG-CCTGAAACCTGTCACAATAACTGC
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_42:3-211 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GTTATTGTGA Num.seqs=4
Similarity=0.863248
49 T-TTTTCTTGACAGC-TTTGGGCTAT-GT-AC-CTTGAAAGCTGTCACAATAACTAC
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_100:44990-45353
Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=GTTATTGTGA Num.seqs=6
Similarity=0.841026 49
T-TTTTCTTGACAGC-TTTTCCGTGT-TC-GC-CCCCAAACCTGTCACAATAACGGC
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_60:30-342 Satlength=313 Nr
of Repeats=5 RepeatLength=52 seed=AAAGCTGTCA Num.seqs=4
Similarity=0.764403
69 T-CTTTCTTGACAGC-TTTTCGCTCTATC-NCACCCAAACCTGTCACAATAACGAC
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_89:4898-5417 Satlength=520
Nr of Repeats=9 RepeatLength=52 seed=GAAAAGCTGT Num.seqs=6
Similarity=0.771279 71
T-TTTTCTTGACAGC-TTTTC-CTCA-TCAGC-ATCCAAACCTGTCACGATTACCTC
Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_1:28106-28314 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=TTATTTTGAC Num.seqs=4
Similarity=0.881027 47
TCT-TTCTTGACAACCTTTTGCCCTTT-TC-AC--CTGAAAGTTGTCAAATAACCTC

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Consensus:

TTTCTTGACAgCTTTgCGTctttaccctgAAAcCTGTCACAATAACgGCTT

>Bacillus_Fam_59_55_8 Nr. of seq. 8 Alignment length(with gaps) = 57
Alignment score = 0.625731
GCF_000708755.2_ASM70875v2_genomic.fna_6:281885-282097 Satlength=213 Nr
of Repeats=4 RepeatLength=53 seed=CGCCACAAAC Num.seqs=4
Similarity=0.890985
13 CTAC-GG-GGAATGACGCCACAAAC-ATGGATGCTTTCACATG-AAAAGTGGCAGCA
GCF_000709935.2_ASM70993v2_genomic.fna_15:188408-188619 Satlength=212 Nr
of Repeats=4 RepeatLength=53 seed=CGCCACAAAC Num.seqs=3
Similarity=0.899371
13 CTAC-GG-GGAATGACGCCACAAAC-ATGGATGCTTTCACATG-AAAAGTGGCGGCA
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_22:121820-122085
Satlength=266 Nr of Repeats=5 RepeatLength=53 seed=TGGCGTCATT Num.seqs=5
Similarity=0.899371 18
CTTC-GC-GGAATGACGCCACAAAC-A-AGAACCCTTCTCCGGCAAAAGTGGCAGCA
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_24:232406-232777
Satlength=372 Nr of Repeats=7 RepeatLength=53 seed=TGGCGTCATT Num.seqs=7
Similarity=0.901767 18
CTAC-GC-GGAATGACGCCACAAAC-N-AGAACCCTTCTCTGGCAAAAGTGGCAGCA
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_1:491832-492044
Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=ATCCTAGTTT Num.seqs=4
Similarity=0.809671 29
CTACAGC--GAATGACGCCACAACTA-GGATCC-AACTACGATAAAAGTGGCACCA
GCF_000709935.2_ASM70993v2_genomic.fna_5:571905-572276 Satlength=372 Nr
of Repeats=7 RepeatLength=53 seed=ACGAATGACG Num.seqs=7

Similarity=0.841869

58 CTACAAC--GAATGACGCCACTAACCA-TCATCC-ATCTCTGGTAAAAGTGGCGGCA
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_4:195544-195756
Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=CCACTTTTTTC Num.seqs=4
Similarity=0.895178 48
CTA-AGCT-GAATGACGCCACAAATGA-GGATCC-ATCACTGGAAAAAGTGGCGTCA
GCF_000709935.2_ASM70993v2_genomic.fna_15:32457-32775 Satlength=319 Nr of
Repeats=5 RepeatLength=53 seed=CACTACCGCG Num.seqs=4 Similarity=0.756813
51 CTACCGC--GAATGACGCCACAAATGA-GCATTC-ATCAAAGGCAAAAGTGGCGCCA

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Consensus:

CGCCACAAAcnAggAtcCnaTCacngGnAAAAGTGGCagCACTACnGcgGAATGA

>Bacillus_Fam_60_52_8 Nr. of seq. 8 Alignment length(with gaps) = 56
Alignment score = 0.673044
GCF_000708755.2_ASM70875v2_genomic.fna_1:172527-172891 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=ATGGCACTTA Num.seqs=7
Similarity=0.787546
0 ATGGCACTTATCCGGNAGAATAGAACCCTCAAGCAGAGAAAT-CTC--AGAGTTG
GCF_000709935.2_ASM70993v2_genomic.fna_1:173354-173666 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=GCACTTATCC Num.seqs=6
Similarity=0.810256
3 ATGGCACTTATCCGGGAGAATAGAACCCTCAAGCAGAGNAAT-CAC--AGAGTTG
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:379262-379469
Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=GATAAGTGCC Num.seqs=3
Similarity=0.783951 12
AGGGCACTTATCAGGAAGTCTAGAACCATCAAACTGAAGGATTCTC--AG-GTTG
GCF_000708755.2_ASM70875v2_genomic.fna_5:265879-266243 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=ACCATCAAAA Num.seqs=7
Similarity=0.811966
24 ATGGCACTTATCGGGGAGAACAGTACCATCAAAAGGAAGAATGTTT--TG-GTTG
GCF_000709935.2_ASM70993v2_genomic.fna_13:199669-200033 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=ACCATCAAAA Num.seqs=7
Similarity=0.781441
24 ATGGCACTTATCNGGGAGAACAGAACCATCAAAAGGAAGAATGTTC--TG-GTTG
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_7:77605-78021 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=TTTTGATGGT Num.seqs=8
Similarity=0.850517 34
ATGGCACTTATCCGGAAGAATAGAACCATCAAAAAGAAGAATCCAC--AG-GTTG
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_19:84981-85241
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTTTGATGGT Num.seqs=5
Similarity=0.838462 34
ATGGCACTTATCCGGAAGAATAGAACCATCAAAAAGAAGATNTAC--AG-GTTG
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_19:30893-31257
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=CCTCTGTTGA Num.seqs=5
Similarity=0.815385 38
GTGGTACTTATCAGGGAGAATAGAACCATCAA-CAGAGG-AT-CTCGTTTG-GTTG

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Consensus:

ATGGCACTTATCcGGgAGAAAtAGAACCAtCAAAAAgAagaATnctCaGGTTG

Similarity=0.790598
 43 GGTACTAGTCATACGGACTAAACCCCTCTGAACAGAGAAAAA---GAAACAGAG
 Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2545989-2546197
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CCCTCTGTTT Num.seqs=4
 Similarity=0.790598 54
 GGTACTAGTCATGCGGACTAAGACCCTCTGAACGGTGAAAAA---GAAACAGAG
 GCF_000153365.1_ASM15336v1_genomic.fna_72:65371-65750 Satlength=380 Nr of
 Repeats=5 RepeatLength=52 seed=AAAAAAGAAA Num.seqs=3 Similarity=0.829060
 88 GGTCTTAGTCAAGGCCACTAAGACCCTCTGACCAG-GAAAAAA-G-AAAACAGAT
 GCF_000473245.1_ASM47324v1_genomic.fna_1:1667185-1667564 Satlength=380 Nr
 of Repeats=5 RepeatLength=52 seed=AAAAAAGAAA Num.seqs=3
 Similarity=0.829060 88
 GGTCTTAGTCAAGGCCACTAAGACCCTCTGACCAG-GAAAAAA-G-AAAACAGAT
 GCF_000153365.1_ASM15336v1_genomic.fna_16:461270-461740 Satlength=471 Nr
 of Repeats=9 RepeatLength=52 seed=GGTCTTAGTC Num.seqs=7
 Similarity=0.854701
 0 GGTCTTAGTCAGTGCGACTAACACCATCT-AGCCA-CAGAAAA-GCGAATCAGAC
 Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2350437-2350907
 Satlength=471 Nr of Repeats=9 RepeatLength=52 seed=CTGACTAAGA Num.seqs=7
 Similarity=0.854701 12
 GGTCTTAGTCAGTGCGACTAACACCATCT-AGCCA-CAGAAAA-GCGAATCAGAC

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Consensus:

GGTctTAGTcAagccgACTAanACCtCTgAnccggAaAAAAggAAaCAGAg

>Bacillus_Fam_63_52_8 Nr. of seq. 8 Alignment length(with gaps) = 54
 Alignment score = 0.661155
 GCF_001278705.1_ASM127870v1_genomic.fna_1:569178-569542 Satlength=365 Nr
 of Repeats=7 RepeatLength=52 seed=GATGAAGGAC Num.seqs=7
 Similarity=0.862027
 0 GATGAAGGACATTTCTTTGGCTATC-TTGCCTCATTTTGTCTTCAGCACCCG-
 Rev.of_GCF_001278705.1_ASM127870v1_genomic.fna_1:2433779-2434247
 Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=ATGTCCTTCA Num.seqs=9
 Similarity=0.754274 12
 AATGAAGGACATTTCTCTGNCTCAC-TTGCCTCATTTTGTCTTCATAACCCG-
 Rev.of_GCF_001278705.1_ASM127870v1_genomic.fna_1:577894-578363
 Satlength=470 Nr of Repeats=9 RepeatLength=52 seed=GAAGGACAAA Num.seqs=8
 Similarity=0.786388 44
 TATGAAGGACTTTTCTCGAGCTCTC-TTACTCTTTTTTGTCTTCCTTCACTACCCG-
 Rev.of_GCF_001278705.1_ASM127870v1_genomic.fna_1:3589135-3589394
 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=TGAAGGACAA Num.seqs=4
 Similarity=0.777778 45
 GATGAAGGACTTTTCTCTGGCTCTT-TTACGCCTTTTTGTCTTCATGACCCG-
 Rev.of_GCF_001278705.1_ASM127870v1_genomic.fna_1:3837620-3837827
 Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=GTTCTGAAGG Num.seqs=3
 Similarity=0.965812 49
 TATGAAGGACTTTTCCTTGGATTTC-CTGCTCCTTTTTGTCTTCAGAACCCCT-
 GCF_001636425.1_ASM163642v1_genomic.fna_1:3113621-3114088 Satlength=468
 Nr of Repeats=9 RepeatLength=52 seed=TTGTCCTTCA Num.seqs=8
 Similarity=0.810984 87
 TATGAAGGACGTTTCCCTGGATTCTCT-CACGGTTTTGTCTTCATCACCCCT-

GCF_001278705.1_ASM127870v1_genomic.fna_1:1906710-1907023 Satlength=314
Nr of Repeats=5 RepeatLength=52 seed=TGAAGGACTT Num.seqs=3
Similarity=0.982906 1
G-TGAAGGACTTTTCTCTGGATCTA-TTCCCTCTTTTCGTCCTTCAGCTCCCCCT
GCF_001278705.1_ASM127870v1_genomic.fna_1:2231666-2231875 Satlength=210
Nr of Repeats=4 RepeatLength=52 seed=TTTCTCTGG Num.seqs=3
Similarity=0.897436 9
GATGATGGACTTTTCTCTGGATCTT-TTCCCTCTTTTGTCTTCAGAACCCC-

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Consensus:

gATGAAGGACtTTTctcTGGaTcTctTnCncctTTTTGTCCCTTCagnACCCg

>Bacillus_Fam_64_45_8 Nr. of seq. 8 Alignment length(with gaps) = 45
Alignment score = 0.881481
GCF_000007825.1_ASM782v1_genomic.fna_1:2082917-2083097 Satlength=181 Nr
of Repeats=4 RepeatLength=45 seed=TTTTTGCTCT Num.seqs=4
Similarity=0.901235
0 TTTTTGCTCTTCTTGTTGCTTACGAGCTTGCTCATCAGCTAGACG
GCF_000007845.1_ASM784v1_genomic.fna_1:2006658-2006928 Satlength=271 Nr
of Repeats=6 RepeatLength=45 seed=TCTTGTTGTT Num.seqs=4
Similarity=0.812500
7 TTTTTGTTCTTCTTGTTGTTTACGAGCTTGTTTCATCAGCCTGGCG
GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_1:1160788-1161253
Satlength=466 Nr of Repeats=8 RepeatLength=45 seed=TCTTGTTGTT Num.seqs=5
Similarity=0.806944 7
TTTTTGTTCTTCTTGTTGTTTACGAGCTTGTTTCATCAGCCTGGCG
GCF_000831065.1_ASM83106v1_genomic.fna_1:1900224-1900491 Satlength=268 Nr
of Repeats=6 RepeatLength=45 seed=TTACGAGCTT Num.seqs=5
Similarity=0.988148 19
TTTTTGCTCTTCTTGTTGTTTACGAGCTTGTTTCATCAGCCTGACG
Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:3728877-3729057
Satlength=181 Nr of Repeats=4 RepeatLength=45 seed=GCTGATGAAC Num.seqs=4
Similarity=0.930864 39
TTTTTGCTCTTCTTGTTGTTTACGAGCCTGTTTCATCAGCTTGCG
Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_12:642752-643016
Satlength=265 Nr of Repeats=5 RepeatLength=45 seed=GATGAACAAG Num.seqs=4
Similarity=0.916049 81
TTTTTGCTCTTCTTGTTGTTTACGAGCTTGTTTCATCAGCTTGCG
GCF_000161455.1_ASM16145v1_genomic.fna_1:1905065-1905245 Satlength=181 Nr
of Repeats=4 RepeatLength=45 seed=GCTTGACGTT Num.seqs=4
Similarity=0.911111 37
TTTTTGCTCTTCTTGTTGTTTTTGTAGCTTGTTCTCAGCTTGACG
Rev.of_GCF_000299035.1_ASM29903v1_genomic.fna_2:20736-20973 Satlength=238
Nr of Repeats=5 RepeatLength=45 seed=GAACAAGCTC Num.seqs=4
Similarity=0.837037 78
TTGTTGCTCTTCCTGTTGTTTACGAGCTTGTTCTTCAGCTTGACG

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Consensus:

TTTTTGcTCTTCTTGTTGTTTACGAGCTTGTTCaTCAGctTgaCG

>Bacillus_Fam_65_26_8 Nr. of seq. 8 Alignment length(with gaps) = 26
Alignment score = 0.630495
GCF_000181495.1_ASM18149v1_genomic.fna_175:18883-19008 Satlength=126 Nr of Repeats=5 RepeatLength=25 seed=AACTGAGCCA Num.seqs=5
Similarity=0.807692
0 AACTGAGCCAGGCTCAAAAGGTGTG-
GCF_000181495.1_ASM18149v1_genomic.fna_181:9837-9962 Satlength=126 Nr of Repeats=5 RepeatLength=25 seed=TCTGAGCCAG Num.seqs=5 Similarity=0.740741
1 ATCTGAGCCAGGCTCAAAAGG-GTGG
Rev.of_GCF_001877785.1_PlanoSAMB_genomic.fna_96:412299-412474
Satlength=176 Nr of Repeats=7 RepeatLength=25 seed=TTTGTGCCTG Num.seqs=7
Similarity=0.910867 18
ATTTGAGCCAGGCACAAAAGG-GTTG
GCF_001877785.1_PlanoSAMB_genomic.fna_106:16546-16696 Satlength=151 Nr of Repeats=6 RepeatLength=25 seed=TTTGAGCCAG Num.seqs=6 Similarity=0.655967
1 GTTTGAGCCAGGCTCAAAAGGTGTA-
Rev.of_GCF_001877785.1_PlanoSAMB_genomic.fna_96:184758-184883
Satlength=126 Nr of Repeats=4 RepeatLength=25 seed=GTGCCTGGCT Num.seqs=3
Similarity=0.964444 15
ATTTGAGCCAGGCACAAACGCCCTG-
GCF_001877785.1_PlanoSAMB_genomic.fna_128:45834-46035 Satlength=202 Nr of Repeats=8 RepeatLength=25 seed=GCCAGGCACA Num.seqs=7 Similarity=0.838217
31 ATTTGAGCCAGGCACAAACGTGATG-
Rev.of_GCF_001877785.1_PlanoSAMB_genomic.fna_139:90007-90157
Satlength=151 Nr of Repeats=6 RepeatLength=25 seed=TTTGAGCCTG Num.seqs=6
Similarity=0.621811 17
ATC-GAGCCAGGCTCAAAACGCCAC
Rev.of_GCF_001877785.1_PlanoSAMB_genomic.fna_117:70844-70944
Satlength=101 Nr of Repeats=4 RepeatLength=25 seed=TTTGAGCCTG Num.seqs=4
Similarity=0.850427 17
ATCTGAGCCAGGCTCAAACCAGCCGA

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Consensus:

ATcTGAGCCAGGCTCAAAaggngtgn

>Bacillus_Fam_66_21_8 Nr. of seq. 8 Alignment length(with gaps) = 24
Alignment score = 0.630208
GCF_000508325.1_BAVI_1_genomic.fna_132:10204-10328 Satlength=125 Nr of Repeats=4 RepeatLength=21 seed=TTCGCAAATA Num.seqs=3 Similarity=0.583333
0 -TTCGCAAATAANA--CAGGNGAA
GCF_001591805.1_ASM159180v1_genomic.fna_27:26552-26636 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCAAAT Num.seqs=4 Similarity=0.676768
0 ATTCGCAAATAAAA--CNGGAGAT
GCF_000612665.1_FF4_genomic.fna_70:25409-25493 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCAAAT Num.seqs=4 Similarity=0.563131
20 -TTCGCAAATAAAA-TC-GACAAA
GCF_001591665.1_ASM159166v1_genomic.fna_6:121036-121119 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTCGCAAATA Num.seqs=3
Similarity=0.545455
20 -TTCGCAAATAAAACNC-GTCAA-
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_57:31859-31943
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTTATTGCG Num.seqs=4

Similarity=0.635266 33
 -TTCGCAAATAAAN--CGGATAAA
 Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_59:63831-63915
 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTTATTTGCG Num.seqs=4
 Similarity=0.582071 33
 -TTCGCAAATAA--CGGATTAA
 GCF_001591805.1_ASM159180v1_genomic.fna_21:4565-4670 Satlength=106 Nr of
 Repeats=5 RepeatLength=21 seed=TCGCAAATAA Num.seqs=5 Similarity=0.709091
 43 -TTCGCAAATAA--CNGGTANA
 GCF_001591805.1_ASM159180v1_genomic.fna_27:83451-83535 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=TCGCAAATAA Num.seqs=4 Similarity=0.622475
 63 -TTCGCAAATAA--CAGGNAAA

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Consensus:

TTCGCAAATAAAACnGgnaAa

>Bacillus_Fam_67_21_8 Nr. of seq. 8 Alignment length(with gaps) = 21
 Alignment score = 0.806689
 GCF_000007825.1_ASM782v1_genomic.fna_1:871016-871268 Satlength=253 Nr of
 Repeats=11 RepeatLength=21 seed=TGAAGGAACA Num.seqs=10
 Similarity=0.865961
 0 TGAAGGAACAGGAAAACCAGG
 GCF_000007845.1_ASM784v1_genomic.fna_1:880306-880558 Satlength=253 Nr of
 Repeats=11 RepeatLength=21 seed=AAGAAACAGA Num.seqs=10
 Similarity=0.957672
 2 TGAAGAAACAGAAAAGCCAGG
 GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_1:43675-44110
 Satlength=436 Nr of Repeats=15 RepeatLength=21 seed=AAGAAACAGA
 Num.seqs=13 Similarity=0.894180 2
 TGAAGAAACAGAAAAGCCAGG
 GCF_000831065.1_ASM83106v1_genomic.fna_1:719782-719908 Satlength=127 Nr
 of Repeats=6 RepeatLength=21 seed=TGAAGGAACA Num.seqs=6
 Similarity=0.894180
 21 TGAAGGAACAGAAAAGCCAGG
 GCF_001645555.1_ASM164555v1_genomic.fna_48:126076-126286 Satlength=211 Nr
 of Repeats=10 RepeatLength=21 seed=GAAGAAACAG Num.seqs=8
 Similarity=0.861678 22
 TGAAGAAACAGAAAACCAGG
 GCF_001889165.1_ASM188916v1_genomic.fna_1:134977-135082 Satlength=106 Nr
 of Repeats=4 RepeatLength=21 seed=GGAACAGATA Num.seqs=3
 Similarity=0.851852
 4 NGAAGGAACAGATAACCCAGG
 GCF_000496285.1_ASM49628v1_genomic.fna_1:3488675-3488864 Satlength=190 Nr
 of Repeats=9 RepeatLength=21 seed=ACACCAGGTG Num.seqs=9
 Similarity=0.925926 13
 TGGAGGAACAGAAACACCAGG
 Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:4861442-4861757
 Satlength=316 Nr of Repeats=15 RepeatLength=21 seed=CTCCACCTGG
 Num.seqs=15 Similarity=0.958881
 26 TGGAGAGACAGAAACACCAGG

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Consensus:

TGaAGaAACAGAAaCCAGG

>Bacillus_Fam_68_52_7 Nr. of seq. 7 Alignment length(with gaps) = 54
Alignment score = 0.639624
GCF_000759675.1_ASM75967v1_genomic.fna_13:145209-145417 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CGGTCACCTTA Num.seqs=4
Similarity=0.730084
0 CGGTCACCTTATAGCCCTTATTAGTGACCACTTTTTTCGAATTCCTT-TGATTA-
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_155:58436-59008
Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=TGGTAACTAA
Num.seqs=11 Similarity=0.890452
29 CGGTCACCTTATAGCCTCTATTAGTTACCACTTTTTTCG-ATTTTTTC-TCATTTT
GCF_000759675.1_ASM75967v1_genomic.fna_57:134608-134868 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=ATTTCGGTCA Num.seqs=5
Similarity=0.794969
48 CGGTCACCTTATAGCCTTCATTAGTGACCACTCTTCT-ATTTTAAACAAGATTT-
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_134:29911-30379
Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=TATGAGTGAC Num.seqs=9
Similarity=0.912393 64
CGGTCACCTCATAGCCTTTATGAGTGACCACTTTTTTAA-ATTTAAACAAGATTA-
GCF_000759675.1_ASM75967v1_genomic.fna_85:197429-198209 Satlength=781 Nr
of Repeats=15 RepeatLength=52 seed=AGCCTTCATG Num.seqs=15
Similarity=0.914530 63
CGGTCACCTCATAGCCTTCATGAGTGCCCGGTTTTCCA-ATTCTAACAAGATTC-
GCF_000759675.1_ASM75967v1_genomic.fna_73:261668-261928 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=ATTTCGGTCA Num.seqs=5
Similarity=0.583929
48 CGGTCAACNATAGCACTCATTGATGACCACTTTCTCT-ATTTCAACCANATTT-
GCF_000759675.1_ASM75967v1_genomic.fna_153:33935-34143 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TTGGTTACCA Num.seqs=4
Similarity=0.816239
71 CGGTCACTATAGTCCTCATTGGTTACCACTTTCTCT-ATTCCAACCAGATTT-

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Consensus:

CGGTCACtTATAGCCTtTcATtAGTgACCACTTTtTCnATTtnaaCnagATTt

>Bacillus_Fam_69_52_7 Nr. of seq. 7 Alignment length(with gaps) = 54
Alignment score = 0.627572
GCF_000813125.1_ASM81312v1_genomic.fna_25:23691-23951 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=GGACAACCTTT Num.seqs=5 Similarity=0.928205
0 GGACAACCTTTTC-GTTCTTTTCCT-CTAAACCTGTCTGAAGTTGCACCTCCTTC
GCF_000934845.1_ASM93484v1_genomic.fna_4:21973-22597 Satlength=625 Nr of
Repeats=12 RepeatLength=52 seed=GTTCCGACTA Num.seqs=10
Similarity=0.788889
48 GGACTACTTTTC-G-CCTTTTCCTGCAAAACCTGTCCGAAGTTGGCTCTTGTTTC
Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_57:39159-39367
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CAACTTCGGA Num.seqs=4
Similarity=0.770576 94
GGACTGCTTTTC-G-CTTTTCCGACAAAACCAGTCCGAAGTTGGCTCTAGTTC

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_64:18546-18857
 Satlength=312 Nr of Repeats=5 RepeatLength=52 seed=ACAGGTTTGG Num.seqs=4
 Similarity=0.676440 33
 TGACAGCTTTTCTG-GCTTTCCT-CCAAACCTGTCTGAAGTTGGGCGATGTTC
 GCF_000813125.1_ASM81312v1_genomic.fna_75:60242-60554 Satlength=313 Nr of
 Repeats=6 RepeatLength=52 seed=GACAGCTTTT Num.seqs=6 Similarity=0.788034
 1 TGACAGCTTTTC-C-ACTTCTTCCTCCAAACCTGTCCGAACTTGGGGCTACTTC
 Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_92:118219-118635
 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=GGAAAAGCTG Num.seqs=8
 Similarity=0.619260 13
 TGACAGCTTTTC-C-TCTTNCCCCGACCAAACCTGTCCGAACTTGGNGCTTCTTT
 GCF_000813125.1_ASM81312v1_genomic.fna_133:9463-9775 Satlength=313 Nr of
 Repeats=5 RepeatLength=52 seed=CTGACAGCTT Num.seqs=4 Similarity=0.690329
 51 TGACAGCTTTTC-C-TCNGTTCCTCATCAAACCTGTCCGAACTTGCCTCTACTTC

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 Consensus:

tGACagCTTTTCgnCTTtCCnnCcAAACCTGTcGAAgTTGgnnCTncTTC

>Bacillus_Fam_70_52_7 Nr. of seq. 7 Alignment length(with gaps) = 54
 Alignment score = 0.638448
 GCF_001636345.1_ASM163634v1_genomic.fna_1:931350-932077 Satlength=728 Nr
 of Repeats=14 RepeatLength=52 seed=AATCTGGAAA Num.seqs=13
 Similarity=0.791566 0
 AATCTGGAAAATGGTGTCTGTA-AAAGGGAAGAAACACCCCTCTATAATCCAN-
 GCF_001636345.1_ASM163634v1_genomic.fna_1:1522369-1522681 Satlength=313
 Nr of Repeats=6 RepeatLength=52 seed=CAGTATCTGG Num.seqs=6
 Similarity=0.885470 49
 TATCTGGAAAATGGTGTCTGTA-AAAGGAGAGAAACACCCCTCTAAAGTCCAG-
 Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:3881060-3881632
 Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=GGTGTCTTCTC
 Num.seqs=11 Similarity=0.874126
 38 AAAAAGGTAAACAGTGTCTGCGA-AAAGCAGAGAAACACCCCTCTATAATCCAG-
 Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:4336082-4336445
 Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=GGGGTGTTC Num.seqs=6
 Similarity=0.835897 40
 AATCTAGAAAATAGAGTCGCGG-AAAGGGGAGAAACACCCCGTGGAATCCAG-
 Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:3624890-3625255
 Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=AGGGGTGTTT Num.seqs=6
 Similarity=0.870085 40
 AAAAGGGAAAAT-GTGTCTTGATTAAGG-GAGAAACACCCCTCTGAAATCCAGA
 Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:3412758-3413277
 Satlength=520 Nr of Repeats=10 RepeatLength=52 seed=CTGTTTTCTGA
 Num.seqs=9 Similarity=0.849715
 27 -AAATGGTAAATGGTGTCTCGA-AAACAGNGGAAACACCCCACTAAAAACCACT
 GCF_001636345.1_ASM163634v1_genomic.fna_1:1414565-1414877 Satlength=313
 Nr of Repeats=6 RepeatLength=52 seed=TCCAGAAAAA Num.seqs=6
 Similarity=0.822222 47
 AAAAAGGAAAATGGTGTCTGCGG-AAACNGATAAACACACCCGTAAAGTCCAG-

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 Consensus:

aAaatGGaAAATgGTGTcGcGaAAAggngAGAAACACCCctcTaaAaTCCAG

>Bacillus_Fam_71_52_7 Nr. of seq. 7 Alignment length(with gaps) = 54
Alignment score = 0.641387
GCF_002019645.1_ASM201964v1_genomic.fna_1:579578-581402 Satlength=1825 Nr
of Repeats=35 RepeatLength=52 seed=TGCTGAAGT Num.seqs=34
Similarity=0.899173 0
TGTCTGAAGTAGC-CTCGNGTTCGGACAGCTTTGA-TTGTTTAGAAGTAAAAGC
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:2223040-2223404
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GCTACTTCAG Num.seqs=7
Similarity=0.912088 13
TGTCTGAAGTAGC-CTCGGGTTCGGACAGCTTTGA-TTGTTTTAAAGCAAAAGC
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:4753408-4753928
Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=GCTACTTCAG
Num.seqs=10 Similarity=0.850142
13 TGTCTGAAGTAGC-GTTGGGTTCGGACAGGTTTGG-TTGGTTTTAGGCTAAAGC
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:1988468-1989404
Satlength=937 Nr of Repeats=18 RepeatLength=52 seed=AAGCTGTCCG
Num.seqs=18 Similarity=0.815904
31 TGTCTGAAGTTGC-CTTGGGTTCGGACAGC-TTGAATTCATTTCTTGCTAAAGC
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:2086406-2086926
Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=TTAGACAGC
Num.seqs=10 Similarity=0.776068
8 TGTCTGAAGTTCC-CTCCACTTCGGACAGCTTTGA-TTCGTTCTGGGCCAAAGC
GCF_002019645.1_ASM201964v1_genomic.fna_1:1098526-1099150 Satlength=625
Nr of Repeats=12 RepeatLength=52 seed=TGTCGAAGT Num.seqs=12
Similarity=0.860917 0
TGTCGAAGTTGCTCT-GAGTTCAGACAGGTTTAG-GGGTTTGAAGCAAAAGC
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:4437435-4438782
Satlength=1348 Nr of Repeats=26 RepeatLength=52 seed=TACTTCAGAC
Num.seqs=24 Similarity=0.790994
11 TGTCTGAAGTAGCTCT-GTGTTCGGACAGCTTTG-TGCTTTACAAGGCAAAGT

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Consensus:

TGTCTGAAGTaGCCTnGnGTTTCGGACAGcTTTgaTtgtTTnnaaGcnAAAGC

>Bacillus_Fam_72_52_7 Nr. of seq. 7 Alignment length(with gaps) = 52
Alignment score = 0.731380
GCF_002019645.1_ASM201964v1_genomic.fna_1:2495463-2495723 Satlength=261
Nr of Repeats=4 RepeatLength=52 seed=CATAGGCCTT Num.seqs=3
Similarity=0.811966 0
CATAGGCCTTCTATGATTTAGTTGTCTGAGCGAAAACAAGGAGAAAGTAAAT
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:4542766-4542973
Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=CAGGCAACTT Num.seqs=3
Similarity=0.761006 28
CATAGGCCTTCTATGATCAAGTTGCCTGGACGAAAACGAGGAGNAAGTAAAC
GCF_002019645.1_ASM201964v1_genomic.fna_1:2741337-2741701 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=AAGGAGGAAG Num.seqs=7
Similarity=0.854701 37
CATACNCCCTCTATGATCCAGTTGCCGAGGCGAAACCAAGGAGGAAGTGAAT

Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:3938951-3939315
 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GCCTATGATT Num.seqs=7
 Similarity=0.866427 59
 CATAGGCCTTCTATGAGTCAGTTGCCGAAGCGAAAAACAAGGAGGAAGTGAAT
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:3790499-3790810
 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=TTTCTCCTTG Num.seqs=5
 Similarity=0.838462 46
 CATAGGCTCTCTATGATTGAGTTGCTGAGGCAAAAACAAGGAGAAAGTGAAT
 GCF_002019645.1_ASM201964v1_genomic.fna_1:5108997-5109209 Satlength=213
 Nr of Repeats=4 RepeatLength=52 seed=AAGTGAATCA Num.seqs=3
 Similarity=0.897436 96
 CATTGGCTCTCTATGATTGAGTTGCTAAAGCGGAAAACAAGGAGAAAGTGAAT
 GCF_002019645.1_ASM201964v1_genomic.fna_1:4292665-4292873 Satlength=209
 Nr of Repeats=4 RepeatLength=52 seed=AGGAACTCAA Num.seqs=4
 Similarity=0.910256 41
 CATAGACCTGCTTTGATCCAGTTGCAGAAGCAAAAACAAGGAGAACTCAAT

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Consensus:

CATAGgCctTCTATGATtCAGTTGCcgaaGCgAAAACAAGGAGnAAGTgAAT

>Bacillus_Fam_73_20_7 Nr. of seq. 7 Alignment length(with gaps) = 22
 Alignment score = 0.655123
 GCF_001315165.1_ASM131516v1_genomic.fna_64:18994-19094 Satlength=101 Nr
 of Repeats=5 RepeatLength=20 seed=TTTTATAGCG Num.seqs=5
 Similarity=0.515278
 0 TTTTAT-AGCGA--NTTTCNAT
 Rev.of_GCF_001591625.1_ASM159162v1_genomic.fna_70:0-79 Satlength=80 Nr of
 Repeats=4 RepeatLength=20 seed=TCGCTGATAA Num.seqs=4 Similarity=1.000000
 12 TTTTATCAGCGA--CTTTCCT
 Rev.of_GCF_001591625.1_ASM159162v1_genomic.fna_110:11874-11954
 Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=GGGAAAGTCG Num.seqs=4
 Similarity=1.000000 19
 TTTTATCAGCGA--CTTTCCT
 Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_3:8732-8832 Satlength=101
 Nr of Repeats=5 RepeatLength=20 seed=TCGCTATAAA Num.seqs=5
 Similarity=0.631746 11
 TTTTAT-AGCGA-NTTNTCNT
 Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_53:86-186 Satlength=101 Nr
 of Repeats=5 RepeatLength=20 seed=TCGCTATAAA Num.seqs=5
 Similarity=0.631746 11
 TTTTAT-AGCGA-NTTTTNCNT
 GCF_001315165.1_ASM131516v1_genomic.fna_77:6171-6271 Satlength=101 Nr of
 Repeats=5 RepeatLength=20 seed=TTTATAGCGA Num.seqs=5 Similarity=0.661905
 21 TTTTAT-AGCGA-GTTTTACTT
 Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_213:71-191 Satlength=121
 Nr of Repeats=6 RepeatLength=20 seed=CGCTATAAAA Num.seqs=6
 Similarity=0.631313 31
 TTTTAT-AGCGNAATTTTNCTT

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Consensus:

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>Bacillus_Fam_74_21_7 Nr. of seq. 7 Alignment length(with gaps) = 22
Alignment score = 0.698413
GCF_001591425.1_ASM159142v1_genomic.fna_1:10873-11167 Satlength=295 Nr of
Repeats=14 RepeatLength=21 seed=TTTATTTATC Num.seqs=14
Similarity=0.725275
0 TTTATTTATCACCGCACTCCG-
Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_40:10038-10143
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TGATAAATAA Num.seqs=5
Similarity=0.733333 11
TTTATTTATCACCGACCNCNG-
Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_40:16835-16961
Satlength=127 Nr of Repeats=6 RepeatLength=21 seed=TGATAAATAA Num.seqs=6
Similarity=0.762963 11
TTTATTTATCACCGACCCCCG-
Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_40:19702-19849
Satlength=148 Nr of Repeats=7 RepeatLength=21 seed=TGATAAATAA Num.seqs=7
Similarity=0.794407 11
TTTATTTATCACCGAACGCNT-
Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_40:23367-23615
Satlength=249 Nr of Repeats=12 RepeatLength=21 seed=TGATAAATAA
Num.seqs=11 Similarity=0.710245
11 TTTATTTATCANCANGANCTCNN-
Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_62:9174-9363 Satlength=190
Nr of Repeats=9 RepeatLength=21 seed=TGATAAATAA Num.seqs=9
Similarity=0.514245 11
TTTATTTATCAACGA-CTCCNA
GCF_001591425.1_ASM159142v1_genomic.fna_54:21619-21808 Satlength=190 Nr
of Repeats=9 RepeatLength=21 seed=TTATTTATCA Num.seqs=9
Similarity=0.576892
1 TTTATTTATCACCC-AACNCNAG

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TTTATTTATCAcCGAnCnCnn

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>Bacillus_Fam_75_22_7  Nr. of seq. 7 Alignment length(with gaps) = 22
Alignment score = 0.622655
GCF_001645685.2_ASM164568v2_genomic.fna_1:3341360-3341445 Satlength=86 Nr
of Repeats=4 RepeatLength=21 seed=TTTACTCGCC Num.seqs=3
Similarity=0.686869 0
TTTACTCGCCAATTTAGCGAC-
Rev.of_GCF_001645685.2_ASM164568v2_genomic.fna_1:4482743-4483219
Satlength=477 Nr of Repeats=13 RepeatLength=21 seed=TGGCGAGTAA
Num.seqs=11 Similarity=0.662534
11 TTTACTCGCCAAATTAGCGNG-
Rev.of_GCF_001645685.2_ASM164568v2_genomic.fna_1:4454332-4454416
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTGGCGAGTA Num.seqs=4
Similarity=0.682540 12
TTTACTCGCCAAATTTG-GATG

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GCF_001645685.2_ASM164568v2_genomic.fna_1:4248891-4249324 Satlength=434
 Nr of Repeats=5 RepeatLength=21 seed=ACTCGCCAAT Num.seqs=3
 Similarity=0.957672 3
 TTTACTCGCCAA-TTCAGCACT
 GCF_001645685.2_ASM164568v2_genomic.fna_1:4241205-4241656 Satlength=452
 Nr of Repeats=10 RepeatLength=21 seed=TTACTCGCCA Num.seqs=6
 Similarity=0.818687 23
 TTTACTCGCCAATTTGNGCACT
 Rev.of_GCF_001645685.2_ASM164568v2_genomic.fna_1:4466835-4466919
 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TCGCGAGTAA Num.seqs=4
 Similarity=0.596618 11
 TTTACTCGCGAATTTGTCNACT
 GCF_001591665.1_ASM159166v1_genomic.fna_66:6860-6944 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=TTTACTCGCG Num.seqs=4 Similarity=0.600242
 0 TTTACTCGCGAATTCTGNCATN

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Consensus:

TTTACTCGCcAAtTTngnnAcn

>Bacillus_Fam_76_21_7 Nr. of seq. 7 Alignment length(with gaps) = 21
 Alignment score = 0.702948
 GCF_001591425.1_ASM159142v1_genomic.fna_25:49292-49439 Satlength=148 Nr
 of Repeats=7 RepeatLength=21 seed=TTACTTAACA Num.seqs=7
 Similarity=0.550725
 0 TTACTTAACAAGTNTTGAAA-
 Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_38:25074-25221
 Satlength=148 Nr of Repeats=7 RepeatLength=21 seed=TGTTAAGTAA Num.seqs=7
 Similarity=0.761149 10
 TTACTTAACANGTANTGAAAA
 Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_88:2823-2970 Satlength=148
 Nr of Repeats=7 RepeatLength=21 seed=TGTTAAGTAA Num.seqs=7
 Similarity=0.667423 10
 TTACTTAACANGTATTNAAAN
 Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_5:44236-44383
 Satlength=148 Nr of Repeats=7 RepeatLength=21 seed=CTGTTAAGTA Num.seqs=5
 Similarity=0.659420 11
 ATACTTAACAGCTTTTCAAAA
 GCF_001591425.1_ASM159142v1_genomic.fna_161:2289-2478 Satlength=190 Nr of
 Repeats=9 RepeatLength=21 seed=TTACTTAACA Num.seqs=9 Similarity=0.738977
 21 TTACTTAACAGCNTTTCAAAA
 GCF_001591425.1_ASM159142v1_genomic.fna_16:280-445 Satlength=166 Nr of
 Repeats=6 RepeatLength=21 seed=ACTTAACAGA Num.seqs=4 Similarity=0.622475
 23 TTACTTAACAAATTGACAAAA
 GCF_001591425.1_ASM159142v1_genomic.fna_34:0-104 Satlength=105 Nr of
 Repeats=5 RepeatLength=21 seed=TTACTTAACA Num.seqs=5 Similarity=0.746032
 42 TTACTTAACAACCTTTCCAAAT

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Consensus:

TTACTTAACAnnTtttcAAAa

>Bacillus_Fam_77_15_7 Nr. of seq. 7 Alignment length(with gaps) = 16
Alignment score = 0.610119
GCF_000009825.1_ASM982v1_genomic.fna_1:3550903-3551497 Satlength=595 Nr
of Repeats=11 RepeatLength=15 seed=CCTGGTTCTT Num.seqs=7
Similarity=0.741799
0 CCTGGTTCTTCAGTN-
Rev.of_GCF_000305495.1_BacPsy2.0_genomic.fna_17:24629-24719 Satlength=91
Nr of Repeats=6 RepeatLength=15 seed=GGTACTGAAA Num.seqs=6
Similarity=0.946667 2
CCTGGTTTTCAGTA-
GCF_002019645.1_ASM201964v1_genomic.fna_1:2043017-2043122 Satlength=106
Nr of Repeats=7 RepeatLength=15 seed=CCAGGCTCTT Num.seqs=7
Similarity=0.915344 0
CCAGGCTCTTCAGTA-
GCF_900142675.1_IMG-
taxon_2654588196_annotated_assembly_genomic.fna_7:329335-329959
Satlength=625 Nr of Repeats=10 RepeatLength=15 seed=TCGGTGCCTG
Num.seqs=8 Similarity=0.888889 9
CCTGGCTCTTCGGTG-
Rev.of_GCF_001591585.1_ASM159158v1_genomic.fna_18:75061-75166
Satlength=106 Nr of Repeats=7 RepeatLength=15 seed=GGAGCAGAAG Num.seqs=7
Similarity=0.881481 1 -
CCGGTTCTTCTGCTC
GCF_002019645.1_ASM201964v1_genomic.fna_1:5231068-5231188 Satlength=121
Nr of Repeats=7 RepeatLength=15 seed=TCTTCTGTTC Num.seqs=6
Similarity=0.851852 5
-CCGGTTCTTCTGTTC
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:422359-422539
Satlength=181 Nr of Repeats=11 RepeatLength=15 seed=GATCCAGGAA
Num.seqs=10 Similarity=0.796543
7 -CTGGATCTTCTGTTC

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Consensus:

cCtGGtTCTTCnGTn

>Bacillus_Fam_78_12_7 Nr. of seq. 7 Alignment length(with gaps) = 12
Alignment score = 0.830688
GCF_000025805.1_ASM2580v1_genomic.fna_1:1178251-1178455 Satlength=205 Nr
of Repeats=12 RepeatLength=12 seed=CGGCGAGTAG Num.seqs=8
Similarity=0.908730 0
CGGCGAGTAGAA
GCF_000025825.1_ASM2582v1_genomic.fna_1:1189082-1189262 Satlength=181 Nr
of Repeats=12 RepeatLength=12 seed=CGAGTAGAAC Num.seqs=11
Similarity=0.919192 3
CGGCGAGTAGAA
Rev.of_GCF_000225265.1_ASM22526v1_genomic.fna_1:3779323-3779479
Satlength=157 Nr of Repeats=13 RepeatLength=12 seed=CTACTCGCCG
Num.seqs=13 Similarity=0.854701
10 CGGCGAGTAGAA
GCF_000025805.1_ASM2580v1_genomic.fna_1:1377397-1377736 Satlength=340 Nr
of Repeats=26 RepeatLength=12 seed=AGAACGGCGA Num.seqs=24

```

Similarity=0.884461 8
CGGCGAGAAGAA
GCF_000025805.1_ASM2580v1_genomic.fna_1:1377397-1377820 Satlength=424 Nr
of Repeats=29 RepeatLength=12 seed=AGAACGGCGA Num.seqs=24
Similarity=0.884461 8
CGGCGAGAAGAA
Rev.of_GCF_000242895.2_ASM24289v3_genomic.fna_1:2771381-2771945
Satlength=565 Nr of Repeats=41 RepeatLength=12 seed=CTACTCGTCG
Num.seqs=35 Similarity=0.758242
10 CGACGAGTAGAG
Rev.of_GCF_000956595.1_ASM95659v1_genomic.fna_17:23745-23997
Satlength=253 Nr of Repeats=21 RepeatLength=12 seed=CTACTCGCCG
Num.seqs=21 Similarity=0.863492
10 CGGCGAGTAGTG

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Consensus:

CGGCGAGtAGAA

>Bacillus_Fam_79_12_7 Nr. of seq. 7 Alignment length(with gaps) = 12
Alignment score = 0.640212
GCF_000331575.1_ASM33157v1_genomic.fna_1:153900-154010 Satlength=111 Nr
of Repeats=7 RepeatLength=12 seed=ATTTTGATT Num.seqs=5
Similarity=0.777778
0 ATTTTGATTTTG
GCF_000331575.1_ASM33157v1_genomic.fna_4:18792-18873 Satlength=82 Nr of
Repeats=5 RepeatLength=12 seed=GTGTGATGTTG Num.seqs=4 Similarity=1.000000
2 ATGTGTGATGTTG
Rev.of_GCF_001591625.1_ASM159162v1_genomic.fna_36:9709-9757 Satlength=49
Nr of Repeats=4 RepeatLength=12 seed=TCAAAGTCAA Num.seqs=4
Similarity=0.702991 1
ACTTTGACTTTG
Rev.of_GCF_000496285.1_ASM49628v1_genomic.fna_1:1498693-1498783
Satlength=91 Nr of Repeats=5 RepeatLength=12 seed=CAATATCAAC Num.seqs=3
Similarity=0.851852 0
CTGTTGATATTG
Rev.of_GCF_001315085.1_ASM131508v1_genomic.fna_9:7125-7221 Satlength=97
Nr of Repeats=7 RepeatLength=12 seed=CAACAACAGC Num.seqs=5
Similarity=0.800000 9
CTGTTGTTGTTG
Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:771792-772062
Satlength=271 Nr of Repeats=8 RepeatLength=12 seed=TCAACAGCAA Num.seqs=5
Similarity=0.911111 7
CTGTTGACCTTG
Rev.of_GCF_001420595.1_ASM142059v1_genomic.fna_11:2152936-2153020
Satlength=85 Nr of Repeats=7 RepeatLength=12 seed=TCAACAACAA Num.seqs=7
Similarity=0.851852 7
TTGTTGAGTTTG

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Consensus:

nTgTTGAtnTTG

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>Bacillus_Fam_80_52_6 Nr. of seq. 6 Alignment length(with gaps) = 58
Alignment score = 0.624904
GCF_000759675.1_ASM75967v1_genomic.fna_125:36622-37090 Satlength=469 Nr
of Repeats=9 RepeatLength=52 seed=CGGTCACTCA Num.seqs=9
Similarity=0.875356
0 -CGGTCACTCATAG--GGTAGATGAGAGCCCGAGAATAGTTAAAAGAAGGAAG-TG--
GCF_000759675.1_ASM75967v1_genomic.fna_130:33497-34016 Satlength=520 Nr
of Repeats=10 RepeatLength=52 seed=AGATGAGAGC Num.seqs=9
Similarity=0.860399
16 -CGGTCACTCATAG--GGTAGATGAGAGCCCGTGAATAGCTAAAAGAAGGAAG-AG--
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_134:133322-134102
Satlength=781 Nr of Repeats=15 RepeatLength=52 seed=AGTGACCGCT
Num.seqs=15 Similarity=0.888889
8 -CGGTCACTCATAA--AGTAGATGAGAGCCCGNGAATAGCAAAAAGAAGAAAG-AG--
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_134:112507-112871
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=ATGAGTGACC Num.seqs=7
Similarity=0.958486 11 -
TGGTCACTCATAGC-GGT-TATGAGAGCCCGGAAACAGCAAAAAGGAGAAAG-AG--
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_151:23767-24183
Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=TCATCACCTT Num.seqs=8
Similarity=0.877289 22 -
CGGTCACTCATAA-AGGT-GATGAGAGCCCGAAGACTGCAAAAAGAAG--AGCTGA-
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_153:338216-338424
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TAAGATTACG Num.seqs=4
Similarity=0.965812 38
GCGGTCACTCATAA-GGGTA-ATGAGAGCCCGT-AAT-CTTATAATAAG--AGCAGAA

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Consensus:

CGGTCACTCATAAgGTagATGAGAGCCCGngAAtaGcaAAAAGAAGnaAGaG

>Bacillus_Fam_81_52_6 Nr. of seq. 6 Alignment length(with gaps) = 57
Alignment score = 0.684016
GCF_000621445.1_ASM62144v1_genomic.fna_2:115234-115494 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=ATGAAGGACA Num.seqs=5
Similarity=0.823899
75 GAGAAAGTGCCTTCATAAAGG-GAATGAAGGACAAAAGTAGT--GAGAAAC-AG-AG
GCF_000621445.1_ASM62144v1_genomic.fna_2:130298-130558 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TGAAGGACAA Num.seqs=5
Similarity=0.920513
75 CAAAAGTGCCTTCATAAAGGNGA-TGAAGGACAAAACAAG---GAGAAAC-CGAAG
Rev.of_GCF_000621445.1_ASM62144v1_genomic.fna_3:128510-128771
Satlength=262 Nr of Repeats=5 RepeatLength=52 seed=ATGAAGGACA Num.seqs=4
Similarity=0.901709 119
CAAAAGTGCCTTCATAAAGGTGA-TGAAGGACAAAACAAG---GAGAAAG-CGAAG
Rev.of_GCF_000621445.1_ASM62144v1_genomic.fna_3:303079-303287
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TATGAAGGAC Num.seqs=4
Similarity=0.888889 120
CGAAAGTGCCTTCATAAAGGCGA-TGAAGGACAAAAGAAG---GAGAAAA-CGAAG
GCF_000621445.1_ASM62144v1_genomic.fna_20:46586-46794 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=AGAAAGTGTC Num.seqs=4 Similarity=0.828189
103 --AAAGTGCCTTCATAAAGGCGA-TGAAGGACAAAACGAG-AGGAAAAACTTG-AG

Rev.of_GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_19:114955-115475
Satlength=521 Nr of Repeats=9 RepeatLength=52 seed=ATGAAGGACT Num.seqs=7
Similarity=0.797766 83 --AGTGAATC-AGATGGAAAA-
AGTCCTTCATAGAGCTGA-TGAAGGACAAAACCAG

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Consensus:

GGAGAAAccGaAGcaAAAGTGTCTTCATAAAGGnGATGAAGGACAAAcaA

>Bacillus_Fam_82_52_6 Nr. of seq. 6 Alignment length(with gaps) = 57
Alignment score = 0.644444
GCF_000153365.1_ASM15336v1_genomic.fna_10:208343-208606 Satlength=264 Nr
of Repeats=5 RepeatLength=53 seed=AAAAGGAGCA Num.seqs=3
Similarity=0.855967
0 AAAAG-GAGCAGTCATGTATCCCGGGAGGAGTGC GGGATGCATGAG-TG-G-GTCGA
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2810130-2811347
Satlength=1218 Nr of Repeats=23 RepeatLength=53 seed=GA CTGCTCCT
Num.seqs=21 Similarity=0.867984
13 AAAAG-GAGCAGTCATGTATCCCGGGAGGAGTGC GGGATACATGAG-TG-G-GTCGA
GCF_000153365.1_ASM15336v1_genomic.fna_12:72983-73301 Satlength=319 Nr of
Repeats=6 RepeatLength=53 seed=TCATGTATTC Num.seqs=6 Similarity=0.948008
9 -GAAG-G-GCAGTCATGTATTCCGGGAGCGTTCCGGGATACATGAGCTGTG-CTCGG
GCF_000473245.1_ASM47324v1_genomic.fna_1:1054274-1054592 Satlength=319 Nr
of Repeats=6 RepeatLength=53 seed=TCATGTATTC Num.seqs=6
Similarity=0.948008 9
-GAAG-G-GCAGTCATGTATTCCGGGAGCGTTCCGGGATACATGAGCTGTG-CTCGG
Rev.of_GCF_000153365.1_ASM15336v1_genomic.fna_18:460556-461987
Satlength=1432 Nr of Repeats=27 RepeatLength=53 seed=ACTCATGTAC
Num.seqs=25 Similarity=0.833795
46 AAAAGAG-GAAGTCATGTATGCCGGGATCGTTTTGGAGTACATGAG-TG-GTGT-GA
GCF_000473245.1_ASM47324v1_genomic.fna_1:491395-492826 Satlength=1432 Nr
of Repeats=27 RepeatLength=53 seed=GTACATGAGT Num.seqs=27
Similarity=0.833934 89
AAAAGAG-GAAGTCATGTATGCCGGGATCGTTTTGGAGTACATGAG-TG-GTGT-GA

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Consensus:

aaAAGGGcAGTCATGTATnCcGGGAgcgtTncGGgaTACATGAGTGGgTcGa

>Bacillus_Fam_83_52_6 Nr. of seq. 6 Alignment length(with gaps) = 56
Alignment score = 0.775397
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_23:1814-2438
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=AACCCATTTT
Num.seqs=12 Similarity=0.899276
0 AACC--CA-TTTTCGCGAAATCCTCTTCATTTTCGGCTCATAG-ACTCACTCTATG
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_23:79057-79681
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=TTCTATGAAC
Num.seqs=12 Similarity=0.757766
45 AACC-AC--TTTTCGCGAAATCCTCATCATTTTNGGCTCATAGAACTC-TTCTATG
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_24:6181-8365
Satlength=2185 Nr of Repeats=42 RepeatLength=52 seed=TTCTATGAAC

Num.seqs=42 Similarity=0.829254
 45 AACC-AC--TTTTCGCGAAATCCACATCATTTTCGGCTCATAGAACTC-TTCTATG
 GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_24:948-3548
 Satlength=2601 Nr of Repeats=50 RepeatLength=52 seed=TTCTATGAAC
 Num.seqs=50 Similarity=0.770286
 45 AACC-AC--TTTTCGTGAAATCCNCATCATTTTNGGCTCATAGAACTC-TTCTATG
 Rev.of_GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_41:405982-
 406190 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GGTTCATAGA
 Num.seqs=4 Similarity=0.769392 56
 AACCNAC--TTTTCGCGGAATCCCCATCATTTTCGGCTCATAGCACTC-TTCTATG
 Rev.of_GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_41:77609-78025
 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=GGTTCATAGA Num.seqs=8
 Similarity=0.812390 4 AACC--C-
 TTTTTTGC GGAATCCCAATCATTTTTGGCTCATAGANCAC-TTCTATG

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 Consensus:

AACCaCTTTTCGCGaAATCCnCATCATTTTcGGCTCATAGaACTCTTCTATG

>Bacillus_Fam_84_53_6 Nr. of seq. 6 Alignment length(with gaps) = 56
 Alignment score = 0.659127
 GCF_000708755.2_ASM70875v2_genomic.fna_2:1053748-1054173 Satlength=426 Nr
 of Repeats=8 RepeatLength=53 seed=CTTTGCTTAC Num.seqs=7
 Similarity=0.857442 0
 CTTTGCTTACCCTGCTNACCCGTTTTT-TCCGCT-TTGCTGGGTAAGATTC-CTCC
 GCF_000709935.2_ASM70993v2_genomic.fna_4:308519-308731 Satlength=213 Nr
 of Repeats=4 RepeatLength=53 seed=CTTTGCTTAC Num.seqs=4
 Similarity=0.836478
 0 CTTTGCTTACCCTGCTCACCCTTTTTT-TCCGCT-TTGCGGGTAGGATTC-CTCC
 GCF_000708755.2_ASM70875v2_genomic.fna_6:66915-67179 Satlength=265 Nr of
 Repeats=5 RepeatLength=53 seed=GGGTACGATT Num.seqs=4 Similarity=0.878407
 38 CTTTGCTTACCCTGCCATGCCGTTTT-T-CACTCTTGCTGGGTACGATTC-ATCC
 Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_1:463602-463814
 Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=AGGGTAAGCA Num.seqs=4
 Similarity=0.878407 66
 TTTTGCTTACCCTCCCAATTCGGTTTTT-T-CGCTCTTGCTGGGTACGATTC-CGGC
 Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_22:9836-10048 Satlength=213
 Nr of Repeats=4 RepeatLength=53 seed=AAAAACGGTT Num.seqs=4
 Similarity=0.823899 26
 -TTTGCTTACCCACCCCAACCGTTTTT-T-CGGTCTAGCTGGGTACGATTCACCTCC
 GCF_000709935.2_ASM70993v2_genomic.fna_5:333641-333853 Satlength=213 Nr
 of Repeats=4 RepeatLength=53 seed=TTTGCTTACC Num.seqs=4
 Similarity=0.844864
 54 -TTTGCTTACCCTCCACCACC-TGGTTTTT-CGGCTTGCTGGGTACGATTCACCTCC

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 Consensus:

cTTTGCTTACCCTcCccAncCgtTTTTTCGcTcTTTGCTGGGTAcGATTCCTCC

>Bacillus_Fam_85_52_6 Nr. of seq. 6 Alignment length(with gaps) = 55
 Alignment score = 0.734949

GCF_000177235.2_ASM17723v2_genomic.fna_1:18889-19512 Satlength=624 Nr of Repeats=10 RepeatLength=52 seed=CACTCAACGA Num.seqs=7
 Similarity=0.815403
 0 CACTCAACGAAGGTAATCAT--AGTAAGCCAATGCTACCCCAAAA-CCAAACCCG
 GCF_000177235.2_ASM17723v2_genomic.fna_1:2263203-2263619 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=AAGGTAATCA Num.seqs=8
 Similarity=0.794974 9
 CACTCAACAAAGGTAATCATA-AGCAAG-CAATGCTACCCCAAAA-CCAAACCCG
 GCF_000177235.2_ASM17723v2_genomic.fna_1:44519-44779 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CAATGCTACC Num.seqs=5 Similarity=0.752830
 27 CACTCAACGAAGGTCATCATA-NGCAAG-CAATGCTACCCCAAAA-GCTAATCCT
 GCF_000177235.2_ASM17723v2_genomic.fna_1:113351-113768 Satlength=418 Nr of Repeats=8 RepeatLength=52 seed=AAGGTCATCA Num.seqs=7
 Similarity=0.714286
 61 CACTCAACGAAGGTCATCATA-AGCAAG-CAATGCTNCCCCAAAA-CCAAANCCN
 Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:2555929-2556137
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AGCATTGCTT Num.seqs=4
 Similarity=0.691468 34
 CATTCAACGAAGGTCATCATAGAG-AAG-CAATGCTGCCCCAAAAGCCAAACCT-
 Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:2730527-2730944
 Satlength=418 Nr of Repeats=8 RepeatLength=52 seed=CTATGATGAC Num.seqs=7
 Similarity=0.678424 74
 CAATCCACGAAGGTCATCATAGAG-AAG-CAATGCTGCCCCGAAAATCCAAAANN-

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Consensus:

CAcTCAACGAAGGTcATCATAAGcAAGCAATGCTaCCCCAAAACCAAACcn

>Bacillus_Fam_86_53_6 Nr. of seq. 6 Alignment length(with gaps) = 55
 Alignment score = 0.654545
 GCF_001636335.1_ASM163633v1_genomic.fna_1:186192-186660 Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=CTAGATTTTC Num.seqs=9
 Similarity=0.938746
 0 CTAGA-TTTTCTGTTTCGTTTCGGGGTTCAATAGACCT-TATAGAAGCCCCCTTTTCG-
 GCF_001636335.1_ASM163633v1_genomic.fna_1:3084736-3085256 Satlength=521
 Nr of Repeats=10 RepeatLength=52 seed=AAGACTCTTT Num.seqs=10
 Similarity=0.920798 40
 CTGGATTTTTCG-TCGTTTCGGGGTTCTATACACCT-TATTGAAGACTCTTTTCG-
 Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:1182339-1183064
 Satlength=726 Nr of Repeats=14 RepeatLength=52 seed=TCAATAAGGT
 Num.seqs=12 Similarity=0.878399
 40 C--GATTTTCTGTTCATTTCAGGGCTCTATACACCT-TATTGAAGACTCTTTCAA
 GCF_001636335.1_ASM163633v1_genomic.fna_1:3149857-3150741 Satlength=885
 Nr of Repeats=17 RepeatLength=52 seed=ATTGAGGACT Num.seqs=17
 Similarity=0.854638 87
 CT-GA-TTTTCTGTTTCGTTTCGGGCCTCTATACGGCT-GATTGAGGACTCTTTTCAT
 Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_2:190727-191455
 Satlength=729 Nr of Repeats=14 RepeatLength=52 seed=AACGAAAAAA
 Num.seqs=14 Similarity=0.822203
 13 CT-ATTTTTTC-GTTCGTTTCGGGGTTCTAT-CTGCNCTATTGAGGACTCTTTTCG
 Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_2:192943-193202
 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=AAGAGTCCTC Num.seqs=4

Similarity=0.914530

48

CT-GTTTTTTC-GTTCGTTTCGGGGTCTAT-CTGCTCTATTGAGGACTCTTCCGC

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Consensus:

CTGatTTTTcTGTTCGTTTCGGGGtTCTATaCacCTTATTGAaGACTCTTTCgn

>Bacillus_Fam_87_52_6 Nr. of seq. 6 Alignment length(with gaps) = 53

Alignment score = 0.628512

GCF_001636315.1_ASM163631v1_genomic.fna_1:2367649-2367858 Satlength=210

Nr of Repeats=4 RepeatLength=52 seed=TCTACGTTAC Num.seqs=3

Similarity=0.717172

0

TCTACGTTACCCAA-GCC-CTATTTTTCTCCGNTTCGGGCACCTAGAACCCC

GCF_001636315.1_ASM163631v1_genomic.fna_1:247094-247354 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=AACCTCTCTA Num.seqs=5

Similarity=0.910256

46 TCTACGTGACCACACGAC-CACATTTTCATCCGGTTCGGTCACGTAGAACCTC

GCF_001636315.1_ASM163631v1_genomic.fna_1:263113-263529 Satlength=417 Nr

of Repeats=8 RepeatLength=52 seed=ACCTTTTCT Num.seqs=8

Similarity=0.888278

70 TCTACGTGACCCAACATC-ACCTTTTCTTCNGCTACGGTCACGTAGAACCTC

GCF_001636315.1_ASM163631v1_genomic.fna_1:4729327-4729587 Satlength=261

Nr of Repeats=5 RepeatLength=52 seed=TCTACGTGAC Num.seqs=5

Similarity=0.871795

104

TCTACGTGACCGAACAAAC-CCCTTTTTCTTCGGCTACGGTCACGTAGAACCTC

GCF_000612665.1_FF4_genomic.fna_50:1971-2335 Satlength=365 Nr of

Repeats=6 RepeatLength=52 seed=TGTTTTTCGGT Num.seqs=5 Similarity=0.897436

29 TCTACGTGACCCATTTTCATTCTTTCTTCT-GTTTTTCGGTCGCGTAGAACCCC

GCF_000612665.1_FF4_genomic.fna_72:27-391 Satlength=365 Nr of Repeats=7

RepeatLength=52 seed=TCTACGTGAC Num.seqs=7 Similarity=0.823300

53 TCTACGTGACCC-GTGTCACTGGTTTTTATCCATTTCGGTCGCGTAGAACCTC

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Consensus:

TCTACGTGACCcaacgtCctctTTTTcnTCcgnTtCGGTCaCGTAGAACcTc

>Bacillus_Fam_88_52_6 Nr. of seq. 6 Alignment length(with gaps) = 53

Alignment score = 0.782809

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:97548-97860

Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GTCAATCGTT Num.seqs=6

Similarity=0.803145

0

GTCAATCGTTACCGTTTTCACAGTAGATCAACTCATTACGGGCACGATTC-ACC

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2964303-2964563

Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CAATCGTTAC Num.seqs=5

Similarity=0.928205

2

GTCAATCGTTACCGTTTTCACAGAAGATCAGCTCATTACGGGCACGATTC-AGT

Rev.of_GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3681028-3687820

Satlength=6793 Nr of Repeats=123 RepeatLength=52 seed=AATGAGTTGA

Num.seqs=122 Similarity=0.935809

36

GTCAATCGTTACCGTTTTCACAGAAGTTCAACTCATTATGGGCACGATTC-AGT

Rev.of_GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3691066-3691326

Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GAATCGTGCC Num.seqs=5

Similarity=0.900000 49
GTCAATCGTTACCGTTTCACAGAAGTTCAACTCATTATGGGCACGATTC-AGT
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:1865881-1866297
Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=AGAAGATCAG Num.seqs=8
Similarity=0.939560 20
GTCAATCGTTACCATTTTCACAGAAGATCAGTGCATTACGGGCACGATTC-AGC
Rev.of_GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3933103-3935130
Satlength=2028 Nr of Repeats=39 RepeatLength=52 seed=GAATCGTTCC
Num.seqs=38 Similarity=0.998650 48 CT-
TATCGTTACCGTTTTTCCGGAGTTCATCACATAACGGGAACGATTCAAGA

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Consensus:

GTCAATCGTTACCGTTTCACAGaAGaTCAaCtCATTAcGGGCACGATTCAGt

>Bacillus_Fam_89_53_6 Nr. of seq. 6 Alignment length(with gaps) = 53
Alignment score = 0.780503
GCF_001439965.1_ASM143996v1_genomic.fna_104:39216-39670 Satlength=455 Nr
of Repeats=9 RepeatLength=52 seed=AGCAAAAATG Num.seqs=7
Similarity=0.803235
0 AG-CAAAAATGTGTGTCCAAGGCGGAAGTGGAGACACATTACGAAGGAAAAAC
GCF_001887185.1_ASM188718v1_genomic.fna_175:122798-123214 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=AGTGGAGACA Num.seqs=8
Similarity=0.709821 25
AG-CAACAATGTGTGTCCAAGGCGNAAGTGGAGACACATGACGAAGGAAAAAC
GCF_002009555.1_ASM200955v1_genomic.fna_90:39540-39956 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=AGTGGAGACA Num.seqs=8
Similarity=0.709821
25 AG-CAACAATGTGTGTCCAAGGCGNAAGTGGAGACACATGACGAAGGAAAAAC
GCF_001439965.1_ASM143996v1_genomic.fna_125:141897-142307 Satlength=411
Nr of Repeats=8 RepeatLength=52 seed=AAAAATGTGTG Num.seqs=7
Similarity=0.755189 5
GGTCAAAAATGTGTGTCCAAGGNGAGAGTGGAGACAGATAATGAGGAAAAAA-
Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_334:40008-40529
Satlength=522 Nr of Repeats=10 RepeatLength=52 seed=TGTCTCCACT
Num.seqs=9 Similarity=0.772792
36 GGTCAAAAATGTGTGTCTCAGAGGNGAGAGTGGAGACAGATAATGAGGAAAAAA-
GCF_001887185.1_ASM188718v1_genomic.fna_106:36381-37057 Satlength=677 Nr
of Repeats=13 RepeatLength=52 seed=AGTGGAGACA Num.seqs=13
Similarity=0.812623 26
GGNCAAAAATGTGTGTCCAAGGCAAGAGTGGAGACAGATAATGAGGGAAAAA-

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Consensus:

aGnCAAaAATGTGTGTCCAAGGcGaaAGTGGAGACAcATaAcGAaGgAAAAAc

>Bacillus_Fam_90_42_6 Nr. of seq. 6 Alignment length(with gaps) = 42
Alignment score = 0.812169
GCF_000007825.1_ASM782v1_genomic.fna_1:4624384-4624759 Satlength=376 Nr
of Repeats=9 RepeatLength=42 seed=TCTTCCACTT Num.seqs=8
Similarity=0.875283
0 TCTTCCACTTGTGGTTCTACTACCACCTGCTGCACTGGGCGT

GCF_000831065.1_ASM83106v1_genomic.fna_1:4382555-4382849 Satlength=295 Nr of Repeats=7 RepeatLength=42 seed=TCTTCCACTT Num.seqs=7
 Similarity=0.860922 0
 TCTTCCACTTGTGGTTCTGCTACTACTTGCTGCACTGGGTGC
 GCF_000007845.1_ASM784v1_genomic.fna_1:4485994-4486366 Satlength=373 Nr of Repeats=9 RepeatLength=42 seed=TCTTCCACTT Num.seqs=7
 Similarity=0.900227
 0 TCTTCCACTTGTGGTTCCACTACTACTTGCTGCACTGGGTTTT
 Rev.of_GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_2:177294-177504 Satlength=211 Nr of Repeats=5 RepeatLength=42 seed=GAACCACAAG Num.seqs=5 Similarity=0.892063 17
 TCTTCCACTTGTGGTTCCACTACTACTTGCTGCACTGGGTTTT
 Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:1288569-1288821 Satlength=253 Nr of Repeats=6 RepeatLength=42 seed=TGCAGCAAGT Num.seqs=6 Similarity=0.833850 34
 TCTTCCACTTGNGGTTCTACTACCACTTGCTGCATCGGTTTT
 Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:181687-181855 Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=TGCAGCAAGT Num.seqs=4 Similarity=0.825397 34
 TCTTCTGCTTGTGGTTCTACTACCACTTGCTGCATTGGCTTT

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Consensus:

TCTTCCACTTGTGGTTCTACTACcACTTGCTGCACtGGtTtT

>Bacillus_Fam_91_20_6 Nr. of seq. 6 Alignment length(with gaps) = 22
 Alignment score = 0.625758
 GCF_001712755.1_ASM171275v1_genomic.fna_4:95498-95778 Satlength=281 Nr of Repeats=14 RepeatLength=20 seed=AATTTAATTG Num.seqs=14
 Similarity=0.761120
 8 ATACCCGGAA-TTTAATTGC-G
 GCF_001712755.1_ASM171275v1_genomic.fna_4:102562-102861 Satlength=300 Nr of Repeats=14 RepeatLength=20 seed=GAAATTAATT Num.seqs=13
 Similarity=0.916239 27
 ATTCACGGAA-ATTAATTGC-G
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_32:127615-127715 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=GCAATTAAAT Num.seqs=3
 Similarity=0.866667 19
 ATTCTCTTAA-TTTAATTGC-G
 GCF_001712755.1_ASM171275v1_genomic.fna_2:242324-242407 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTTAATTGCA Num.seqs=3
 Similarity=0.626263
 31 ATTCNCTAGA-TTTAATTGCAG
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_13:327923-328123 Satlength=201 Nr of Repeats=10 RepeatLength=20 seed=CGCAATTAAA Num.seqs=8 Similarity=0.668831
 41 ATTCTCTAGATTTTAATTGC-G
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_32:95561-95681 Satlength=121 Nr of Repeats=6 RepeatLength=20 seed=GCAATTAAAA Num.seqs=4
 Similarity=0.753968 19
 GTTTTTCGG-ATTTTAATTGC-G

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Consensus:

aATTTAATTGCGATTCTcgg

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>Bacillus_Fam_92_21_6  Nr. of seq. 6 Alignment length(with gaps) = 22
Alignment score = 0.633333
GCF_000175075.1_ASM17507v1_genomic.fna_2:18020-18125 Satlength=106 Nr of
Repeats=5 RepeatLength=21 seed=AAGTCGGAAT Num.seqs=5 Similarity=0.828571
0   AAGTCGGAAT-TCGGCGGAATA
GCF_000307875.1_BABA1.0_genomic.fna_123:41009-41093 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=4 Similarity=0.506667
10  AACTAGAAAG-TTGGCGGAATA
Rev.of_GCF_001591445.1_ASM159144v1_genomic.fna_38:10093-10301
Satlength=209 Nr of Repeats=7 RepeatLength=21 seed=ATTCCGCCAA Num.seqs=5
Similarity=0.556944                                     20
AACTAGTAAN-TTGGCGGAATA
GCF_001591665.1_ASM159166v1_genomic.fna_21:145523-145647 Satlength=125 Nr
of Repeats=4 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=3
Similarity=0.516908                                     10
AACT-CAAANNTTGGCGGAATN
GCF_001591665.1_ASM159166v1_genomic.fna_16:71486-71593 Satlength=108 Nr
of Repeats=5 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=4
Similarity=0.585648
10  AAAGTCAAAN-TTGGCGGAATA
GCF_001591665.1_ASM159166v1_genomic.fna_21:87303-87605 Satlength=303 Nr
of Repeats=11 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=10
Similarity=0.478905                                     10
AANGNANAAG-TTGGCGGAATA
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Consensus:

AActngaAAAnTTGGCGGAATA

```
>Bacillus_Fam_93_21_6  Nr. of seq. 6 Alignment length(with gaps) = 22
Alignment score = 0.603030
GCF_001889165.1_ASM188916v1_genomic.fna_1:473933-474227 Satlength=295 Nr
of Repeats=14 RepeatLength=21 seed=ATCGCGGAAT Num.seqs=14
Similarity=0.849294                                     0
ATCGCG-GAAAGGAGTGCCGGA
GCF_001889165.1_ASM188916v1_genomic.fna_1:757324-757654 Satlength=331 Nr
of Repeats=6 RepeatLength=21 seed=GAATCGCGGA Num.seqs=5
Similarity=0.873016
19  ATCGCG-GAAAGAGGTGCCGGA
Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:3509098-3509350
Satlength=253 Nr of Repeats=12 RepeatLength=21 seed=TCCGCGATTA
Num.seqs=12 Similarity=0.755599
29  ATCGCG-GAAAGAGGTGCCGTA
GCF_001889165.1_ASM188916v1_genomic.fna_1:684231-684378 Satlength=148 Nr
of Repeats=7 RepeatLength=21 seed=GAATCGCGGA Num.seqs=7
Similarity=0.927438
19  ATCGCG-GAAAGAGAGGTCCGGA
Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:3632787-3633039
Satlength=253 Nr of Repeats=12 RepeatLength=21 seed=TCCGCGATTCT
```

Num.seqs=12 Similarity=0.772957

8 ATCGCG-GATAGGAGNGTCGGA

Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:3348404-3348982

Satlength=579 Nr of Repeats=18 RepeatLength=21 seed=CTTTCGCGA

Num.seqs=16 Similarity=0.700116

3 AAGGGGTGATGGAATCG-CGGA

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Consensus:

ATCGCGGAaAGaagtGcCGGA

>Bacillus_Fam_94_21_6 Nr. of seq. 6 Alignment length(with gaps) = 21

Alignment score = 0.647619

GCF_000508325.1_BAVI_1_genomic.fna_103:54980-55146 Satlength=167 Nr of Repeats=7 RepeatLength=21 seed=ATTTGCGCAA Num.seqs=6 Similarity=0.517460

0 ATTTGCGCAAACCTNACGNTTA

GCF_001591805.1_ASM159180v1_genomic.fna_7:208460-208544 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTATTTCGCC Num.seqs=4

Similarity=0.640212

19 ATTTGCGCAAACCTCAGGATTT

GCF_001591805.1_ASM159180v1_genomic.fna_5:205275-205400 Satlength=126 Nr of Repeats=6 RepeatLength=21 seed=ATTTGCGCAA Num.seqs=5

Similarity=0.822222

0 ATTTGCGCAAACCNAGCAATA

GCF_001591445.1_ASM159144v1_genomic.fna_22:80175-80280 Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=ATTCCGCCAA Num.seqs=5

Similarity=0.473611

0 ATTCCGCCAAATNNCNGATTT

Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_21:177804-177908

Satlength=105 Nr of Repeats=5 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=3 Similarity=0.727273 10

ATTCCGCCAAACTTCGGATTA

Rev.of_GCF_001591445.1_ASM159144v1_genomic.fna_25:3465-3548 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=3

Similarity=0.430556 10

ATTCCGCCAANTNGCNATTT

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Consensus:

ATTcCGCCAAACtnaggATTa

>Bacillus_Fam_95_20_6 Nr. of seq. 6 Alignment length(with gaps) = 20

Alignment score = 0.731111

GCF_000374565.1_ASM37456v1_genomic.fna_3:124095-124776 Satlength=682 Nr of Repeats=32 RepeatLength=20 seed=ATACTCTTCA Num.seqs=22

Similarity=0.695355 0

ATACTCTTCACATTTGCGAA

GCF_000374565.1_ASM37456v1_genomic.fna_18:12540-13648 Satlength=1109 Nr of Repeats=51 RepeatLength=20 seed=ATACTCTTCA Num.seqs=33

Similarity=0.575442 0

ATACTCTTCANAATTCAGAA

Rev.of_GCF_000374565.1_ASM37456v1_genomic.fna_4:170298-171100
 Satlength=803 Nr of Repeats=32 RepeatLength=20 seed=AAGAGTATTT
 Num.seqs=23 Similarity=0.639118
 8 ATACTCTTCACTTTCAAGNA
 Rev.of_GCF_000374565.1_ASM37456v1_genomic.fna_30:38245-38545
 Satlength=301 Nr of Repeats=14 RepeatLength=20 seed=AAGTGAAGAG
 Num.seqs=13 Similarity=0.779487
 13 ATACTCTTCACTTTTCGGGAA
 GCF_000374565.1_ASM37456v1_genomic.fna_34:28543-28664 Satlength=122 Nr of
 Repeats=5 RepeatLength=20 seed=TACTCTTCAC Num.seqs=3 Similarity=0.777778
 21 TTACTCTTCACTTTTCGAGAA
 Rev.of_GCF_000374565.1_ASM37456v1_genomic.fna_38:0-139 Satlength=140 Nr
 of Repeats=7 RepeatLength=20 seed=AAGTGAAGAG Num.seqs=7
 Similarity=0.888889
 13 ATACTCTTCACTTTCCGCAA

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Consensus:

ATACTCTTCACTTTcgaGAA

>Bacillus_Fam_96_15_6 Nr. of seq. 6 Alignment length(with gaps) = 15
 Alignment score = 0.751111
 GCF_000007825.1_ASM782v1_genomic.fna_1:953796-953898 Satlength=103 Nr of
 Repeats=4 RepeatLength=15 seed=TAAACAAGAA Num.seqs=3 Similarity=0.644444
 0 TAAACAAGAAAATAC
 GCF_000831065.1_ASM83106v1_genomic.fna_1:794707-794809 Satlength=103 Nr
 of Repeats=4 RepeatLength=15 seed=TAAACAAGAA Num.seqs=3
 Similarity=0.644444
 0 TAAACAAGAAAATAC
 Rev.of_GCF_000831065.1_ASM83106v1_genomic.fna_2:182684-182786
 Satlength=103 Nr of Repeats=4 RepeatLength=15 seed=TTCTTGTTTA Num.seqs=3
 Similarity=0.644444 10
 TAAACAAGAAAATAC
 GCF_000225265.1_ASM22526v1_genomic.fna_1:1128295-1128356 Satlength=62 Nr
 of Repeats=4 RepeatLength=15 seed=AAAAGAAAAA Num.seqs=3
 Similarity=0.847222
 3 TGAAAAAGAAAAAGC
 GCF_000474275.1_Bmar1.0_genomic.fna_8:157466-157541 Satlength=76 Nr of
 Repeats=5 RepeatLength=15 seed=AAATAGAAAA Num.seqs=5 Similarity=1.000000
 17 TAAATAGAAAAAGC
 Rev.of_GCF_000712615.1_ASM71261v1_genomic.fna_2:274011-274086
 Satlength=76 Nr of Repeats=5 RepeatLength=15 seed=TCTTCTTTTT Num.seqs=5
 Similarity=0.822222 12
 TAAAAAAGAAGAAGC

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Consensus:

TAAAaAAGAAAAaC

>Bacillus_Fam_97_12_6 Nr. of seq. 6 Alignment length(with gaps) = 12
 Alignment score = 0.807407

GCF_000311725.1_ASM31172v1_genomic.fna_9:43921-43981 Satlength=61 Nr of Repeats=5 RepeatLength=12 seed=GGTTCTGGCT Num.seqs=5 Similarity=1.000000
0 GGTCTGGCTTT
Rev.of_GCF_001700275.1_ASM170027v1_genomic.fna_45:377163-377241
Satlength=79 Nr of Repeats=4 RepeatLength=12 seed=CCAAAGCCAG Num.seqs=3
Similarity=1.000000 2
GGTCTGGCTTT
Rev.of_GCF_001439635.1_ASM143963v1_genomic.fna_175:44104-44236
Satlength=133 Nr of Repeats=9 RepeatLength=12 seed=GAACCAGAAC Num.seqs=6
Similarity=0.814815 5
GGTCTGGCTTT
GCF_000972245.2_ASM97224v2_genomic.fna_1:3422882-3423134 Satlength=253 Nr of Repeats=21 RepeatLength=12 seed=GGATTTGGTT Num.seqs=21
Similarity=0.971429 6
GGTCTGGATTT
Rev.of_GCF_001742425.1_ASM174242v1_genomic.fna_25:16787-17924
Satlength=1138 Nr of Repeats=16 RepeatLength=12 seed=CCAGAACCAA
Num.seqs=10 Similarity=0.775309
8 GGTCTGGTTTT
Rev.of_GCF_000612805.1_FF3_genomic.fna_1:431588-431636 Satlength=49 Nr of Repeats=4 RepeatLength=12 seed=CCAGAGCCAA Num.seqs=4 Similarity=0.888889
2 GGCTTTGGCTCT

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Consensus:

GGTCTGGcTTT

>Bacillus_Fam_98_52_5 Nr. of seq. 5 Alignment length(with gaps) = 61
Alignment score = 0.610929
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_2:72771-73392
Satlength=622 Nr of Repeats=12 RepeatLength=52 seed=TCATGGCGAC 78
Num.seqs=10 Similarity=0.852422
TNTCA-ATTTT-CGGCTT-CATG-AA-CCC-TTCATGGCGACCA--TTTTCT-TCTCTGGT
Rev.of_GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_9:73399-73710 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=GAAAAATGGT
Num.seqs=5 Similarity=0.848718 95 TC-
CTGATTTT-CGGCTT-CATG-AAGCGC-T-CATGGCGACCAT-TTTTCT--CTTTGCT
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:1168663-1168919
Satlength=257 Nr of Repeats=5 RepeatLength=52 seed=GAAAAATGGT Num.seqs=3
Similarity=0.811966 95 TC-
CTGATTTT-CGGCTT-CATG-AAGTGC-T-CATGGCGACCAT-TTTTCT--CTTTGCT
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:900085-900448
Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=TGAAGCCGAA Num.seqs=6
Similarity=0.810256 121
TC-CT--TTTT-CGGCTT-CATG--AGAGCTT-CATGGCGACCAT-TTTTCTGGCTCTGGT
Rev.of_GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_4:197835-198199 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=ATGAAGCCGA
Num.seqs=7 Similarity=0.710758 83
TTTCT---TATCGCTNC-ACG-ACTTTTCGGCTTCATG-ACTGC-CT-CATGGCGACCG-T

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Consensus:

tttctnctctGnTTcCtatTtTcggcttCatgaagngctcatgGcgaccatT

>Bacillus_Fam_99_61_5 Nr. of seq. 5 Alignment length(with gaps) = 61
Alignment score = 0.663934
GCF_000161455.1_ASM16145v1_genomic.fna_1:4024244-4024484 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=CCTGTTTGCA Num.seqs=4
Similarity=0.752205 0
CCTGTTTGCAATGCTCCGCTTCCGTTGAAGTAGTACCATGTACCG-TTAATTGCTTGCCAG
Rev.of_GCF_000496285.1_ASM49628v1_genomic.fna_1:4380225-4380585
Satlength=361 Nr of Repeats=6 RepeatLength=60 seed=GCGATGCAAA Num.seqs=6
Similarity=0.896296 14
CCTGTTTGCAATGCTCCGCTTCCGTTGAAGTAATACCATGTCCGTTTACCTGC-TGCCAA
GCF_000712595.1_ASM71259v1_genomic.fna_14:75165-75465 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=TTTGCAATTGC Num.seqs=5 Similarity=0.806557
4 CCTTTTTGCATTGCACCGTTTCCATTAAAGTAGTACCATGTCCATTTA-TTGCTTGCCAA
Rev.of_GCF_000712595.1_ASM71259v1_genomic.fna_10:96270-96750
Satlength=481 Nr of Repeats=8 RepeatLength=60 seed=ACATGGTACT Num.seqs=8
Similarity=0.801587 41
CCTGTTTGCAATGTACCGTTTTTCGTTTAAAGTAGTACCATGTCCACCAATTTG-TTTCCAT
Rev.of_GCF_000496285.1_ASM49628v1_genomic.fna_1:3570725-3571145
Satlength=421 Nr of Repeats=7 RepeatLength=60 seed=TGGCAATCAA Num.seqs=7
Similarity=0.880423 59
CCNGTTAACATTGCACCTTCACCATTTAAGTAGTACCATTTACCACCTA-TTGATTGCCAA

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Consensus:

CCTgTTtgCATtGcaCCgttttcCgTTnAAGTAgTACCATGgttCCanttAntTGctTgCCAA

>Bacillus_Fam_100_52_5 Nr. of seq. 5 Alignment length(with gaps) = 59
Alignment score = 0.628531
GCF_000759675.1_ASM75967v1_genomic.fna_48:7-215 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AGAGTGTGCC Num.seqs=4 Similarity=0.888889
0 AG-AGTGTGCCTAGTGACC-AAAAG---TAAGAT-AGGAATCCATAGAAAGTGGTCACA-
GCF_000759675.1_ASM75967v1_genomic.fna_150:19-279 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GTGACCAAAA Num.seqs=5 Similarity=0.866667
12 AG-AGTGCCTAGTGACC-AAAAG---TAAGCT-CGGAATCCATAGAAAGTGGTCACA-
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_164:20-228 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=ACCACTTCTA Num.seqs=4
Similarity=0.850427 48
AG-AGTGTGTCTTGTGACC-AAAAG---TAAGCT-CGGAATCCATAGAAAGTGGTCACA-
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_151:544090-544350
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CTTGTGACCA Num.seqs=5
Similarity=0.879487 2
AGAAGTGA-CCTTGTGACC-AAACGCTGTAA--T--TGAAATCATAAAAGTGGTCACA-
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_154:26046-26254
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=ATGTGACCAC Num.seqs=4
Similarity=0.829060 52
AG-AGCGT-CCTTGTGACCAAAAAGC---AA--TGGTGATTTCATCAAAGTGGTCACAT

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Consensus:

AGAGtGtgcCTtGTGACCAAAaGtAAgnTngGAatcCAtagAAGTGGTCACA

>Bacillus_Fam_101_51_5 Nr. of seq. 5 Alignment length(with gaps) = 58
Alignment score = 0.637356
GCF_000813125.1_ASM81312v1_genomic.fna_86:7113-7633 Satlength=521 Nr of
Repeats=10 RepeatLength=52 seed=GGAATCGTGA Num.seqs=10
Similarity=0.880342
5 ACCTCGGAATCGTGACAGGTTTGGGTGT---G-AAA-GCCGAAAAGCTGTCAAGAAA
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_129:103315-103679
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TTTTCTTGAC Num.seqs=7
Similarity=0.802198 53
AGCCCGGAATCGTGACAGGTTNGGCAGT---G-AAA-GCCGAAAAGCTGTCAAGAAA
GCF_001315165.1_ASM131516v1_genomic.fna_31:17940-18200 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=AAAGCTGTCA Num.seqs=5
Similarity=0.887179
37 AGCACGGAATTATGACAGGTTT-GAAGTG--G-AAA-GCGGAAAAGCTGTCAAGAAA
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_134:126961-127481
Satlength=521 Nr of Repeats=9 RepeatLength=52 seed=CCAAAGCTGT Num.seqs=8
Similarity=0.808625 24
ACGAAGGAATTATGACAGCTTT-GGAGT---GTAAATGAAGAAAAGCTGTCAAGAAA
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_122:32607-32815
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TTTCTTGACA Num.seqs=4
Similarity=0.858974 52
ACAAAGGAATTGTGACAGGTAT-GAGGT-TCTG---A-GACCAAAAGCTGTCAAGAAA

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Consensus:

GGAATtgTGACAGgTttGnaGTGaaAGccgAAAAGCTGTCAAGAAAAccac

>Bacillus_Fam_102_52_5 Nr. of seq. 5 Alignment length(with gaps) = 58
Alignment score = 0.601149
GCF_001636315.1_ASM163631v1_genomic.fna_1:3520892-3521308 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=AGCCTATTGG Num.seqs=8
Similarity=0.868486 0
-AGCCTATTGGCGACATTTCTCTTAG-C-AAAAA--CAACAAAAGTGTTTCCAATAA-
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:3785428-3785688
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTGGAAACAC Num.seqs=5
Similarity=0.820513 49 -
GGCCTATTGGCGACATTTCTCTTAG-C-AAAAG--CAACAAAAGTGTTTCCAATGG-
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:3568862-3569174
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=ATAGAAATGT Num.seqs=6
Similarity=0.849573 21 -AG-
CTATTGGCGACATTTCTATT--CAAAAAGT-CAACATAAGTGTTTCCAATGGC
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:3535170-3535534
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GTTGTAATTT Num.seqs=7
Similarity=0.894994 35 CGG-
CTATTGCCGACAATACT-CTAG--AAAATTACAACCAAAGTGTTTCCAATGG-
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:3851718-3851925
Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=CTATTGGAAA Num.seqs=3
Similarity=0.897436 52 CCG-
GTATTGGCGACAATACT-TGAGTT-AAAATTGGA--CAAAGTGTTTCCAATAG-

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Consensus:

nGcTATTGgCGACAtTtCTnttagcAAAAntcAacaaAAGTGTTTCCAATgg

>Bacillus_Fam_103_53_5 Nr. of seq. 5 Alignment length(with gaps) = 57
Alignment score = 0.626901
GCF_000708755.2_ASM70875v2_genomic.fna_1:37544-37809 Satlength=266 Nr of
Repeats=4 RepeatLength=53 seed=CACTCGGTGT Num.seqs=3 Similarity=0.730453
0 CACTCGGTGT-AGTGGCGCCACAAACAAGG-NTCCAAGT-NCGAG-AAAAGTGGTAT
GCF_000709935.2_ASM70993v2_genomic.fna_1:37723-37935 Satlength=213 Nr of
Repeats=4 RepeatLength=53 seed=CACTCGGTGT Num.seqs=4 Similarity=0.715278
0 CACTCGGTGT-AGTGGCGCCACAAACAAGG-ATCCAAGT-GCAGG-AAAAGTGGCAT
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:860672-860884
Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=TCATTTGTGG Num.seqs=4
Similarity=0.790356 27
CACTCTGGGT-AGTGGTGCCACAAATGAGGTAAAC---TCACGAGAAAAAGTGGCAG
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_4:114946-115370
Satlength=425 Nr of Repeats=8 RepeatLength=53 seed=CTGCCACTTT Num.seqs=6
Similarity=0.817191 53
CACTCGGGGT-AATGGTGCCACAAATGAGGTAAAC---TCACGAGAAAAAGTGGCAG
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_5:581943-582154
Satlength=212 Nr of Repeats=4 RepeatLength=53 seed=CTGCCACTTT Num.seqs=3
Similarity=0.714885 53
CACTC-GAGTGAGTGGCGCCAGAAAAGAGG-ATCC-A-TCACCTGAAAAAGTGGCAG

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Consensus:

CACTCgGnGTAgTGGcGCCAcAAAngAGGatcCaTcaCgaGaAAAAAGTGGcAg

>Bacillus_Fam_104_52_5 Nr. of seq. 5 Alignment length(with gaps) = 56
Alignment score = 0.618750
GCF_000813125.1_ASM81312v1_genomic.fna_40:52980-53241 Satlength=262 Nr of
Repeats=5 RepeatLength=52 seed=ATGACGGACA Num.seqs=4 Similarity=0.852201
0 ATGACGGACACTTTTCCTC--TGT-TTCCTTCGATTTCTGTCCGTCATG-GCCTTG
GCF_000813125.1_ASM81312v1_genomic.fna_88:27406-27823 Satlength=418 Nr of
Repeats=8 RepeatLength=52 seed=GATGACGGAC Num.seqs=7 Similarity=0.837607
51 ATGACGGACAGTTTT-NTCGAT-T-TTCCATCGATTTGTGTCCGTCATG-GCCTTG
GCF_000813125.1_ASM81312v1_genomic.fna_75:30268-30683 Satlength=416 Nr of
Repeats=8 RepeatLength=52 seed=CTGTCCGTCA Num.seqs=7 Similarity=0.828092
34 ATGACGGACACTTTTT-C-CGGNAC-TTCTCTAATTTCTGTCCGTCATG-ACCTTG
GCF_000813125.1_ASM81312v1_genomic.fna_122:22295-22555 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GATGACGGAC Num.seqs=5
Similarity=0.798148
51 ATGACGGACACTTTTT--TC-ATGAGTTCACGNGATTTCTGTCCGTCATA-GCCTNG
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_3:27965-28173
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=ATGACGGACA Num.seqs=4
Similarity=0.839099 96
ATGACGGACACTTTTT--GC-TTCTGTTTCGGTGATTTCTGTCCGTCATACCCCTT-

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Consensus:

ATGACGGACAcTTTTntCntntTTcCntngaTTTcTGTCCGTCATggCCTtg

>Bacillus_Fam_105_53_5 Nr. of seq. 5 Alignment length(with gaps) = 56
Alignment score = 0.664286
GCF_000153365.1_ASM15336v1_genomic.fna_15:302007-302379 Satlength=373 Nr
of Repeats=7 RepeatLength=53 seed=AGTCATGTAT Num.seqs=6
Similarity=0.859119
0 AGTCATGTATCCCAACAAGCA-TCC-GGGATACATAACAAGGCTGAGAAAAGAG-A
GCF_000473245.1_ASM47324v1_genomic.fna_1:1507348-1507827 Satlength=480 Nr
of Repeats=9 RepeatLength=53 seed=AGTCATGTAT Num.seqs=7
Similarity=0.868224 0
AGTCATGTATCCCACCGGGCA-TCC-GGGATACATAACCAGGCTGAGAAAAGAG-A
GCF_000153365.1_ASM15336v1_genomic.fna_16:360419-360896 Satlength=478 Nr
of Repeats=9 RepeatLength=53 seed=GGGATACATG Num.seqs=7
Similarity=0.940102
24 AGTCATGTACTTCAACAGGC--TCCTGGGATACATGACCCGGCCGTGCAAAGGG-A
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2449207-2449684
Satlength=478 Nr of Repeats=9 RepeatLength=53 seed=CCCTTTGCAC Num.seqs=9
Similarity=0.938505 52
AGTCATGTACTTCAACAGGC--TCCTGGGATACATGACCCGGCCGTGCAAAGGG-A
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:4524426-4525114
Satlength=689 Nr of Repeats=11 RepeatLength=53 seed=CTGCTTTTGG
Num.seqs=9 Similarity=0.870021
21 ACTCATGTATCCCAA-AAGCAGTCT-GAGATACATGACCCGGC-GAAAAAAGCGCA

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Consensus:

AgTCATGTAtccCAacagGCaTCcGgGATACATgACccGGCnGagaAAAAGnGA

>Bacillus_Fam_106_53_5 Nr. of seq. 5 Alignment length(with gaps) = 56
Alignment score = 0.671429
GCF_900156865.1_PRJEB18960_genomic.fna_3:359545-359916 Satlength=372 Nr
of Repeats=7 RepeatLength=53 seed=ATGGATAAAA Num.seqs=7
Similarity=0.881402
0 ATGGATAAAAATAGGAGAAAGCGAACCAGNAAAGGC-G-T-TAATCATCCACGCAA
Rev.of_GCF_900156865.1_PRJEB18960_genomic.fna_3:1976860-1977284
Satlength=425 Nr of Repeats=8 RepeatLength=53 seed=TCTCCTAATT Num.seqs=8
Similarity=0.739443 18
TTGGATGAAATTAGGAGAAAGCGAACCAGTAAAGTN-G-T-GAATCGTCCTCGCAC
Rev.of_GCF_900156865.1_PRJEB18960_genomic.fna_3:2163225-2163596
Satlength=372 Nr of Repeats=7 RepeatLength=53 seed=TCTCCTAATT Num.seqs=7
Similarity=0.766397 18
ATGGATGAAATTAGGAGAAAGCGAACCAGTAAAGT--G-TCGAATCATCCTCGCAA
GCF_900156865.1_PRJEB18960_genomic.fna_3:759210-759634 Satlength=425 Nr
of Repeats=8 RepeatLength=53 seed=TTGGATAAAA Num.seqs=8
Similarity=0.710097
0 TTGGATAAAAATTAGGNAAAGCGAACCCGCAAACTCNG-T--AATCATCCTTGCAA
Rev.of_GCF_900156865.1_PRJEB18960_genomic.fna_3:3854012-3854277
Satlength=266 Nr of Repeats=4 RepeatLength=53 seed=ATGCAAGGAC Num.seqs=3
Similarity=0.874214 0
TTGGGTAAATTTAGGAGAATGCGGACCTGTAAAGGCNGCT---TTCGTCCTTGCA

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Consensus:

tTGGaTaAAaAtTAGGaGAAaGCGaACCaGtAAAgTcGTnaaTCaTCcTcGCAa

>Bacillus_Fam_107_52_5 Nr. of seq. 5 Alignment length(with gaps) = 55
Alignment score = 0.752727
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:422934-423246 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=GAGTAAAGTA Num.seqs=6 Similarity=0.905660
0 GAGTAAAGTA-ACGAAAAGAGCCGAACGAGACAGTTACTCGGG-GGAAGTGAGA-
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_3:348761-349177 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=GAGTAAAGTA Num.seqs=8 Similarity=0.867925
0 GAGTAAAGTA-ACGAAAAGAGCCGAACGAGACAGTTACTCGAG-GGAAGTGAGT-
Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:81732-82096 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=AGTAACTGAC Num.seqs=7
Similarity=0.762204 38
GAGTAAAGTA-ACGAAAAGGGCNGAACGTGTCTAGTTACTCGAG-GGAAGTGAGT-
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:122808-123431 Satlength=624 Nr of
Repeats=12 RepeatLength=52 seed=GTAAAGTAAC Num.seqs=11
Similarity=0.794282 2
GAGTAAAGTA-ACGAAAAGAGGCGAACGAGNCAGTTACTCGAG-GGAAGT-AGNT
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:538341-538653 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=TGTCAGTTAC Num.seqs=6 Similarity=0.738272
27 AAGT-AAGTACACGAAAAGAGCTGAACATGTCTAGTTACT-GAGTGGTAGGGAGG-

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Consensus:

gAGTaAAGTAACGAAAAGaGccGAACgaGnCAGTTACTcGaGGGaAGtgAGn

>Bacillus_Fam_108_52_5 Nr. of seq. 5 Alignment length(with gaps) = 55
Alignment score = 0.681818
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:93343-93855 Satlength=513 Nr of
Repeats=9 RepeatLength=52 seed=TAATGTGCAG Num.seqs=8 Similarity=0.848160
0 TAATGTGCAGATACTGAG-GAGAAGAG-GGTAGTATCTGCACAAAGA-GGAGGC
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:78874-79289 Satlength=416 Nr of
Repeats=8 RepeatLength=52 seed=TTAATGTGCA Num.seqs=7 Similarity=0.858341
51 TAATGTGCAGATACGGAA-GAGAGAAG-GGAGAGTAACTGCACAAAGA-GGCGTT
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:376488-377061 Satlength=574 Nr of
Repeats=11 RepeatLength=52 seed=TAATGTGCAG Num.seqs=10
Similarity=0.793621 0
TAATGTGCAGATANGGAA-GAGAAAAG-AGCTAGTATCTGAACAAAAAGGGCGAT
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:354718-354978 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=GTATCTGCAC Num.seqs=5 Similarity=0.846154
31 TTATGTGCAGATAAGGAA-GAGT-AAGTAGCCGGTATCTGCACAAAGA-GTCGGT
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_16:108274-109024 Satlength=751 Nr
of Repeats=14 RepeatLength=52 seed=AGGCGGTTTA Num.seqs=13
Similarity=0.902435 45
TTATGTGCAGATACGGAAGGAGA-AAG-GGCTGGTATCTGTACAAAGA-GGCGGT

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Consensus:

Consensus:

TGGTAGTTAATCgAGAnGaaTAACGACGAAAAagacgaaggTCnAaGGAAaA

>Bacillus_Fam_111_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.714815
GCF_000708755.2_ASM70875v2_genomic.fna_2:1062403-1062663 Satlength=261 Nr
of Repeats=4 RepeatLength=52 seed=TTTGCTACCC Num.seqs=3
Similarity=0.777778 0
TTTGCTACCCCATATTTACCCG-CTCCGTTTTATAAGGATGCATTTTCTT-CT
GCF_000709935.2_ASM70993v2_genomic.fna_5:8490-8905 Satlength=416 Nr of
Repeats=7 RepeatLength=52 seed=TTTGCTACCC Num.seqs=5 Similarity=0.771069
0 TTTGCTACCCCATATTTACCCG-CTCCGTTTTATAAGGATGCATTTTCTT-CT
GCF_000708755.2_ASM70875v2_genomic.fna_6:445956-446216 Satlength=261 Nr
of Repeats=4 RepeatLength=52 seed=TTTCTTCCTT Num.seqs=3
Similarity=0.897436
43 TTTGCTACCCTATATTCGCTCA-CTCCGATTTATAAGGCAGCA-TTTCTTCCT
GCF_000709935.2_ASM70993v2_genomic.fna_5:651406-651666 Satlength=261 Nr
of Repeats=4 RepeatLength=52 seed=TTTCTTCCTT Num.seqs=3
Similarity=0.897436
43 TTTGCTACCCTATATTCGCTCA-CTCCGATTTATAAGGCAGCA-TTTCTTCCT
GCF_000709935.2_ASM70993v2_genomic.fna_15:49878-50085 Satlength=208 Nr of
Repeats=4 RepeatLength=52 seed=CCCATATTTTC Num.seqs=3 Similarity=0.725367
8 TTTGATACCCCATATTTTC-CGCATCCCATTTTTATAGGGATGCATTTTCNC-NT

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Consensus:

TTTGcTACCCcATATTtCnCnCaCtCcgTtTTATAaGGatGCAtTTTcttcT

>Bacillus_Fam_112_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.676543
GCF_000708755.2_ASM70875v2_genomic.fna_2:1371598-1372014 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=ACTTATCTCG Num.seqs=8
Similarity=0.817766 0
ACTTATCTCGTTTTTC-AGTACCACCAATTTCGGTCTTCCCCTT-CCTTGATGGC
GCF_000708755.2_ASM70875v2_genomic.fna_2:1674648-1674960 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=ACTTATCTCG Num.seqs=6
Similarity=0.808386 0
ACTTATCTCGGAGTTC-AGAACCACCAACACGCAGATTTCCCTT-TTTTGATGGC
GCF_000709935.2_ASM70993v2_genomic.fna_3:97017-97277 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=GATGGCACTT Num.seqs=5 Similarity=0.882051
46 ACTTATCTCGGAGTTC-AGAACCACCAACACGCAGATTTCCCTT-TTTTGATGGC
GCF_000708755.2_ASM70875v2_genomic.fna_6:335157-335781 Satlength=625 Nr
of Repeats=12 RepeatLength=52 seed=TTGATGGCAC Num.seqs=10
Similarity=0.807977 44
ACTTATCNCG-CTTACAAGTACCACCAA-ACTCAGAAATCCTTCTCTTGATGGC
GCF_000709935.2_ASM70993v2_genomic.fna_5:541475-541891 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=TTGATGGCAC Num.seqs=8
Similarity=0.799451
44 ACTTATCTCG-CTTACAAGTACCACCAA-ACTCAGAAATCCTTCTCTTGATGGC

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Consensus:

ACTTATCtCGnntTtCAGtACCACCAAnaCgcagatntCCTTtcTTGATGGC

>Bacillus_Fam_113_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.609877
GCF_001636315.1_ASM163631v1_genomic.fna_1:1832094-1832406 Satlength=313
Nr of Repeats=5 RepeatLength=52 seed=GACAGTTTTG Num.seqs=4
Similarity=0.846154 0
GACAGTTTTGCTAGTTTTTTGAAC-TG-GTTTTGTCTTCAAGAACTTATTGAA
GCF_001636315.1_ASM163631v1_genomic.fna_1:2472381-2472589 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=CTTATTGAAG Num.seqs=4
Similarity=0.897436 43
GACAGTTTTAGTAGTTTTTCGCAG-CG-GTTTTGTCTCCAAGAGGCCTTATTGAA
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:2851663-2851975
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GCATAAAAAA Num.seqs=6
Similarity=0.938462 24
GACAGTTTCGATGATTTTTTTATG-CT-GTTTTGTCTTCAAGACGGCTTATTGAA
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:2942377-2942588
Satlength=212 Nr of Repeats=4 RepeatLength=52 seed=AAACTGTCTT Num.seqs=3
Similarity=0.702306 8
GACAGTTTCTC-AATTTTTGTAG-GGCNGTTTGTCTCCAAGAANCCTTATTGAA
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:3763475-3763890
Satlength=416 Nr of Repeats=8 RepeatLength=52 seed=TGTCTTTAAT Num.seqs=5
Similarity=0.848718 4
GACA-TTTTCATAAGTTCCTAGGCCG-GGTTTGTCTTCTAGAAGCCTTATTAAA

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Consensus:

GACAgTTTnntaatTTttgaagcggTTTGTCTtCaAGAagcCTTATTgAA

>Bacillus_Fam_114_52_5 Nr. of seq. 5 Alignment length(with gaps) = 54
Alignment score = 0.701235
GCF_900156875.1_PRJEB18969_genomic.fna_11:799820-800080 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GATGAGAACC Num.seqs=5
Similarity=0.915385
51 ATGAGAACCGAAACAAACGAAACAAGAGAA-GGAAA-CGGTCTTCATCAAGGGG
GCF_900156875.1_PRJEB18969_genomic.fna_11:864748-865216 Satlength=469 Nr
of Repeats=9 RepeatLength=52 seed=TGAGAACCGA Num.seqs=9
Similarity=0.790598
53 ATGAGAACCGAAACAACCGCAACAAGAGAA-GGAAC-CGGTCTTCATCAAGAGG
Rev.of_GCF_900156875.1_PRJEB18969_genomic.fna_11:1169427-1169687
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=ATGAAGACCG Num.seqs=5
Similarity=0.884615 97
ATGAGAACCGAAACAATCGCAGCACGAGAA-GGGAA-CGGTCTTCATTAAGGGA
Rev.of_GCF_900156875.1_PRJEB18969_genomic.fna_11:892286-897590
Satlength=5305 Nr of Repeats=101 RepeatLength=52 seed=GATGAAGACC
Num.seqs=100 Similarity=0.834986
98 ATGAGAACCGTAACCTATCACTGCATGAGAA-GGAAA-CGGTCTTCATCATGGAG
Rev.of_GCF_900156875.1_PRJEB18969_genomic.fna_11:2645550-2646025
Satlength=476 Nr of Repeats=9 RepeatLength=53 seed=ACCGCTTTCC Num.seqs=7
Similarity=0.833921 92
ATGAAGACCGAAACCA-GGTAGGAAGAGAAGGGAAAGCGGTCTTCATNAAGAGA

Consensus :

gATGAgAACCGaAACaAncgcagcAaGAGAAGGaAaCGGTCTTCATcAaGgg

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>Bacillus_Fam_115_53_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.694969
GCF_001590785.1_ASM159078v1_genomic.fna_38:115242-115452 Satlength=211 Nr
of Repeats=4 RepeatLength=52 seed=GGTCAAAAGG Num.seqs=3
Similarity=0.445355 0
GGTCAAAAGGAGNAGCNCTATTACCCGAAAAGCGAG-CGNACCAAGAA--AC
GCF_001590785.1_ASM159078v1_genomic.fna_5:48221-48618 Satlength=398 Nr of
Repeats=8 RepeatLength=52 seed=AACGGTCAAA Num.seqs=6 Similarity=0.712103
49 GGTCAAAAGGAGAAGCGCTATTACCCGAAAAGAGAGCCGCATCA-GAAGAAC
Rev.of_GCF_001590785.1_ASM159078v1_genomic.fna_23:40421-40734
Satlength=314 Nr of Repeats=6 RepeatLength=52 seed=CCTTTTGACC Num.seqs=5
Similarity=0.883019 61
GGTCAAAAGGAGAAGCGCTATTACCCGAAAAGAGAGCCGCACCACGAAA-AC
GCF_001590785.1_ASM159078v1_genomic.fna_25:115-322 Satlength=208 Nr of
Repeats=4 RepeatLength=52 seed=GGTCAAAAGG Num.seqs=3 Similarity=0.675052
0 GGTCAAAAGGCGAAGCTCTATTACCCGAAAAAGGAGCTG-ANCNAGTAGAAC
Rev.of_GCF_001590785.1_ASM159078v1_genomic.fna_3:106756-107171
Satlength=416 Nr of Repeats=7 RepeatLength=52 seed=CCTTTTGACC Num.seqs=6
Similarity=0.797531 10
GGTCAAAAGGAAGAGCTCTATTACCTGAAAAAGNTGGTGAGCCAAGAA-AAG
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Consensus :

GGTCAAAGGagaAGCnCTATTCACcGAAAAqngaGccGnacCaaGaAnaAc

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>Bacillus_Fam_116_51_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.735220
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:381197-381605 Satlength=409 Nr of
Repeats=8 RepeatLength=51 seed=GAGTAACCCC Num.seqs=8 Similarity=0.881525
29 AATCGCGGGGTTGCTGG-TGAAAAA-AGNGGGAGTAACCCCGAGCAAACGGAG
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_10:100326-100580 Satlength=255 Nr
of Repeats=5 RepeatLength=51 seed=AACCCCGAGC Num.seqs=4
Similarity=0.839623 33
AATCGCGGGGTTGCGGG-CGTAAAA-AGAAGGAGTAACCCCGAGCAAACGGTG
Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:367038-367242
Satlength=205 Nr of Repeats=4 RepeatLength=51 seed=CCGTTTGCTC Num.seqs=4
Similarity=0.865385 49
AATCTCGGGGTACGGGCTGGAAAA-AGCAGGAGGAACCCCGAGCAAACGGAG
Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:392539-392794
Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=TTGCTCGGGT Num.seqs=5
Similarity=0.869281 45
AATCTCGGGGTTGCAGT-CGGAAAA-AGCAGGAGTAAACCCCGAGCAAACGTGG
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:184414-184771 Satlength=358 Nr of
Repeats=7 RepeatLength=51 seed=CCCGAGCAAA Num.seqs=7 Similarity=0.809219
7 GAGTAACCCCGAGCAAATGGA-AATACGCGGGGTTGCGAG-CAGAAAAAGNGG
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Consensus:

aAtcncggttgCnggnGnaAAaaGcaGGagtaacccccgAGcAAAcGgnG

>Bacillus_Fam_117_52_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.725786
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:475827-476186 Satlength=360 Nr of
Repeats=7 RepeatLength=51 seed=AGTAACTGAC Num.seqs=5 Similarity=0.926923
0 AGTAACTGACACGTTTCAGGCGTTTTTCGTGTAGTTACTCACGCC-ACCCCTCC-
Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_4:117009-117217
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GAGTAACTAC Num.seqs=4
Similarity=0.948718 38
AGTAACTGTCATGTTTCAGCCTTTTTTCGTGTAGTTACTCACCTT-CTTCCTTCG
Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:101702-102015
Satlength=314 Nr of Repeats=6 RepeatLength=52 seed=GTGACAGTTA Num.seqs=5
Similarity=0.816352 64
AGTAACTGTCACCTTCAGCCTNNTTTCGTGTGCTTACTCACCTT-CTTCCTCCG
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:91832-92092 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=AGTTACTCAC Num.seqs=5 Similarity=0.883019
82 AGTAACTGACATGTTTGGCCTTTTTTCGTGCAGTTACTCACGCT-TTTCCTTTG
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:344904-345112 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=AGTAACTGAC Num.seqs=4 Similarity=0.756813
105 AGTAACTGACATGATTGGCCTTTTTTCGTGCAGTTACTCACCTATTCCCTTCG

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Consensus:

AGTAACTGaCatgtTcaGcCttTTTCGTGtaGTTACTCACcctnttCCTtcg

>Bacillus_Fam_118_52_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.699371
GCF_001439965.1_ASM143996v1_genomic.fna_125:65382-65694 Satlength=313 Nr
of Repeats=5 RepeatLength=52 seed=AGGTTACCGA Num.seqs=4
Similarity=0.752137
0 AGGTTACCGAGCCCCCGCCATTTACTCCATCCCGGTAACCAAACCTCTCTCTT-
Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_197:48906-49947
Satlength=1042 Nr of Repeats=17 RepeatLength=52 seed=GTTCGGTAAC
Num.seqs=12 Similarity=0.836981
12 TGGTTACCGAACGCGCGCAATATCGTCCATCCGGGTAACCAATCCCTCTCAA-
Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_62:29140-29922
Satlength=783 Nr of Repeats=14 RepeatLength=52 seed=CGGGAATAA
Num.seqs=12 Similarity=0.786382
8 -AGTTCCCGTGTCCGCGTAAATCCTCCATCAAGGTAACCAAACGCACTCATT
GCF_002009555.1_ASM200955v1_genomic.fna_166:5014-5326 Satlength=313 Nr of
Repeats=5 RepeatLength=52 seed=ATTAGTTCCC Num.seqs=4 Similarity=0.884615
49 -AGTTCCCGAGCCGCGAAAAATCCTCCATCAAGGTAACCAAACGCACTCATT
GCF_002009555.1_ASM200955v1_genomic.fna_217:22-438 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=CTCCATCAAG Num.seqs=8 Similarity=0.788745
23 -AGTTCCCGTGCCGCGGAAAAATCCTCCATCAAGGTAACCAATCGCACTCATT

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Consensus:

aGTTcCCGagccCgGnaAaaTccTCCATCaaGGTAACCAAaCgCaTCatt

>Bacillus_Fam_119_52_5 Nr. of seq. 5 Alignment length(with gaps) = 53
Alignment score = 0.620755
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_7:4560-4976 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=GTTTTGTCTA Num.seqs=8
Similarity=0.776675 0
GTTTTGTCTAATAGAGCTCTTCTATTGAACAAAACCATTCCTCCGAGA-CATGT
Rev.of_GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_31:30740-31103
Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=TTTGTCCGAT Num.seqs=6
Similarity=0.818449 33
GTTTTGTCTATTAGAGGGCTTCTATCGGACAAAACCATTGCTC-AGACCATGA
Rev.of_GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_29:79068-79380
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TCTATTAGAC Num.seqs=6
Similarity=0.824948 15
GTTTTGTCTAATAGAGNCCGTCTATTGGACAAATTCCTTGCTC-ACAACAGGG
Rev.of_GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_25:114221-114585
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GCTCTATTGG Num.seqs=7
Similarity=0.892552 17
GTTTTGTCCAATAGAGCTGTCCTATCGAACATAATCTTTGCTC-GGACCTGGT
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_19:27781-28613
Satlength=833 Nr of Repeats=16 RepeatLength=52 seed=CTATTGGACA
Num.seqs=16 Similarity=0.823113 21
GGTTTGTCTAATAAAGACCCCCTATTGGACAGAATCATCACTCNGGA-CATGT

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Consensus:

GtTTTTGTCTAaTAgaGnncttCTATtGgACAAaAatCaTtgCtCagAnCatGt

>Bacillus_Fam_120_52_5 Nr. of seq. 5 Alignment length(with gaps) = 52
Alignment score = 0.853846
GCF_001439965.1_ASM143996v1_genomic.fna_95:54401-54661 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=ACACATTTTT Num.seqs=5
Similarity=0.800000
0 ACACATTTTTTCGCTTCTCCCCATGATAATCTGTCTCAGGCATGGCTTCTGAC
GCF_001887185.1_ASM188718v1_genomic.fna_5:448-656 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TGATAATCTG Num.seqs=4 Similarity=0.987179
22 ACACATTTTTTCGCTTCTCCCCATGATAATCTGTCTCAGGCATGGCTTCTGAC
Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_11:16345-16813
Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=TGAGACAGAT Num.seqs=9
Similarity=0.792181 37
ACACATTTTTTCGCTTNTCCCCATGATAATCTGTCTCAGGCATGGCTTCTGAC
GCF_001439965.1_ASM143996v1_genomic.fna_95:56169-56429 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=AATCTGTCTC Num.seqs=5
Similarity=0.810256
26 ACACATTTTTGACCTTTACCTTTGATAATCTGTCTCANGCATGGCCTCTGAC
GCF_002009555.1_ASM200955v1_genomic.fna_56:33-448 Satlength=416 Nr of
Repeats=8 RepeatLength=52 seed=AATCTGTCTC Num.seqs=7 Similarity=0.846154
26 ACACATTTTTGGCCTTTACCTTTGATAATCTGTCTCAAGTATGGCCTCTGAC

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Consensus:

ACACATTTTTcgCtTnTcCCcaTGATAATCTGTCTCagGcATGGCtTCTGAC

>Bacillus_Fam_121_52_5 Nr. of seq. 5 Alignment length(with gaps) = 52

Alignment score = 0.823077

GCF_001636335.1_ASM163633v1_genomic.fna_1:206310-206778 Satlength=469 Nr

of Repeats=9 RepeatLength=52 seed=TTATTGAACC Num.seqs=9

Similarity=0.753258

0 TTATTGAACCCCGAGCAGGCGAAAAAAGCATCAAAGAGTCTTCAATAGGTG

Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:210863-211279

Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=CTATTGAAGA Num.seqs=8

Similarity=0.879155

49

GGATTGAACCCCGAAGTGGCGAAAAAAGCATCAAAGAGTCTTCAATAGAGG

Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:3030262-3031197

Satlength=936 Nr of Repeats=17 RepeatLength=52 seed=ATTGAAGACT

Num.seqs=14 Similarity=0.826042

99 CTATTGAACCCCGAACAAGCGAAAAAAGCANCAAAGAGTCTTCAATAGAGG

Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:2795926-2796445

Satlength=520 Nr of Repeats=10 RepeatLength=52 seed=TATTGAGGAC

Num.seqs=9 Similarity=0.870720

48 TCATTGAACCCCGAACAAGCGAAAAAACCGTCAAAGCGTCCTCAATAGGGG

Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:2827224-2827795

Satlength=572 Nr of Repeats=11 RepeatLength=52 seed=AGGACTCTTT

Num.seqs=10 Similarity=0.822222

95 TCCTTGAACCCCGAACAGGCGAAAAAATCGTCAAAGAGTCCTCAATAGGGG

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Consensus:

tnaTTGAACCCCGAaCagGCGAAAAAAgCatCAAAGaGTcTCAATAGggG

>Bacillus_Fam_122_45_5 Nr. of seq. 5 Alignment length(with gaps) = 48

Alignment score = 0.736806

GCF_000007845.1_ASM784v1_genomic.fna_1:3515122-3515563 Satlength=442 Nr

of Repeats=9 RepeatLength=45 seed=ACTGGACCTC Num.seqs=7

Similarity=0.874427

0 ACTGGACCTCAAGGTGTTCAAGG--A-CCAGCAGGTGCTACCGGTGCT

GCF_000008505.1_ASM850v1_genomic.fna_1:3540669-3543189 Satlength=2521 Nr

of Repeats=56 RepeatLength=45 seed=ACTGGACCTC Num.seqs=45

Similarity=0.827814

0

ACTGGACCTCAAGGTGTTCAAGG--A-CCAGCAGGTGCTACTGGTGCC

Rev.of_GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_3:327060-

327582 Satlength=523 Nr of Repeats=11 RepeatLength=45 seed=CCTTGAGGTC

Num.seqs=9 Similarity=0.787842

14

ACTGGACCTCAAGGTGTTCAAGG--A-CCGGCGGGTGCTACTGGTGCT

GCF_000831065.1_ASM83106v1_genomic.fna_1:3427920-3429909 Satlength=1990

Nr of Repeats=47 RepeatLength=45 seed=ACTGGACCTC Num.seqs=29

Similarity=0.774327

0

ACTGGACCTCAAGGTGTTCAAGGT-A-ACA-CNGGTGCTACTGGTGCC

GCF_000017425.1_ASM1742v1_genomic.fna_1:2475569-2477171 Satlength=1603 Nr

of Repeats=43 RepeatLength=45 seed=GGACCTCAAG Num.seqs=30

Similarity=0.881073

3

ACTGGACCTCAAGGGCCTCAAGG-CATCCA--AGGACCTACAGGGGCT

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Consensus:

ACTGGACCTCAAGGtgtTCAAGGAcCagcaGGtgCTACtGGtGcT

>Bacillus_Fam_123_39_5 Nr. of seq. 5 Alignment length(with gaps) = 42

Alignment score = 0.642857

GCF_000017425.1_ASM1742v1_genomic.fna_1:3517703-3517985 Satlength=283 Nr

of Repeats=8 RepeatLength=36 seed=TTCTTCTATA Num.seqs=6

Similarity=0.987654

0 TTCTTCT-AT-ACGCTGC-TCTTCTTGCTTGCGTTTTTC---

Rev.of_GCF_001719185.1_ASM171918v1_genomic.fna_1:3645533-3645689

Satlength=157 Nr of Repeats=4 RepeatLength=39 seed=AAGCAAGAGG Num.seqs=4

Similarity=0.897436

30

TTCTGCTAATCGCGCTTCTTCCTCTTGCTTGCGTTTTTC---

GCF_000008505.1_ASM850v1_genomic.fna_1:3065080-3065314 Satlength=235 Nr

of Repeats=7 RepeatLength=39 seed=TGCTCTTCTT Num.seqs=5

Similarity=0.938462

13 TTCTACT-CT-TTGCTGC-TCTTCTTGCTTACGTTTTTCTTC

Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:1202055-1202214

Satlength=160 Nr of Repeats=4 RepeatLength=39 seed=AAACGTAAGC Num.seqs=3

Similarity=0.977208

33

CTCTACT-CT-TTGTTGC-TCTTCCTGCTTACGTTTTTCTTC

GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_1:2060357-2060513

Satlength=157 Nr of Repeats=4 RepeatLength=39 seed=TTTGTTGCTC Num.seqs=4

Similarity=0.874644

47

TTCTGCT-CT-

TTGTTGC-TCTTCTTGCTTACGCTTCTCTTC

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Consensus:

tTCTnCTcTttGcTgCTCtTcTGCTTaCGtTTtTcTtc

>Bacillus_Fam_124_40_5 Nr. of seq. 5 Alignment length(with gaps) = 42

Alignment score = 0.684127

GCF_000285535.1_ASM28553v1_genomic.fna_2:812840-813040 Satlength=201 Nr

of Repeats=5 RepeatLength=40 seed=ATTTGCGTCT Num.seqs=5

Similarity=0.753333

0 ATTTGCGTC-TCCTCTANGATTTTTGCGTCGGTTTTCTCAC-

GCF_000285535.1_ASM28553v1_genomic.fna_31:3-163 Satlength=161 Nr of

Repeats=4 RepeatLength=40 seed=TTTTCTCACA Num.seqs=4 Similarity=0.905556

31 ATTTGCGTC-TCCCCAGCGATTTTTGCGTCGGTTTTCTCAC-

Rev.of_GCF_000285535.1_ASM28553v1_genomic.fna_51:18-258 Satlength=241 Nr

of Repeats=7 RepeatLength=40 seed=AGACGCAAAT Num.seqs=5

Similarity=0.743089

50 ATTTGCGTC-TCCCCAGCGATTTTTGCGTCGATTTTCTCAN-

GCF_000285535.1_ASM28553v1_genomic.fna_2:954754-954914 Satlength=161 Nr

of Repeats=5 RepeatLength=40 seed=TTTTTGCCTC Num.seqs=3

Similarity=0.796748

19 ATTTGCGTC-TTCTCCCTGATTTTTGCGTCGATATCCGCGG-

Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_105:62151-62311
Satlength=161 Nr of Repeats=5 RepeatLength=40 seed=CGACGCAAAT Num.seqs=3
Similarity=0.777778 10
ATTTGCGTCGTGCTC-GAGATTTATGCGTCGTTTGC-CAAT

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Consensus:

ATTTGCGTCTcCtCngnGATTTtTGCGTCGgTtTtCtCan

>Bacillus_Fam_125_42_5 Nr. of seq. 5 Alignment length(with gaps) = 42
Alignment score = 0.888889
GCF_000496285.1_ASM49628v1_genomic.fna_1:3159834-3160296 Satlength=463 Nr
of Repeats=11 RepeatLength=42 seed=AAAGAAGAAG Num.seqs=11
Similarity=0.894949 0
AAAGAAGAAGTAAAAGAGCCGGTAAAAGAAGTTGAAGAAACG
Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:4810089-4810866
Satlength=778 Nr of Repeats=5 RepeatLength=42 seed=TCTTCTTTTG Num.seqs=4
Similarity=0.841270 8
AAAGAAGAAGTAAAAGAGCCGGTAAAAGAAGTTGAAGAAACA
GCF_000831065.1_ASM83106v1_genomic.fna_1:383609-384197 Satlength=589 Nr
of Repeats=14 RepeatLength=42 seed=AAAGAAGAAG Num.seqs=14
Similarity=0.913134 0
AAAGAAGAAGTGAAAGAACCGGTAAAAGAAGTTGAAGGAACA
Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:5196965-5197301
Satlength=337 Nr of Repeats=8 RepeatLength=42 seed=CGGCTCTTTT Num.seqs=8
Similarity=0.907029 21
AAAGAAGAAGTAAAAGAGCCGGTAAAAGAAGTTGAAGAAACA
GCF_001645555.1_ASM164555v1_genomic.fna_2:16394-16667 Satlength=274 Nr of
Repeats=8 RepeatLength=42 seed=GAAGTAAAAG Num.seqs=5 Similarity=0.828571
6 AAAGAAGAAGTAAAAGAGCCAACAAAAGAAGTTGAAGGANCG

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Consensus:

AAAGAAGAAGTaAAAGAgCCggtAAAAGAAGTTGAAGaAaCa

>Bacillus_Fam_126_39_5 Nr. of seq. 5 Alignment length(with gaps) = 39
Alignment score = 0.788034
GCF_000007825.1_ASM782v1_genomic.fna_1:4664228-4664735 Satlength=508 Nr
of Repeats=13 RepeatLength=39 seed=TAAGCAACAA Num.seqs=13
Similarity=0.780769 0
TAAGCAACAAAGTNCTAAACAAGANGATTCTCTCAGGA
GCF_000831065.1_ASM83106v1_genomic.fna_1:4422505-4422934 Satlength=430 Nr
of Repeats=11 RepeatLength=39 seed=GCTAAACAAG Num.seqs=11
Similarity=0.854545 13
TAAGCAACAAAGTGCTAAACAAGATGATTCTNTCTCAAGA
GCF_000496285.1_ASM49628v1_genomic.fna_1:1925714-1926104 Satlength=391 Nr
of Repeats=10 RepeatLength=39 seed=TCTCATGAGA Num.seqs=10
Similarity=0.889079 31
GAAACAACAAAATTCTAAACAAGACGATTCTCTCATGA
Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:143645-144191
Satlength=547 Nr of Repeats=13 RepeatLength=39 seed=TTAGAATTTT

Num.seqs=12 Similarity=0.852370
18 CAAGCAGCAAAATTCTAAGCAAGATGATTCTTCTCAAAA
Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:1250277-1250745
Satlength=469 Nr of Repeats=15 RepeatLength=39 seed=CTTGTTTAGA
Num.seqs=9 Similarity=0.840456
23 CAAACAGCAAAGTTCTAAACAAGAGGATTCTTCTCAAGA

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Consensus:

nAAgCAaCAAAGTtCTAAaCAAGAnGATTcNtCTCAagA

>Bacillus_Fam_127_36_5 Nr. of seq. 5 Alignment length(with gaps) = 36
Alignment score = 0.792593
GCF_000007825.1_ASM782v1_genomic.fna_1:4624379-4625096 Satlength=718 Nr
of Repeats=5 RepeatLength=36 seed=GTTGCTCTTC Num.seqs=4
Similarity=0.925926
0 GTTGCTCTTCTACGACTGGCGCTTCTTCTACAACCTC
GCF_000496285.1_ASM49628v1_genomic.fna_1:1885490-1886414 Satlength=925 Nr
of Repeats=18 RepeatLength=36 seed=TGGTTGTTCT Num.seqs=12
Similarity=0.956229 34
GTTGTTCTTCAGCGACTGGCCCTTCTTCTGCAACTG
GCF_000007845.1_ASM784v1_genomic.fna_1:4486380-4486794 Satlength=415 Nr
of Repeats=8 RepeatLength=36 seed=TTGTTCTTCT Num.seqs=5
Similarity=0.837037
1 GTTGTTCTTCTACGACCGGTGCTTCTCTGCAACTG
GCF_000008505.1_ASM850v1_genomic.fna_1:4481591-4482005 Satlength=415 Nr
of Repeats=11 RepeatLength=36 seed=TTGTTCTTCT Num.seqs=10
Similarity=0.853498 1
GTTGTTCTTCTACGACCGGTGTTTCTCTGCAACTG
Rev.of_GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_2:176867-
177083 Satlength=217 Nr of Repeats=7 RepeatLength=36 seed=AGAAGAACAA
Num.seqs=5 Similarity=0.829630 11
ATTGTTCTTCTGCGACCGGTGTTTCTTCTACAACCTG

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Consensus:

gTTGtTCTTCTaCGACcGGtgcTTcTtCTgCAACTg

>Bacillus_Fam_128_36_5 Nr. of seq. 5 Alignment length(with gaps) = 36
Alignment score = 0.874074
GCF_000007825.1_ASM782v1_genomic.fna_1:4625342-4625852 Satlength=511 Nr
of Repeats=15 RepeatLength=36 seed=CTTCCACTTC Num.seqs=10
Similarity=0.893827 0
CTTCCACTTCTTCTGACTCTTTCGCTTCCGCAATTA
GCF_000831065.1_ASM83106v1_genomic.fna_1:4383407-4384004 Satlength=598 Nr
of Repeats=16 RepeatLength=36 seed=GCAATTACTT Num.seqs=14
Similarity=0.859178 29
CTTCNACTTCTTCTGACTCTTCTGCTTCCGCAATTA
GCF_000007845.1_ASM784v1_genomic.fna_1:4486994-4487255 Satlength=262 Nr
of Repeats=7 RepeatLength=36 seed=CTTCTGTTTC Num.seqs=5
Similarity=0.896296
18 CTCTACTTCTTCTGACTCTTCTGTTTCTGCAATTA

GCF_000008505.1_ASM850v1_genomic.fna_1:4482205-4482457 Satlength=253 Nr
of Repeats=7 RepeatLength=36 seed=CTTCTGTTTC Num.seqs=7
Similarity=0.890653
18 CTTCCACTTCTTCTAACTCTTCTGTTTCTGCAATTA
Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_4:74869-75013
Satlength=145 Nr of Repeats=4 RepeatLength=36 seed=GAAACAGAAG Num.seqs=4
Similarity=0.827160 28
CTTCCACTTCTTCTGGCTCTTCTGTTTCCGCAATTA

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Consensus:

CTTCcACTTCTTCTGaCTCTTctGtTTCcGCAATTA

>Bacillus_Fam_129_29_5 Nr. of seq. 5 Alignment length(with gaps) = 30
Alignment score = 0.824444
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_16:61242-61589
Satlength=348 Nr of Repeats=5 RepeatLength=29 seed=GAGCAGCGGA Num.seqs=3
Similarity=1.000000 0
GAGCAGCGGAGCGTACATCACA-CGTACGT
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_17:131859-132214
Satlength=356 Nr of Repeats=5 RepeatLength=29 seed=GAGCAGCGGA Num.seqs=3
Similarity=0.908046 0 GAGCAGCGGAGCGTACAAGGAA-
CGTACGA
Rev.of_GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_32:48473-49200
Satlength=728 Nr of Repeats=5 RepeatLength=29 seed=CTCCGCTGCT Num.seqs=3
Similarity=1.000000 11 GAGCAGCGGAGCGTACAAGGGA-
CGTACGT
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_51:15077-15428
Satlength=352 Nr of Repeats=5 RepeatLength=29 seed=TGAGCAGCGC Num.seqs=3
Similarity=0.969349 28
GAGCAGCGCAGCGTACAAGGGA-CGTACGT
Rev.of_GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_43:86875-87225
Satlength=351 Nr of Repeats=5 RepeatLength=30 seed=CTCCGCTGCT Num.seqs=3
Similarity=0.970370 11
GAGCAGCGGAGCGTACAAGAGATCGTACGT

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Consensus:

GAGCAGCGgAGCGTACAaggACGTACGt

>Bacillus_Fam_130_21_5 Nr. of seq. 5 Alignment length(with gaps) = 24
Alignment score = 0.626389
GCF_000813125.1_ASM81312v1_genomic.fna_65:36039-36144 Satlength=106 Nr of
Repeats=5 RepeatLength=21 seed=TCGACCACAT Num.seqs=5 Similarity=0.733333
0 TCGACCACATTCC--AAG-ATAAT
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_109:33798-33903
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TGGTCAATT Num.seqs=5

Similarity=0.707937 7
 TCGACCACATNTC-NAAT--TAAT
 Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_40:56922-57048
 Satlength=127 Nr of Repeats=6 RepeatLength=21 seed=ATGTGGTTGA Num.seqs=6
 Similarity=0.778283 10
 TCGACCACATTTT-GAANT-TAAT
 GCF_001315165.1_ASM131516v1_genomic.fna_25:29879-29963 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=AATAATTCGA Num.seqs=4 Similarity=0.828283
 16 TCGACCACATTTTCGAAA--TAAT
 Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_144:1991-2075 Satlength=85
 Nr of Repeats=4 RepeatLength=21 seed=TGGTCGAATT Num.seqs=4
 Similarity=0.756614 7
 TCGACCAGATTTA-GGAT--TAAT

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 Consensus:

TCGACCACATttnngaAnTAAT

>Bacillus_Fam_131_24_5 Nr. of seq. 5 Alignment length(with gaps) = 24
 Alignment score = 0.822222
 GCF_000007845.1_ASM784v1_genomic.fna_1:1480940-1481189 Satlength=250 Nr
 of Repeats=8 RepeatLength=24 seed=AGCTTCTTCT Num.seqs=5
 Similarity=0.822667
 0 AGCTTCTTCTTCAGCTTTTTTTGT
 GCF_000008505.1_ASM850v1_genomic.fna_1:1505384-1505633 Satlength=250 Nr
 of Repeats=8 RepeatLength=24 seed=AGCTTCTTCT Num.seqs=5
 Similarity=0.822667
 0 AGCTTCTTCTTCAGCTTTTTTTGT
 GCF_000496285.1_ASM49628v1_genomic.fna_1:4094822-4095035 Satlength=214 Nr
 of Repeats=5 RepeatLength=24 seed=AGCTTCTTCT Num.seqs=3
 Similarity=0.795556 0
 AGCTTCTTCTTCAGCTTTTTTTCTT
 Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:4215062-4215365
 Satlength=304 Nr of Repeats=6 RepeatLength=24 seed=GCTGACGAAG Num.seqs=4
 Similarity=0.851852 15
 AGCTTCTTCTGTCAGCTTTTTTTCTT
 GCF_000175075.1_ASM17507v1_genomic.fna_2:117151-117274 Satlength=124 Nr
 of Repeats=5 RepeatLength=24 seed=GCTTCTTTCT Num.seqs=3
 Similarity=0.925926
 13 AGCTTGCTCTTCGGCTTCTTTCTT

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 Consensus:

AGCTTctTctTCaGCTTtTTTctT

>Bacillus_Fam_132_21_5 Nr. of seq. 5 Alignment length(with gaps) = 23
 Alignment score = 0.630435
 GCF_000242895.2_ASM24289v3_genomic.fna_1:1703717-1703819 Satlength=103 Nr
 of Repeats=5 RepeatLength=20 seed=AGTCGAGCAT Num.seqs=3
 Similarity=0.866667 0
 AGTCGAGCATA-AAACCT-GAG-

GCF_000242895.2_ASM24289v3_genomic.fna_1:1503263-1503366 Satlength=104 Nr
of Repeats=5 RepeatLength=21 seed=AGTCGAGCAT Num.seqs=3
Similarity=0.808081 0
AGTCGAGCATA-AACCCT-CAAA
GCF_000242895.2_ASM24289v3_genomic.fna_1:1982125-1982248 Satlength=124 Nr
of Repeats=5 RepeatLength=21 seed=GTCGAGCATA Num.seqs=3
Similarity=0.690821 1
AGTCGAGCATANNACCCC-GAA-
Rev.of_GCF_000242895.2_ASM24289v3_genomic.fna_1:4665131-4665236
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TATGCTCGAC Num.seqs=5
Similarity=0.824242 11
AGTCGAGCATA-AAT-CTCGAAA
Rev.of_GCF_000242895.2_ASM24289v3_genomic.fna_1:1951392-1951496
Satlength=105 Nr of Repeats=5 RepeatLength=21 seed=ATATATGCTC Num.seqs=4
Similarity=0.818182 14
AGTTGAGCATA-TATCCTCGAAA

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Consensus:

AGTcGAGCATAaAncCtgAaa

>Bacillus_Fam_133_21_5 Nr. of seq. 5 Alignment length(with gaps) = 23
Alignment score = 0.650725
GCF_000294775.2_ASM29477v2_genomic.fna_1:5051016-5051119 Satlength=104 Nr
of Repeats=5 RepeatLength=21 seed=TGCAAATAAA Num.seqs=3
Similarity=0.440000 0
TGCAAATAAACNG-GTNGAA-CC
GCF_001712755.1_ASM171275v1_genomic.fna_2:340961-341149 Satlength=189 Nr
of Repeats=9 RepeatLength=21 seed=TGCAAATAAA Num.seqs=8
Similarity=0.655329
0 TGCAAATAAAAAAGGTGAAA-C-
GCF_001712755.1_ASM171275v1_genomic.fna_37:106859-106987 Satlength=129 Nr
of Repeats=6 RepeatLength=21 seed=TGCAAATAAA Num.seqs=4
Similarity=0.513889 0
TGCAAATAAAAAA-GTGAAATC-
GCF_001712755.1_ASM171275v1_genomic.fna_3:168469-168573 Satlength=105 Nr
of Repeats=4 RepeatLength=21 seed=TGCAAATAAA Num.seqs=3
Similarity=0.621212
0 TGCAAATAAAAAATCCTGAAA-C-
GCF_001712755.1_ASM171275v1_genomic.fna_5:11567-11647 Satlength=81 Nr of
Repeats=4 RepeatLength=21 seed=TGCAAATAAA Num.seqs=3 Similarity=0.661616
0 TGCAAATAAAAAATAGTAAAA-C-

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Consensus:

TGCAAATAAAaanngTgaAAC

>Bacillus_Fam_134_21_5 Nr. of seq. 5 Alignment length(with gaps) = 23
Alignment score = 0.628986
GCF_000508325.1_BAVI_1_genomic.fna_121:21154-21237 Satlength=84 Nr of
Repeats=4 RepeatLength=21 seed=TTTATCAGCG Num.seqs=3 Similarity=0.525253
0 TTTATCAGCGGATNTN-GNNCT-

GCF_001591665.1_ASM159166v1_genomic.fna_16:4578-4661 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTTATCAGCG Num.seqs=3 Similarity=0.727273
0 TTTATCAGCGAATTTC-ACGCT-
GCF_001591805.1_ASM159180v1_genomic.fna_23:27706-27789 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTTATCAGCG Num.seqs=3 Similarity=0.727273
0 TTTATCAGCGAATTTT-ATACT-
GCF_000508325.1_BAVI_1_genomic.fna_64:16791-16874 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=ATCAGCGAAT Num.seqs=3 Similarity=0.681818
3 TTTATCAGCGAATTTTGATAGT-
GCF_001591805.1_ASM159180v1_genomic.fna_9:281564-281647 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTTATCAGCG Num.seqs=3
Similarity=0.500000
0 TTTATCAGCGGAATTC-A-NCTG

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Consensus:

TTTATCAGCGaAttTnannCT

>Bacillus_Fam_135_21_5 Nr. of seq. 5 Alignment length(with gaps) = 23
Alignment score = 0.630435
GCF_001889165.1_ASM188916v1_genomic.fna_1:3505433-3505516 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TTTATTTTCG Num.seqs=3
Similarity=0.626263 0
TTTATTTTCGG-NTTTGAGTCA-
GCF_001889165.1_ASM188916v1_genomic.fna_1:3842895-3843000 Satlength=106 Nr of Repeats=4 RepeatLength=21 seed=TTTATTTTCG Num.seqs=3
Similarity=0.562222 0
TTTATTTTCGA-ATTTNA-TTNG
GCF_001889165.1_ASM188916v1_genomic.fna_1:4154491-4154573 Satlength=83 Nr of Repeats=4 RepeatLength=21 seed=TTTATTTTCG Num.seqs=3
Similarity=0.671498 0
TTTATTTTCGA-ATTTGA-TCAT
GCF_001889165.1_ASM188916v1_genomic.fna_1:3860025-3860109 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTTATTTTCG Num.seqs=4
Similarity=0.646465 0
TTTATTTTCGANATTTCA-TCGN
Rev.of_GCF_002019605.1_ASM201960v1_genomic.fna_1:4136408-4136513
Satlength=106 Nr of Repeats=4 RepeatLength=21 seed=AAGTTGAAAA Num.seqs=3
Similarity=1.000000 14
TTTATTTTCAA-CTTTGC-TCAA

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Consensus:

TTTATTTTCgaaTTTgaTcan

>Bacillus_Fam_136_20_5 Nr. of seq. 5 Alignment length(with gaps) = 22
Alignment score = 0.613636
GCF_000007845.1_ASM784v1_genomic.fna_1:4468427-4468527 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=GATATATTTT Num.seqs=5
Similarity=0.733333
0 GATAT-ATTTTGATAAT-CGCT

GCF_000831065.1_ASM83106v1_genomic.fna_1:4854120-4854260 Satlength=141 Nr of Repeats=6 RepeatLength=20 seed=GATATATTTT Num.seqs=5
 Similarity=0.713333 0
 GATAT-ATTTTAANAAT-CGCT
 Rev.of_GCF_000008505.1_ASM850v1_genomic.fna_1:4898752-4898852
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TATATCAGCG Num.seqs=5
 Similarity=0.636508 6
 GATAT-ATTTNGGNAAT-CGCT
 Rev.of_GCF_000008505.1_ASM850v1_genomic.fna_1:2760175-2760255
 Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=TATATCAGCG Num.seqs=4
 Similarity=0.555556 6
 GATATATATTAG-AAATNCGCT
 GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_4:613849-613969
 Satlength=121 Nr of Repeats=5 RepeatLength=20 seed=GATATAATTT Num.seqs=4
 Similarity=0.687831 22 GATAT-
 AATTAGAAAATGCGCC

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 Consensus:

GATATatTTnganAATCGct

>Bacillus_Fam_137_20_5 Nr. of seq. 5 Alignment length(with gaps) = 22
 Alignment score = 0.633333
 GCF_000242895.2_ASM24289v3_genomic.fna_1:4197965-4198045 Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=CCGATATAAT Num.seqs=4
 Similarity=0.711640
 0 CCGATATA-ATCGAGATTTTA-
 Rev.of_GCF_000311725.1_ASM31172v1_genomic.fna_2:106659-106759
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TATATCGGCG Num.seqs=5
 Similarity=0.552174 8
 CCGATATA-ATT-AAATTTTCG
 GCF_001578185.1_ASM157818v1_genomic.fna_1:4205454-4205534 Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=AGATATAATT Num.seqs=4
 Similarity=0.822222 21
 CAGATATA-ATT-CGATTTTCG
 Rev.of_GCF_000311725.1_ASM31172v1_genomic.fna_2:362483-362583
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=TATATCGGCG Num.seqs=3
 Similarity=0.525253 8
 CCGATATA-NTC-AGAATATCG
 GCF_000311725.1_ASM31172v1_genomic.fna_4:83330-83410 Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=CGCCGATATA Num.seqs=4 Similarity=0.603535
 19 CCGATATATCTC-AGATTTTCG

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 Consensus:

CcGATATAaTcagAtTtTcg

>Bacillus_Fam_138_20_5 Nr. of seq. 5 Alignment length(with gaps) = 22
 Alignment score = 0.601515
 GCF_000401235.1_BacNeaAAU1_genomic.fna_37:7-109 Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=TATCAGCCAA Num.seqs=3 Similarity=1.000000
 0 TATC-AGCCAAACTTTCC-ATT

GCF_001591585.1_ASM159158v1_genomic.fna_21:18-404 Satlength=387 Nr of Repeats=19 RepeatLength=20 seed=TCAGCCAAAC Num.seqs=13 Similarity=0.965812
 2 TTTC-AGCCAAACTTCAG-ATT
 GCF_001591585.1_ASM159158v1_genomic.fna_43:11976-12101 Satlength=126 Nr of Repeats=6 RepeatLength=21 seed=TATCAGCCAA Num.seqs=5 Similarity=0.784127
 21 TATC-AGCCAAACTTCAGTACT
 GCF_000508325.1_BAVI_1_genomic.fna_156:10891-11119 Satlength=229 Nr of Repeats=7 RepeatLength=21 seed=ATCTCGCCAA Num.seqs=5 Similarity=0.556522
 1 NATCTCGCCAAACTTNGA-ATT
 Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_199:5141-5284 Satlength=144 Nr of Repeats=5 RepeatLength=21 seed=TTGGCGAGAT Num.seqs=3 Similarity=0.505050
 11 TATCTCGCCAAACTTTNA-GTT

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Consensus:

taTCaGCCAAACTTnnnatT

>Bacillus_Fam_139_21_5 Nr. of seq. 5 Alignment length(with gaps) = 22
 Alignment score = 0.645455
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:1986285-1988125
 Satlength=1841 Nr of Repeats=92 RepeatLength=20 seed=TTCGGATTTT Num.seqs=92 Similarity=1.000000 0
 TTCG-GATTTTATGAGCGAGA-
 Rev.of_GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3077746-3079526
 Satlength=1781 Nr of Repeats=89 RepeatLength=20 seed=CTCGCTCATA Num.seqs=89 Similarity=1.000000 19
 TTCG-GATTTTATGAGCGAGT-
 Rev.of_GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2460775-2461355
 Satlength=581 Nr of Repeats=28 RepeatLength=20 seed=AGATCTCGCT Num.seqs=25 Similarity=0.779524 2 CT-
 GTGA-TATATGAGCGAGAT
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4065733-4066073
 Satlength=341 Nr of Repeats=17 RepeatLength=20 seed=GATATATGAG Num.seqs=17 Similarity=0.847059 5
 -TCGTGA-TATATGAGCAAGAA
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4271828-4272328
 Satlength=501 Nr of Repeats=25 RepeatLength=20 seed=ATATGAGCGA Num.seqs=25 Similarity=0.836000 8
 -TCGNGA-TATATGAGCGAGAT

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Consensus:

nTcGnGATaTATGAGCgAGan

>Bacillus_Fam_140_22_5 Nr. of seq. 5 Alignment length(with gaps) = 22
 Alignment score = 0.630303
 GCF_001315045.1_ASM131504v1_genomic.fna_21:8-820 Satlength=813 Nr of Repeats=5 RepeatLength=21 seed=TTTATTGTCC Num.seqs=4 Similarity=0.530193
 0 TTTATTGTCC-GATGACCCACA

Rev.of_GCF_001315045.1_ASM131504v1_genomic.fna_25:32585-32669
 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=GGACAATAAA Num.seqs=4
 Similarity=0.622475 10
 TTTATTGTCC-GATTCGCGCCA
 Rev.of_GCF_001315045.1_ASM131504v1_genomic.fna_35:25565-25649
 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=GGACAATAAA Num.seqs=4
 Similarity=0.696970 10
 TTTATTGTCCAGATGAGCTCCA
 Rev.of_GCF_001315045.1_ASM131504v1_genomic.fna_25:36402-36485
 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=GGACAATAAA Num.seqs=3
 Similarity=0.462963 10
 TTTATTGTCCNGTT-CGTNACA
 GCF_001315045.1_ASM131504v1_genomic.fna_150:1706-1790 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=TTTATTGTCC Num.seqs=4 Similarity=0.445473
 21 TTTATTGTCCAGAT-CACAGCA

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Consensus:

TTTATTGTCCnGaTncgcnnCA

>Bacillus_Fam_141_20_5 Nr. of seq. 5 Alignment length(with gaps) = 21
 Alignment score = 0.666667
 GCF_000311725.1_ASM31172v1_genomic.fna_7:70953-71160 Satlength=208 Nr of
 Repeats=4 RepeatLength=20 seed=ATCGGTCTAA Num.seqs=3 Similarity=0.644444
 0 ATCGGTCTAAT-TTCAAATAT
 GCF_900156875.1_PRJEB18969_genomic.fna_10:321051-321132 Satlength=82 Nr
 of Repeats=4 RepeatLength=20 seed=TATATCGGTC Num.seqs=3
 Similarity=0.671958
 17 ATCGGTCTCAGAT-TTNNAATAT
 GCF_002019645.1_ASM201964v1_genomic.fna_1:898029-898267 Satlength=239 Nr
 of Repeats=12 RepeatLength=20 seed=TATCGGTCTA Num.seqs=8
 Similarity=0.771429 19
 ATCGGTCTAAC-TAGAAAAAT
 GCF_002019645.1_ASM201964v1_genomic.fna_1:1325761-1326158 Satlength=398
 Nr of Repeats=20 RepeatLength=20 seed=TATCGGTCTA Num.seqs=17
 Similarity=0.704482 19
 ATCGGTCTAAC-TCAAGATAT
 GCF_002019645.1_ASM201964v1_genomic.fna_1:1553541-1553821 Satlength=281
 Nr of Repeats=13 RepeatLength=20 seed=TATCGGTCTA Num.seqs=12
 Similarity=0.763348 19
 ATCGGTCTAACTTTAAGATAT

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Consensus:

ATCGGTCTaAcTtnaaAtAT

>Bacillus_Fam_142_20_5 Nr. of seq. 5 Alignment length(with gaps) = 20
 Alignment score = 0.746667
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:224994-228602
 Satlength=3609 Nr of Repeats=180 RepeatLength=20 seed=TTTCTCTATC
 Num.seqs=179 Similarity=0.998519 0
 TTTCTCTATCCAAGAGTATT

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:1933173-1933473
 Satlength=301 Nr of Repeats=15 RepeatLength=20 seed=ATACGAGAGT
 Num.seqs=15 Similarity=0.818292 7
 CCTCGCTATACGAGAGTATC
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2574155-2574275
 Satlength=121 Nr of Repeats=6 RepeatLength=20 seed=GAGAGTATTT Num.seqs=6
 Similarity=0.853333 11
 TCACGCTATACGAGAGTATT
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3800918-3801078
 Satlength=161 Nr of Repeats=7 RepeatLength=20 seed=GAGAGTATTT Num.seqs=6
 Similarity=0.675556 11
 TCGCGCTATACGAGAGTATT
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2578467-2578567
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=GAGAGTATTT Num.seqs=5
 Similarity=0.726667 11
 TCTCGCTATGTGAGAGTATT

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Consensus:

tctCgCTATacgAGAGTATt

>Bacillus_Fam_143_20_5 Nr. of seq. 5 Alignment length(with gaps) = 20
 Alignment score = 0.686667
 GCF_001591645.1_ASM159164v1_genomic.fna_5:153867-154047 Satlength=181 Nr
 of Repeats=9 RepeatLength=20 seed=CGCAAATAAA Num.seqs=7
 Similarity=0.746032
 0 CGCAAATAAATTCTCAGGAT
 GCF_001712755.1_ASM171275v1_genomic.fna_5:39192-39789 Satlength=598 Nr of
 Repeats=27 RepeatLength=20 seed=GCAAATAAAA Num.seqs=22
 Similarity=0.724675
 1 GGCAAATAAAATCNTGGAAT
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_35:198476-198815
 Satlength=340 Nr of Repeats=17 RepeatLength=20 seed=TTTTATTTGC
 Num.seqs=16 Similarity=0.675694
 11 CGCAAATAAAATTTGGAAT
 GCF_001712755.1_ASM171275v1_genomic.fna_37:245563-245843 Satlength=281 Nr
 of Repeats=11 RepeatLength=20 seed=ATCGCAAATA Num.seqs=9
 Similarity=0.706349 18
 CGCAAATAAAACTGGAAT
 GCF_001712755.1_ASM171275v1_genomic.fna_10:18587-18827 Satlength=241 Nr
 of Repeats=11 RepeatLength=20 seed=GAATCGCAAA Num.seqs=10
 Similarity=0.716755 16
 CGCAAATAAAANGCCGAAT

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Consensus:

cGCAAATAAAanctngGaAT

>Bacillus_Fam_144_18_5 Nr. of seq. 5 Alignment length(with gaps) = 18
 Alignment score = 0.718518
 GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_1:1402612-1402892
 Satlength=281 Nr of Repeats=11 RepeatLength=18 seed=GGAGCAACAG

Num.seqs=7 Similarity=0.816579 0
GGAGCAACAGGCCCAACA
GCF_900156865.1_PRJEB18960_genomic.fna_3:459675-459846 Satlength=172 Nr
of Repeats=10 RepeatLength=18 seed=GGCCCAACAG Num.seqs=8
Similarity=0.896825
9 GGTCCAACAGGCCCAACA
GCF_000408885.1_ASM40888v1_genomic.fna_1:903316-904711 Satlength=1396 Nr
of Repeats=62 RepeatLength=18 seed=GGAGCAACCG Num.seqs=39
Similarity=0.802069 0
GGAGCAACCGNCCGACA
GCF_000712615.1_ASM71261v1_genomic.fna_9:136496-136568 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=GGAGAAACCG Num.seqs=4 Similarity=0.913580
0 GGAGAAACCGGCCCAACG
Rev.of_GCF_900096965.1_IMG-
taxon_2671180223_annotated_assembly_genomic.fna_5:86873-87080
Satlength=208 Nr of Repeats=9 RepeatLength=18 seed=CACCCGTTGG Num.seqs=6
Similarity=0.935802 4 GGTGTAACGGGCCCAACG

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Consensus:

GGagcAACnGGcCCaACa

>Bacillus_Fam_145_12_5 Nr. of seq. 5 Alignment length(with gaps) = 12
Alignment score = 0.811111
GCF_000153365.1_ASM15336v1_genomic.fna_16:276957-277038 Satlength=82 Nr
of Repeats=6 RepeatLength=12 seed=GAAGACGAAG Num.seqs=4
Similarity=0.851852
0 GAAGACGAAGAT
GCF_000153365.1_ASM15336v1_genomic.fna_16:276984-277131 Satlength=148 Nr
of Repeats=12 RepeatLength=12 seed=GAAGATGAAG Num.seqs=9
Similarity=0.833333 0
GAAGATGAAGAT
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2532988-2533135
Satlength=148 Nr of Repeats=11 RepeatLength=12 seed=TCTTCATCTT
Num.seqs=7 Similarity=0.830688
5 GAAGATGAAGAT
GCF_000299035.1_ASM29903v1_genomic.fna_1:1278771-1279065 Satlength=295 Nr
of Repeats=21 RepeatLength=12 seed=GAAGATGAAG Num.seqs=16
Similarity=0.892593 0
GAAGAAGAAGAA
Rev.of_GCF_000956595.1_ASM95659v1_genomic.fna_52:22021-22282
Satlength=262 Nr of Repeats=21 RepeatLength=12 seed=TCTTCCTCTT
Num.seqs=13 Similarity=0.931624
2 GAAGAAGANGAA

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Consensus:

GAAGAnGAaGAt

>Bacillus_Fam_146_52_4 Nr. of seq. 4 Alignment length(with gaps) = 58
Alignment score = 0.652778

GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_6:238667-238927
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GTTCGGACTG Num.seqs=5
 Similarity=0.796226 18
 TGTCCGAAGTTGCATC-AG--GTTCGGACT-GCT-CTGA-ACGGGTTTCCTCTTCTCC
 Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:859052-859364
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=ACTTCGGACA Num.seqs=6
 Similarity=0.783857 62
 TGTCCGAAGTTGCATCTAG--GTTCGGACT-GCT-CTGA-ACGGGTTTCCTCTTCTCC
 GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_14:48997-49307
 Satlength=311 Nr of Repeats=6 RepeatLength=52 seed=GTTCGGACTC Num.seqs=5
 Similarity=0.762963 18
 TGTCCGAAGTTGCACC-GG--GTTCGGACTCTCTCCTG---CGGATTTCTTCTTCTCC
 Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:477876-478136
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GTGAGTCCGA Num.seqs=5
 Similarity=0.866667 29
 TGTCCGAATAAGCA-C-TGTG-TTCGGACT--CA-CCAAC TCGGTTTTCTTCTTCTCC

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 Consensus:

gTTCGGACTgCtCtgaacGGgTTTctTCTTCTCCTGTCCGAagtGCAAtCaG

>Bacillus_Fam_147_54_4 Nr. of seq. 4 Alignment length(with gaps) = 57
 Alignment score = 0.632554
 GCF_000401235.1_BacNeaAAU1_genomic.fna_155:14912-15172 Satlength=261 Nr
 of Repeats=5 RepeatLength=52 seed=TTCATCCACT Num.seqs=5
 Similarity=0.791195
 0 TTCATCCACTCGATGAACACCACTTTTCTCCT--G-CTTCCTCTACTT--TTTGGTG
 GCF_001591585.1_ASM159158v1_genomic.fna_2:273831-274142 Satlength=312 Nr
 of Repeats=6 RepeatLength=52 seed=CACTTTTCCT Num.seqs=5
 Similarity=0.886792
 20 TTCATCCCTTTGATGAAAACCACTTTT--CCT--G-CTTCTTCTGGTTATTTTGGTG
 Rev.of_GCF_001591585.1_ASM159158v1_genomic.fna_18:26242-26552
 Satlength=311 Nr of Repeats=6 RepeatLength=52 seed=TGGTGTTCAT Num.seqs=5
 Similarity=0.784615 22
 TTCATCCGCTTGATGAACACCACTTTT-TCCTCNGCCTTC--CTGGAT--TGTGGTT
 Rev.of_GCF_001591585.1_ASM159158v1_genomic.fna_18:28113-28373
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GTTCATCAAG Num.seqs=5
 Similarity=0.817949 70
 TTCATTTGCTTGATGAACACCATTTTT-TCCTCGGTCTTC--CTGGAT--TGTGGTG

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 Consensus:

TTCATccgcTtGATGAACACCAcTTTTtCCTcnGnCTTCntCTggaTTgTGGTg

>Bacillus_Fam_148_52_4 Nr. of seq. 4 Alignment length(with gaps) = 57
 Alignment score = 0.626218
 GCF_000759675.1_ASM75967v1_genomic.fna_13:55319-55837 Satlength=519 Nr of
 Repeats=10 RepeatLength=52 seed=GCTCTTGGTG Num.seqs=8
 Similarity=0.807952
 0 GCTCTTGGTGACCGATA-TCCAAGGGAA-ATCG-AA-ATTGTGGTCACCAAGG-AGT
 Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_151:356127-356582
 Satlength=456 Nr of Repeats=4 RepeatLength=52 seed=GATTTTCCTT Num.seqs=3

Similarity=0.914530 30
 GCTCTTGGTGACCGAAA-TCAAAGGAAA-ATCG-AA-AAAGTGGTAACCAAGA-AGG
 Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_164:44908-45116
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GTCATCAAGA Num.seqs=4
 Similarity=0.854701 12
 GCTCTTGATGACCGAAA-TCC--GGAAA-AAAGTAAGAAAGTGGTTACCAAGA-AGG
 Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_57:123377-123693
 Satlength=317 Nr of Repeats=6 RepeatLength=53 seed=ATTGGTTACC Num.seqs=4
 Similarity=0.890985 48 -
 CTATTGGTGACCGAAACAGCAAGGGAAGATAG--A-AAAGTGGTAACCAATAGAGG

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Consensus:

gCTcTTGgTGACCGAaAtccaaGGaAAAtaGaAAaaGTGGTaACCAAGaAGg

>Bacillus_Fam_149_53_4 Nr. of seq. 4 Alignment length(with gaps) = 57
 Alignment score = 0.627680
 GCF_002019645.1_ASM201964v1_genomic.fna_1:1958292-1959384 Satlength=1093
 Nr of Repeats=21 RepeatLength=52 seed=GACAGCTTTG Num.seqs=21
 Similarity=0.736162 48
 GCTTTGGCT-ATATCAACA-A-GAAAGCTGTCCGAACCT-AGG-TAGACTTCGGACA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:1960889-1961149 Satlength=261
 Nr of Repeats=5 RepeatLength=52 seed=AAGCTGTCCG Num.seqs=5
 Similarity=0.846541 73
 GCTTTGGCT-ANATCAACA-A-GAAAGCTGTCCGAACCT-AGG-TAGACTTCGGACA
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:5249431-5249898
 Satlength=468 Nr of Repeats=9 RepeatLength=52 seed=CTGTTCAGAC Num.seqs=8
 Similarity=0.826923 88
 GCTTTAGCT-AGA--AAAAGAGGGAAGCTGTCTGAACAG-AGCGCA-ACTTCGGACA
 GCF_002019645.1_ASM201964v1_genomic.fna_1:5267087-5267710 Satlength=624
 Nr of Repeats=11 RepeatLength=52 seed=ACTTCGGACA Num.seqs=10
 Similarity=0.699802 94
 GCTTCAGCNCTCA--AACAGA-GAAAGCTGTCCGAACACAAGC-CA-ACTTCGGACA

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Consensus:

GACAGCTTtaGCTanAtcAAcAgAGaAAGCTGTCCGAACatAGccAgACTTCG

>Bacillus_Fam_150_53_4 Nr. of seq. 4 Alignment length(with gaps) = 56
 Alignment score = 0.619048
 GCF_000294775.2_ASM29477v2_genomic.fna_1:4687252-4687712 Satlength=461 Nr
 of Repeats=9 RepeatLength=51 seed=GATTAACCTAC Num.seqs=8
 Similarity=0.729654 39
 TTTT--TCTT--TGACCCCTT-ATTTTCGGCGTTAATCCCTCCGATTAACCTACCA
 GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_3:854190-854829
 Satlength=640 Nr of Repeats=12 RepeatLength=52 seed=ATTAACCTCCC
 Num.seqs=9 Similarity=0.824074 40
 TTTTC-TCTT-GAGCA--CCTTCATTTTGGGCGTTATTCCCACTGATTAACCTCCA
 Rev.of_GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_5:200856-
 201375 Satlength=520 Nr of Repeats=10 RepeatLength=52 seed=GACGAAATTG
 Num.seqs=9 Similarity=0.878205 79
 TTTTCGCCCTTACTCCA---CTC-AATTTTCGTCGTTATTCCATGTGATTAACCTACCA

GCF_000294775.2_ASM29477v2_genomic.fna_1:2711828-2712087 Satlength=260 Nr
of Repeats=5 RepeatLength=52 seed=ATTAACTACC Num.seqs=4
Similarity=0.772013 92
TTTTCGCCTTACTCCA---CTC-AATTTTCGTCGTAAATCCATGTGATTA ACTACCA

Consensus:

GATTAAC TaCCATTTTcg cCTTactcCAcCTcAaTTTcGgCGTtAaTCCatct

>Bacillus_Fam_151_52_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.669643
GCF_000169195.2_ASM16919v2_genomic.fna_1:485549-485757 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TTATGAAGGA Num.seqs=4
Similarity=0.794872
0 TTATGAAGGACATTTTCAGACT--GCGG--TTTGCACCCCTTTGTCCTTCATCCCGC
GCF_000169195.2_ASM16919v2_genomic.fna_1:2293568-2294088 Satlength=521 Nr
of Repeats=10 RepeatLength=52 seed=TTTGTCTTC Num.seqs=10
Similarity=0.789937 35
TTATGAAGGACATTTTCAGCTT--GCGG--TTCGTCCCCTTTGTCCTTCATCCCGT
Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:2365732-2366096
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=CGGGATGAAG Num.seqs=7
Similarity=0.912088 51
TTATGAAGGACATTTCAACCT--GCAG--CTCGCNACCTTTTGTCTTCATCCCGC
Rev.of_GCF_001591485.1_ASM159148v1_genomic.fna_169:2077-2544
Satlength=468 Nr of Repeats=9 RepeatLength=52 seed=ATGAAGGACA Num.seqs=6
Similarity=0.583236 47
TTATGAAGGACAATTC---TTGNGCGGCNTTCATAA-CATTTGTCTTCATCCGGC

Consensus:

TTATGAAGGACATTTcagccTGCgGtTcgcaacCtTTTGTCTTCATCCcGc

>Bacillus_Fam_152_53_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.633929
GCF_000177235.2_ASM17723v2_genomic.fna_1:299755-299963 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CTGAAGGTCA Num.seqs=4
Similarity=0.867521
0 CTGAAGGTCATCATA-GAAGCG-CAATGCTTACCGAGAAAACAAGA-AGAAG-CAC
GCF_000177235.2_ASM17723v2_genomic.fna_1:1015273-1015845 Satlength=573 Nr
of Repeats=11 RepeatLength=52 seed=AAAGCAGAAA Num.seqs=11
Similarity=0.933800 34
-TGAAGGTCATCATACG-AG-GTCAATGCTACCCGAAAAAGCAGAAAAAATG-TTC
Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:4124120-4124692
Satlength=573 Nr of Repeats=10 RepeatLength=52 seed=CTTTCTCGGG
Num.seqs=9 Similarity=0.791495
38 -TGAAGGTCATCATACGAAG-G-CAATGCTACCCGAGAAAGTAAACTGAAG-CGN
Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:4072932-4073556
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=GTATGATGAC
Num.seqs=12 Similarity=0.743874
67 --GACGGTCATCATACGAAG-GNCAATGCTGCCCGAGAAATCAAACTGAAGTCGC

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tGAaGGTCATCATAcGaAGGnCAATGCTacCCGAgAAAgcAaaAcagAaGcgc

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Consensus:

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Consensus:

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>Bacillus_Fam_155_54_4 Nr. of seq. 4 Alignment length(with gaps) = 56
Alignment score = 0.630952
```

GCF_001636325.1_ASM163632v1_genomic.fna_1:1582614-1583134 Satlength=521
Nr of Repeats=10 RepeatLength=52 seed=CCTGAAACAC Num.seqs=10
Similarity=0.912251 0
CCTGAAACACTCTGCGATCAC-TC-T-CTTCAGAGGAATAAAT-CATCTTTATTCA
Rev.of_GCF_001636325.1_ASM163632v1_genomic.fna_2:51162-51682
Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=GAATAAAGAT
Num.seqs=10 Similarity=0.944729
51 CCTGAAACACTCTGCAATCAC-TC-T-CTTCAGAGGAATAAAT-CATCTTTATTCA
GCF_001636325.1_ASM163632v1_genomic.fna_1:2294800-2295110 Satlength=311
Nr of Repeats=6 RepeatLength=52 seed=TTACCTGAA Num.seqs=4
Similarity=0.858974 48
CCTGAAGCGC--TCCGAT-TCTTCTTCCTTCAGGTGAATAAACGCA-CTTTATTCA
Rev.of_GCF_001636325.1_ASM163632v1_genomic.fna_3:1067228-1067852
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=GAAGCAGAGA
Num.seqs=12 Similarity=0.882673
80 CCTGAAGCGCTTTCTTAT-TC-TC-TGCTTCAGAGGAATAAATGCG-CGTTATCCA

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Consensus:

CCTGAAaCaCtcTccgAtcaCTCTnCTTCAGagGAATAAAtgCatCtTTATtCA

>Bacillus_Fam_156_51_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.623232
GCF_000292245.2_ASM29224v2_genomic.fna_2:106784-107395 Satlength=612 Nr
of Repeats=12 RepeatLength=51 seed=ATTGGTAATG Num.seqs=11
Similarity=0.743396 0
-ATTGGTAATGNAATT-TTCGCTTTC--CTCCGTTTTCGGTGCGTATTACTCTGA
GCF_000292245.2_ASM29224v2_genomic.fna_60:13365-13773 Satlength=409 Nr of
Repeats=8 RepeatLength=51 seed=CGGTGCGTAT Num.seqs=8 Similarity=0.820728
33 -ATTGGTAATGTAATT-TTCACTTTC-TCT-CTTTTACGGTGCGTATTATCCNCA
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_57:11835-12090
Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=CATTACCAAT Num.seqs=5
Similarity=0.562346 10
-ATTGGTAATGNANAT-TTCGNGTTCNTCT--TTTTACGGTGCGTATTAACCTGGA
GCF_000292245.2_ASM29224v2_genomic.fna_35:28784-28988 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=TAATGAAAAT Num.seqs=4 Similarity=0.925926
6 TATTCGTAATGAAAATCCTGAC-TTC-TCT-CTTTTACGGTGCGTATTATCCTT-

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Consensus:

ATTgGTAATGnAaaTtTcactTTCTtCTctTTTaCGGTGCGTATTAtcctga

>Bacillus_Fam_157_53_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.639899
GCF_000292245.2_ASM29224v2_genomic.fna_33:5368-5572 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=CTTTTTTCGC Num.seqs=4 Similarity=0.864924
47 TTTCGCTCCCTAATTT--CTGCGATCCTCGATTCTCATTACCTATCAC-GCT-TT
GCF_000292245.2_ASM29224v2_genomic.fna_61:11632-11836 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=TTTTTCATTAC Num.seqs=4 Similarity=0.895425
80 TTTCGCACCCTTATTT--CTGCAAGCCGCGATTTTCATTACCTATCAC-A-TGCT

GCF_000292245.2_ASM29224v2_genomic.fna_58:26892-27198 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=CAATTTTCAT Num.seqs=6 Similarity=0.919017
77 ATTCGCACCCTAATTTGGCTTC-A-CCTCAATTTTCATTACCAATCAC-GCT-TT
GCF_000292245.2_ASM29224v2_genomic.fna_94:1889-2195 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=ATTTTCATTA Num.seqs=6 Similarity=0.748428
79 ATTCGCACCCTAATTTGACTAC-ATACACCATTTTCATTACCTATCACAGC--TN

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Consensus:

ctttaTTCGCaCCCTaATTTGnCTgCnAtcCtCgATTtTCATTACctATCACg

>Bacillus_Fam_158_51_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.638384
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_5:259376-259584
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AGTCCGAACC Num.seqs=4
Similarity=0.789308 0
AGTCCGAACCTGCCACGACTTCGGACAGA-AA-AAGGAGAAAAT-CCCTTGCCAG
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:2652246-2652610
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=CTGTCCGAAG Num.seqs=5
Similarity=0.871795 28
AGTCCGAACCTGCCACGACTTCGGACAGT-AA-AAGGA-AAAATCCCCGTGCCAG
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:2731628-2731940
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TTCTCTGTCC Num.seqs=6
Similarity=0.847863 32
AGTCCGAACCTGGGCAACTTCGGACAGAGAA-ATCGA-AAAAC-CCGGTGTGAG
Rev.of_GCF_001591465.1_ASM159146v1_genomic.fna_7:42047-42307
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTCCGACTCT Num.seqs=5
Similarity=0.720606 61
AGTCCGAACCNGGNTCAACTTCTGACACA-ACCAGCGA-AAAAA-CCGGAGTCAG

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Consensus:

AGTCCGAACctGccaCaACTTCgGACAgAaAacGAAAAAtCCcgtGccAG

>Bacillus_Fam_159_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.621212
GCF_000331575.1_ASM33157v1_genomic.fna_1:1399302-1400446 Satlength=1145
Nr of Repeats=22 RepeatLength=52 seed=GTTCGGACAC Num.seqs=22
Similarity=0.894416 0
GTTCGGACACAATTT--TGC-TACTACGGCCGTTTTCTGTCCGAACCTACCACCAA
GCF_000331575.1_ASM33157v1_genomic.fna_1:1688744-1689472 Satlength=729 Nr
of Repeats=14 RepeatLength=52 seed=TTCTGTGCCG Num.seqs=14
Similarity=0.876021 30
GTTCGGACTCGATTT--CGC-TTCTNCGGCCTTTTTCTGTCCGAATTCGCACCTA
Rev.of_GCF_000331575.1_ASM33157v1_genomic.fna_3:122725-123817
Satlength=1093 Nr of Repeats=21 RepeatLength=52 seed=GTCCGAACCTA
Num.seqs=21 Similarity=0.898291
59 GTTCGGACTCGATTT--CGCTTTCTTCTACCTT-TTCTGTCCGAACCTACCCCTA
GCF_000331575.1_ASM33157v1_genomic.fna_1:1781562-1782030 Satlength=469 Nr
of Repeats=9 RepeatLength=52 seed=TCCTGTCCGA Num.seqs=9
Similarity=0.876068 31
GTTCGGACACCATTTGGTGC-TTATGCTAAAAT--CCTGTCCGAACCTACCACCAA

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Consensus:

GTTCGGACaCgATTTcGCTtcTnCgacctTtttCTGTCCGAACtacCaCCaA

>Bacillus_Fam_160_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55

Alignment score = 0.711616

GCF_000708755.2_ASM70875v2_genomic.fna_2:551545-552118 Satlength=574 Nr

of Repeats=11 RepeatLength=52 seed=GATAAGTGCC Num.seqs=10

Similarity=0.772080

0

GATAAGTGCCACCAAGAACAGAGATTNCAGTT-TTGATGGTTCCTTTC-TG-CTG

GCF_000708755.2_ASM70875v2_genomic.fna_2:805597-805857 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=AGAGATTCCCT Num.seqs=5

Similarity=0.874359

18 -ATAAGTGCCATCAACAACAGAGATTCTGGT-TTGGTGGTTCCTTTC-TGCCTG

GCF_000709935.2_ASM70993v2_genomic.fna_4:61155-61415 Satlength=261 Nr of

Repeats=5 RepeatLength=52 seed=AGAGATTCCCT Num.seqs=5 Similarity=0.874359

18 -ATAAGTGCCATCAACAACAGAGATTCTGGT-TTGGTGGTTCCTTTC-TGCCTG

GCF_000708755.2_ASM70875v2_genomic.fna_6:56917-57385 Satlength=469 Nr of

Repeats=9 RepeatLength=52 seed=TGGTTCTTAT Num.seqs=9 Similarity=0.820130

35 -TTAAGTGCCATCAAGCAC-NAGATTTCTNCTGTTGGTGGTTCCTTATCACG-CTG

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Consensus:

aTAAGTGCCAtCAAcACagAGATTcCtggTTTGgTGGTTCcTtTcTcGcCTG

>Bacillus_Fam_161_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55

Alignment score = 0.627778

GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_17:112081-112497

Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=CTCAAGTTTT Num.seqs=8

Similarity=0.883700

0

CTCAAG-

TTTTCGCAAAATCNGGCTCATAGAACACTT-CTATGAACCCAAAATC-

GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_24:70990-71406

Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=GTTTACGCGA Num.seqs=8

Similarity=0.815934

5

CTGAAG-TTTACGCGAAAACGGGCGCATACAAC-CTTCCTATAAGCCCAAAATT-

GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_24:160764-161336

Satlength=573 Nr of Repeats=10 RepeatLength=52 seed=TCTATGAACC

Num.seqs=9 Similarity=0.789832

35

CTNAGG-TTTACGCGAAAANGGNGCATAGAAC-CTTCTATGAACCTAAAATC-

Rev.of_GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_45:75443-75911

Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=TTTTATCGAA Num.seqs=9

Similarity=0.833333

17

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CACGATTTTCGATAAAACGGGATTATAGAAC-CTTCCTATGAACCCATTATTC

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Consensus:

ctcAaGTTTaCGcgAAAacgGGcgCATAgAACCTTcCTATgAaCCcAaaATc

>Bacillus_Fam_162_53_4 Nr. of seq. 4 Alignment length(with gaps) = 55

Alignment score = 0.636364

Similarity=0.842100 4
GCGTTCCATA-CACCTTCTATGACACGCGAACTC--CTCTCGCTCTCCTCTTTTC
GCF_001648575.1_ASM164857v1_genomic.fna_62:58957-59580 Satlength=624 Nr
of Repeats=12 RepeatLength=52 seed=TCTATGACAC Num.seqs=9
Similarity=0.816737
15 GCGTTCCATT-CACCTTCTATGACACGCGTTTTCA-CTCCCGCTCT-CTACTTTC
GCF_001648575.1_ASM164857v1_genomic.fna_67:75226-75644 Satlength=419 Nr
of Repeats=8 RepeatLength=52 seed=TGACACGCGT Num.seqs=6
Similarity=0.782922
19 GCGTTTCATT-CACCTCCTATGACACGCGTTTTCA-CTNCCGCTCT-CGAAGTTT

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Consensus:

GCGTTcCATtCACcttCTATGACACgCGttttCaCTccCGCTCtCtattTTc

>Bacillus_Fam_165_52_4 Nr. of seq. 4 Alignment length(with gaps) = 55
Alignment score = 0.602525
GCF_002019645.1_ASM201964v1_genomic.fna_1:2030290-2031330 Satlength=1041
Nr of Repeats=20 RepeatLength=52 seed=GTTTCAGACAG Num.seqs=20
Similarity=0.811784 3
AAGGTTTCAGACAGCTTTTAGCGTCTGG-CTCGANAAGCTGTCCGAAGTNGAGC--
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:5152559-5153287
Satlength=729 Nr of Repeats=14 RepeatLength=52 seed=AAAAGCTGTC
Num.seqs=14 Similarity=0.904480
17 AAG-TTCAGACAGCTTTTGCCGCATGG-CTCCTAAAGCTGTCCGAAGTAG-GCTC
GCF_002019645.1_ASM201964v1_genomic.fna_1:2116675-2117143 Satlength=469
Nr of Repeats=9 RepeatLength=52 seed=GAAAGCTGTC Num.seqs=9
Similarity=0.798043 31
CGGGTTCAGACAGCTTTTCCGTCCGAG-CACGGAAAGCTGTCCGAAGTTG-GN-C
GCF_002019645.1_ASM201964v1_genomic.fna_1:4452843-4453467 Satlength=625
Nr of Repeats=12 RepeatLength=52 seed=GTTTCAGACAG Num.seqs=12
Similarity=0.821290 54
CGGGTTCAGACAGCTTTTGCCTCCTAGCCACCG-AACCTGTCCGAAGTTG-AC-T

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Consensus:

gTTCAGACAGCTTTTgccgcctaGCaCcgaAAgCTGTCCGAAGtTgccaaG

>Bacillus_Fam_166_52_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.626543
GCF_000292245.2_ASM29224v2_genomic.fna_5:78606-78963 Satlength=358 Nr of
Repeats=7 RepeatLength=51 seed=TTTCATTACC Num.seqs=7 Similarity=0.737528
0 -TTTCATTACCTATCCCA-GCTTTTTTCGCACTCTAATC-CCA-CAACCCACAAG
GCF_000292245.2_ASM29224v2_genomic.fna_2:36979-37183 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=TTTCATTACC Num.seqs=4 Similarity=0.860566
0 -TTTCATTACCTATCACA-GCTTTTTTCGCACTCTAATCTCGA-CATCCCCCAAC
GCF_000292245.2_ASM29224v2_genomic.fna_17:33217-33472 Satlength=256 Nr of
Repeats=5 RepeatLength=51 seed=TTTTCATTAC Num.seqs=5 Similarity=0.783007
0 TTTTCATTACTTATCACC-ACTTTTTTCGCACCGTAATC-CCAGCACCACGCGG-
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_16:189-393 Satlength=205 Nr
of Repeats=4 RepeatLength=51 seed=GATAAGTAAT Num.seqs=4

Similarity=0.769231

15

TTTTTCATTACTTATCACCTACTTATTCGTACCCTAATT-CCGGCATCTCAAAA-

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Consensus:

tTTTCATTACcTATCaCaaCTTtTTCGcACccTAATcCcagCATCcCacaan

>Bacillus_Fam_167_52_4 Nr. of seq. 4 Alignment length(with gaps) = 54

Alignment score = 0.618827

GCF_001636325.1_ASM163632v1_genomic.fna_2:1366189-1366546 Satlength=358

Nr of Repeats=7 RepeatLength=51 seed=AAAAATGGTC Num.seqs=7

Similarity=0.891636

0

AAAAATGGTCATAGAGAGCGAAACTGGAACCAAAAATCCACG-AG--AAAACGA

GCF_001636325.1_ASM163632v1_genomic.fna_2:868067-868429 Satlength=363 Nr

of Repeats=7 RepeatLength=52 seed=GAAGTGAAC Num.seqs=5

Similarity=0.871795

20 AAAAATGGTCATAGAGTGAGGAAGTGAACCAAAAAGGCTCG-AGC-AAAGTGC

Rev.of_GCF_001636325.1_ASM163632v1_genomic.fna_1:1668035-1668348

Satlength=314 Nr of Repeats=5 RepeatLength=52 seed=CTTCCCTGCA Num.seqs=3

Similarity=0.897436

50

CAAAATGGTCATAGATTGAGAACTGGAACCAAAAATGGTTGCAGG-GAAG-GT

GCF_001636325.1_ASM163632v1_genomic.fna_1:898598-898859 Satlength=262 Nr

of Repeats=5 RepeatLength=52 seed=AACTGGAACC Num.seqs=4

Similarity=0.846154

20 -AAAATGGTCATAGATATACAAACTGGAACCAAAAATCGAGCG-GGCTGAAGCCA

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Consensus:

aAAAAATGGTCATAGAgagagaAACTGGAACCAAAAatgctcGaGcaAAgcga

>Bacillus_Fam_168_50_4 Nr. of seq. 4 Alignment length(with gaps) = 54

Alignment score = 0.652778

GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_16:149617-150076

Satlength=460 Nr of Repeats=9 RepeatLength=51 seed=TTTTGTCTTT Num.seqs=9

Similarity=0.819801

24 ACTTTTCTTGAGTCT-CCAC-C-

GATTTTGTCTTTCATAGNCTTGATGAAAG

Rev.of_GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_29:94987-95243

Satlength=257 Nr of Repeats=5 RepeatLength=51 seed=ATGAAAGACA Num.seqs=4

Similarity=0.745807

36 ACTTTTCCAAAAGAT-CCAC-CGGAT-

TTTGTCTTTCATAGCCTCGATGAAAG

GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_19:193092-193875

Satlength=784 Nr of Repeats=7 RepeatLength=51 seed=ACTTTTCTT Num.seqs=5

Similarity=0.963399

50 ACTTTTCTTCTAGCT-CAACTC-

AAT-TTTGTCTTTCATAAGCTCGATGAAAG

Rev.of_GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_25:18116-18765

Satlength=650 Nr of Repeats=6 RepeatLength=51 seed=AAAATAGCTG Num.seqs=4

Similarity=0.891068

27 ACTTTTTCACGTGCTTACCAG-C-TAT-

TTTGTCTTTCATAAGCTTGATGAAGG

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Consensus:

TTTGTCTTTCATAagCTcGATGAAaGACTTTTTTcttgaagcTcAcCgAT

>Bacillus_Fam_169_54_4 Nr. of seq. 4 Alignment length(with gaps) = 54

Alignment score = 0.745885

GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_4:107252-107511

Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=GCCGAAAATG Num.seqs=4

Similarity=0.709644 0

GCCGAAAATGTGATAGGGAAG-AG-GAAAAGGGTAGTTAATCAACCGGATTAAC

Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:3523470-3523938

Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=ACATTTTCGG Num.seqs=9

Similarity=0.804682 11

GCCGAAAATGTGGAGGGGAGG-AG-GAAACTGGTAGTTAATCGACTGGATTAAC

GCF_000294775.2_ASM29477v2_genomic.fna_1:910807-911429 Satlength=623 Nr

of Repeats=12 RepeatLength=52 seed=AACGACGAAA Num.seqs=10

Similarity=0.832054 49

GACGAAAACGTGG-AGAGA-GTAGAGAAAATGGTAGCTAATCAACCGGATTAAC

Rev.of_GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_6:186939-

187251 Satlength=313 Nr of Repeats=5 RepeatLength=52 seed=TTTTCGTCGT

Num.seqs=4 Similarity=0.930818 60

GACGAAAACGTGG-AGAGAGGTAGAGAAAATGGTAGCTAATCAACCGGATTAAC

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Consensus:

GaCGAAAACGTGgnaGaGAgGtAGaGAAAatGGTAGcTAATCaACcGGATTAAC

>Bacillus_Fam_170_52_4 Nr. of seq. 4 Alignment length(with gaps) = 54

Alignment score = 0.600823

GCF_000430765.1_ASM43076v1_genomic.fna_6:155335-155595 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=GGACTACTTT Num.seqs=5

Similarity=0.862893

0 GGACTACTTTCTCCTC--CTGCCGCTCAACCTGTCCGAACAGAGACCGCCTTC

GCF_000430765.1_ASM43076v1_genomic.fna_14:144417-144731 Satlength=315 Nr

of Repeats=6 RepeatLength=52 seed=TTCCGACTAC Num.seqs=5

Similarity=0.830769

49 GGACTACTTTCTCCGC--CNCCCGCTTCAACCTGTCCGAACCTGGACCGACTTC

GCF_002019645.1_ASM201964v1_genomic.fna_1:287166-287842 Satlength=677 Nr

of Repeats=13 RepeatLength=52 seed=CTTCGACAG Num.seqs=13

Similarity=0.833333 48

GGACAGCTTTAACCGC--NTGGCTCCTCAACCTGTCTGAACTTACTCTGACTTC

GCF_002019645.1_ASM201964v1_genomic.fna_1:4704557-4705493 Satlength=937

Nr of Repeats=18 RepeatLength=52 seed=TGAACCTGTC Num.seqs=18

Similarity=0.826714 76

GGACAGCTTT--CGGCTTCTGGCGCATGAACCTGTCCGAACCTGCCTTCACTTC

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Consensus:

GGACaaCTTTctCcgCctgcCgCcTcAACCTGTCCGAACttacaccgaCTTC

>Bacillus_Fam_171_53_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.641975
GCF_001636315.1_ASM163631v1_genomic.fna_1:3109160-3109628 Satlength=469
Nr of Repeats=9 RepeatLength=52 seed=GTCGCCTATA Num.seqs=9
Similarity=0.729167 0
GTCGCCTATAAGGCGTATACGCGACCG-AACGGNAGCCAAAA-AGAGTCCCTCG
GCF_001636315.1_ASM163631v1_genomic.fna_1:3775783-3776095 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=GTCGCATAGA Num.seqs=6
Similarity=0.782906 0
GTCGCATAGAAGGGGTATACGCGCCCG-AGCGGCGGAAAAAATGGAGGTGC-CG
GCF_001636315.1_ASM163631v1_genomic.fna_1:5059185-5059445 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=AGAAAAAGAA Num.seqs=5
Similarity=0.792308 33
GTCGCATAGAAAGAGTATATGCGACTG-AGCGGCAGAAAAAGAAGAGNNGC-CG
GCF_001636315.1_ASM163631v1_genomic.fna_1:4975737-4976309 Satlength=573
Nr of Repeats=11 RepeatLength=52 seed=GTCGCATAGA Num.seqs=9
Similarity=0.720798 0
GTCGCATAGAAGGCGTATACGCGACCGAAGCGGC-GAAAAAATCGTG-AGCTCG

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Consensus:

GTCGCaTagAAgGcGTATAcGCGaCcGAgCGGcaGaaAAAataGaGnngCtCG

>Bacillus_Fam_172_53_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.720165
GCF_001636425.1_ASM163642v1_genomic.fna_1:2633742-2634106 Satlength=365
Nr of Repeats=6 RepeatLength=52 seed=ATGAAGGACT Num.seqs=5
Similarity=0.677576 0
ATGAAGGACTTTTCGCGCTCTTCTTGA-CCTGGTTTTGGCCTTCATAAGCCTN-
Rev.of_GCF_001636425.1_ASM163642v1_genomic.fna_1:4369053-4369313
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AAAGTCCTTC Num.seqs=5
Similarity=0.776543 11 -
TGAAGGACTTTGCTCGTCTTCTTGA-CCTGGTTTTGGTCTTCATTAGCTCGA
Rev.of_GCF_001636425.1_ASM163642v1_genomic.fna_1:4370800-4371268
Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=AAAGTCCTTC Num.seqs=9
Similarity=0.820513 11 -
TGAAGGACTTTGCTCGCTCTTCTTGA-CCGGGTTTTGGCCTTCATTAGCTTGA
GCF_001636425.1_ASM163642v1_genomic.fna_1:3011924-3012184 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=TTTTGTCCCTT Num.seqs=5
Similarity=0.730818 32
ATGAAGGACTTTTCTCGTTATTCTCCAGCCT-GTTTTGTCCCTTCATTCACTTT-

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Consensus:

aTGAAGGACTTTgCtCGcTcTTcttgACctgGTTTTGgcCTTCATtagCttga

>Bacillus_Fam_173_52_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.661523
GCF_002019665.1_ASM201966v1_genomic.fna_1:300861-301737 Satlength=877 Nr
of Repeats=11 RepeatLength=52 seed=ATCGTGCCCT Num.seqs=9
Similarity=0.871795 12
GATCAAGCCGC-GATCGTGCCCTCTAAACGCCGAAAACG-AGAAAACAGGTAAC

GCF_002019665.1_ASM201966v1_genomic.fna_1:548830-549350 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=TCAAAACAAG Num.seqs=10
 Similarity=0.955556 21
 GATGAAG-CGTTGATCGTGCCCTCAAAACAAGAAAAACGAAAAATCG-GGTAAC
 GCF_002019665.1_ASM201966v1_genomic.fna_1:2070270-2070894 Satlength=625
 Nr of Repeats=12 RepeatLength=52 seed=AAAATAGAGG Num.seqs=12
 Similarity=0.897436 38
 GATGAAG-AGCGGATCGTGCCCTCTAAACGAGAAAAATG-AAAATAGAGGGAAC
 Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:4148016-4148588
 Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=TTTTCAGGGC
 Num.seqs=11 Similarity=0.835897
 79 GATGGAG-NGCTGATCGTGCCCTGAAAANNTGAAAAACG-AAAATAGAGGAAAC

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Consensus:

ATCGTGCCCTcaAAAcgagaAAAACGAaAatagaGGtAACGATgaAGcGctG

>Bacillus_Fam_174_54_4 Nr. of seq. 4 Alignment length(with gaps) = 54
 Alignment score = 0.763375
 GCF_000153365.1_ASM15336v1_genomic.fna_16:423251-424048 Satlength=798 Nr of Repeats=15 RepeatLength=53 seed=GTCATGTATC Num.seqs=13
 Similarity=0.864861 0
 GTCATGTATCCCATCAGGTTCCCGGAATACATGAGTA-GGGAGAAAAAAGGATG
 Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2388131-2388928
 Satlength=798 Nr of Repeats=15 RepeatLength=53 seed=GATACATGAC
 Num.seqs=13 Similarity=0.864861
 10 GTCATGTATCCCATCAGGTTCCCGGAATACATGAGTA-GGGAGAAAAAAGGATG
 GCF_000153365.1_ASM15336v1_genomic.fna_74:127356-128149 Satlength=794 Nr of Repeats=13 RepeatLength=53 seed=CGGGATACAT Num.seqs=10
 Similarity=0.875891 22
 GTCATGTATGCCAACAGGTTTCCGGGATACATG-GTATGACTGCAAGAAGGCTA
 GCF_000473245.1_ASM47324v1_genomic.fna_1:2184010-2184804 Satlength=795 Nr of Repeats=13 RepeatLength=53 seed=CGGGATACAT Num.seqs=11
 Similarity=0.875586 22
 GTCATGTATGCCAACAGGTTTCCGGGATACATG-GTATGACTGCAAGAAGGCTA

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Consensus:

GTCATGTATcCCAaCAGGTTcCCGgaATACATGaGTAtGacaGaAAaAAGGaTa

>Bacillus_Fam_175_54_4 Nr. of seq. 4 Alignment length(with gaps) = 54
 Alignment score = 0.627572
 GCF_000311725.1_ASM31172v1_genomic.fna_1:927879-928355 Satlength=477 Nr of Repeats=9 RepeatLength=53 seed=CATGAAACAT Num.seqs=8
 Similarity=0.891285
 0 CATGAAACATACTTT-CCCTACAAATCCGCTCTTCTCTTGTCTCATGAACCCCT
 Rev.of_GCF_000311725.1_ASM31172v1_genomic.fna_2:132590-132855
 Satlength=266 Nr of Repeats=5 RepeatLength=53 seed=ACATAAGTTG Num.seqs=5
 Similarity=0.886420 40
 CATGAGACATACATT-CTCTAAGAATGTGCTCAACTTATGTTCCATGAGCCCTT
 GCF_000311725.1_ASM31172v1_genomic.fna_3:662414-662785 Satlength=372 Nr of Repeats=7 RepeatLength=53 seed=TGTATCATGA Num.seqs=7

Similarity=0.855046
37 CATGTGACATACTTTCCTCTTCCAACCACCT-AACTTATGTATCATGAACCCTT
GCF_000311725.1_ASM31172v1_genomic.fna_4:562666-563196 Satlength=531 Nr
of Repeats=10 RepeatLength=53 seed=AGTTTGTGTT Num.seqs=10
Similarity=0.865269
CATGTGACATACTTTCCTCTGAAAACACCCT-GAGTTTGTGTTTCATGAACCCTT

85

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Consensus:

CATGagACATACtTtCtCtTaaaAAccccCTcaacTtaTGTttCATGAaCCcTt

>Bacillus_Fam_176_53_4 Nr. of seq. 4 Alignment length(with gaps) = 54
Alignment score = 0.659465
GCF_900156865.1_PRJEB18960_genomic.fna_3:147620-148044 Satlength=425 Nr
of Repeats=8 RepeatLength=53 seed=GATAAAATTA Num.seqs=8
Similarity=0.733099
0 GATAAAATTAGGAAAAAGCGAACCAGCAAACCCG-AAATGCAGGTACGCATTTG
GCF_900156865.1_PRJEB18960_genomic.fna_3:564737-565055 Satlength=319 Nr
of Repeats=6 RepeatLength=53 seed=GGATAAAATT Num.seqs=6
Similarity=0.814815
52 GATAAAATTAGGAAACGGCAAACCCGCAAACGAG-AGATACAGGTTCGCATTTG
GCF_900156865.1_PRJEB18960_genomic.fna_3:163814-164132 Satlength=319 Nr
of Repeats=6 RepeatLength=53 seed=CTTAACAGGT Num.seqs=6
Similarity=0.833128
34 GAAGAAATTAGGGAACACCGAACCCGCAAAGGCTCTTA-ACAGGTTCGCATATG
GCF_900156865.1_PRJEB18960_genomic.fna_3:535365-535736 Satlength=372 Nr
of Repeats=7 RepeatLength=53 seed=ATACAGGTTC Num.seqs=7
Similarity=0.746914
36 TAAAAAATTAGGGAANNCGAACCAGTAAAAGCG-ATATACAGGTTCGCAAATG

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Consensus:

gAaaAAATTAGGaAAAagCgAACCaGcAAAcgcatAtaCAGGTtCGCAtaTG

>Bacillus_Fam_177_51_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.768344
GCF_000242895.2_ASM24289v3_genomic.fna_1:507909-508266 Satlength=358 Nr
of Repeats=7 RepeatLength=51 seed=AAAAATGGGA Num.seqs=7
Similarity=0.820728
0 AAAAATGGGAACGAAAGAGCCGCAATAATGCCCAAAATCCAAGAGTCG-C-AG
Rev.of_GCF_000242895.2_ASM24289v3_genomic.fna_1:4381175-4381532
Satlength=358 Nr of Repeats=7 RepeatLength=51 seed=ATTTTGGGCA Num.seqs=7
Similarity=0.828991 38
AAAAATGGGAACCAAGAGCCGCAATGATGCCCAAAATCCAAGAGTCG-C-GG
Rev.of_GCF_000242895.2_ASM24289v3_genomic.fna_1:1303702-1303957
Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=GATTTTGGGC Num.seqs=5
Similarity=0.750000 39
AAAAATGGGAATCAAAGAGCCTCANTGATGCCCAAAATCCGAGAGTCG-C-GG
Rev.of_GCF_000242895.2_ASM24289v3_genomic.fna_1:2430720-2430925
Satlength=206 Nr of Repeats=4 RepeatLength=51 seed=ATTTTGGGCA Num.seqs=3
Similarity=0.912854 38
AAAAACGGGAACGAAAGAGCCGTATTGATGCCCAAAATTC--GAGGCGACTGG

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Consensus:

AAAAAtGGGAAccAAAGAGCCgcAaTgATGCCCCAAATcCaaGAGtCGCgG

>Bacillus_Fam_178_52_4 Nr. of seq. 4 Alignment length(with gaps) = 53

Alignment score = 0.633124

GCF_001636325.1_ASM163632v1_genomic.fna_1:40630-41088 Satlength=459 Nr of Repeats=9 RepeatLength=51 seed=ATAAGAAAGC Num.seqs=8 Similarity=0.916900
0 ATAAGAAAGCGCCGATTTCGCTCAAGAAACCCG-CCA-CTTGAGTCAAGTTG

GCF_001636325.1_ASM163632v1_genomic.fna_1:516349-516757 Satlength=409 Nr of Repeats=8 RepeatLength=51 seed=AGTTGATAAG Num.seqs=8
Similarity=0.798319

46 ATAAGAAAGTGCCGATTCCCATCAAGAAAACGGCCCA-C-CGAGTAAAGTTG

GCF_001636325.1_ASM163632v1_genomic.fna_3:614885-615192 Satlength=308 Nr of Repeats=6 RepeatLength=51 seed=GATAAGAAAG Num.seqs=5
Similarity=0.921569

50 ATAAGAAAGAGCCGTATTTCCATCAAGAACCCCG--AAGCCCGAATAAAGATG

Rev.of_GCF_001636325.1_ASM163632v1_genomic.fna_1:2096119-2096476

Satlength=358 Nr of Repeats=7 RepeatLength=51 seed=TACAGATTTTC Num.seqs=7
Similarity=0.927793 43

ATAAGAAAGCACNGGATTCTCATCAAGAAAATCG-AAATC-TGTATAAAGCTG

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Consensus:

ATAAGAAAGcgCcGgATTccCaTCAAGAAaaccGcaAnCncGaaTaAAGtTG

>Bacillus_Fam_179_53_4 Nr. of seq. 4 Alignment length(with gaps) = 53

Alignment score = 0.742138

GCF_000153365.1_ASM15336v1_genomic.fna_12:126684-126892 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CTTAGTCAGC Num.seqs=4
Similarity=0.876068

0 CTTAGTCAGCTGGACTAGAGCCCTCTG-TAAGGCAATTAAGAGTCCAGAGGGC

GCF_000473245.1_ASM47324v1_genomic.fna_1:1107975-1108183 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CTTAGTCAGC Num.seqs=4
Similarity=0.876068 0

CTTAGTCAGCTGGACTAGAGCCCTCTG-TAAGGCAATTAAGAGTCCAGAGGGC

GCF_000153365.1_ASM15336v1_genomic.fna_16:507322-507582 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GGGTCTTAGT Num.seqs=5
Similarity=0.876923

48 CTTAGTCGGCTGAACTAGTACCCTCTGATTTGAGAATTGCTAG-CCAGAGGGT

Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2304596-2304856

Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GACTAAGACC Num.seqs=5
Similarity=0.876923 59

CTTAGTCGGCTGAACTAGTACCCTCTGATTTGAGAATTGCTAG-CCAGAGGGT

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Consensus:

CTTAGTCaGCTGaACTAGaaCCCTCTGaTaaGacAATTaagAGtCCAGAGGGc


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>Bacillus_Fam_184_52_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.692872
GCF_001591665.1_ASM159166v1_genomic.fna_18:122146-122559 Satlength=414 Nr
of Repeats=8 RepeatLength=52 seed=TCCAATAACC Num.seqs=6
Similarity=0.849573 0
TCCAATAACCCCTATTGGATAC-CTTTTCTCCCACTTTTGCCTCCGTACGGGT
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_53:24940-25253
Satlength=314 Nr of Repeats=6 RepeatLength=52 seed=GGTATCCAAT Num.seqs=5
Similarity=0.712821 23
TCCAATATGCCCGATTGGATACCCCTTTT-TCCNATNTTCTANCGGAACGGGN
GCF_001591665.1_ASM159166v1_genomic.fna_76:10574-10937 Satlength=364 Nr
of Repeats=7 RepeatLength=52 seed=ACCTTTTCTC Num.seqs=6
Similarity=0.870085
73 TCCAATAAGGCCGATTGGAAAC-CTTTTCTCCGATTTTTCCGGTGGAAACGGGT
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GCF_001591805.1_ASM159180v1_genomic.fna_26:68567-68984 Satlength=418 Nr of Repeats=8 RepeatLength=52 seed=GGCTCCAATC Num.seqs=7
Similarity=0.870574
102 TCCAATCAAGCCTATTGGATAC-CTTTTCTCCAATTTTCCAGTGGAACGGGC

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Consensus:

TCCAATaagcCCgATTGGAtACCTTTTcTCCnAttTTTccagcgGaACGGGt

>Bacillus_Fam_185_52_4 Nr. of seq. 4 Alignment length(with gaps) = 53
Alignment score = 0.707547
GCF_001636315.1_ASM163631v1_genomic.fna_1:1920272-1920895 Satlength=624
Nr of Repeats=14 RepeatLength=52 seed=TTTGTCCCTT Num.seqs=9
Similarity=0.760684 0
TTTTGTCCCTTCATCNGCCTTATGAAGACCATTTTGGACCT-GGCTCACGCCTG
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:2936759-2937122
Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=GATGAAGGAC Num.seqs=6
Similarity=0.921368 14
TTTTGTCCCTTCATCAGCCTTATGAAGACCATTTTGAACCT-GGATCCCGCCTG
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:2922406-2923185
Satlength=780 Nr of Repeats=15 RepeatLength=52 seed=ATGAAGACCA
Num.seqs=14 Similarity=0.825021
13 TTTTGGTCTTCATCCNGCTTATGAAGACCATTTTCGTTCCCTCGGC-CACGGCTG
GCF_001636315.1_ASM163631v1_genomic.fna_1:1954829-1955089 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=TATGAAGGAC Num.seqs=5
Similarity=0.933333 19
TTTTGGTCTTCATCGGGCTTATGAAGGACATTTTGAACCC-GGGTCCCAGCTA

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Consensus:

TTTTGgcCTTCATCngcCTTATGAAGacCATTTtGaaCctGGctCaCgcCTg

>Bacillus_Fam_186_51_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.607906
GCF_000292245.2_ASM29224v2_genomic.fna_4:29318-29828 Satlength=511 Nr of Repeats=10 RepeatLength=51 seed=GCACCGTAAT Num.seqs=10
Similarity=0.784242
0 GCACCGTAATTTTCNGCTCCCANCTTTTTCATTACCTATTCCT-TTTTATCC
GCF_000292245.2_ASM29224v2_genomic.fna_4:4185-4491 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=TTTTTCATTA Num.seqs=6 Similarity=0.780342
24 GCACCNTAATCACGGCAACTCAACTTTTTCATTACCTATTCCTACCCTATTC
GCF_000292245.2_ASM29224v2_genomic.fna_14:17182-17488 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=TCATTACCTA Num.seqs=6 Similarity=0.750763
28 GCTCCCTAATTTCTAAACCCCACTAGTTTCATTACCTATTCAC-CGTTATTC
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_31:19400-19655
Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=ATTGGTAATG Num.seqs=5
Similarity=0.803922 39
GCACCGTAATTTTGGGATTCTCCTGTTTCATTACCAATTCAN-CGTTATTC

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Consensus:

GCaCCgTAATttcggcacccCacctgTTTCATTACcTATTCatcgtTATtC

>Bacillus_Fam_187_51_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.695513
GCF_000292245.2_ASM29224v2_genomic.fna_7:14915-15272 Satlength=358 Nr of
Repeats=7 RepeatLength=51 seed=TTTCATTACT Num.seqs=7 Similarity=0.601190
0 TTTCATTACTTATCNCNGTTTTTCGCACCCTAATT-CTGCNAATCTCNAAN
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_21:11408-11714
Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=GATAAGTAAT Num.seqs=6
Similarity=0.803050 14
TTTCATTACTTATCCTAGGTTTTTCGCACCCTAATTCCGGCAAATCTC-AAG
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_31:11-419 Satlength=409 Nr
of Repeats=8 RepeatLength=51 seed=GTAATGAAAA Num.seqs=8
Similarity=0.774043
9 TTTCATTACCTATCCCGGTTTTTCGCACCCTAATCATGCTAAATTT-AAT
GCF_000292245.2_ASM29224v2_genomic.fna_46:27-231 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=ATTTTCATTA Num.seqs=4 Similarity=0.814637
49 TTTCATTACCTATCCCAAGTTTTTCGAACCCTAATCCCTGCAAACTT-CAT

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Consensus:

TTTCATTACcTATCccagGTTTTTCGcACCcTAATccctGCaAAacTcaAt

>Bacillus_Fam_188_52_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.668803
GCF_000307875.1_BABA1.0_genomic.fna_182:7089-7293 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=TGAAGGACAA Num.seqs=4 Similarity=0.904139
0 TGAAGGACAAAACCTCTGTAAAAAT-CGGAAGAAATGTCCTTCATGAAGCCAA
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_73:164831-165091
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AAGGACATTT Num.seqs=5
Similarity=0.876923 41
TGAAGGACAAAACCCCGTAGGAATACAGGAGAAATGTCCTTCATAAAGCCGA
GCF_000759675.1_ASM75967v1_genomic.fna_155:210755-211118 Satlength=364 Nr
of Repeats=6 RepeatLength=52 seed=AAAGAAATGT Num.seqs=4
Similarity=0.854701 27
TGAAGGACAAAACGCTGAAGAAAACCAAAGAAATGTCCTTCATAAGGTCTGA
GCF_001420715.1_ASM142071v1_genomic.fna_22:535021-535281 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=AGGAAAAAGTG Num.seqs=5
Similarity=0.979487 26
TGAAGGACAAAACCCGATAGTAAATAGGAAAAGTGTCCTTCATCTTGTTAA

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Consensus:

TGAAGGACAAAACcCtgtAgaAAaacagaAgAAaTGTCTTCATaaaGccaA

>Bacillus_Fam_189_52_4 Nr. of seq. 4 Alignment length(with gaps) = 52
Alignment score = 0.784188
GCF_000153365.1_ASM15336v1_genomic.fna_18:361319-361684 Satlength=366 Nr
of Repeats=7 RepeatLength=52 seed=GGTTCTAGTC Num.seqs=6
Similarity=0.835897
0 GGTTCTAGTCGAGCGAACTAAGACCCTCTATCCTCCAAAATGTGATTCAGAG

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Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:590850-591215
Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=GACTAGAACC Num.seqs=6
Similarity=0.835897 10
GGTTCTAGTCGAGCGAACTAAGACCCTCTATTCTCCAAAATGTGATTTCAGAG
GCF_000153365.1_ASM15336v1_genomic.fna_59:11476-11844 Satlength=369 Nr of
Repeats=7 RepeatLength=52 seed=CACCCTCTAT Num.seqs=5 Similarity=0.687180
21 GGCCTTAGTCGGNCGGACTAACACCCTCTATTCTCNGCAAATGACTTTCAGAG
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:1841148-1841516
Satlength=369 Nr of Repeats=7 RepeatLength=52 seed=ATAGAGGGTG Num.seqs=5
Similarity=0.697436 31
GGCCTTAGTCGGNCGGACTAACACCCTCTATTCTCNGCAAATGACTTTCAGAG

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GGcccTAGTCGagCGaACTAAcACCCTCTATtCtcCAAATGacaTTCAGAG

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Consensus:

AAAATGTGTCTCAacCcqGTCaATGGAAaCACATAAcAAGaGATtaTGCTcA

Rev.of_GCF_001636325.1_ASM163632v1_genomic.fna_2:1233431-1233639
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GTGTAGGCAA Num.seqs=4
Similarity=0.901709 100
TTTTGGTTCCAGTTACTCAATCTATGACCATTTTCTGTTGCCTACACCTAA

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Consensus:

ttTTGGTTCCAGTTAcaCaatCTAtGACCATTTTctGcttgaCtaCACCcaA

>Bacillus_Fam_192_45_4 Nr. of seq. 4 Alignment length(with gaps) = 45
Alignment score = 0.887654
GCF_000832605.1_ASM83260v1_genomic.fna_1:3713478-3713688 Satlength=211 Nr
of Repeats=5 RepeatLength=45 seed=CAAAATCCAT Num.seqs=3
Similarity=0.597222 0
CAAAATCCATATGCAGCANC GC-AACTCAAGAACAACAATATCAG
Rev.of_GCF_000007825.1_ASM782v1_genomic.fna_1:2093339-2093558
Satlength=220 Nr of Repeats=5 RepeatLength=45 seed=CATATGGATT Num.seqs=4
Similarity=0.876543 13
CAAAATCCATATGTAGCACCACAAAACCAAGAACAACAATATCAA
Rev.of_GCF_000831065.1_ASM83106v1_genomic.fna_1:1910267-1910531
Satlength=265 Nr of Repeats=6 RepeatLength=45 seed=CATATGGATT Num.seqs=5
Similarity=0.905185 13
CAAAATCCATATGCAGCACCACAAAACCAAGAACAACAATATCAA
GCF_001645555.1_ASM164555v1_genomic.fna_12:630892-631111 Satlength=220 Nr
of Repeats=5 RepeatLength=45 seed=CAAAATCCAT Num.seqs=4
Similarity=0.742754 45
CAAAATCCATATGCAGCACCACAAAATCAAGAACAACAATATCAA

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Consensus:

CAAAATCCATATGcAGCAcCaCaAAacCAAGAACAACAATATCAa

>Bacillus_Fam_193_42_4 Nr. of seq. 4 Alignment length(with gaps) = 43
Alignment score = 0.714470
GCF_001591425.1_ASM159142v1_genomic.fna_67:17-228 Satlength=212 Nr of
Repeats=5 RepeatLength=42 seed=TGGCCGAAAA Num.seqs=4 Similarity=0.830688
0 TGGCCG-AAAAGCGACTGCAGTTGGCGCGAAAGCAAGTTGGGT
GCF_001591425.1_ASM159142v1_genomic.fna_102:7924-8407 Satlength=484 Nr of
Repeats=14 RepeatLength=42 seed=TTGGCGTGAA Num.seqs=9
Similarity=0.848325
20 TGGCCGAAAAAGCGT-CGCAGTTGGCGTGAAAGTGAGCTCAGT
GCF_001591425.1_ASM159142v1_genomic.fna_150:3-528 Satlength=526 Nr of
Repeats=11 RepeatLength=42 seed=GGCCGAAAAA Num.seqs=9
Similarity=0.739506
43 TGGCCGAAAAAGCGA-TGCAGTTGGCGTGAAAGTGAGTTCGGT
GCF_001591425.1_ASM159142v1_genomic.fna_97:4685-4958 Satlength=274 Nr of
Repeats=7 RepeatLength=42 seed=TGGCCGAAAA Num.seqs=6 Similarity=0.815873
0 TGGCCGAAAAAGTAA-CCCAGTTGGCGCAAAAGTCCGTTCAGT

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Consensus:

TGGCCGaAAAAGcgacgCAGTTGGCGcgAAAGtgaGtTcaGT

>Bacillus_Fam_194_40_4 Nr. of seq. 4 Alignment length(with gaps) = 40
Alignment score = 0.730556
GCF_000153365.1_ASM15336v1_genomic.fna_18:178288-178478 Satlength=191 Nr
of Repeats=5 RepeatLength=38 seed=AAAAGAGCCA Num.seqs=3
Similarity=0.906433
0 AAAAGAGCCAACGGAACCGTCCCCCTGGCCCAGTTTCA--
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:774018-774208
Satlength=191 Nr of Repeats=5 RepeatLength=38 seed=TTGGCTCTTT Num.seqs=3
Similarity=0.906433 11
AAAAGAGCCAACGGAACCGTCCCCCTGGCCCAGTTTCA--
GCF_000153365.1_ASM15336v1_genomic.fna_18:449580-449794 Satlength=215 Nr
of Repeats=5 RepeatLength=40 seed=GGTCTGTCCC Num.seqs=3
Similarity=0.911111
13 AAATGAGCCATGGGGTCTGTCCCCCGGCCCTGCTCCAAA
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:503588-503802
Satlength=215 Nr of Repeats=5 RepeatLength=40 seed=GGGACAGACC Num.seqs=3
Similarity=0.911111 23
AAATGAGCCATGGGGTCTGTCCCCCGGCCCTGCTCCAAA

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Consensus:

AAAaGAGCCAacGGaaCcGTCCCCcGGCCCaGcTcCAaa

>Bacillus_Fam_195_40_4 Nr. of seq. 4 Alignment length(with gaps) = 40
Alignment score = 0.661111
GCF_000612665.1_FF4_genomic.fna_56:12424-12580 Satlength=157 Nr of
Repeats=4 RepeatLength=39 seed=GTAAAGCGGT Num.seqs=4 Similarity=0.880342
0 GTAAAGCGGTGATGCGCTGGGGGCCAGTCCCCCGCT-AAG
Rev.of_GCF_000612665.1_FF4_genomic.fna_72:69320-69476 Satlength=157 Nr of
Repeats=4 RepeatLength=39 seed=CTTACCGCT Num.seqs=4 Similarity=0.863248
13 -TAAAGCGGTGAAGCGCTGGGGGACAGGCCCCCGCTGAAG
Rev.of_GCF_000612665.1_FF4_genomic.fna_72:117051-117206 Satlength=156 Nr
of Repeats=4 RepeatLength=39 seed=CTGTCCCCCA Num.seqs=3
Similarity=0.977208
27 ATAAAGCGTTACTGTGATGGGGGACAGGCCCCCGCT-GTG
Rev.of_GCF_000612665.1_FF4_genomic.fna_72:111644-111839 Satlength=196 Nr
of Repeats=5 RepeatLength=39 seed=GGGGGCCTGT Num.seqs=5
Similarity=0.829060
32 -TAAAGCAGTAACGCACTGAGGGACAGGCCCCACCCAAG

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Consensus:

nTAAAGCggTaatGcgctGgGGGaCAGgCCCCgCtnaaG

>Bacillus_Fam_196_40_4 Nr. of seq. 4 Alignment length(with gaps) = 40
Alignment score = 0.686111
GCF_000285535.1_ASM28553v1_genomic.fna_7:68195-68355 Satlength=161 Nr of
Repeats=5 RepeatLength=40 seed=GAGACGCAAA Num.seqs=3 Similarity=0.731707
0 GAGACGCAAAATCTTAATTTGACGCAAAATCCTCAGAAAT

GCF_000285535.1_ASM28553v1_genomic.fna_7:68195-69241 Satlength=1047 Nr of Repeats=16 RepeatLength=40 seed=GAGACGCAAA Num.seqs=12
 Similarity=0.745455
 0 GAGACGCAAAAATCTGAGTTATGACGCAAATCTTCAGAAC
 Rev.of_GCF_000285535.1_ASM28553v1_genomic.fna_56:13-336 Satlength=324 Nr of Repeats=8 RepeatLength=40 seed=TTTTTGCGTC Num.seqs=5
 Similarity=0.739683
 12 CAGACGCAAAAATAAGGATTTTCGACGCAAATCCGTGGANG
 GCF_000285535.1_ASM28553v1_genomic.fna_57:33-354 Satlength=322 Nr of Repeats=8 RepeatLength=40 seed=GACGCAAAAA Num.seqs=7 Similarity=0.723810
 42 CAGACGCAAAAATTAGGATTTTCGACGCAAATCCNTGGGCG

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 Consensus:

cAGACGCAAAAATcagaaTTtcGACGCAAATCctcaGaag

>Bacillus_Fam_197_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
 Alignment score = 0.608025
 GCF_000007825.1_ASM782v1_genomic.fna_1:2540573-2540735 Satlength=163 Nr of Repeats=5 RepeatLength=36 seed=CCAGTCGGTC Num.seqs=4
 Similarity=0.833333
 0 CCAGTCGGTCCAGTAATACCAGTCCTTCCAGTAACA
 GCF_000017425.1_ASM1742v1_genomic.fna_1:1048468-1048891 Satlength=424 Nr of Repeats=11 RepeatLength=36 seed=CCAGTAATAC Num.seqs=9
 Similarity=0.962963
 CCAGTTGGTCCAGTAATACCAGTTTCTCCTGTAGGT
 Rev.of_GCF_001895885.1_ASM189588v1_genomic.fna_1:1987676-1989071
 Satlength=1396 Nr of Repeats=31 RepeatLength=36 seed=GGGATCACTG
 Num.seqs=26 Similarity=0.727521
 20 CCAGTTGATCCAGTGATCCCTGTNGCNCCAGTAGGT
 GCF_000715205.1_SOAPdenovo_v1.05_genomic.fna_25:483-1086 Satlength=604 Nr of Repeats=10 RepeatLength=36 seed=CCCGTGTTTC Num.seqs=6
 Similarity=0.802469
 CCAGTCGGACCACTTGTACCCGTGTTTCTGTGCA

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 Consensus:

CCAGTcGgtCCAgTaaTaCCaGTntctCCaGTagca

>Bacillus_Fam_198_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
 Alignment score = 0.804012
 GCF_000007845.1_ASM784v1_genomic.fna_1:2735864-2736314 Satlength=451 Nr of Repeats=12 RepeatLength=36 seed=TCTTCCTTAG Num.seqs=11
 Similarity=0.805387
 TCTTCCTTAGGTTTNGCTACTTCTTGGACTTTCACT
 Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_51:179190-179442
 Satlength=253 Nr of Repeats=7 RepeatLength=36 seed=GAAAGTCCAA Num.seqs=7
 Similarity=0.915344
 TCTTCCTTAGGCTTTACTACTTCTTGGACTTTTCGCT
 GCF_000008505.1_ASM850v1_genomic.fna_1:2775427-2776093 Satlength=667 Nr of Repeats=18 RepeatLength=36 seed=CTTCTTCCTT Num.seqs=17


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Similarity=0.784314
TCTTCCTTAGCTTTNGCTATTTCTTGTGCTTTTGCT
GCF_000496285.1_ASM49628v1_genomic.fna_1:232428-232860 Satlength=433 Nr
of Repeats=10 RepeatLength=36 seed=GCTATTCTT Num.seqs=8
Similarity=0.873016
51 TCTTCCTTAGCCTTTGCTATTTCTTGGGCTTTCGCT

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Consensus:

TCTTCCTTAGccTTtgCTAcTTCTTGgaCTTTcgCT

>Bacillus_Fam_199_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
Alignment score = 0.658951
GCF_000775975.1_ASM77597v1_genomic.fna_1:1148498-1150349 Satlength=1852
Nr of Repeats=44 RepeatLength=36 seed=CCCGTGTTAC Num.seqs=28
Similarity=0.803155
CCCGTGTTACCTTGAGCNCCTTGAGGTCCAGTAGCA
Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_45:36-216 Satlength=181 Nr
of Repeats=5 RepeatLength=36 seed=TCAAGGTAAC Num.seqs=3
Similarity=0.851852
CCCGTGTTACCTTGAGCACCTTGAGGTCCAGTAGCG
GCF_001645555.1_ASM164555v1_genomic.fna_50:0-323 Satlength=324 Nr of
Repeats=9 RepeatLength=36 seed=GTGTTACCTT Num.seqs=9 Similarity=0.797297
3 CCCGTGTTACCTTGAGGTCCAGTAGCACCGGTAGCG
GCF_001439635.1_ASM143963v1_genomic.fna_165:51610-51799 Satlength=190 Nr
of Repeats=5 RepeatLength=36 seed=CCCTTATCTC Num.seqs=4
Similarity=0.827160
9 CCTGTGTCACCCTTATCTCCTTGTGGTCCTGTTGCT

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Consensus:

CCcGTGTtACcTtGAgctCcttgaGgtCCaGTaGCg

>Bacillus_Fam_200_36_4 Nr. of seq. 4 Alignment length(with gaps) = 36
Alignment score = 0.780864
GCF_001439635.1_ASM143963v1_genomic.fna_69:47-182 Satlength=136 Nr of
Repeats=4 RepeatLength=36 seed=CCAGTAGGTC Num.seqs=3 Similarity=0.851852
0 CCAGTAGGTCCAGTGTTNCCAGTAAATCCNGTAGCC
GCF_001439635.1_ASM143963v1_genomic.fna_173:47-182 Satlength=136 Nr of
Repeats=4 RepeatLength=36 seed=CCAGTAGGTC Num.seqs=3 Similarity=0.925926
0 CCAGTAGGTCCAGTGTTCCCAGTAAATCCGGTAGCC
GCF_001439635.1_ASM143963v1_genomic.fna_175:55401-55545 Satlength=145 Nr
of Repeats=4 RepeatLength=36 seed=GTAAATCCGG Num.seqs=4
Similarity=0.889640
21 CCAGTAGGCCAGTGATTCCGGTAAATCCGGTAGCC
Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_8:14-248 Satlength=235 Nr
of Repeats=5 RepeatLength=36 seed=ACTGGAACA Num.seqs=4
Similarity=0.787538
5 CCAGTAGGTCCGGTGATGCCGGTAGATCCAGTGTTTC

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Consensus:

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CCAGTAGGtCCaGTGaTnCCaGTAAATCCgGTagcC

>Bacillus_Fam_201_33_4 Nr. of seq. 4 Alignment length(with gaps) = 35
Alignment score = 0.651587
GCF_001578185.1_ASM157818v1_genomic.fna_1:3749385-3749913 Satlength=529
Nr of Repeats=16 RepeatLength=33 seed=CCTCCCATCA Num.seqs=16
Similarity=0.768919 0
-CCTCCCATCATTCCTGGTTGACCTCCTGGATGG-
GCF_001578185.1_ASM157818v1_genomic.fna_1:3749385-3750507 Satlength=1123
Nr of Repeats=33 RepeatLength=33 seed=CCTCCCATCA Num.seqs=32
Similarity=0.696781 0
-CCTCCCATCATNCCTGGNTGGCCTCCTTGATGA-
GCF_001578185.1_ASM157818v1_genomic.fna_1:3750017-3750692 Satlength=676
Nr of Repeats=16 RepeatLength=33 seed=CATCATGCCT Num.seqs=12
Similarity=0.815211 5
-CTTCCCATCATGCCTGAATGGCTTCCTTGATGAC
GCF_001645685.2_ASM164568v2_genomic.fna_1:3344937-3345585 Satlength=649
Nr of Repeats=19 RepeatLength=33 seed=CCGCCCATCA Num.seqs=12
Similarity=0.884910 1
ACCGCCCATCATGCCGGGCTGACCTCCATTTG--

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Consensus:

CctCCCATCATgCcTggnTGaCcTCcTtgaTGa

>Bacillus_Fam_202_27_4 Nr. of seq. 4 Alignment length(with gaps) = 28
Alignment score = 0.646825
GCF_000262045.1_KCTC_13613_01_genomic.fna_51:24-285 Satlength=262 Nr of
Repeats=7 RepeatLength=27 seed=CCAGTTACTC Num.seqs=5 Similarity=0.945679
0 -CCAGTTACTCCTGTTGCTCCTGTTGGA
GCF_001712755.1_ASM171275v1_genomic.fna_9:108050-108311 Satlength=262 Nr
of Repeats=11 RepeatLength=27 seed=GCTCCTGTCTG Num.seqs=7
Similarity=0.985891 7
TCCAGTTGCTCCTGTCTGCTCCAGCTGT-
Rev.of_GCF_000706725.1_ASM70672v1_genomic.fna_1:1393225-1394061
Satlength=837 Nr of Repeats=18 RepeatLength=27 seed=TTAGATGGAG
Num.seqs=13 Similarity=0.953150
8 -CCATCTAATCCTGTCTGGTCCCGTTGCT
GCF_002019765.1_ASM201976v1_genomic.fna_1:2612055-2612922 Satlength=868
Nr of Repeats=22 RepeatLength=27 seed=TCCATCTAAT Num.seqs=18
Similarity=0.917050 26
-CCATCTAATCCTGTCTGGTCCCGTTGCT

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Consensus:

CCAgcTaaTCCTGTcGcTCCcGtTGct

>Bacillus_Fam_203_27_4 Nr. of seq. 4 Alignment length(with gaps) = 27
Alignment score = 0.711934

BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:129261-129369 Satlength=109 Nr of Repeats=4 RepeatLength=27 seed=GGAGTAACCG Num.seqs=4 Similarity=0.893004
0 GGAGTAACCGGAGCGACAGGAATGCCA
GCF_000007845.1_ASM784v1_genomic.fna_1:2280509-2280779 Satlength=271 Nr of Repeats=9 RepeatLength=27 seed=GGAATAACGG Num.seqs=8
Similarity=0.821869
18 GGAGTGACAGGTCCAACAGGAATAACG
GCF_000008505.1_ASM850v1_genomic.fna_1:2328181-2328613 Satlength=433 Nr of Repeats=14 RepeatLength=27 seed=GGAATAACGG Num.seqs=12
Similarity=0.831650 18
GGAGCAACAGGTCCGACGGGAATAACG
Rev.of_GCF_000017425.1_ASM1742v1_genomic.fna_1:3294429-3294681
Satlength=253 Nr of Repeats=9 RepeatLength=27 seed=GTTGCTCCTG Num.seqs=8
Similarity=0.987654 35
GGAGCAACCGGTCCAACGGGAATAACA

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Consensus:

GGAGcaACaGGtcCaACaGGAATaaCa

>Bacillus_Fam_204_25_4 Nr. of seq. 4 Alignment length(with gaps) = 25
Alignment score = 0.617778
GCF_000175075.1_ASM17507v1_genomic.fna_44:33119-33407 Satlength=289 Nr of Repeats=11 RepeatLength=24 seed=GCTGCTGCTT Num.seqs=10
Similarity=0.851852
0 GCTGCTGCTTCTGCCTCCGC-TTTG
Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:273946-274090
Satlength=145 Nr of Repeats=6 RepeatLength=24 seed=GCCAAAGCGA Num.seqs=6
Similarity=0.911111 2
GCCTCTGCTTCTGCCTTCGC-TTTG
Rev.of_GCF_000321185.1_ASM32118v1_genomic.fna_111:34583-34703
Satlength=121 Nr of Repeats=5 RepeatLength=24 seed=CAGGCAAAAG Num.seqs=5
Similarity=0.933333 4 -
CCTGCGCCTCTGCTTCAGCTTTTG
Rev.of_GCF_000430785.1_ASM43078v1_genomic.fna_23:12805-12925
Satlength=121 Nr of Repeats=5 RepeatLength=24 seed=AAAGCAGAGG Num.seqs=5
Similarity=0.977778 22
-CTTTCGCATCTGCCTCTGCTTTTG

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Consensus:

gCctccGctTCTGCcTccGctTTTG

>Bacillus_Fam_205_24_4 Nr. of seq. 4 Alignment length(with gaps) = 24
Alignment score = 0.805556
GCF_000007825.1_ASM782v1_genomic.fna_1:1044010-1044106 Satlength=97 Nr of Repeats=4 RepeatLength=24 seed=CCTGGAACAC Num.seqs=4 Similarity=0.824074
0 CCTGGAACACCAGATCCAGAAAAA
GCF_000831065.1_ASM83106v1_genomic.fna_1:894250-894442 Satlength=193 Nr of Repeats=7 RepeatLength=24 seed=ATCCAGAAAA Num.seqs=6
Similarity=0.881481
13 CCTGGAACACCAGATCCAGAAAAA

Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:3721872-3721992
 Satlength=121 Nr of Repeats=5 RepeatLength=24 seed=TCTGGATCTG Num.seqs=5
 Similarity=0.833333 20
 CCGGAAAAACCAGATCCAGAAAAA
 Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_16:33671-33767
 Satlength=97 Nr of Repeats=4 RepeatLength=24 seed=TCTGGATCCG Num.seqs=4
 Similarity=0.935185 20
 CCAGAAACAACGGATCCAGAGAAA

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Consensus:

CCtGaAAcAcCaGATCCAGaAAA

>Bacillus_Fam_206_20_4 Nr. of seq. 4 Alignment length(with gaps) = 23
 Alignment score = 0.718599
 GCF_001877785.1_PlanoSAMB_genomic.fna_33:9772-9852 Satlength=81 Nr of
 Repeats=4 RepeatLength=20 seed=TATGATCCAT Num.seqs=4 Similarity=0.542929
 0 TATGATCCATT--CTGAAATTA
 Rev.of_GCF_900094975.1_IMG-
 taxon_2617270721_annotated_assembly_genomic.fna_4:70413-70513
 Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=AATGGATCAT Num.seqs=5
 Similarity=0.693939 11 TATGATCCATT-T-CNGAAATA-
 GCF_001877785.1_PlanoSAMB_genomic.fna_85:133615-133695 Satlength=81 Nr of
 Repeats=4 RepeatLength=20 seed=TATGATCCAT Num.seqs=4 Similarity=0.671958
 21 TATGATCCATT-TCCAGAAATA-
 GCF_001877785.1_PlanoSAMB_genomic.fna_106:22377-22457 Satlength=81 Nr of
 Repeats=4 RepeatLength=20 seed=TATGATCCAT Num.seqs=4 Similarity=0.683862
 21 TATGATCCATTCT-CAGAAATT-

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Consensus:

TATGATCCATTtCaGAAATa

>Bacillus_Fam_207_21_4 Nr. of seq. 4 Alignment length(with gaps) = 23
 Alignment score = 0.642512
 GCF_000612805.1_FF3_genomic.fna_1:291005-291088 Satlength=84 Nr of
 Repeats=4 RepeatLength=21 seed=AACATGGAAT Num.seqs=3 Similarity=0.809524
 0 AACATGGAATAAA-C-TCCGNAA
 GCF_000612805.1_FF3_genomic.fna_1:447160-447244 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=CATGGAATAA Num.seqs=4 Similarity=0.654040
 2 TTCATGGAATAAA-C-TCTGAAA
 GCF_000612805.1_FF3_genomic.fna_8:67783-67867 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=TGGAATAAAC Num.seqs=4 Similarity=0.732323
 4 AACATGGAATAAA-CNTCTGANA
 GCF_000612805.1_FF3_genomic.fna_3:573446-573530 Satlength=85 Nr of
 Repeats=4 RepeatLength=21 seed=GTAGAATAAA Num.seqs=4 Similarity=0.646465
 3 AATGTAGAATAAANC-TCCGAAA

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Consensus:

aacaTgGAATAAACTCcGaaA

>Bacillus_Fam_208_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.604798
GCF_000294775.2_ASM29477v2_genomic.fna_1:4944734-4944837 Satlength=104 Nr
of Repeats=5 RepeatLength=21 seed=TCTATTTGCA Num.seqs=3
Similarity=0.490741 0
TCTATTTGCAG-NTTNCGGC-
Rev.of_GCF_001591465.1_ASM159146v1_genomic.fna_37:37195-37419
Satlength=225 Nr of Repeats=10 RepeatLength=20 seed=CTGCAAATAG
Num.seqs=6 Similarity=0.659788
10 CCTATTTGCAG--TTCCGGTT
Rev.of_GCF_000986785.1_ASM98678v1_genomic.fna_5:144649-145040
Satlength=392 Nr of Repeats=15 RepeatLength=21 seed=GCAAATAGAA
Num.seqs=11 Similarity=0.592496
9 TCTATTTGCCG-NTTTCNANT
Rev.of_GCF_000986785.1_ASM98678v1_genomic.fna_4:84896-85225 Satlength=330
Nr of Repeats=12 RepeatLength=21 seed=GCAAATAGAA Num.seqs=8
Similarity=0.590278 9
TCTATTTGCCGATTTTCNCATT

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Consensus:

tCTATTTGCaGnTTTccgatt

>Bacillus_Fam_209_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.651515
GCF_000401235.1_BacNeaAAU1_genomic.fna_227:43989-44111 Satlength=123 Nr
of Repeats=6 RepeatLength=20 seed=AGTCGCAAGT Num.seqs=4
Similarity=0.837302
0 AGTCGCAAGTAAGAG-GG-GAG
Rev.of_GCF_000401235.1_BacNeaAAU1_genomic.fna_157:4403-4508 Satlength=106
Nr of Repeats=5 RepeatLength=21 seed=TTACTTGCGA Num.seqs=5
Similarity=0.715151 12
AGTCGCAAGTAAAG-GGTGAA
Rev.of_GCF_000401235.1_BacNeaAAU1_genomic.fna_154:1239-1364 Satlength=126
Nr of Repeats=6 RepeatLength=21 seed=CTTGCGACTC Num.seqs=5
Similarity=0.743939 9
AGTCGCAAGAAAAAGTGTCGG-
Rev.of_GCF_000401235.1_BacNeaAAU1_genomic.fna_164:34058-34338
Satlength=281 Nr of Repeats=13 RepeatLength=21 seed=TTACTTGCGA
Num.seqs=12 Similarity=0.826840
12 AGTCGCAAGTAAAGGTGGGGA-

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Consensus:

AGTCGCAAGtAAaaGtGgnGan

>Bacillus_Fam_210_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.650253
GCF_000986785.1_ASM98678v1_genomic.fna_3:201618-201723 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=GTAGAGTAAA Num.seqs=5

Similarity=0.442667

0 GTAGAGTAAACT-AANAAATT-

GCF_001315085.1_ASM131508v1_genomic.fna_38:31481-31582 Satlength=102 Nr of Repeats=4 RepeatLength=20 seed=TTAGTAGATA Num.seqs=3

Similarity=0.631313

17 GTAGA-TAAAAT-CAGAAATTA

GCF_000986785.1_ASM98678v1_genomic.fna_25:55323-55428 Satlength=106 Nr of Repeats=4 RepeatLength=21 seed=GTAGAGTAAA Num.seqs=3 Similarity=0.505050

0 GTAGAGTAAANTNCTGAAANT-

GCF_000986785.1_ASM98678v1_genomic.fna_39:16547-16652 Satlength=106 Nr of Repeats=4 RepeatLength=21 seed=GTAGAGTAAA Num.seqs=3 Similarity=0.505050

0 GTAGAGTAAANTNCTGAAANT-

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Consensus:

GTAGAgTAAAnTncagAAAtT

>Bacillus_Fam_211_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22

Alignment score = 0.656566

GCF_001636335.1_ASM163633v1_genomic.fna_1:2068723-2068964 Satlength=242

Nr of Repeats=12 RepeatLength=20 seed=TTTGCGAATT Num.seqs=9

Similarity=0.766667

0

TTTGCGAATTTCATT-C-TTTA

Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_111:18515-18598 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCTAAT Num.seqs=3

Similarity=0.626263

9

TTAGCGAATTTCNAA-CATTTA

Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_30:250624-250707 Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=TCGCTAATAA Num.seqs=3

Similarity=0.746032

29

TTAGCGAA-

TTCAAAGCATTTA

Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_18:190500-190624 Satlength=125 Nr of Repeats=6 RepeatLength=21 seed=TCGCTAATAA Num.seqs=4

Similarity=0.666667

28

TTAGCGATTTCAAT-CACTTA

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Consensus:

TTaGCGAatTTCaaaCatTTA

>Bacillus_Fam_212_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22

Alignment score = 0.631313

GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_16:258288-258369

Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TATCTACGAA Num.seqs=3

Similarity=0.777778

0

TATCTACG-AAA-ATACAGATA

Rev.of_GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_22:509247-509328

Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TTTCGTTAGAT Num.seqs=3

Similarity=0.777778

11

TATCTACG-AAATTTAAA-ATA

Rev.of_GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_22:513986-514066

Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=TTCGTAGATA Num.seqs=4
Similarity=0.636243 30 TATCTACG-AAATTTAGA-ATA
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_19:516952-517036
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TATCTACACA Num.seqs=4
Similarity=0.461353 0
TA-CTACGAAAATGTGTAGATA

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

Consensus:

TAtCTACGAAAttTanAgATA

>Bacillus_Fam_213_21_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.611111
GCF_000171615.1_ASM17161v1_genomic.fna_75:39270-39436 Satlength=167 Nr of
Repeats=7 RepeatLength=21 seed=TAAAAACAGA Num.seqs=5 Similarity=0.666667
0 TAAAAACAGAAATGCAAGAGG-
GCF_001591425.1_ASM159142v1_genomic.fna_42:3633-3717 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=ATGAAAGCAG Num.seqs=4 Similarity=0.724868
10 -ACAAACTGAAATGAAAGCAGA
GCF_001591465.1_ASM159146v1_genomic.fna_37:32146-32471 Satlength=326 Nr
of Repeats=6 RepeatLength=21 seed=GAAATGAAAA Num.seqs=4
Similarity=0.862434
28 -ACAACAAGAAATGAAAAAAGA
Rev.of_GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_21:114898-115087
Satlength=190 Nr of Repeats=8 RepeatLength=21 seed=TCTTGTTTCA Num.seqs=7
Similarity=0.806500 42 -ACTACAAGAAATGAAACAAGA

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Consensus:

AcaAaaaGAAATGaAAgaaGa

>Bacillus_Fam_214_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.623737
GCF_000331575.1_ASM33157v1_genomic.fna_1:1705037-1705121 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=ATTTATTGTC Num.seqs=4
Similarity=0.548309
0 ATTTATTGTCCGAAACAAGG-
GCF_000331575.1_ASM33157v1_genomic.fna_4:111890-112405 Satlength=516 Nr
of Repeats=18 RepeatLength=21 seed=TTTATTGTCC Num.seqs=13
Similarity=0.806268 1
TTTTATTGTCCGGAATCAAAT-
Rev.of_GCF_001315045.1_ASM131504v1_genomic.fna_25:44801-44885
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=GGACAATAAA Num.seqs=4
Similarity=0.453704 11
ATTTATTGTCC-GATTCTAGTG
GCF_001315045.1_ASM131504v1_genomic.fna_42:24951-25035 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTTATTGTCC Num.seqs=4 Similarity=0.420940
22 -TTTATTGTCCAGATACTCATG

***** ** *

Consensus:

aTTTATTGTCCgGAaaCaaatg

>Bacillus_Fam_215_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.694444
GCF_000401235.1_BacNeaAAU1_genomic.fna_108:5084-5249 Satlength=166 Nr of
Repeats=8 RepeatLength=21 seed=ATCAGCCAAA Num.seqs=5 Similarity=0.809524
12 AATGAG-GGGGAAATCAGCCAA
Rev.of_GCF_001591585.1_ASM159158v1_genomic.fna_22:73236-73362
Satlength=127 Nr of Repeats=6 RepeatLength=21 seed=TTTGGCTGAT Num.seqs=6
Similarity=0.771717 21
AGTGAGTGGGGAA-TCAGCCAA
Rev.of_GCF_001591585.1_ASM159158v1_genomic.fna_40:17715-17818
Satlength=104 Nr of Repeats=5 RepeatLength=21 seed=TTTGGCTGAT Num.seqs=3
Similarity=0.809524 22
AGTAAG-ANGGAAATCAGCCAA
Rev.of_GCF_001591585.1_ASM159158v1_genomic.fna_3:180090-180216
Satlength=127 Nr of Repeats=6 RepeatLength=21 seed=CTTTGGCTGA Num.seqs=6
Similarity=0.839153 22
AGCGGGGAGGGAA-TCAGCCAA

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Consensus:

aTCAGCCAAAgtgaGnagGGAA

>Bacillus_Fam_216_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.702020
GCF_000948175.1_BFA_2_A_genomic.fna_31:29597-29723 Satlength=127 Nr of
Repeats=6 RepeatLength=21 seed=ATCTCTCGGT Num.seqs=6 Similarity=0.911111
0 ATCTCTCGGTTTTGCG-CTTTA
GCF_000948175.1_BFA_2_A_genomic.fna_185:0-83 Satlength=84 Nr of Repeats=4
RepeatLength=21 seed=AATCTCTCGG Num.seqs=4 Similarity=0.968254
20 ATCTCTCGGTTTTGCG-CTTTA
Rev.of_GCF_000948175.1_BFA_2_A_genomic.fna_39:8694-8799 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=AAACCGAGAG Num.seqs=5
Similarity=0.847619
12 ATCTCTCGGTTT-GCGGGAATA
GCF_000948175.1_BFA_2_A_genomic.fna_14:18049-18299 Satlength=251 Nr of
Repeats=12 RepeatLength=21 seed=AATCTCTCGG Num.seqs=10
Similarity=0.679461
21 ATCTCTCGGTTTCGCGTCGNGA

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Consensus:

ATCTCTCGGTTTtGCGnctttA

>Bacillus_Fam_217_22_4 Nr. of seq. 4 Alignment length(with gaps) = 22
Alignment score = 0.601010
GCF_001591485.1_ASM159148v1_genomic.fna_6:6108-6192 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TATTTGCGAA Num.seqs=4 Similarity=0.597884
11 T-TAGCACCTTTTATTTGCGAA

Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_53:38984-39068
 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCAAAT Num.seqs=4
 Similarity=0.735450 22
 T-TGGGGGCGTTTATTTGCGAA
 Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_78:8523-8607 Satlength=85
 Nr of Repeats=4 RepeatLength=21 seed=TTTCGCAAATA Num.seqs=4
 Similarity=0.671958 20
 TCTATGACGTTT-ATTTGCGAA
 GCF_001591805.1_ASM159180v1_genomic.fna_15:21542-21647 Satlength=106 Nr
 of Repeats=5 RepeatLength=21 seed=TTATTTGCGA Num.seqs=5
 Similarity=0.683333
 30 TCTAACNCTNTT-ATTTGCGAA

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Consensus:

tATTTGCGAATcTagcacctTT

>Bacillus_Fam_218_20_4 Nr. of seq. 4 Alignment length(with gaps) = 21
 Alignment score = 0.669312
 GCF_001439915.1_ASM143991v1_genomic.fna_94:254056-254153 Satlength=98 Nr
 of Repeats=5 RepeatLength=19 seed=TTGCGCTTTA Num.seqs=3
 Similarity=0.953216
 0 TTGCG-CTTT-AGCCACATAT
 GCF_000153365.1_ASM15336v1_genomic.fna_11:41215-41295 Satlength=81 Nr of
 Repeats=4 RepeatLength=20 seed=TATATTTGCG Num.seqs=4 Similarity=0.648148
 15 TTGCGAGTTT-CTCCATATAT
 GCF_000473245.1_ASM47324v1_genomic.fna_1:3661356-3661436 Satlength=81 Nr
 of Repeats=4 RepeatLength=20 seed=TATATTTGCG Num.seqs=4
 Similarity=0.648148
 15 TTGCGAGTTT-CTCCATATAT
 Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:2663845-2663929
 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TCGCAGATAT Num.seqs=4
 Similarity=0.593434 26
 CTGCGAGTTTAGTCAATATAT

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Consensus:

tTGCGagTTTctCcAtATAT

>Bacillus_Fam_219_20_4 Nr. of seq. 4 Alignment length(with gaps) = 21
 Alignment score = 0.671958
 GCF_000401235.1_BacNeaAAU1_genomic.fna_6:1275-1356 Satlength=82 Nr of
 Repeats=4 RepeatLength=20 seed=ATGATCCAAA Num.seqs=3 Similarity=0.822222
 0 ATGATCCAAA-ATCAAATAT
 GCF_900094975.1_IMG-
 taxon_2617270721_annotated_assembly_genomic.fna_9:33588-33669
 Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TATTATCAAA Num.seqs=3
 Similarity=0.644444 19 ATTATCAAAA-
 NNCAATTAT
 GCF_900094975.1_IMG-
 taxon_2617270721_annotated_assembly_genomic.fna_9:41410-41491
 Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TATTATCAAA Num.seqs=3

Similarity=0.666667

19 ATTATCAAAAA-

TNGAATTAT

GCF_001877785.1_PlanoSAMM_genomic.fna_74:382717-382798 Satlength=82 Nr of
Repeats=4 RepeatLength=20 seed=TATTATCAAA Num.seqs=3 Similarity=0.603175
19 ATTATCAAAAACAAGNATTAT

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Consensus:

ATtATCaAAAAanCaAtTAT

>Bacillus_Fam_220_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21

Alignment score = 0.625661

GCF_000429705.1_ASM42970v1_genomic.fna_2:37535-37615 Satlength=81 Nr of
Repeats=4 RepeatLength=20 seed=AATTGGCGGA Num.seqs=4 Similarity=0.805556
0 AATTGGCGGAGTTATTTATG-

Rev.of_GCF_000307875.1_BABA1.0_genomic.fna_7:97-181 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=ATTCCGCCAA Num.seqs=4 Similarity=0.571256
12 AGTTGGCGGAATTACTTNTGA

GCF_001591665.1_ASM159166v1_genomic.fna_21:113671-113776 Satlength=106 Nr
of Repeats=4 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=3
Similarity=0.505050 23

ATTTGGCGGAATTANTGGCGA

Rev.of_GCF_000948175.1_BFA_2_A_genomic.fna_71:44838-44964 Satlength=127

Nr of Repeats=5 RepeatLength=21 seed=AACTCCGTAA Num.seqs=4

Similarity=0.548309 4

AGTTCGCGGTNTTATTTACGG

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Consensus:

AgTTgGCGGaaTTAtTtacGa

>Bacillus_Fam_221_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21

Alignment score = 0.634921

GCF_000181495.1_ASM18149v1_genomic.fna_184:58106-58409 Satlength=304 Nr
of Repeats=5 RepeatLength=21 seed=ACTCGTCGAT Num.seqs=3
Similarity=0.787879

0 ACTCGTCGATAGAACCGCAAN

GCF_001591445.1_ASM159144v1_genomic.fna_34:15168-15252 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=CGCCAATAGA Num.seqs=4 Similarity=0.724868
3 ATTCGCCAATAGAACCGCAA

Rev.of_GCF_001274935.1_ASM127493v1_genomic.fna_37:44679-44969

Satlength=291 Nr of Repeats=7 RepeatLength=21 seed=TTCTATCGAT Num.seqs=5
Similarity=0.733333 14

ANTGATCGATAGAAAAGCAA

GCF_001439635.1_ASM143963v1_genomic.fna_74:26703-26787 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TGACGGATAG Num.seqs=4 Similarity=0.733586
23 ACTGACGGATAGAACTCAA

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Consensus:

AcTcaccgATAGAAacgCAaA

>Bacillus_Fam_222_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.701058
GCF_000508325.1_BAVI_1_genomic.fna_8:57470-57985 Satlength=516 Nr of
Repeats=16 RepeatLength=21 seed=TGTCGTAAAGT Num.seqs=10
Similarity=0.553704
0 TGTCGTAAAGTGTGCGAAAAATN
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_65:32-187 Satlength=156 Nr
of Repeats=6 RepeatLength=21 seed=ACTTACGACA Num.seqs=5
Similarity=0.809524 10
TGTCGTAAAGTGGCTGAAAATA
GCF_001591665.1_ASM159166v1_genomic.fna_77:44-199 Satlength=156 Nr of
Repeats=6 RepeatLength=21 seed=TGTCGTAAAGT Num.seqs=5 Similarity=0.765079
21 TGTCGTAAAGTNGCTGAAAATG
GCF_001591445.1_ASM159144v1_genomic.fna_24:47680-47785 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=ATGTAATAAG Num.seqs=5
Similarity=0.713636
20 TGTAAATAAGNNTCCGAAAATA

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Consensus:

TGTcgTAAGtggCtgAAAATa

>Bacillus_Fam_223_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.666667
GCF_000508325.1_BAVI_1_genomic.fna_47:49007-49090 Satlength=84 Nr of
Repeats=4 RepeatLength=21 seed=TATCAGCGAA Num.seqs=3 Similarity=0.545455
0 TATCAGCGAATNTNCACNATA
GCF_000508325.1_BAVI_1_genomic.fna_89:42322-42405 Satlength=84 Nr of
Repeats=4 RepeatLength=21 seed=TATCAGCGAA Num.seqs=3 Similarity=0.682540
0 TATCAGCGAATCTAANCAATA
GCF_001591445.1_ASM159144v1_genomic.fna_67:12088-12172 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTCTATCAGC Num.seqs=4 Similarity=0.767196
18 TATCAGCGAATTTAACCATT
Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_95:8292-8375 Satlength=84 Nr of
Repeats=4 RepeatLength=21 seed=CGCTGATAAA Num.seqs=3 Similarity=0.565657
8 TATCAGCGNATTTCCGCANTT

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Consensus:

TATCAGCGaAtTtAanCaaTa

>Bacillus_Fam_224_21_4 Nr. of seq. 4 Alignment length(with gaps) = 21
Alignment score = 0.724868
GCF_000508325.1_BAVI_1_genomic.fna_48:140-287 Satlength=148 Nr of
Repeats=7 RepeatLength=21 seed=TTTACTGTCC Num.seqs=7 Similarity=0.611833
0 TTTACTGTCCACTTCTGNCCA
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_53:13657-14008
Satlength=352 Nr of Repeats=10 RepeatLength=21 seed=GGACAGTAAA
Num.seqs=7 Similarity=0.608225
10 TTTACTGTCCACTTTTANNCA

Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_27:47504-47609
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=GGACAGTAAA Num.seqs=5
Similarity=0.571014 10

TTTACTGTCCGGTTTTANCNA

GCF_001591805.1_ASM159180v1_genomic.fna_35:13044-13128 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TCCGGTTTTG Num.seqs=4 Similarity=0.767196
28 TTTACTGTCCGGTTTTGACGA

***** ** *

Consensus:

TTTACTGTCCacTTtTancca

>Bacillus_Fam_225_20_4 Nr. of seq. 4 Alignment length(with gaps) = 20
Alignment score = 0.666667

GCF_000181495.1_ASM18149v1_genomic.fna_104:725-825 Satlength=101 Nr of
Repeats=5 RepeatLength=20 seed=TTATCGGCGA Num.seqs=5 Similarity=0.682540
0 TTATCGGCGATTTCTGAATT

Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:1148631-1149011

Satlength=381 Nr of Repeats=19 RepeatLength=20 seed=TCGCAAATAA

Num.seqs=17 Similarity=0.694742

10 TTATTTGCGATTTTCNNATTT

GCF_001712755.1_ASM171275v1_genomic.fna_23:187080-187438 Satlength=359 Nr
of Repeats=17 RepeatLength=20 seed=TTTATTTGCG Num.seqs=13

Similarity=0.688441

19

TTATTTGCGATTNCTGATAT

GCF_001645685.2_ASM164568v2_genomic.fna_1:4106820-4106922 Satlength=103

Nr of Repeats=5 RepeatLength=20 seed=TTTATCTAC Num.seqs=3

Similarity=0.735450

18

TTATCTACGAATTCTGCNTT

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Consensus:

TTATctgCGAtTtCtgattT

>Bacillus_Fam_226_20_4 Nr. of seq. 4 Alignment length(with gaps) = 20
Alignment score = 0.788889

GCF_001648575.1_ASM164857v1_genomic.fna_58:901-1002 Satlength=102 Nr of
Repeats=4 RepeatLength=20 seed=TTTCAGGATA Num.seqs=3 Similarity=0.636364
0 TTTCAGGATAAATCCCAAAA

Rev.of_GCF_001648575.1_ASM164857v1_genomic.fna_61:70721-70900

Satlength=180 Nr of Repeats=8 RepeatLength=20 seed=TTATCCTGAA Num.seqs=6

Similarity=0.630688

11

TTTCAGGATAAATCCGAAAT

Rev.of_GCF_001648575.1_ASM164857v1_genomic.fna_67:67316-67396

Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=TTTATCCTGA Num.seqs=4

Similarity=0.805556

12

ATTTCAGGATAAATCTCAAAA

Rev.of_GCF_001877785.1_PlanoSAMM_genomic.fna_150:75986-76073 Satlength=88

Nr of Repeats=4 RepeatLength=20 seed=TTTATGCTGA Num.seqs=3

Similarity=0.555556

12

ATTTCAGCATAAATCTAAAAA

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Consensus:

aTTCAGgATAAATCccAAAa

>Bacillus_Fam_227_18_4 Nr. of seq. 4 Alignment length(with gaps) = 19
Alignment score = 0.688596
GCF_000161455.1_ASM16145v1_genomic.fna_1:2935090-2935216 Satlength=127 Nr
of Repeats=6 RepeatLength=18 seed=TCGCCTTGAG Num.seqs=5
Similarity=0.837037 0
TCGCCTTGAGGTCCTGGT-
GCF_000299035.1_ASM29903v1_genomic.fna_1:825324-826476 Satlength=1153 Nr
of Repeats=60 RepeatLength=18 seed=CCTTGTTTCGC Num.seqs=49
Similarity=0.850214 12
TCGCCCTGAGGTCCTTGT-
GCF_000334155.1_L1_genomic.fna_44:19664-22112 Satlength=2449 Nr of
Repeats=125 RepeatLength=18 seed=TGAGGCCCTT Num.seqs=117
Similarity=0.883486
6 TCNCCTTGAGGCCCTTGT-
Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:1011858-1012110
Satlength=253 Nr of Repeats=9 RepeatLength=18 seed=GGTCCACAAG Num.seqs=6
Similarity=0.886420 14
TCTCCTTGTTGGACCT-GTT

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Consensus:

TCgCctTGaGGtCCTtGT

>Bacillus_Fam_228_18_4 Nr. of seq. 4 Alignment length(with gaps) = 18
Alignment score = 0.641975
GCF_000008505.1_ASM850v1_genomic.fna_1:2327569-2327767 Satlength=199 Nr
of Repeats=9 RepeatLength=18 seed=GTGATGCCTG Num.seqs=7
Similarity=0.922399
0 GTGATGCCTGTAGGACCA
Rev.of_GCF_001587375.1_ASM158737v1_genomic.fna_6:3784-4054 Satlength=271
Nr of Repeats=15 RepeatLength=18 seed=CCTACTGGCG Num.seqs=15
Similarity=0.882892 14
GTTACGCCAGTAGGTCCA
Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_12:312575-312683
Satlength=109 Nr of Repeats=6 RepeatLength=18 seed=TTACTGGACC Num.seqs=6
Similarity=0.885965 4
GTAATACCTGTGGGTCCA
Rev.of_GCF_900096965.1_IMG-
taxon_2671180223_annotated_assembly_genomic.fna_22:69506-70175
Satlength=670 Nr of Repeats=15 RepeatLength=18 seed=ACTGGTGCTA
Num.seqs=14 Similarity=0.797667 2 GTGACCCCGGTAGCACCA

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Consensus:

GTgAcgCCtGTaGgACCA

>Bacillus_Fam_229_18_4 Nr. of seq. 4 Alignment length(with gaps) = 18
Alignment score = 0.716049
GCF_000177235.2_ASM17723v2_genomic.fna_1:713412-713628 Satlength=217 Nr
of Repeats=11 RepeatLength=18 seed=CCAGGAGAAC Num.seqs=10
Similarity=0.899588 0
CCAGGAGAACCAAGTGAC
GCF_900096965.1_IMG-
taxon_2671180223_annotated_assembly_genomic.fna_7:2615-2903 Satlength=289
Nr of Repeats=15 RepeatLength=18 seed=CCAGGAGATC Num.seqs=12
Similarity=0.841751 0 CCAGGAGATCCGGGCGAC
Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_2:899-971 Satlength=73 Nr
of Repeats=4 RepeatLength=18 seed=TTGCTTGGAT Num.seqs=4
Similarity=0.802469
17 CCAGGGGATCCAAGCAAA
Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_105:8418-8580
Satlength=163 Nr of Repeats=9 RepeatLength=18 seed=TTGCTTGGAT Num.seqs=9
Similarity=0.823045 17
CCAGGAGATCCAAGCAAA

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Consensus:

CCAGGaGAtCCaaGcaAa

>Bacillus_Fam_230_18_4 Nr. of seq. 4 Alignment length(with gaps) = 18
Alignment score = 0.864198
GCF_000526655.1_ASM52665v1_genomic.fna_3:175348-175420 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=AGACCATTCG Num.seqs=4 Similarity=0.864198
0 AGACCATTCGGGTTTGGC
GCF_000724485.1_ASM72448v1_genomic.fna_1:630902-631064 Satlength=163 Nr
of Repeats=9 RepeatLength=18 seed=GACCATTTGG Num.seqs=9
Similarity=0.925926
1 AGACCATTTGGTTTTGGC
Rev.of_GCF_000724485.1_ASM72448v1_genomic.fna_1:2776674-2776836
Satlength=163 Nr of Repeats=9 RepeatLength=18 seed=GCCAAAACCA Num.seqs=9
Similarity=0.946502 18
AGACCATTTGGTTTTGGC
GCF_001273755.1_ASM127375v1_genomic.fna_17:1520653-1520719 Satlength=67
Nr of Repeats=4 RepeatLength=18 seed=ATTTGGATTT Num.seqs=3
Similarity=0.901235 5
AGACCATTTGGATTTGGG

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Consensus:

AGACCATTTtGGtTTTGGc

>Bacillus_Fam_231_15_4 Nr. of seq. 4 Alignment length(with gaps) = 15
Alignment score = 0.700000
GCF_000175075.1_ASM17507v1_genomic.fna_36:203990-204113 Satlength=124 Nr
of Repeats=4 RepeatLength=15 seed=ACCAAAACAA Num.seqs=3
Similarity=0.881481
0 ACCAAAACAAGAAGC

Rev.of_GCF_000299035.1_ASM29903v1_genomic.fna_4:202303-202378
 Satlength=76 Nr of Repeats=5 RepeatLength=15 seed=TTAGGCTCTT Num.seqs=5
 Similarity=0.756250 6
 GCCTAANAAAGAAGA
 GCF_000724485.1_ASM72448v1_genomic.fna_1:1494972-1495197 Satlength=226 Nr
 of Repeats=15 RepeatLength=15 seed=CGAAAAAAGC Num.seqs=15
 Similarity=0.925503 17
 ACCGAAAAAGCAGA
 GCF_000724485.1_ASM72448v1_genomic.fna_1:1494984-1495281 Satlength=298 Nr
 of Repeats=20 RepeatLength=15 seed=AACCGAAAAA Num.seqs=17
 Similarity=0.901961 29
 ACCGAAAAAGCAGA

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Consensus:

aCCgAAaaAGaAGa

>Bacillus_Fam_232_12_4 Nr. of seq. 4 Alignment length(with gaps) = 12
 Alignment score = 0.888889
 GCF_000153365.1_ASM15336v1_genomic.fna_71:47849-47909 Satlength=61 Nr of
 Repeats=5 RepeatLength=12 seed=GGCAACGGCA Num.seqs=5 Similarity=0.866667
 0 GGCAACGGCAAT
 GCF_000473245.1_ASM47324v1_genomic.fna_1:3082960-3083020 Satlength=61 Nr
 of Repeats=5 RepeatLength=12 seed=GGCAACGGCA Num.seqs=5
 Similarity=0.866667
 0 GGCAACGGCAAT
 Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_1:111557-111623
 Satlength=67 Nr of Repeats=5 RepeatLength=12 seed=TTGCCATTAC Num.seqs=4
 Similarity=1.000000 5
 GGCAACGGTAAT
 GCF_900156865.1_PRJEB18960_genomic.fna_3:344931-345015 Satlength=85 Nr of
 Repeats=7 RepeatLength=12 seed=GGCAACGGCA Num.seqs=7 Similarity=0.820106
 0 GGCAACGGCAAC

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Consensus:

GGCAACGGcAAt

>Bacillus_Fam_233_234_3 Nr. of seq. 3 Alignment length(with gaps) = 234
 Alignment score = 0.864198
 GCF_000169195.2_ASM16919v2_genomic.fna_1:908315-909719 Satlength=1405 Nr
 of Repeats=6 RepeatLength=234 seed=CCAAAACAAC Num.seqs=6
 Similarity=0.860589 0
 CCAAAAACAACGACGAAGTATGTCAATGTGGACAAAGGCTCCCATTTAATATTGCGCTCNAAGCCTCCACTTC
 GTCCAGCATTTTAGCAAGCTTGGCAAGAGGAGAAAAAGTGACGGTTTACTCCATTTCCGGGGATTGGGCAAAA
 GTAAAAGCCGGGAGCAAAACGGGCTATGTTTCATGCATCTTTTGGCGAACTCAAATCCCACAGCAATGCAG
 AACTTCTACTCCGG
 Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:416000-417405
 Satlength=1406 Nr of Repeats=6 RepeatLength=234 seed=ACATTGACAT
 Num.seqs=5 Similarity=0.718207
 28
 CCAAAAACAACGACGAAGTATGTCAATGTGGATAAAGGNTCCCATTTAATATTACGTTCGAAAGCCTCCAAAAAC

GTCCAGCATTTTtagcaagCTTGGCAAGAGGNAAAAAGTGACGGTTTACTCTATTTCCGGGGANTGGGCAAAA
GTAAAAGCCGGGAGCAAAACGGGCTATGTTTCATGCATCTTTTTTGACGAACTCAAATCCCgATAGCAATGCAG
GCACTTCAACCCCAAG

Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:2760090-2761260

Satlength=1171 Nr of Repeats=5 RepeatLength=234 seed=TTTTTCGCCTC

Num.seqs=5 Similarity=0.877637

109

CCAAAACAACGACGAAGTATGTCAATGTGGATAAGGGTTCACATCTAATCTTACGTTCAAAGCCTCCGAAAC
GTCCAGCATTTTGGACAGCTTGCCAAGAGGCGAAAAGGTGACGGTGACTCTATTTCCGGGGACTGGGCGAAA
GTAAAAGCCGGCAGCAAAACGGGCTATGTTTCATGCATCTTTTTTGCGGAATTCAAATCCTGATAGCAGTGCAG
ATACTTCTACTCCAG

Consensus:

CCAAAACAACGACGAAGTATGTCAATGTGGATAAaGGnTCCcATtTAATaTTaCGtTCnAAAGCCTCCaaaaC
GTCCAGCATTTTaGcaAGCTTGgCAAGAGGngAAAAaGTGACGGTtTACTCtATTTCCGGGGAnTGGGCaAAA
GTAAAAGCCGGgAGCAAAACGGGCTATGTTTCATGCATCTTTTTTGgCGAAcTCAAATCCcGAtAGCAaTGCAG
acACTTCTACTCCaG

>Bacillus_Fam_234_213_3 Nr. of seq. 3 Alignment length(with gaps) = 222

Alignment score = 0.719720

GCF_001420645.1_ASM142064v1_genomic.fna_7:2736-4618 Satlength=1883 Nr of
Repeats=10 RepeatLength=213 seed=TTAAACCTTC Num.seqs=7

Similarity=0.788528

0

TTAAACCTTCGGTCGGGTGCTGGCACGTCTCATCGNGTTTTAACGACCCTTCCTGTTGGACAGAAGCTTGAGC
TTCTTCAAAAACAAGGCAATTGGTATCAAGTTAAAGCTGGTAACCAAACCTGGCTGGGTCTCCGCTGATTTTCAT
TAAAACAAATGGTAATAATGTCGAAGACAA-----CAAGC--
CTTCTCTTGGCTCTGCGACGACTACAGCTCGC

Rev.of_GCF_002019765.1_ASM201976v1_genomic.fna_1:1075884-1077375

Satlength=1492 Nr of Repeats=8 RepeatLength=213 seed=CGAAGGTTTA

Num.seqs=6 Similarity=0.765152

11

TTAAACCTTCGGTCGGGTGCTGGTACGTCTCATCGNGTTTTAACGACTCTTCCGGTTGGACAGAAGCTTGAGC
TTCTTCAAAAACAAGGCAATTGGTATCAAGTTAAAGCTGGTAACCAAACCTGGCTGGGTTTCTGCTGATTTTCAT
TAAAACAGATGGTAATAATGTCGAAGACAA-----CAAGC--
CTTCTCTTGGCTCTGCGACGACTACAGCTCGC

GCF_002019705.1_ASM201970v1_genomic.fna_1:1608983-1610081 Satlength=1099

Nr of Repeats=5 RepeatLength=219 seed=TGGTATCAAG Num.seqs=3

Similarity=0.861999

93

TTAAACTTGCGCACTGGGGCTGGCACAAACCACCGTATTATTACAACGCTACCTGTTGGGCAAAAGCTGGAAC
TTCTTAAAAAAGAAGGCAATTGGTATCAAGTTAAAGCCGGGTCTCATACGGGATGGGTTTCTGCTGACTTTAT
TAAATCTGACGGCAAT--GGTGAAG-
CAATGTCGGGCAATCTTCTTCTATCGGCTCTGCCACTACCACTGCTCGC

Consensus:

TTAAACcTtCGgtCgGGtGCTGGcACgtctCatCGngTTtTaACgACnCTtCctGTTGGaCAGAGCTtGAgC
TTCTTcAAAAAcAAGGCAATTGGTATCAAGTTAAAGCtGGtaacCAaActGGcTGGGTtTctGCTGAtTTcAT
TAAaAaCagAtGGtAATaatGTcGAAGaCAACAAGCCTTCTcTtGGCTCTGCgACgActACaGCTCGC

>Bacillus_Fam_235_166_3 Nr. of seq. 3 Alignment length(with gaps) = 168
Alignment score = 0.659392

GCF_001742425.1_ASM174242v1_genomic.fna_64:52962-53922 Satlength=961 Nr
of Repeats=5 RepeatLength=159 seed=CTTGATTCTGT Num.seqs=4
Similarity=0.724668

0 CTTGA-TTC-GTTCCCTATATTCCCGTCCCCAAGCTGACCATAATAGTT--
ACTTCCCCACGCATACATCGTTCCATCACTTGCTAATGCTACTGAGTGAAAGATTCTACAGCTACTTGTTTCG
ATCTTGGCTCCTTCGGGCATTGTGATCGCTGTGCGGACTAG----

GCF_001742425.1_ASM174242v1_genomic.fna_64:66225-67212 Satlength=988 Nr
of Repeats=6 RepeatLength=165 seed=CCATCACTTG Num.seqs=4
Similarity=0.642857

71 AATAACTCCANATCCACTATCCCGTCTCCCAACTGACCAAAATCGTT--
NTCNTCCCCACGTATACAACGTCCCATCACTTGCTAACGCTATTGTATGATCTCCCCCTGCTGTTACTTGTTTC
GATACTGGCTCCTCCGGGGATCGAAATCGCTATCGGACTAGCTTG

GCF_001742425.1_ASM174242v1_genomic.fna_64:68080-68896 Satlength=817 Nr
of Repeats=5 RepeatLength=165 seed=CATCACTTGC Num.seqs=4
Similarity=0.742275

72 ATCAACTCCCCATCCACTATTACCGTCTCCCAGCTGACC-
ANATCGTTATTTCTCCCCACGTATACACCGTTCATCACTTGCTAACGCTACTGTGTGGGCAAATCCTGCCG
ATACTTGTTTCGATCTTGCTCCTCCAGGGATAGGGATCACTGTGCGGACTAGATTG

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Consensus:

attaAcTcCnnaTCCacTATtcCCGTctCCcAgCTGACCaaaATcGTTntCttCCCCACgtATACAnCGTtCC
ATCACTTGCTAAcGCTAcTgtgTGancnantCCTgCnGnTACTTGTTTCGATctTGGCTCCTcCgGGgATnGng
ATCgCTgTTCGGACTAGnttg

>Bacillus_Fam_236_151_3 Nr. of seq. 3 Alignment length(with gaps) = 159
Alignment score = 0.705101

GCF_001636425.1_ASM163642v1_genomic.fna_1:3237226-3237826 Satlength=601
Nr of Repeats=4 RepeatLength=150 seed=GCCGATGACC Num.seqs=4
Similarity=0.986667

GCCGATGACCAAGGTGCTTCCTCTTTTC--
TCTGTCTAGCTCCACGCGCTATCGGCTAGCGGATTTCTCCGTCTCCTCCCTACGATAAGTCAACATCAGCTC-
---GT-CCCTCGCTGTGT-TTCCTTTATCTCAGTCGTAGATTCTGAAATCCGTAC

GCF_001636425.1_ASM163642v1_genomic.fna_1:571154-571780 Satlength=627 Nr
of Repeats=4 RepeatLength=157 seed=CTCGCTGTGT Num.seqs=3
Similarity=1.000000

GCCGATGAGCAAGGCGCTTGTGCTTTTCT--
TCTGTCTAGCTCCAGCGCGCTATCGGCTAGCGGATTTCTACGTCTTCTCCCTGCGATAAGTCAACATCAGCTCG
TGAGTGACCTCGCTGTGTGTCGTCCTTTATCTCAGTCGAAGACTCTGAAATCCGTAC

GCF_001636425.1_ASM163642v1_genomic.fna_1:4465616-4467134 Satlength=1519
Nr of Repeats=10 RepeatLength=152 seed=AGCTCCAGCG Num.seqs=8
Similarity=1.000000

GCCGATCACGAAGCTCCTCCCGTCTTTCTGAT-

37

TGTCTAGCTCCAGCGCCTATCGGCTCGCGGGCTTCTCCGTCTCCTCCCTGCGATAAGGCAACATCAGCTC---
-GT-ACCTCGCTGTGT-ATCCTTGATCTCAGGCCACCCCTACGGTACCCGCAC

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Consensus:

GCCGATgAccAAGgtgCTtccgctTTTCTtTcTGTCTAGCTCCAgCGCCTATCGGCTaGCgGatTTCTtCGTCT
cCTCCCTgCGATAAGtCAACATCAGCTCGTaCCTCGCTGTGTnTCCTTtATCTCAGtCgnAgacTctGaaAtC
CGtAC

>Bacillus_Fam_237_144_3 Nr. of seq. 3 Alignment length(with gaps) = 148
Alignment score = 0.644895

GCF_000474275.1_Bmar1.0_genomic.fna_56:91616-92192 Satlength=577 Nr of
Repeats=4 RepeatLength=144 seed=TTGGTGGGACG Num.seqs=4
Similarity=0.470569

0 -TTGGTGGGACGGCTGAAGGTGGAGCAGGTGGGAAAATCTTGGCGCGCCGCAAGGNNGA-
TTGAAGGCTCNGCC--GAGCTGTCNTCATGGGCACCAAATCGTATCGACTGCTTTGTTCAG-
GGAGCGTAATAATCAGATGTGGCATAAA

GCF_000005825.2_ASM582v2_genomic.fna_1:430629-431349 Satlength=721 Nr of
Repeats=5 RepeatLength=144 seed=TGTGGCATAA Num.seqs=5
Similarity=0.515711

133 -
TTGGTGGGACGGNCGCAGATGGAGCGANTGGGAAAATCTNNGTTTACCGCAAGGAGGATTTGATGGCTC-
GCCAGGTGCTGTC-TCNTGGGGNCCAAATCGNATCGACTGTTTTGTTCAG-
GGGAAGAAATAATCANATGTGGCATAAA

Rev.of GCF_000175075.1_ASM17507v1_genomic.fna_4:29270-29846 Satlength=577
Nr of Repeats=4 RepeatLength=144 seed=TTGTGCCACA Num.seqs=4
Similarity=0.519371

0
ATGGTGGGATGGACAACGTTGGAGTCAGTGGGAGAATCTTGGTTCCCCACGTGGTGGCTTTGAAGGTNC-
GCCAGCTGCAGTT-TCATGGGGAGCAAATCGNATCGACTGTTTTGTAAGAGGGATG-
NACAAGCGCATGTGGCACAA-

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Consensus:

TTGGTGGGAcGGncgaaGnTGGAGcnagTGGGAaAATCTtGGttCnCCgCaaGGnGGatTTGAaGGctCGCCag
gtGcTGTcTCaTGGGgacCAAATCGnATCGACTGtTTTGTcAGGGganGnaAtAAtCanATGTGGCAtAAa

>Bacillus_Fam_238_122_3 Nr. of seq. 3 Alignment length(with gaps) = 125
Alignment score = 0.682667

GCF_000299035.1_ASM29903v1_genomic.fna_4:356724-357203 Satlength=480 Nr
of Repeats=4 RepeatLength=122 seed=GGCTCGTTCA Num.seqs=3
Similarity=0.985428

0 GGCTCGTTCAGAATGGGAGGAGGATGGAGCT-TCTGCCGTAGAGGCGCTTTTTGCCTCGTAGGA-
AGACGCGAAGCCACCGACCGTTCTTGCCCCTGGAGCTGGATATC-TTTAAAAGCGGAATT

GCF_000831065.1_ASM83106v1_genomic.fna_1:4750262-4750754 Satlength=493 Nr
of Repeats=4 RepeatLength=123 seed=AAAAGCGAAA Num.seqs=4
Similarity=0.813333

111
GGCTCGCTCAGAATGTGAGGTGGATGGAGCT-TCTGACCTTGAGGCGCTTTTGCCTCTGGGGA-
AGAAGCGAAGCCGCCGAACATTCTAGCCACTGTAGCTGGATTCCAATTAAAAGCGAAAGT

Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:4477828-4478573
Satlength=746 Nr of Repeats=6 RepeatLength=122 seed=GAGCCGCTTC
Num.seqs=4 Similarity=0.798387
5 GGCTCGCTCAGAATCGCAGGACATTGGAGCTCTC-
GACCTTGAAGCGCTTTTTCGCTTCGAGCGAGAGA-
GCGAAATGACCGGAGATTCTAGCCACTGGAGCTGGATATC-ATTAAAAGCGGAAGC

Consensus:

GGCTCGcTCAGAATgggAGGaggaTGGAGCTTcTgACcTtGAgGCGCTtTTTGcTCgnggGAAGAnGCGAAg
ccaCCGaacaTTCTaGCCaCTGgAGCTGGATatCaTTAAAAGCGgAAgt

>Bacillus_Fam_239_104_3 Nr. of seq. 3 Alignment length(with gaps) = 104
Alignment score = 0.978632
GCF_001420645.1_ASM142064v1_genomic.fna_41:140954-141471 Satlength=518 Nr
of Repeats=5 RepeatLength=103 seed=ATGCTAGAAA Num.seqs=3
Similarity=0.870550
ATGCTAGAAACTGATTCAAAGCTTGAACAAGAATATCTGTAAACATAAGATCCACCTCCAGTTTGAAAATAA
GGAAAAA-AGAATTAGCCAAGAGTGCCGATA
Rev.of_GCF_000706725.1_ASM70672v1_genomic.fna_1:3741837-3742252
Satlength=416 Nr of Repeats=4 RepeatLength=104 seed=GTTTCTAGCA
Num.seqs=3 Similarity=0.829060

11
ATGCTAGAAACTGATTCAAAGCTTGAACAAGAATATCTGTAAACATAAGATCCACCTCCAGTTTGAAAATAA
GGAAAAAGAGAATTAGCCAAGAGTGCCGATA
GCF_002019765.1_ASM201976v1_genomic.fna_1:254081-254703 Satlength=623 Nr
of Repeats=6 RepeatLength=104 seed=ATGCTAGAAA Num.seqs=4
Similarity=0.952991
ATGCTAGAAACTGATTCAAAGCTTGAACAAGAATATCTGTAAACATAAGATCCACCTCCAGTTTGAAAATAA
GGAAAAAGAGAATTACCCAAGAGTGCCGATA

Consensus:

ATGCTAGAAACTGATTCAAAGCTTGAACAAGAATATCTGTAAACATAAGATCCACCTCCAGTTTGAAAATAA
GGAAAAAgAGAATTAgCCAAGAGTGCCGATA

>Bacillus_Fam_240_84_3 Nr. of seq. 3 Alignment length(with gaps) = 84
Alignment score = 0.825397
GCF_001654695.1_ASM165469v1_genomic.fna_26:0-419 Satlength=420 Nr of
Repeats=5 RepeatLength=84 seed=AAGAGTTTTC Num.seqs=5 Similarity=0.834921
0
AAGAGTTTTTCAGAGATGCTTGAAGAAAGATCTCCCGAATGTGAAGAGTCTGAATCAATCAAAGAAGAGGATAC
TTCATTAGAAG
Rev.of_GCF_001654695.1_ASM165469v1_genomic.fna_34:68-566 Satlength=499 Nr
of Repeats=6 RepeatLength=84 seed=AAACTCTTC Num.seqs=4
Similarity=0.814815
AAGAGTTTTTCAGAGATGCTTGAAGAAAGATCTCCTGAATGTGATGATTGTGAATTAATCAAAGAAGAAGATAC
TTCATTAGAAG
Rev.of_GCF_001654695.1_ASM165469v1_genomic.fna_34:67-985 Satlength=919 Nr
of Repeats=11 RepeatLength=84 seed=GAAAACTCTT Num.seqs=7

Similarity=0.726237 10
AAGAGTTTTTCAGCGATGCTTGAAGAAAGATCTCCCGAATGGGATGAGTCTGAATCAATNAANGAGGAAGTCAC
ATCACTAGAAA

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Consensus:

AAGAGTTTTCaGaGATGCTTGAAGAAAGATCTCCcGAATGtGAtGAGtCtGAATcAATcAAaGAaGAaGatAC
tTCAtTAGAAg

>Bacillus_Fam_241_59_3 Nr. of seq. 3 Alignment length(with gaps) = 66
Alignment score = 0.611111
GCF_000508325.1_BAVI_1_genomic.fna_42:2128-2428 Satlength=301 Nr of
Repeats=4 RepeatLength=60 seed=GGCTGGGTCA Num.seqs=3 Similarity=0.733333
0 GGCTGGGT-CAAAGTGAAGGAANA-TGGTATTACCTTAA--TNGTAAT--GGAGCTATGCAAACC
GCF_001591805.1_ASM159180v1_genomic.fna_14:1768-2128 Satlength=361 Nr of
Repeats=4 RepeatLength=60 seed=AAATGGTATT Num.seqs=3 Similarity=0.702509
21 GGCTGGCTGCAAACAG-GNCGCAA-TGGTATTACCTCAA--TC--AATCAGGTGCGATGCAAAC
GCF_000508325.1_BAVI_1_genomic.fna_45:33463-33823 Satlength=361 Nr of
Repeats=6 RepeatLength=60 seed=AAGTGGTATT Num.seqs=4 Similarity=0.483165
22 GGCTGGGTGCAAACCTG-GCGGCAAAGTGGTATTACCTTAACATC--NAGC-GGCGCGATGCAAACC

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Consensus:

GGCTGGgTgCAAActGgnGGcAaATGGTATTACCTtAATcaAtcGGnGCgATGCAAACc

>Bacillus_Fam_242_66_3 Nr. of seq. 3 Alignment length(with gaps) = 66
Alignment score = 0.752525
GCF_001591805.1_ASM159180v1_genomic.fna_24:108668-109031 Satlength=364 Nr
of Repeats=5 RepeatLength=60 seed=ACTGGCTGGG Num.seqs=4
Similarity=0.479167 0
ACAGGCTGGGCAAAAGTAGGAGGTAAATGGTACTTCCTTGATGC-AA-G-CGGT--GCAATGAAA
Rev.of_GCF_000299035.1_ASM29903v1_genomic.fna_2:1035187-1035517
Satlength=331 Nr of Repeats=5 RepeatLength=66 seed=TAGTACCATT Num.seqs=5
Similarity=0.727363 35
ACAGGNTGGGNACAAGTAGATGGAAAATGGTACTACCTAGATGCAAATGATGGTGGAGCAATGAAA
Rev.of_GCF_000299035.1_ASM29903v1_genomic.fna_2:1035252-1037684
Satlength=2433 Nr of Repeats=17 RepeatLength=66 seed=GTAGTACCAT
Num.seqs=15 Similarity=0.705306
36 ACAGGCTGGGNACAAGTAGANGGNAATGGTACTACCTAGATGGAAATGATGGTGGAGCAATGAAA

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Consensus:

ACAGGcTGGGnAcAAGTAGanGGnAAATGGTACTaCCTaGATGcaAAAtGatGGTggaGCAATGAAA

>Bacillus_Fam_243_66_3 Nr. of seq. 3 Alignment length(with gaps) = 66
Alignment score = 1.000000
GCF_001887185.1_ASM188718v1_genomic.fna_65:9688-9951 Satlength=264 Nr of
Repeats=4 RepeatLength=66 seed=GGGGTCTGAC Num.seqs=3 Similarity=0.865320
0 GGGGTCTGACCCCGTTTGTATAATCAAGAGCTACGAACCCTTGTCTTTCCTGGAATTAACGCTTG

Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_362:0-329 Satlength=330 Nr
of Repeats=5 RepeatLength=66 seed=GGGGTCAGAC Num.seqs=5
Similarity=0.975758 13
GGGGTCTGACCCCGTTTGTATAATCAAGAGCTACGAACCCTTGTCTTTCCTGGAATTAACGCTTG
Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_48:948-1343 Satlength=396
Nr of Repeats=6 RepeatLength=66 seed=GGGGTCAGAC Num.seqs=5
Similarity=0.886869 13
GGGGTCTGACCCCGTTTGTATAATCAAGAGCTACGAACCCTTGTCTTTCCTGGAATTAACGCTTG

Consensus:

GGGGTCTGACCCCGTTTGTATAATCAAGAGCTACGAACCCTTGTCTTTCCTGGAATTAACGCTTG

>Bacillus_Fam_244_55_3 Nr. of seq. 3 Alignment length(with gaps) = 58
Alignment score = 0.607280
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_16:309953-310163
Satlength=211 Nr of Repeats=4 RepeatLength=53 seed=TATTGGTGAC Num.seqs=3
Similarity=0.865828 0 TATTGGTGACCTTTC-
TCCTCTCG-GGCGAC--CCCACTTAGGGCACCAA-GAGACCT
Rev.of_GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_26:134607-134815
Satlength=209 Nr of Repeats=4 RepeatLength=53 seed=AGGAAGAAAG Num.seqs=3
Similarity=0.882600 20 TGTGGTGACCTTTCCTC-AG--AC-
TCTTCCCACTTTGGGCACCAATGGG-CCT
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_36:66229-66446
Satlength=218 Nr of Repeats=4 RepeatLength=53 seed=ATTGGTGACC Num.seqs=3
Similarity=0.773663 54
TATTGGTGACCTTTCCTTGTCTAGCAAC-ACTT--ACTTTGGGCACCAATGAG-CCT

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Consensus:

TaTTGGTGACCTTTCtTccTctaGnaCaCttcccACTTtGGGCACCAAtGaGCCT

>Bacillus_Fam_245_53_3 Nr. of seq. 3 Alignment length(with gaps) = 57
Alignment score = 0.606238
GCF_000181495.1_ASM18149v1_genomic.fna_167:17100-17312 Satlength=213 Nr
of Repeats=4 RepeatLength=53 seed=TGGCCCATTT Num.seqs=4
Similarity=0.865828
0 TGGCCCATTTACCACC-TTATTGGCCCAACATC-C-T-CTCATAACTTGATTCTCAT
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_186:351607-352031
Satlength=425 Nr of Repeats=8 RepeatLength=53 seed=AGATATAGAA Num.seqs=6
Similarity=0.854088 44
TGGGCCATTTA-CACCTTTAATGGCCCAACATCTCTT-CT-ATATCTT-ATTCTCAT
GCF_000181495.1_ASM18149v1_genomic.fna_186:601490-601914 Satlength=425 Nr
of Repeats=6 RepeatLength=53 seed=TGGCCCATTT Num.seqs=4
Similarity=0.616162 0
TGGCCCATTTAGCTCT-TAAATGGGCCAACATC---TACTCAAAAATGGAATCTCAA

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Consensus:

TGGcCCATTTAnCaCcTtAaTGGcCCAACATCcTCTcAtAacTtgAtTCTCAt

```
>Bacillus_Fam_246_53_3  Nr. of seq. 3 Alignment length(with gaps) = 56
Alignment score = 0.684524
GCF_000708755.2_ASM70875v2_genomic.fna_1:523918-524339 Satlength=422 Nr
of Repeats=8 RepeatLength=53 seed=AAAAGTGGCG Num.seqs=5
Similarity=0.856604
0   AAAAGTGGCGCCATTcAGNAGAGTGTGCCACATTT-GAGGTGA--AGACCCCCGN
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_6:246542-246807
Satlength=266 Nr of Repeats=5 RepeatLength=53 seed=GCAGAATGGC Num.seqs=5
Similarity=0.859119                                     17   -
-AAGTGGCGCCATTCTGCACAGTGGTGCCACTTTTCGA-GTGATGAGATTCTCAA
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_15:163135-163347
Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=GAATGGCGCC Num.seqs=4
Similarity=0.878407                                     67   --
AAGTGGCGCCATTCTGCGTAGTGGTGCCACTTTTCGA-GTGAAGAGACTCTCAA
```

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Consensus:

AAGTGGCGCCATTCTGcanAGTGgTGCCACTTTTcGAGTGAngAGActCtCaa

```
>Bacillus_Fam_247_50_3  Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.630303
GCF_000292245.2_ASM29224v2_genomic.fna_15:25962-26268 Satlength=307 Nr of
Repeats=5 RepeatLength=51 seed=TTTTcATTAC Num.seqs=4 Similarity=0.604663
0   TTTTCATTACCTATTAACCTGTATTGCGACCGTAATTTcGCT-CTGCTTG-GA--
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_128:7207-7563 Satlength=357
Nr of Repeats=7 RepeatLength=51 seed=GTAATGAAAA Num.seqs=6
Similarity=0.813508                                     10
TTTTcATTACCTATTcACCTTGATTcGAACCGTAA-TTCGAC-CAGCTCGTGC--
GCF_000292245.2_ASM29224v2_genomic.fna_83:12733-12989 Satlength=257 Nr of
Repeats=5 RepeatLength=51 seed=TTTTcATTAC Num.seqs=4 Similarity=0.702306
2   TTTTCATTACCAATTAACCTTTATTGCGACTCTAA-TTCACCGCANCTCG-CATT
```

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Consensus:

TTTTcATTACcTATTaACCTttATTcGcACcgTAATTcGccCagCTcGga

```
>Bacillus_Fam_248_51_3  Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.612121
GCF_000175075.1_ASM17507v1_genomic.fna_2:945-1361 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=GGTAACAGAG Num.seqs=8 Similarity=0.769558
0   GGTAACAGAGA-GGGCTTCTCAAAGCCCCGAATCGAGTTGAGAATA-GCAAA-AC
Rev.of_GCF_000175075.1_ASM17507v1_genomic.fna_29:154879-155190
Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=TCTCTCTGTT Num.seqs=5
Similarity=0.851572                                     13
GGTAACAGAGAGA-GCGTCTCAAGGCCCGAAGCAAG-AAGCGAAGCGTCTAA-AC
GCF_000175075.1_ASM17507v1_genomic.fna_35:6050-6310 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=AACAGAGAAG Num.seqs=5 Similarity=0.943590
56   GGTAACAGAGA-AGGCGTCTCAAGGCCCGAAGCAAG-CAACGAAAC-CCGAAGAC
```

Consensus :

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>Bacillus_Fam_249_53_3  Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.616162
```

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Consensus :

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>Bacillus_Fam_250_51_3  Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.620202
GCF_000181495.1_ASM18149v1_genomic.fna_100:912-1381 Satlength=470 Nr of
Repeats=9 RepeatLength=52 seed=GTTTCTTCTT Num.seqs=8 Similarity=0.828704
0      GTTTCTTCTT-GAATCTTACCATTATAAA-AC-GGTTTCCCTGCTGTAGGGGTAC
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_175:57618-58242
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=GGTACGATTA
Num.seqs=12 Similarity=0.799145
```

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Consensus :

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>Bacillus_Fam_251_52_3  Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.634343
```

GCF_000292245.2_ASM29224v2_genomic.fna_15:39283-39543 Satlength=261 Nr of
Repeats=4 RepeatLength=52 seed=TACCACTTTT Num.seqs=3 Similarity=0.914530
0 TACCACTTTT--TCACTTCACT-CTTCCTCTTTTTTTGTTTCCATCTCCCTTTGGA
GCF_000292245.2_ASM29224v2_genomic.fna_107:33-293 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=CCTTTTCTTG Num.seqs=5 Similarity=0.861635
24 TACCTCTTTTCTCCA--CGCTCCTTCC-CTTTTCTTGCTCCATCCTTGTTTGGT

Similarity=0.848720
48 TTGGCTACCGTTCTCTTCGCGAT-TC-CTCGGT-TTCGGGATCCATCACACCTCT
Rev.of_GCF_000787375.1_ASM78737v1_genomic.fna_12:89119-89327
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CGGGGGAGAG Num.seqs=4
Similarity=0.854701 28
TTGGCTACCGTTCT-TACGC--TCTCCCCGCTTTTCGGGCTCCAACCTACCTCT

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Consensus:

TTGGCTaCCGTTCTTtcGCnnTcTcNcTcggtTTCGGGatCCAtCacACCTCT

>Bacillus_Fam_255_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.660606
GCF_000813125.1_ASM81312v1_genomic.fna_40:47668-47876 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TTAGACATTT Num.seqs=4 Similarity=0.726496
39 CAGCT-TACCAGCCT-TGAAATGTCCATTAAACACCTCTT-TTTAGACATTTTCAT
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_138:81898-82158
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GTCTAATAAA Num.seqs=5
Similarity=0.828205 44 -
AGCTACAACAGTTTCTGAAATGTCTATTAAACACCTTTTAT-TAGACATTTTCA-
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_21:7080-7288 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=AAATGTCTAA Num.seqs=4
Similarity=0.829060 48
-ATCCCCATCAGCTTCTGAAATGTCTATTAAATCCCTTTTAT-TAGACATTTTA-

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Consensus:

TAGACATTTcAAgCtnCAnCAGctTcTGAAATGTCTATTAAAcacCTtTTaT

>Bacillus_Fam_256_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.668687
GCF_001636315.1_ASM163631v1_genomic.fna_1:379346-379554 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CCTCTATGTG Num.seqs=4
Similarity=0.816239
0 CCTCTATGTGCACTT-AACAAGC-TTTTTCAATCGATTTCGTGTTCATTG-AGAC
GCF_001636315.1_ASM163631v1_genomic.fna_1:2299724-2300141 Satlength=418
Nr of Repeats=8 RepeatLength=52 seed=GGTTTCGTGT Num.seqs=7
Similarity=0.839173 31
-CTCTATGTGCACTT-TCCTCGC-TTTTTTCATTGGTTTCGTGTTCATTGAAGAC
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:4170771-4171031
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AAGAAGTGTC Num.seqs=5
Similarity=0.871795 17 -
CTCTATGGACACTTCTTC-CGCTTTTTTTTCA-CGATTTCGTGTTCATTGAGGAC

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Consensus:

CTCTATGtgCACTTtnCncGCTTTTTtcAtcGaTTTCGTGTTCATTGaaGAC

>Bacillus_Fam_257_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.634343

GCF_001636315.1_ASM163631v1_genomic.fna_1:2912216-2912475 Satlength=260
 Nr of Repeats=5 RepeatLength=52 seed=TGCATTGCCC Num.seqs=4
 Similarity=0.841880 0
 TGCATTGCCCCAAAAACGG-GA--AGAGCCACTAATTTGGTCAAAGGAAGAGGGA
 GCF_001636315.1_ASM163631v1_genomic.fna_1:3674698-3674906 Satlength=209
 Nr of Repeats=4 RepeatLength=52 seed=AAACGAGGTG Num.seqs=4
 Similarity=0.867521 11
 TGCATTGCCCCAAACGAGGTGA-TACATCAA--AATTTGGTCAATGGAAGAGGGG
 GCF_001636315.1_ASM163631v1_genomic.fna_1:4951452-4952180 Satlength=729
 Nr of Repeats=14 RepeatLength=52 seed=ATTGCCCAAA Num.seqs=12
 Similarity=0.924631 55
 TGCATTGCCCCAAAATCGGTGATTAGATGGA--AA-TTGGTCAATGGACGGGGCT

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Consensus:

TGCATTGCCCCAAAancGGtGAtAgAtcnAAAtTTGGTCAAtGGAaGaGGgn

>Bacillus_Fam_258_51_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.612121
 GCF_001636325.1_ASM163632v1_genomic.fna_1:443016-443432 Satlength=417 Nr
 of Repeats=8 RepeatLength=52 seed=GTTTATTCCT Num.seqs=8
 Similarity=0.880952
 0 GTTTATTCCTCTAAAGCTTCAAAATATG--A-ATGCCTTCAGGTGAATAAATGGG
 Rev.of_GCF_001636325.1_ASM163632v1_genomic.fna_1:2689693-2690109
 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=AGAGGAATAA Num.seqs=8
 Similarity=0.879409 12
 ATTTATTCCTCTGAAGCTGTAGAAGTCGTCA-A-G-CTTCAGGTGAAGAAACGAG
 GCF_001636325.1_ASM163632v1_genomic.fna_3:480673-481035 Satlength=363 Nr
 of Repeats=7 RepeatLength=52 seed=CTAAAGCAGC Num.seqs=6
 Similarity=0.924786
 62 ATTTCTTCCTCTAAAGCAGCAAAATTCG-CAGA-G-CTTGAGGTGAATAACAGAG

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Consensus:

aTTTaTTCCTCTaAAGCtgcaAAAttcGcAAGCTTcAGGTGAAtAAanGaG

>Bacillus_Fam_259_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
 Alignment score = 0.723232
 GCF_001887185.1_ASM188718v1_genomic.fna_350:150-462 Satlength=313 Nr of
 Repeats=6 RepeatLength=52 seed=AATGTGTCTC Num.seqs=6 Similarity=0.854927
 0 AATGTGTCTCAAGACTGGATCTTGAGACAGATAAAGAGG---GAGAAAGGAGAAA
 Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_24:43390-43598
 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TGAGACACAT Num.seqs=4
 Similarity=0.864256 11
 AATGTGTCTCAAGACTGGATCTTGAGACAGATAAAGAGG---GGGAAAGGAGAAA
 GCF_002009555.1_ASM200955v1_genomic.fna_548:51305-51513 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=AATGTGTCTC Num.seqs=4
 Similarity=0.656379
 0 AATGTGTCTCAAGACCAGTGCTTGAGACACATAAA-AGGACTGAG-AACTA-AAA

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Consensus:

AATGTGTCTCAAGACTgGatCTTGAGACAgATAAAgAGGGaGaAAAggAgAAA

>Bacillus_Fam_260_52_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.717172
GCF_900156875.1_PRJEB18969_genomic.fna_11:1019409-1020084 Satlength=676
Nr of Repeats=13 RepeatLength=52 seed=ATGAAGACCA Num.seqs=12
Similarity=0.841103 0
ATGAAGACCA-ATTAGCTTCTCGGAACTA-GAAAAACGGTCTTCATCTCCGGC-
GCF_900156875.1_PRJEB18969_genomic.fna_11:1203981-1207193 Satlength=3213
Nr of Repeats=62 RepeatLength=52 seed=AAACGGTCTT Num.seqs=50
Similarity=0.899766 32
ATGAAAACCATTTTTCTCTTC-CGG-AACAAGGAGAAACGGTCTTCAT-GACGGCG
GCF_900156875.1_PRJEB18969_genomic.fna_11:1208970-1209385 Satlength=416
Nr of Repeats=8 RepeatLength=52 seed=AAACGGTCTT Num.seqs=7
Similarity=0.818808 32
ATGAAAACCATTTTTCTCTTC-CGG-AACAAGGAGAAACGGTCTTCAT-GACGGCG

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Consensus:

ATGAaACCAttTTctCTTCCGGAACaAgGAgAAACGGTCTTCATgaCGGCg

>Bacillus_Fam_261_53_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.640404
GCF_001439915.1_ASM143991v1_genomic.fna_83:206289-206524 Satlength=236 Nr
of Repeats=5 RepeatLength=53 seed=ACCGCAAGAA Num.seqs=3
Similarity=0.983229 0
ACCGCAAGAGTGTtTAACGGTACATGCTCAGTCCAAAAAGCAGA--AAGCATGT
GCF_001439915.1_ASM143991v1_genomic.fna_116:178064-178329 Satlength=266
Nr of Repeats=5 RepeatLength=53 seed=TGTACCGCAA Num.seqs=5
Similarity=0.816049 50
ACCGCAAGAGAGGTTTCGTGGTACATGCTCAAT-GAAAAA-AAGCTCAAGCGTGT
Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_122:86523-87001
Satlength=479 Nr of Repeats=9 RepeatLength=53 seed=TGAGCTTGTA Num.seqs=8
Similarity=0.893082 84
ACCGCAAGAACGGTTTCACGGTACAAGCTCACG-CAAAAA-TAGACCTAGCATGT

Consensus:

ACCGCAAGAngGTTTcacGGTACAtGCTCAntcAAAAAnAGancaAGCaTGT

>Bacillus_Fam_262_53_3 Nr. of seq. 3 Alignment length(with gaps) = 55
Alignment score = 0.696970
GCF_002019605.1_ASM201960v1_genomic.fna_1:3456401-3456877 Satlength=477
Nr of Repeats=9 RepeatLength=53 seed=CGGGCACTAT Num.seqs=8
Similarity=0.853549 0
CGGGCACTATGAACCTTTATAGTTACCGCCACCACTTCTTCT-A-TCCCTCCCA
Rev.of_GCF_002019605.1_ASM201960v1_genomic.fna_1:3950268-3950692
Satlength=425 Nr of Repeats=8 RepeatLength=53 seed=CGGTCACTAT Num.seqs=8
Similarity=0.858940 29
CGGGCACTATGAACCTCTATAGTGACCG-C-GAACTACTTGTGACTCCCTCCTG

Rev.of_GCF_002019605.1_ASM201960v1_genomic.fna_1:4323665-4324034
Satlength=370 Nr of Repeats=7 RepeatLength=53 seed=CGGTCACATAT Num.seqs=5
Similarity=0.768553 29
CGGGCACTATGAACTCTCTATAGTGACCG-C-TCTCTTCTTTGACTTCCTCCTG

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Consensus:

CGGGCACTATGAACTCTCTATAGTGACCGCncaCTtCTTnTgAcTcCCTCctg

>Bacillus_Fam_263_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.633745
GCF_000175075.1_ASM17507v1_genomic.fna_32:169519-169779 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GTCAAATAGA Num.seqs=5
Similarity=0.864103
0 GTCAAATAGAA-CGGCTCTATACGCCCCGAACGC-CCGTTAAAAAGAGGAAAACG
GCF_000175075.1_ASM17507v1_genomic.fna_48:8867-9075 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=GCTTCTATAC Num.seqs=4 Similarity=0.877358
12 GTCAAATAGAA-TGCTTCTATACGCCCCGAAGGC-ACGAGGAAAAGCGGTAAACG
GCF_000175075.1_ASM17507v1_genomic.fna_32:398955-399215 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CCAAAGGTCA Num.seqs=5
Similarity=0.943590
46 GTCAAATAGAAGCGG-TCTATATGCCCCGAA-GCGCCGTGAAAGAAAGTCCAAAG

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Consensus:

GTCAAATAGAAcGgnTCTATAcGCCCCGAAnGCcCGtgaAAaAgaGnaAAcG

>Bacillus_Fam_264_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.641975
GCF_000181495.1_ASM18149v1_genomic.fna_105:10535-10847 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=CTCATGACAC Num.seqs=6
Similarity=0.839316
0 CTCATGACACTTTT-CTCTCTCCTTTTTGCCTTTTCATGCCCTTGAGACGCTTC-
GCF_000181495.1_ASM18149v1_genomic.fna_178:76540-76957 Satlength=418 Nr
of Repeats=8 RepeatLength=52 seed=CTCTCTTTTT Num.seqs=7
Similarity=0.867026
16 CTCACGACACTTTT-CCCTCTCTTTTTCTTNTTTCATGTCCTTGAGAAACTTC-
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_146:13461-13667
Satlength=207 Nr of Repeats=4 RepeatLength=52 seed=TCAAGGACAT Num.seqs=3
Similarity=0.636364 44
TTCAAGACACTTTTGCTTTCT-ATTTTGGANTTTGATGTCCTTGAGA-ACTCCC

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Consensus:

cTCAnGACACTTTTCTcTCTcnTTTTngnnTTtCATGtCCTTGAGAnaCTtC

>Bacillus_Fam_265_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.637860
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_2:775846-776164
Satlength=319 Nr of Repeats=6 RepeatLength=52 seed=ACTTCGGACT Num.seqs=5

Similarity=0.675472 0
ACTTCGGACTCACTTCCTCCA-ATTTCTCTCTTTCTGTCTGAA-GNTGCACCT
Rev.of_GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_5:390749-
391008 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=GAGTCCGAAG
Num.seqs=4 Similarity=0.671908 11
ACTTCGGACTCG-TTCCTCTGGATATCCGCTTTTCCTGTCCGAATGGTG-ACCG
GCF_000294775.2_ASM29477v2_genomic.fna_1:2523541-2523749 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CTGTCCGAAT Num.seqs=4
Similarity=0.676101 34
ACTTCGGACTCA-CACCTCCAGATTACCCCTTCTTCTGTCCGAATGATG-ACCA

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Consensus:

ACTTCGGACTCattCCTCcagATttCCnCTttTtCTGTCCGAAtGnTGACCn

>Bacillus_Fam_266_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.699588
GCF_000311725.1_ASM31172v1_genomic.fna_3:146549-147069 Satlength=521 Nr
of Repeats=10 RepeatLength=52 seed=CGGATTCGGA Num.seqs=10
Similarity=0.860867 0
CGGATTCGACAA-CATCACCGAT-TCACCCTGCTTCCCTGTCCGAATATCAAG
GCF_000311725.1_ASM31172v1_genomic.fna_3:585727-586091 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=GATTCGACA Num.seqs=7
Similarity=0.897436
2 CGGATTCGACAA-CATTGCCGGT-TCATCCTGCTTCTCTGTCCGAATATCAAG
GCF_000311725.1_ASM31172v1_genomic.fna_6:313304-313604 Satlength=301 Nr
of Repeats=6 RepeatLength=52 seed=TGTCCGAATA Num.seqs=5
Similarity=0.836478
37 CGGATTCGACAATCCCTACTACTCTC-TCCT-CTTTCCTGTCCGAATATGAAG

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Consensus:

CGGATTCGACAACattaCcgnTTCatCCTgCTTccCTGTCCGAATATcAAG

>Bacillus_Fam_267_53_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.627572
GCF_000430765.1_ASM43076v1_genomic.fna_10:72408-72928 Satlength=521 Nr of
Repeats=10 RepeatLength=52 seed=CTAAAGGACA Num.seqs=10
Similarity=0.738721
0 CTAAAGGACAAAACCTCGGATGGA-GCATCAAAGATAAGTCCATGAGAAG-GGTC
Rev.of_GCF_000430765.1_ASM43076v1_genomic.fna_14:23161-23577
Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=TTGTCCTTTA Num.seqs=8
Similarity=0.826923 10
-TAAAGGACAAAACCTCAGTCGCC-CCAGCAAAGATCTGTCCATGAGAAGCGGTC
GCF_000430765.1_ASM43076v1_genomic.fna_13:190-660 Satlength=471 Nr of
Repeats=9 RepeatLength=52 seed=TAAAGGACAA Num.seqs=7 Similarity=0.639250
1 CTAAAGGACAAAAC-AGGATCAAGGCAGCAAAGATNNGTCCATGATAGGCATT-

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Consensus:

cTAAAGGACAAAACtgcGatgnagCAgCAAAGATnnGTCCATGAgAaGcggTc

>Bacillus_Fam_268_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.633745
GCF_000508325.1_BAVI_1_genomic.fna_31:7329-7537 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=AGTGCCCGTG Num.seqs=4 Similarity=0.880342
0 AGTGCCCGTGCGCATGGAAAAACGCCAA--AGACGGGCACTCTGAGAGGTTCAC
Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_25:13492-13700
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GGGCACTGTG Num.seqs=4
Similarity=0.854701 7
AGTGCCCATGACCATGGGAAAAAGCCAA--GAATGGGCACTCTGAGAGGTCCAC
GCF_001591665.1_ASM159166v1_genomic.fna_53:45335-45543 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GGGCACTCTG Num.seqs=4
Similarity=0.820513
32 AGTGCCCAAACGC--GCGAAAAATCGAAGTGCACGGGCACTCTGAGCGGTTGAC

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Consensus:

AGTGCCCatgcgCatGggAAAAagCcAAgnAcGGGCACTCTGAGaGGTtcAC

>Bacillus_Fam_269_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.625514
GCF_000708755.2_ASM70875v2_genomic.fna_2:68427-68791 Satlength=365 Nr of
Repeats=7 RepeatLength=52 seed=AGTTTTGAGG Num.seqs=7 Similarity=0.893773
0 AGTTTTGAGGGTGCTTATCTGTCTTATAAGTGCCCTCAATTTTTGAT--TTTCA
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_22:217896-218468
Satlength=573 Nr of Repeats=10 RepeatLength=52 seed=TTGAGGGCAC
Num.seqs=9 Similarity=0.781207
39 ATTTTTGAGGGTACTATTCTGCGGTTTTAGTGCCCTCAA--TTTCCTACTTTTCG
Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_5:41766-41974 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=AAAAATGAG Num.seqs=4
Similarity=0.846154 44
GTTTTTGAGGGTACGATTCTGGCTTTTTAGTACCCTCAATTTTTGGT--TTTTG

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Consensus:

atTTTTGAGGGTaCtatTCTGnctTtTtAGTgCCCTCAAttTTTgnTTTTcg

>Bacillus_Fam_270_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.703704
GCF_000708755.2_ASM70875v2_genomic.fna_22:181704-182016 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=GTGGAAATGA Num.seqs=6
Similarity=0.854701
0 GTGGAAATGACCCTTCAG-CAAGATCAAATCTGTGCGAAGGTCACAAAGCCGC-
GCF_000709935.2_ASM70993v2_genomic.fna_24:292765-293078 Satlength=314 Nr
of Repeats=6 RepeatLength=52 seed=TGGAAATGAC Num.seqs=5
Similarity=0.846154
1 GTGGAAATGACCCTTCAG-CATGATCAAATCTGTGCGAAGGTCACAAAGGCGC-
GCF_000709935.2_ASM70993v2_genomic.fna_1:11462-11774 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=TGTCCTTCA Num.seqs=6 Similarity=0.883761
6 -AGGAAATGTCCCTTCAGCCACGCTTGAA-CAGCGTGAAGGTCACAAAAGCGGA

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Consensus:

gtGGAAATGaCCCTTCAGCAnGaTcaAAtCtGtGcGAAGGTCACAAAggCGc

>Bacillus_Fam_271_53_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.600823
GCF_000934845.1_ASM93484v1_genomic.fna_162:31645-32113 Satlength=469 Nr
of Repeats=9 RepeatLength=52 seed=CGGGCACATG Num.seqs=9
Similarity=0.904558
0 CGGGCACATGTTGGCC-TTCTCTGTGACCGTGCTCTCGCTTTTCTTCCTTTT-
GCF_001420595.1_ASM142059v1_genomic.fna_11:2811819-2812081 Satlength=263
Nr of Repeats=5 RepeatLength=52 seed=CTCTTGTTAC Num.seqs=3
Similarity=0.863248 17
CGGGCACATGTGCGCC-CCTCTTGTTACCGCTCTCTTGCTTTTTC-TGCTTCCA
GCF_001420595.1_ASM142059v1_genomic.fna_11:4482129-4482596 Satlength=468
Nr of Repeats=9 RepeatLength=52 seed=AGTTTCTGGC Num.seqs=8
Similarity=0.868132 37
CGGGCACATGTT-GCCTTCTCTTGTTACCATGC-CTTCGAGTTTCTGGCTTTTCG

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Consensus:

CGGGCACATGTtnGCctcTCTTGtTACCgtgCtCTtgcttTTTcttgCTTtcn

>Bacillus_Fam_272_52_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.633745
GCF_001591645.1_ASM159164v1_genomic.fna_2:312008-312320 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=CTCTCTTACC Num.seqs=6
Similarity=0.744235
0 CTCTCTTACCATCCAACCTCTGCTTCCATCACG-AATGGGCACTGA-CAACCACT
Rev.of_GCF_001591645.1_ASM159164v1_genomic.fna_19:50399-50607
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TGGATGGTAA Num.seqs=4
Similarity=0.839623 15
CTCTCTTACCATCC-ACCCTCATTTCTCCCGCAATGGGCACTGA-CAACTTCT
GCF_001591645.1_ASM159164v1_genomic.fna_13:8919-9439 Satlength=521 Nr of
Repeats=10 RepeatLength=52 seed=TCTCTCTTAC Num.seqs=10
Similarity=0.780057
51 CTCTCTTACCATCGTACCCCGTTTACTCTCC-AACGGGCACTGAGCGAC-GCT

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Consensus:

CTCTCTTACCATCcnACcCtnTtccTCnGgAAAtGGGCACTGACaACnnCT

>Bacillus_Fam_273_53_3 Nr. of seq. 3 Alignment length(with gaps) = 54
Alignment score = 0.651235
GCF_001591665.1_ASM159166v1_genomic.fna_16:63845-64053 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TCGGTAAAAG Num.seqs=4
Similarity=0.864256
0 TCGGTAAAAGGAAGAGTGCTCCATTTACCGAAAAGCAG-AAAAGAGAGCTCTC-
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_72:4462-4722 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=CTTTTCATTTA Num.seqs=5
Similarity=0.907692 14
ACGGTAAATGAAAGAGCGGTTTCATTTACCGAAAAG-GGAAAAAAGAGCACTT-

Similarity=0.824691 0
GTGTACCTCTAGAACCATCTTGCGGTACATGCTCCTTCATATTTTCACGCC-AGC
Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_123:2-265 Satlength=264 Nr
of Repeats=5 RepeatLength=53 seed=GGGTGAGCAT Num.seqs=4
Similarity=0.945493 38
ATGTACCGCTAGACTCCTCTTGCGGGACATGCT-CACCCTATTTTCACACCAAGC
Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_126:203282-203547
Satlength=266 Nr of Repeats=5 RepeatLength=53 seed=TGAAATAGGG Num.seqs=5
Similarity=0.876730 45
GTGTACCGCTAGACACTTCATGCGGCACATGCT-CACCCTATTTTCACACCAAGC

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Consensus:

gTGTACCGCTAGACnCTCtTGCGGnACATGCTCacCcTATTTTCaCCaAGC

>Bacillus_Fam_277_51_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.639413
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2695072-2695736
Satlength=665 Nr of Repeats=13 RepeatLength=51 seed=GAATAGAAGC
Num.seqs=12 Similarity=0.816201 0
GAATAGAAGCGCCCTATTTCGACCGTTACA-CG-NGGTTCCACTTCCTTCGGTC
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2711389-2711951
Satlength=563 Nr of Repeats=11 RepeatLength=51 seed=CTATTTCGACC
Num.seqs=10 Similarity=0.819567 13
GAATAGAAGCTTCCTATTTCGACCGTTGCA-CGAGGGTTTCCCTT-CTTCGGGA
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:1751787-1752723
Satlength=937 Nr of Repeats=18 RepeatLength=52 seed=CTATTTCGACC
Num.seqs=18 Similarity=0.885333 13
GAATAGAACCCCTCTATTTCGACCGTTCAATCG-ATTTTTCAATTCTTTCGGGC

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Consensus:

GAATAGAAgCnccCTATTTCGACCGTTncACGnggTTtCacTTccTTCGGgc

>Bacillus_Fam_278_51_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.635220
GCF_001420595.1_ASM142059v1_genomic.fna_11:4524426-4524886 Satlength=461
Nr of Repeats=9 RepeatLength=51 seed=TGTCTGAACT Num.seqs=8
Similarity=0.829132 0
TGTCTGAACTTGAGCTAACTTCGGACTTCTTC-CGGATTTTCTCCTG-ATCT
GCF_001420595.1_ASM142059v1_genomic.fna_11:4601981-4602760 Satlength=780
Nr of Repeats=14 RepeatLength=52 seed=ATCTTGCTCTG Num.seqs=12
Similarity=0.803807 48
TGTCTGAACTTGAACCTAACTTCGGACTCCAGCATGCCTTTTCTNCGG-ATCT
GCF_000934845.1_ASM93484v1_genomic.fna_37:39135-39695 Satlength=561 Nr of
Repeats=11 RepeatLength=52 seed=AAACCTGTCC Num.seqs=9
Similarity=0.792735
47 TGTCCGAACCTTTGGCTAACTTCGGACTACTTT-TGCCTGTTTTNCCTGAAACC

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Consensus:

TGTCtGAACTTgagCTAACTTCGGACTnCttctGccTtTTTctcCtGAtCt

>Bacillus_Fam_279_51_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.681342
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_6:21894-22205
Satlength=312 Nr of Repeats=6 RepeatLength=51 seed=ACTTTATTTT Num.seqs=5
Similarity=0.793590 0 ACTTTATTTTCGATTAT-
TGA-TNGGAAATGTCTTTCATAAGGTCGATGAAGG
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_16:59730-59985
Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=TGAAAATGTC Num.seqs=5
Similarity=0.864052 21 ACTTTATGTT-GATTATATAG-
TTGAAAATGTCTTTCATGAGCTCGATGAAGG
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_10:55052-55308
Satlength=257 Nr of Repeats=5 RepeatLength=51 seed=GACTTTATTTT Num.seqs=4
Similarity=0.777778 50 ACTTTATTTTGGATT-T-
TAACTTAAAAATGTCCTTCATAAGGCTGATGAAAG

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Consensus:

ACTTTATtTnGATtATtTaaTtgaAAATGTCTtTTCATaAGgtcGATGAAGG

>Bacillus_Fam_280_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.666667
GCF_000430765.1_ASM43076v1_genomic.fna_5:240069-240277 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TTTTGTCCTT Num.seqs=4
Similarity=0.880342
0 TTTTGTCTTCATCCCCCTGATGAAGGACCGTTCTCCTGCACGTGAC-CCTGG
Rev.of_GCF_001636425.1_ASM163642v1_genomic.fna_1:4233510-4233770
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GGTCCTTCAT Num.seqs=5
Similarity=0.793711 30
TTTGGGCCTTCATCCGCCTTATGAAGGACCGTTCT-CTGTATTTTCTCTTCG
Rev.of_GCF_001636425.1_ASM163642v1_genomic.fna_1:4415449-4415969
Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=ATGAAGGACA
Num.seqs=10 Similarity=0.782099
65 TTTTGTCTTCATTCCTCCCTATGAAGGACGGTTCA-CTGAATTTTGCACCTCG

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Consensus:

TTTtGtCCTTCATcCcCcttATGAAGGACcGTTCTCTGnAttTtnCnCcTcG

>Bacillus_Fam_281_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.752621
GCF_000708755.2_ASM70875v2_genomic.fna_2:1643369-1643733 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=AGTTTCTGCT Num.seqs=7
Similarity=0.855922 0
AGTTTCTGCTGCTAAATCCAGTTAAGAACACTTTCACCCGCAAAC-CAACCAG

GCF_000709935.2_ASM70993v2_genomic.fna_3:65504-65920 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=GAACACTTTC Num.seqs=8 Similarity=0.821429
25 AGTTTCTGCTGCTAAATCCAGTTAAGAACTTTACCCGCAAAC-CAACCAG
GCF_000708755.2_ASM70875v2_genomic.fna_7:166561-166873 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TTTACAACAC Num.seqs=6
Similarity=0.847863
20 -GTTTCTGCTGCTAACTCTCGTTTACAACACTTTCAACCGCTCACGCTTCAAA

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Consensus:

aGTTTCTGCTGCTAAATCcaGTTaAgAACACTTTTCaCCGCaaACCaaCcAg

>Bacillus_Fam_282_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.746331
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_14:112431-113991
Satlength=1561 Nr of Repeats=30 RepeatLength=52 seed=TACACGAAAA
Num.seqs=30 Similarity=0.924727 0
TACACGAAAACGGCTTATAGAACCT-CTCTATGAACCCAAATTTTATCGAAC
Rev.of_GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_24:24595-25427
Satlength=833 Nr of Repeats=15 RepeatLength=52 seed=GTTCTATGAG
Num.seqs=14 Similarity=0.809626 24
CACATGAAAAGTGGCTCATAGAACCT-NTCTATGAACCCGAATTTGACCGAAA
Rev.of_GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_46:151000-151208
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GGGTTCATAG
Num.seqs=4 Similarity=0.837607 39
CACATGAAAACGGCTCATAGAA-CTCTTCTATGAACCCAAATTTGATCGAAT

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Consensus:

cACAtGAAAAnnGGCTcATAGAAcCTnTCTATGAACCCaAATTTgAtCGAAAn

>Bacillus_Fam_283_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.658281
GCF_000787375.1_ASM78737v1_genomic.fna_1:181126-181438 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TTGACTCCCG Num.seqs=6
Similarity=0.791195
0 TTGACTCCCGTTCTTCCGCCCTTCGCT-TTTTTCGGGAGTCATCACTCCTCT
GCF_000787375.1_ASM78737v1_genomic.fna_25:25502-25762 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CGCTCTTTGG Num.seqs=5 Similarity=0.912821
46 TTGGCTACCGTTCTTCTCTCTTTCTCC-TTTTTCGGGAGCCATCCCCGCTCT
GCF_000787375.1_ASM78737v1_genomic.fna_4:180648-181012 Satlength=365 Nr of Repeats=5 RepeatLength=52 seed=GTTTTTCGGT Num.seqs=4
Similarity=0.880342
27 TTGACTTCCGTTCTTCC-CACGTTCTCCGTTTTTCGGTAGCCAACACATCCCT

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Consensus:

TTGaCTnCCGTTCTTcCnCnCTTCTCcTTTTTCGGgAGcCAAtCaCnnCtCT

>Bacillus_Fam_284_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.618449

GCF_000986785.1_ASM98678v1_genomic.fna_2:158190-158798 Satlength=609 Nr of Repeats=12 RepeatLength=52 seed=CCTCCATCAC Num.seqs=11
 Similarity=0.821911 0
 CCTCCATCACACCCATGGAGGACCTTTTTCTCCNAATTTACGAAAGNTGGG-
 GCF_000986785.1_ASM98678v1_genomic.fna_8:188503-189125 Satlength=623 Nr of Repeats=11 RepeatLength=52 seed=GTCTCCATC Num.seqs=10
 Similarity=0.811966 50
 CCTCCATCACCCCTCATGGAGGACGCTTT-TCCATTTCTCACGCTATTTTCGGT
 GCF_000986785.1_ASM98678v1_genomic.fna_21:12509-12820 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=CCTCCATCAC Num.seqs=5 Similarity=0.882051
 52 CCTCCATCACCCCTCATGGAAGACCTTTTT-TCCTCTTCCTCCCAAAGCGGT

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 Consensus:

CCTCCATCACcCtCATGGAgGACcttTTTTCCnntTctCaCgcnAnntcGGt

>Bacillus_Fam_285_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
 Alignment score = 0.907757
 GCF_001439965.1_ASM143996v1_genomic.fna_89:30076-30284 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AATGTGTGTC Num.seqs=4
 Similarity=0.848008
 0 AATGTGTGTCCAAGAGA-GAGCTTGAAACACATTATAAGAGAAACCGGAGGAA
 GCF_001887185.1_ASM188718v1_genomic.fna_260:30450-30918 Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=TGAAACACAT Num.seqs=9
 Similarity=0.791077
 22 AATGTGTGTCCAAGAGANGAGN-TGAAACACATTATAAGAGAAACCGGAGGAG
 GCF_002009555.1_ASM200955v1_genomic.fna_301:3466-3778 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TGAAACACAT Num.seqs=6 Similarity=0.781151
 22 AATGTGTGTCCAAGAGAGGAGC-TGAAACACATTATAAGAGAAACCGGAGGAG

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 Consensus:

AATGTGTGTCCAAGAGAnGAGcTGAAACACATTATAAGAGAAACCGGAGGAg

>Bacillus_Fam_286_53_3 Nr. of seq. 3 Alignment length(with gaps) = 53
 Alignment score = 0.851153
 GCF_001439965.1_ASM143996v1_genomic.fna_95:72244-72698 Satlength=455 Nr of Repeats=9 RepeatLength=52 seed=ATTGGTTACC Num.seqs=7
 Similarity=0.792430
 0 ATTGGTTACCCGTTGCGC-GATTTCACCCGNACTCGGTCACCTTTCGGCNTG
 Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_11:78-494 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=GGGTAACCAA Num.seqs=8
 Similarity=0.813118 11
 ATTGGTTACCCTGTTGCGCGGATTTACCCGGACTCGGTCACCTTTGGGCNTG
 GCF_001887185.1_ASM188718v1_genomic.fna_43:121-747 Satlength=627 Nr of Repeats=12 RepeatLength=52 seed=TTGGTTACCC Num.seqs=9
 Similarity=0.765898
 1 ATTGGTTACCCGTTG-GCGGATTTACGTGGACTCGGTCACCTTTCGGCNTG

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 Consensus:

ATTGGTTACCCgGTTGcGCgGATTTACccGgACTCGGTCACCTTTcGGCNTG

>Bacillus_Fam_287_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.633124

GCF_001591665.1_ASM159166v1_genomic.fna_53:52093-52301 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TTAAAGACAT Num.seqs=4
Similarity=0.792977

0 TTAAAGACATTTTGAGC-ACATTGATGGGCAGTTATGTCTTTAAGAAAGGCTA

GCF_001591665.1_ASM159166v1_genomic.fna_91:5115-5323 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=ATTAAAGACA Num.seqs=4 Similarity=0.752058

51 TTAAAGACATTTTGGTG-GGTAAGACAGGGAGTTTGTCTTTAAGGAGGGCTA

GCF_001591665.1_ASM159166v1_genomic.fna_54:84694-84902 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GTATTAAAGA Num.seqs=4
Similarity=0.876068

49 TTAAAGACATTTT-AGCTATTTTGTAGAGGTGGTTTGTCTTAAGAAGGGGTA

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Consensus:

TTAAAGACATTTTgagCantttgAnaGGNaGTTtTGTCTTTAAGaAgGGcTA

>Bacillus_Fam_288_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.731656

GCF_001591805.1_ASM159180v1_genomic.fna_5:182944-183204 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CTTATAAGCT Num.seqs=5
Similarity=0.851572

0 CTTATAAGCTACCCAACCTGGATGATTTTCTCGGTTTCGGTAGCTTATAC-CT

GCF_001591805.1_ASM159180v1_genomic.fna_68:9875-10082 Satlength=208 Nr of
Repeats=4 RepeatLength=52 seed=TTATAAGCTA Num.seqs=3 Similarity=0.880342

1 CTTATAAGCTACCCAACCTGGGCGGCTTTCTCGGTTTCGGTCGCTTATAC-CC

Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_63:307-671 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=AAGTTGGGTA Num.seqs=7
Similarity=0.865690

18

-TTATAAGCTACCCAACCTCCGCAAATCCCNCGGCTTCGGTCGCTTATACACC

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Consensus:

cTTATAAGCTACCCAACCTTgggcganTttCtCGGtTTCGGTcGCTTATACCc

>Bacillus_Fam_289_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.645702

GCF_001636315.1_ASM163631v1_genomic.fna_1:834005-834369 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=AAAGTGTTTC Num.seqs=7
Similarity=0.796002

0 AAAGTGTTTCCAATCAAGGCTATTGGCGACATAACTCAGTATAAAAANNTGA-

GCF_001636315.1_ASM163631v1_genomic.fna_1:4300776-4301088 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=GCGACAAAAC Num.seqs=6
Similarity=0.704527

25

GAAGTGATCCAATGAAGGCTATTGGCGACAAAACCTCTGTTGGAAAAGGGGC-

GCF_001636315.1_ASM163631v1_genomic.fna_1:3938063-3939308 Satlength=1246
Nr of Repeats=11 RepeatLength=52 seed=TGGAAACAAA Num.seqs=9

Similarity=0.925926 22
-AAATGTTTCCAATGAGGGCTATTGGAAACAAAACCTCACGAAGAAAGCGGGAG

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Consensus:

nAAgTGtTtCCAATgAaGGCTATTGGcgACAaAACTCagtangAAAanggGa

>Bacillus_Fam_290_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.607966
GCF_001636315.1_ASM163631v1_genomic.fna_1:2347811-2348434 Satlength=624
Nr of Repeats=12 RepeatLength=52 seed=TGGAATCACT Num.seqs=11
Similarity=0.844289 0
TGGAATCACTTTTCTC-TNTTTTTCTCCNAGTTTTGTTTCCAATGACCCTGAT
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:3352830-3353038
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GCGACAAAAG Num.seqs=4
Similarity=0.880342 39
TGGATTCACTTTACTC-TCTTTTGCTCCGGCTTTTGTGCGCCAATAGCCTTCAT
GCF_001636315.1_ASM163631v1_genomic.fna_1:3814968-3815747 Satlength=780
Nr of Repeats=15 RepeatLength=52 seed=TTGGAAACAC Num.seqs=14
Similarity=0.832884 51
TGGAAACACTTTACTCGTATTTT-CACAGAGATTTGTTTCCAATAGGTGCGAT

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Consensus:

TGGAatCACTTTaCTCTnTTTTnTtCcgagtTTTGtTtCCAATagccntgAT

>Bacillus_Fam_291_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.714885
GCF_002019645.1_ASM201964v1_genomic.fna_1:115528-116203 Satlength=676 Nr
of Repeats=13 RepeatLength=52 seed=GCTGTCCGAA Num.seqs=12
Similarity=0.753627 0
GCTGTCCGAAGTTGGCTGAGGTTGAGACAGCTTGAGGAACAAAAGAGAGAAA-
GCF_002019645.1_ASM201964v1_genomic.fna_1:2536105-2536365 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=AAGAGGAAAA Num.seqs=5
Similarity=0.929560 42
GCTGTCCGAAGTGAGGTGAGGTTGAGACAGGTTGAGGGTGAGAAGAG-GAAAA
Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:4937598-4938897
Satlength=1300 Nr of Repeats=25 RepeatLength=52 seed=TACTTCGGAC
Num.seqs=24 Similarity=0.864549
65 GCTGTCCGAAGTAGAGTGAGGTTGAGACAGCTTTGGTGTGCGAAGNG-GAAAA

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Consensus:

GCTGTCCGAAGTnGagTGAGGTTGAGACAGcTTgaGggtgagAAGaGGAAAAa

>Bacillus_Fam_292_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
Alignment score = 0.704403
GCF_002019645.1_ASM201964v1_genomic.fna_1:995262-996146 Satlength=885 Nr
of Repeats=17 RepeatLength=52 seed=AAGGTTCCGA Num.seqs=17
Similarity=0.819570 0
AAGGTTCCGACAGCTTTTGCTCGAAG-GCCCTCGAAGTTGTCCGAAGTNGCCC

Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:4106739-4107991
 Satlength=1253 Nr of Repeats=24 RepeatLength=52 seed=ACTTCGGACA
 Num.seqs=20 Similarity=0.924831
 47 AAGGTTTCGGACAGCTTTAGCTTCCGG-GCATTCTGAAGTTGTCCGAAGTCGCTC
 Rev.of_GCF_002019645.1_ASM201964v1_genomic.fna_1:4426732-4427356
 Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=ACTTCGGACA
 Num.seqs=12 Similarity=0.829060
 47 GGGGTTTCGGACAGCTTTTGGTCTCAGAGGA-TCGAAGTTGTCCGAAGTTGTTC

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Consensus:

aaGGTTCGGACAGCTTTtGcTcncaGGcanTCGAAGTTGTCCGAAGTnGctC

>Bacillus_Fam_293_52_3 Nr. of seq. 3 Alignment length(with gaps) = 53
 Alignment score = 0.637317
 GCF_900104555.1_IMG-
 taxon_2651870172_annotated_assembly_genomic.fna_20:557960-558325
 Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=GTCTGAAGTC Num.seqs=6
 Similarity=0.732510 0 GTCTGAAGTC-
 ACCTTAGGTTTCAGACACAGTTGCATGTGAAATCACCAATCCT
 Rev.of_GCF_900104555.1_IMG-
 taxon_2651870172_annotated_assembly_genomic.fna_22:368575-368885
 Satlength=311 Nr of Repeats=6 RepeatLength=52 seed=CTTCAGACAG Num.seqs=4
 Similarity=0.635288 8 GTCTGAAGTC-
 AGGNTAGGTTTCGGACACGCTTGGATTTGAAATCGCTGATCCT
 GCF_900104555.1_IMG-
 taxon_2651870172_annotated_assembly_genomic.fna_22:384819-385184
 Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=GTCTGAAGT Num.seqs=6
 Similarity=0.741090 51 GTCTGAAGTCGACCCTA-
 GTTCGGACTCTGGTGCACCTTGCAATCACTTCTCTT

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Consensus:

GTCTGAAGTCAccnTAgGTTcGACaCngtTGcAttTGaAATCaCtnaTCcT

>Bacillus_Fam_294_51_3 Nr. of seq. 3 Alignment length(with gaps) = 52
 Alignment score = 0.651709
 GCF_002019605.1_ASM201960v1_genomic.fna_1:184216-184471 Satlength=256 Nr
 of Repeats=5 RepeatLength=51 seed=TATAAGGAAG Num.seqs=3
 Similarity=0.839744
 0 TATAAGGAAGTGATGAGTGCTAAAAGTCAGGATAGCTCATGA-TATTACCAG
 Rev.of_GCF_002019605.1_ASM201960v1_genomic.fna_1:1956898-1957102
 Satlength=205 Nr of Repeats=4 RepeatLength=51 seed=CCTCATACTG Num.seqs=4
 Similarity=0.930283 7
 TATGAGGAAGAAATGAGCGCTAAAGCGAAAGATAGAACACTA-TATTACCAG
 GCF_002019605.1_ASM201960v1_genomic.fna_1:4935750-4936209 Satlength=460
 Nr of Repeats=9 RepeatLength=51 seed=AGTGCTAAAG Num.seqs=9
 Similarity=0.852578 15
 TATAAGTAAGAAATGAGTGCTAAAGCGAGGATAGAGC-TTATTGTTTCCAG

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

Consensus:

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>Bacillus_Fam_295_52_3  Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.707265
GCF_000169195.2_ASM16919v2_genomic.fna_1:649385-650061 Satlength=677 Nr
of Repeats=13 RepeatLength=52 seed=TTAAGGAAGA Num.seqs=13
Similarity=0.725689
TTAAGGAAGATCGAAAAAATCGTCCCTTTCTTAACGTAGANCCGTTCTACG
Rev.of_GCF_000169195.2_ASM16919v2_genomic.fna_1:669488-670145
Satlength=658 Nr of Repeats=10 RepeatLength=52 seed=CTTCCTTAAC
Num.seqs=7 Similarity=0.743590
9 TTAAGGAAGNCCGNNAAAAAGNCNCGCTATCTTAACGTAGAGGCGTTCTATG
GCF_000169195.2_ASM16919v2_genomic.fna_1:2578666-2579497 Satlength=832 Nr
of Repeats=15 RepeatLength=52 seed=GTAAAGGAAG Num.seqs=13
Similarity=0.728270
TAAAGGAAGNCCGCAAAAAGTGTGTCTATCTTAACATAGAGGCGTTCTANG
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Consensus:

TtAAGGAAGncCGnnAAAAgngt cnCTaTCTTAACgTAGAggCGTTCTAnG

```
>Bacillus_Fam_296_52_3  Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.841880
GCF_000171615.1_ASM17161v1_genomic.fna_52:43-615 Satlength=573 Nr of
Repeats=10 RepeatLength=52 seed=GGCGCGCTTA  Num.seqs=9
Similarity=0.811321
0      GGCGCGCTTACCCTAGCGCGNGGCTCTTCTCTCTTTTTTCTTCTTCTTGGGA
GCF_000171615.1_ASM17161v1_genomic.fna_60:29-599 Satlength=571 Nr of
Repeats=8 RepeatLength=52 seed=GCGCTTACCC  Num.seqs=5 Similarity=0.892308
3      GGCGCGCTTACCCTAACGCGGGGCTCTTCTCCCTTTTTTCTTCTTCTTGGGA
Rev.of_GCF_000171615.1_ASM17161v1_genomic.fna_130:149-408 Satlength=260
Nr of Repeats=5 RepeatLength=52 seed=AAGAAGAAAA  Num.seqs=4
Similarity=0.846154
GGGGCGCTGTCCCAAGCGCGTGTCTCTTCTCTCTTTTTTCTTCTTCTTGGGG
```

Consensus:

GGcGCGCTtaCCcTAqCGCGnGqCTCTTCTCtCTTTTTCTTCTTCTTGGGa

```
>Bacillus_Fam_297_52_3  Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.675214
GCF_000177235.2_ASM17723v2_genomic.fna_1:726998-727934 Satlength=937 Nr
of Repeats=18 RepeatLength=52 seed=AAGCGTGTCA  Num.seqs=18
Similarity=0.904475
AAGCGTGTCCATACGAAGGCAATGCCGCATGAAAAATCGGGACGCAGGAAATA
Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:4063448-4064381
Satlength=934 Nr of Repeats=18 RepeatLength=52 seed=CATTGCTCTC
Num.seqs=15 Similarity=0.906227
23  AAGCGTGTCCATACGAGAGCAATGCCACATGAAAAAAGCAAACAAGCAAATA
Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:1193617-1194293
Satlength=677 Nr of Repeats=13 RepeatLength=52 seed=ATGTGTCATT
```


Num.seqs=9 Similarity=0.752970
29 ACNCGTGTGCATACAAGGNCAATGACACATGAAAAATAAGAAGCAATCCAATA

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Consensus:

AagCGTGTGCATACgAgggCAATGcCaCATGAAAAAtaggaAncaAgcaAATA

>Bacillus_Fam_298_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.688034
GCF_000374565.1_ASM37456v1_genomic.fna_3:72207-73350 Satlength=1144 Nr of
Repeats=22 RepeatLength=52 seed=AAACGGTAAC Num.seqs=21
Similarity=0.805750
0 AAACGGTAAC TAATCGTGGGGAAATGTTCCCGTTTTGTGCCTGAGTTCGAAC
GCF_000374565.1_ASM37456v1_genomic.fna_16:37328-37794 Satlength=467 Nr of
Repeats=9 RepeatLength=52 seed=GAAAAAACGG Num.seqs=7 Similarity=0.672252
48 AAACGGGAAC TAATCGTGAGGAAAGGTTACCGGTTGGGGCCCGTGTNGAAA
GCF_000374565.1_ASM37456v1_genomic.fna_3:246080-246600 Satlength=521 Nr
of Repeats=10 RepeatLength=52 seed=CGGTAACTAA Num.seqs=8
Similarity=0.785827
3 AACCGGTAACTAATGGAGAAGAAAGGTGCCCCGCTTTGTGTCCGATTTCGAAA

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Consensus:

AAaCGGtAACTAATcGtGagGAAAgGTtcCCGnTTtGtGcCcGagTTcGAAa

>Bacillus_Fam_299_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.846154
GCF_000708755.2_ASM70875v2_genomic.fna_1:102871-103131 Satlength=261 Nr
of Repeats=4 RepeatLength=52 seed=AAAGTGTTC T Num.seqs=3
Similarity=0.752621
0 AAAGTGTTC TAANCCAGAGTAAGCAGCACAAAGTGAGTAGANCACAGGCTCG
GCF_000709935.2_ASM70993v2_genomic.fna_1:103820-104028 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CAAAGTGT T Num.seqs=4
Similarity=0.786325
50 AAAGTGTTC TAAACCAGAGTTAGCAGCACAAACTGAGTAGAGCACAGGCCCA
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_6:383976-384236
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TGCTAACTCT Num.seqs=5
Similarity=0.853846 25
AAAGTGTTC TAACCCAGAGTTAGCAGCACAAAGTGAGTAGAGCCCGGTCCCG

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Consensus:

AAAGTGTTC TAAnCCAGAGTtAGCAGCACAAAgTGAGTAGAgCaCaGgCcCg

>Bacillus_Fam_300_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.811966
GCF_000708755.2_ASM70875v2_genomic.fna_1:366565-366877 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=GAGTTTGTGC Num.seqs=6
Similarity=0.782906
0 GAGTTTGTGCTGCTAAATCATGTATAGAACACTTTCGGCNGGGCCCCGCACT

Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:47476-47840 Satlength=365
 Nr of Repeats=7 RepeatLength=52 seed=ATGAGTTAGC Num.seqs=7
 Similarity=0.841858 21
 GAGTTTATGCTGCTAACTCATGTTTGAACACTTTTCGCCGCGACCCGCACC
 Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_24:86775-87035
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TAGCAGCACA Num.seqs=5
 Similarity=0.856410 67
 GAGTTTGTGCTGCTAACTCTTGTGTTGAACACTTTNGCCGTGGACCCGCACC

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Consensus:

GAGTTTgTGCTGCTAAcTCaTGtTgGAACACTTTcGcCgnGGaCCCGCACc

>Bacillus_Fam_301_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
 Alignment score = 0.809829
 GCF_000708755.2_ASM70875v2_genomic.fna_6:144195-144506 Satlength=312 Nr
 of Repeats=6 RepeatLength=52 seed=AAGGGTCATA Num.seqs=5
 Similarity=0.784615
 0 AAGGGTCATAANGACACATGATTTAACCCCTTCAGCATGAAGGAAACTCCGTG
 GCF_000709935.2_ASM70993v2_genomic.fna_15:61477-61788 Satlength=312 Nr of
 Repeats=6 RepeatLength=52 seed=TGAAGGGTCA Num.seqs=5 Similarity=0.797436
 50 AAGGGTCATAANGACACATGATTTAACCCCTTCAGCATGAAGGAAACTCCGTG
 Rev.of_GCF_000709935.2_ASM70993v2_genomic.fna_2:33696-33956 Satlength=261
 Nr of Repeats=5 RepeatLength=52 seed=CATGCTGAAG Num.seqs=5
 Similarity=0.842593 38
 AAAGGTCATAAGCCCGCGTGATATAACCCTTCAGCATGAAGGAGAGTGTGTG

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Consensus:

AAgGGTCATAAngaCaCaTGATtTAACCCTTCAGCATGAAGGAaAcTccGTG

>Bacillus_Fam_302_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
 Alignment score = 0.760684
 GCF_000759675.1_ASM75967v1_genomic.fna_13:117550-117862 Satlength=313 Nr
 of Repeats=6 RepeatLength=52 seed=CTGGAGTGAC Num.seqs=6
 Similarity=0.935043
 0 CTGGAGTGACCGTAGATCATATAGAAAATGCTTTTGGGTCAATGCAGATAGG
 Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_19:541006-541370
 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TTCCGGTCACT Num.seqs=7
 Similarity=0.868132 14
 CTGGAGTGACCGAAAAGCATGTAAAAAAGGCATATGGGTCAATGCAGGAAGT
 GCF_000759675.1_ASM75967v1_genomic.fna_136:8346-8709 Satlength=364 Nr of
 Repeats=7 RepeatLength=52 seed=GAGTGACCGA Num.seqs=6 Similarity=0.781197
 55 CTGGAGTGACCGAAAAGCATTAGGAAAAGCATTGGGTCAATGCAGATAGT

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Consensus:

CTGGAGTGACCGaAaAgCATntAgaAAAnGCaTtTGGGTCAATGCAGatAGt

>Bacillus_Fam_303_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
 Alignment score = 0.713675

GCF_000813125.1_ASM81312v1_genomic.fna_102:117072-117487 Satlength=416 Nr of Repeats=8 RepeatLength=52 seed=GACAGCTTTG Num.seqs=7
 Similarity=0.807082 0
 GACAGCTTTGAAGGAAATCAGCGTAAAGCTGTCTGAACTTGGTGCTACTTCT
 Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_83:5-265 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GTCCGAAGTA Num.seqs=5
 Similarity=0.713333
 3 GACTACTTTTACGGAAAAAGGCGGAAACCTGTCCGAACCTGGGCNTACTTCG
 Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_94:227-539 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GCAAAAGCAG Num.seqs=6
 Similarity=0.862055 12
 GACTGCTTTTGCGGAAAAAGGCGGAAAGTGGTCCGAACCTGGGGCTACTTCG

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Consensus:

GACtgCTTTtacGGAAAaagGCGgAAAgctGTCcGAACTTGggcTACTTCg

>Bacillus_Fam_304_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
 Alignment score = 0.675214
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3162845-3163209
 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=AATCGTTACC Num.seqs=7
 Similarity=0.782775 0
 AATCGTTACCGTTTTACATGAGAGCACGTCAAGACGGTAACGAATCAGAGCN
 Rev.of_GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4427320-4431322
 Satlength=4003 Nr of Repeats=77 RepeatLength=52 seed=TGAATCGTTC
 Num.seqs=75 Similarity=0.994622 47
 AATCGTTACCTTTTCATATGCGATCACCGCAATACGGGAACGATTCAGAGCC
 GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4422988-4423300
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GGTAACGATT Num.seqs=6
 Similarity=0.769231 35
 AATCGTGCCCGTTTCGGATGGGANACGGCAACATGGTAACGATTCGGAGTG

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Consensus:

AATCGTtaCCgTTTcanATGnGAnCACggCAAnAcGGtAACGAtTCaGAGcn

>Bacillus_Fam_305_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
 Alignment score = 0.705128
 GCF_001439915.1_ASM143991v1_genomic.fna_83:493100-493309 Satlength=210 Nr of Repeats=4 RepeatLength=52 seed=GGCTTATTCG Num.seqs=3
 Similarity=0.914530 0
 GGCTTATTCGGACAGAACAAGCAAGAAATGCCAATAGAGAGTCCGAATGCAA
 GCF_001439915.1_ASM143991v1_genomic.fna_116:79569-79934 Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=ATTCGGACAG Num.seqs=6
 Similarity=0.789744
 5 GGCTAATTCGGACAGGACAAGCGGAAAAAGTCGGTAGAGAGTCCGAATGCAA
 GCF_001439915.1_ASM143991v1_genomic.fna_123:290092-290300 Satlength=209
 Nr of Repeats=4 RepeatLength=52 seed=ATTTGGACAG Num.seqs=4
 Similarity=0.586420 5
 GGTTCATTTGGACAGACCAATGTAGAACTGCCGNTAGAGAGTCCAAATGCAA

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Consensus:

GGcTnATTcGGACAGaaCAAgcnagAAatGcCgnTAGAGAGTCCgAATGCAA

>Bacillus_Fam_306_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.726496
GCF_001439965.1_ASM143996v1_genomic.fna_56:1630-1890 Satlength=261 Nr of
Repeats=4 RepeatLength=52 seed=TGATTGATTA Num.seqs=3 Similarity=0.794872
0 TGATTGATTACCCTGAAGGNGAAAATTGCATGTGTACGGGAACCATANAGAG
GCF_002009555.1_ASM200955v1_genomic.fna_109:9635-9947 Satlength=313 Nr of
Repeats=5 RepeatLength=52 seed=TGATTGATTA Num.seqs=4 Similarity=0.854701
0 TGATTGATTACCCTGAAGATGAAAATTGCATGTGTACGGGAACCATACAGAG
Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_27:20337-20857
Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=AGGGTAACCA
Num.seqs=10 Similarity=0.871225
14 GGTTTGGTTACCCTGTTGATGGAAATTGCGCCTGTACGGTAACCAATGGGAG

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Consensus:

tGaTTGaTTACCCTGaaGatGaAAATTGCatgTGTACGGgAACCAatanaGAG

>Bacillus_Fam_307_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.899573
GCF_001439965.1_ASM143996v1_genomic.fna_108:192897-193886 Satlength=990
Nr of Repeats=20 RepeatLength=52 seed=GGTAACCATT Num.seqs=17
Similarity=0.698483 0
GGTAACCATTGANGGACTTTGGTGACCCTTTTGGNGGAAAACTCCTTTTCNTC
GCF_001887185.1_ASM188718v1_genomic.fna_193:64604-65229 Satlength=626 Nr
of Repeats=12 RepeatLength=52 seed=AAACTCCTTT Num.seqs=11
Similarity=0.767366 38
GGTAACCATTGAGGGCCTTTGGTGACCCTTTNGGNGGAAAACTCCTTTCTTC
Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_553:44922-45390
Satlength=469 Nr of Repeats=8 RepeatLength=52 seed=AAAGGAGTTT Num.seqs=6
Similarity=0.735185 48
GGTAACCATTGTGGGCCTTTGGTGACCCTTTGGGNGGAAAACTCCTTTCTTC

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Consensus:

GGTAACCATTGagGGcCTTTGGTGACCCTTTnGGNGGAAAACTCCTTTCTTC

>Bacillus_Fam_308_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.929487
GCF_001439965.1_ASM143996v1_genomic.fna_121:22311-22571 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=AGAAAGAGGA Num.seqs=5
Similarity=0.887179
0 AGAAAGAGGAAGAAAGGTAACCAATCGCCCGAAAGGTTCCCGAAACACGAA
GCF_001887185.1_ASM188718v1_genomic.fna_194:35985-36921 Satlength=937 Nr
of Repeats=18 RepeatLength=52 seed=AAAGAAAGAG Num.seqs=18
Similarity=0.771074 50
AGAAAGAGGAAGAAAGGTAACCAATCGCTCGGAAAGGTTACCGAAACTNGAA
GCF_002009555.1_ASM200955v1_genomic.fna_16:8263-9199 Satlength=937 Nr of
Repeats=18 RepeatLength=52 seed=AAAGAAAGAG Num.seqs=18

Similarity=0.771074
50 AGAAAGAGGAAGAAAGGTAACCAATCGCTCGGAAAGGTTACCGAAACTNGAA

Consensus:

AGAAAGAGGAAGAAAGGTAACCAATCGCtCGGAAAGGTTaCCGAAACtnGAA

>Bacillus_Fam_309_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.739316
GCF_001439965.1_ASM143996v1_genomic.fna_121:87820-88132 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=TTGAAACACA Num.seqs=6
Similarity=0.820513
0 TTGAAACACATTATAAGAGAATATTAGAGAAAATGTGTCTCAAGTATAGTGT
Rev.of_GCF_001439965.1_ASM143996v1_genomic.fna_124:121491-121767
Satlength=277 Nr of Repeats=5 RepeatLength=52 seed=CAAAATGTGT Num.seqs=3
Similarity=0.773663 15
TGGATACACATTTTGTGNTAGAAATATTGCGGATAATGTGTCTCAAGGATGGCGG
Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_148:130132-130548
Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=CAAAATGTGT Num.seqs=6
Similarity=0.878632 15
TGGATACACATTTTGTGCGAGAATATTGCAGATAATCTGTCTCAAGGATGGCGG

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Consensus:

TgGAtACACATTTtTgngAGAATATTgcaGAtAATgTGTCTCAAGgATgGcGg

>Bacillus_Fam_310_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.982906
GCF_001439965.1_ASM143996v1_genomic.fna_122:46240-46602 Satlength=363 Nr
of Repeats=7 RepeatLength=52 seed=CTTAAATAGA Num.seqs=6
Similarity=0.780606
0 CTTAAATAGAGGAAACCAAGTGTGTAGGGTAACTAAAGCGAGCGAAAGGTTA
Rev.of_GCF_001887185.1_ASM188718v1_genomic.fna_62:176111-176735
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=TTTAAGTAAC
Num.seqs=12 Similarity=0.876845
6 CTTAAATAGAGGAAACCAGGTGTGTAGGGTAACTAAAGCGAGCGAAAGGTTA
Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_91:21-333 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=TTTAAGTAAC Num.seqs=6
Similarity=0.873504 6
CTTAAATAGAGGAAACCAGGTGTGTAGGGTAACTAAAGCGAGCGAAAGGTTA

Consensus:

CTTAAATAGAGGAAACCAgGTGTGTAGGGTAACTAAAGCGAGCGAAAGGTTA

>Bacillus_Fam_311_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.730769
GCF_001439965.1_ASM143996v1_genomic.fna_125:170548-171172 Satlength=625
Nr of Repeats=11 RepeatLength=52 seed=TGGTTACCGA Num.seqs=10
Similarity=0.670576 0
TGGTTACCGAGTCCNCGAGATATCCACCTTCAGGGTAACCAAACANGTNTTA

GCF_001887185.1_ASM188718v1_genomic.fna_98:26215-26474 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=AAGGTTACCG Num.seqs=4
 Similarity=0.652263
 51 AGGTTACCGAATCCATGAGAAATCCACCTAAAGGGTAACGAAACGAGCGCAA
 Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_334:9897-10157
 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TCGGTAACCT Num.seqs=5
 Similarity=0.744654 62
 AGGTTACCGAATCNATGAGAAATCCACCTANAGGGTAACGAACCCAGCGCAA

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 Consensus:

aGGTTACCGAaTCcatGAGAAATCCACCTanAGGGTAACgAAaCnaGcgcaA

>Bacillus_Fam_312_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
 Alignment score = 0.649573
 GCF_001636325.1_ASM163632v1_genomic.fna_1:60206-60777 Satlength=572 Nr of Repeats=11 RepeatLength=52 seed=AAAGGTAGAA Num.seqs=10
 Similarity=0.805724
 0 AAAGGTAGAAAGAGAGTGTGTCACGCCCATCTGAGGTAGAAAAGAGAAG
 GCF_001636325.1_ASM163632v1_genomic.fna_2:158704-159484 Satlength=781 Nr of Repeats=15 RepeatLength=52 seed=GAAGAGCGAG Num.seqs=15
 Similarity=0.855106 7
 AAAGGAGAAAGAGCGAGCGTCTCATCGCCCATCTGAGCGAGAAGAAGAGTAG
 GCF_001636325.1_ASM163632v1_genomic.fna_2:308084-308398 Satlength=315 Nr of Repeats=6 RepeatLength=52 seed=TGAAAGGAAG Num.seqs=5
 Similarity=0.738462
 50 AAAGGAAGAAGAGAGCACGTCTCAGCGCCCAAGTGATAGAGAATAGCCGATG

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 Consensus:

AAAGGnAGAAGAGaGngcGTcTCAnCGCCCAtcTGAgngAGAAAnAagaGaaG

>Bacillus_Fam_313_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
 Alignment score = 0.675214
 GCF_001636335.1_ASM163633v1_genomic.fna_1:2043697-2044009 Satlength=313
 Nr of Repeats=6 RepeatLength=52 seed=TATGGGACAA Num.seqs=6
 Similarity=0.810256 0
 TATGGGACAAAAGATTACTGATTTCTGCTAATTTTGTCCCATTGAGCTCTCC
 GCF_001636335.1_ASM163633v1_genomic.fna_1:2271770-2272029 Satlength=260
 Nr of Repeats=5 RepeatLength=52 seed=GTCTCATTGA Num.seqs=4
 Similarity=0.931624 35
 TATGGGACACTTGCTTTTCCTTTTTCAGCTTTTTTTGTCTCATTGAGCTCTCC
 GCF_001636335.1_ASM163633v1_genomic.fna_1:2474604-2475436 Satlength=833
 Nr of Repeats=16 RepeatLength=52 seed=TATGGGACAG Num.seqs=16
 Similarity=0.867949 52
 TATGGGACAGTTCCTTCGGCTTCTCGGCTTGTTTTGTCTCATTGAGCCCTCC

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 Consensus:

TATGGGACAnttgCTTncnntTtTCnGCTtnTTTTGTCTcATTGAGCtCTCC

>Bacillus_Fam_314_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.982906
GCF_001645705.1_ASM164570v1_genomic.fna_19:10035-10867 Satlength=833 Nr
of Repeats=16 RepeatLength=52 seed=AAAAGGGAAC Num.seqs=16
Similarity=0.930769 0
AAAAGGGAACATAGAGTCCTTGTATGTACGCGAAACTGGTGGGAAGACTCCG
GCF_001645705.1_ASM164570v1_genomic.fna_57:14-794 Satlength=781 Nr of
Repeats=15 RepeatLength=52 seed=TTGTATGTAC Num.seqs=15
Similarity=0.903804
19 AAAAGGGAACATAGAGTCCTTGTATGTACGCGAAACTGGTGGGAAGACTCCG
GCF_001645705.1_ASM164570v1_genomic.fna_35:14312-14884 Satlength=573 Nr
of Repeats=11 RepeatLength=52 seed=AAAAGGGAAC Num.seqs=11
Similarity=0.938462 0
AAAAGGGAACATAGAGTCCTTGTATGTACGCGAAACTGGTGAGAAGACTCCG

Consensus:

AAAAGGGAACATAGAGTCCTTGTATGTACGCGAAACTGGTGgGAAGACTCCG

>Bacillus_Fam_315_52_3 Nr. of seq. 3 Alignment length(with gaps) = 52
Alignment score = 0.946581
GCF_900156865.1_PRJEB18960_genomic.fna_3:4195877-4197024 Satlength=1148
Nr of Repeats=22 RepeatLength=52 seed=GAGCAAAGAA Num.seqs=20
Similarity=0.876788 0
GAGCAAAGAACATGTCATCATCGANCGGATGAAGACACGAATAGAGGTGTAG
GCF_900156865.1_PRJEB18960_genomic.fna_3:4199517-4200091 Satlength=575 Nr
of Repeats=11 RepeatLength=52 seed=TGTCATCATC Num.seqs=10
Similarity=0.891168 12
GAGCAAAGAACATGTCATCATCGANAGGATGAAGACACGAATAGAAGTGTAG
GCF_900156865.1_PRJEB18960_genomic.fna_3:4202611-4202819 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CAAAGAACAT Num.seqs=4
Similarity=0.914530 55
GAGCAAAGAACATGTCATCATCGAAAGGATGAAGACACGAATAGAAGTGTAG

Consensus:

GAGCAAAGAACATGTCATCATCGAnaGGATGAAGACACGAATAGAAgTGTAG

>Bacillus_Fam_316_48_3 Nr. of seq. 3 Alignment length(with gaps) = 48
Alignment score = 0.981481
GCF_000706725.1_ASM70672v1_genomic.fna_1:2952140-2952854 Satlength=715 Nr
of Repeats=15 RepeatLength=48 seed=TTCTTCTGAT Num.seqs=10
Similarity=0.925309 0
TTCTTCTGATGACGTTGAGAACGACTCAGATGCTGACAGTGACGATGA
Rev.of_GCF_002019765.1_ASM201976v1_genomic.fna_1:1074786-1075170
Satlength=385 Nr of Repeats=8 RepeatLength=48 seed=TCATCAGAAG Num.seqs=8
Similarity=0.870040 12
TTCTTCTGATGACGTTGAGAACGACTCAGATGCTGACAGTGACGATGA
GCF_001420645.1_ASM142064v1_genomic.fna_7:5330-5618 Satlength=289 Nr of
Repeats=6 RepeatLength=48 seed=ATTCTTCTGA Num.seqs=6 Similarity=0.874074
47 TTCTTCTGATGACGTTGAGAACGACTCAGACGCTGACAGTGACGATGA

Consensus:

TTCTTCTGATGACGTTGAGAACGACTCAGAtGCTGACAGTGACGATGA

>Bacillus_Fam_317_45_3 Nr. of seq. 3 Alignment length(with gaps) = 46

Alignment score = 0.666667

GCF_000017425.1_ASM1742v1_genomic.fna_1:1678527-1678779 Satlength=253 Nr

of Repeats=6 RepeatLength=42 seed=GAACAAAAGC Num.seqs=6

Similarity=0.841270

0 GAACAAAAGCCAGAAGATA-C-AAA-AAAACCGAATGACGAAGAC-

GCF_000715205.1_SOAPdenovo_v1.05_genomic.fna_11:26905-27400 Satlength=496

Nr of Repeats=11 RepeatLength=45 seed=AAGCCAGACG Num.seqs=11

Similarity=0.941818

5

GCAC-AAAGCCAGACGATAGCGAAACAAAACCGATGATCAAAACG

Rev.of_GCF_001895885.1_ASM189588v1_genomic.fna_1:3714696-3714876

Satlength=181 Nr of Repeats=5 RepeatLength=45 seed=TCTGGTTTTG Num.seqs=3

Similarity=0.637188

13

GTAC-AAAACCAGACGATAACGAAACAAAGCCGGATGACCAAAACG

* * * * *

Consensus:

GnACAAAgCCAGAcGATAnCgAAAcAAaCCggATGAccAAaACg

>Bacillus_Fam_318_40_3 Nr. of seq. 3 Alignment length(with gaps) = 43

Alignment score = 0.666667

GCF_000612805.1_FF3_genomic.fna_1:485384-485548 Satlength=165 Nr of

Repeats=4 RepeatLength=41 seed=AATTCGCAGA Num.seqs=4 Similarity=0.902439

0 AATTCGCAGATAAGTTAT-GAGAAACCGCAGATAACAC-GTGA

GCF_000612805.1_FF3_genomic.fna_6:82591-82851 Satlength=261 Nr of

Repeats=5 RepeatLength=41 seed=GAAATTCGCA Num.seqs=4 Similarity=0.951219

39 AATTCGCAGATAAATGGT-GA-AAACCGCAGATAACTCAGTGA

Rev.of_GCF_000612805.1_FF3_genomic.fna_2:681994-682158 Satlength=165 Nr

of Repeats=4 RepeatLength=41 seed=TATGACTTAT Num.seqs=4

Similarity=0.869919

19 AAAACGCAGATAAGTCATAGA-AATTCGCAGATAACTC-GGGG

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Consensus:

AAAttCGCAGATAAgTnaTGAAAcCGCAGATAActCGtGa

>Bacillus_Fam_319_39_3 Nr. of seq. 3 Alignment length(with gaps) = 42

Alignment score = 0.722222

GCF_000245315.1_ASM24531v1_genomic.fna_41:263357-263714 Satlength=358 Nr

of Repeats=9 RepeatLength=39 seed=ATAAAAAATC Num.seqs=6

Similarity=0.904274

0 ATAAAAAATCGTACTGTTCTCAC--AAGAGATCCCGCAGCC

GCF_001584325.1_ASM158432v1_genomic.fna_15:65449-65833 Satlength=385 Nr

of Repeats=10 RepeatLength=39 seed=CTCACAAAAG Num.seqs=8

Similarity=0.910867

18 ATAAAAAATCTTTCTGTTCTCAC--AAAAGATCTCGCAGCC

GCF_000245335.1_ASM24533v1_genomic.fna_3:546265-546469 Satlength=205 Nr
of Repeats=5 RepeatLength=42 seed=CGCAGCTACA Num.seqs=3
Similarity=0.894180
35 ACAAAAAGTCTTACTGCTCTCACAAGAAAAGATCACGCAGCT

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Consensus:

AtAAAAAaTcTtTaCTGtTCTCACAAaAGATCnCGCAGCc

>Bacillus_Fam_320_42_3 Nr. of seq. 3 Alignment length(with gaps) = 42
Alignment score = 0.978836

GCF_000161455.1_ASM16145v1_genomic.fna_1:840010-840472 Satlength=463 Nr
of Repeats=11 RepeatLength=42 seed=GCAGAAGAGA Num.seqs=11
Similarity=0.825108

GCAGAAGAGAAAAGTAGCAGAATTAAAACAGACGAAGCAAAAT

GCF_000161455.1_ASM16145v1_genomic.fna_1:840138-840729 Satlength=592 Nr
of Repeats=11 RepeatLength=42 seed=AGAAGAGAAA Num.seqs=8
Similarity=0.866213

2 GCAGAAGAGAAAAGTAGCAGAATTAAAACAGACGAAGCAAAAT

GCF_000712615.1_ASM71261v1_genomic.fna_24:59125-59698 Satlength=574 Nr of
Repeats=13 RepeatLength=42 seed=AGAAGAGAAA Num.seqs=10
Similarity=0.747306

2 GCAGAAGAGAAAAGTATCAGAATTAAAACAGACGAAGCAAAAT

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Consensus:

GCAGAAGAGAAAAGTAgCAGAATTAAAACAGACGAAGCAAAAT

>Bacillus_Fam_321_40_3 Nr. of seq. 3 Alignment length(with gaps) = 40
Alignment score = 0.766667

GCF_000374565.1_ASM37456v1_genomic.fna_1:446313-446554 Satlength=242 Nr
of Repeats=6 RepeatLength=40 seed=TAAGAGTATT Num.seqs=5
Similarity=0.886667

0 TAAGAGTATTTCCCTAATTCCGAAGAGTTTCCCGGCAAAGT

Rev.of_GCF_000374565.1_ASM37456v1_genomic.fna_3:243558-244159

Satlength=602 Nr of Repeats=15 RepeatLength=40 seed=GGATACTCTT

Num.seqs=14 Similarity=0.856410

31 TAAGAGTATTTCCGTTTTCCGAAGAGTATCCTCGCAAAGT

GCF_000374565.1_ASM37456v1_genomic.fna_15:92410-92570 Satlength=161 Nr of
Repeats=4 RepeatLength=40 seed=CAAAGTAAAG Num.seqs=4 Similarity=0.900406

34 AAAGAGTATTTCTGATTTCTGAAGAGTATTCACGCAAAGT

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Consensus:

tAAGAGTATTTCCgatTTCCGAAGAGTaTcCncGCAAAGT

>Bacillus_Fam_322_39_3 Nr. of seq. 3 Alignment length(with gaps) = 39
Alignment score = 0.863248

GCF_000007825.1_ASM782v1_genomic.fna_1:2224382-2224538 Satlength=157 Nr
of Repeats=4 RepeatLength=39 seed=ACGACACCTC Num.seqs=4

Similarity=0.982906
0 ACGACACCTCCAGCAAATAATGGAGGAGGTCAAGGAAAT
GCF_000008505.1_ASM850v1_genomic.fna_1:2199269-2199461 Satlength=193 Nr
of Repeats=5 RepeatLength=39 seed=GGTCAAGGAA Num.seqs=4
Similarity=0.937322
27 ACAACCCCTCCAGCAAATAACGGAGGAGGTCAAGGAAAT
Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_12:477757-477910
Satlength=154 Nr of Repeats=4 RepeatLength=39 seed=GCTGGAGGTG Num.seqs=3
Similarity=0.931624 14
ACACCACCTCCAGCGAATAACGGAGGAGGCCAAGGAAAT

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Consensus:

ACaCaCCTCCAGCaAATAAcGGAGGAGGtCAAGGAAAT

>Bacillus_Fam_323_39_3 Nr. of seq. 3 Alignment length(with gaps) = 39
Alignment score = 0.749288
GCF_000007845.1_ASM784v1_genomic.fna_1:4522244-4522556 Satlength=313 Nr
of Repeats=6 RepeatLength=39 seed=TCAGGGGCAA Num.seqs=4
Similarity=0.792361
0 TCAGGGGCAACAGAAACACTCTAAGCAAGACGACTCCGA
GCF_000008505.1_ASM850v1_genomic.fna_1:4519171-4519561 Satlength=391 Nr
of Repeats=10 RepeatLength=39 seed=TCTAAGCAAG Num.seqs=10
Similarity=0.822222 19
TCAAGGGCAACAGAAACACTCTAAGCAAGACGACTCCAA
Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_4:37147-37492
Satlength=346 Nr of Repeats=9 RepeatLength=39 seed=TGATTCTGAT Num.seqs=7
Similarity=0.873016 9
TCAGAATCAACAACAAAACCTCTAAACAAGACAACCTCGAA

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Consensus:

TCAggggCAACAgAaAcACTCTAAgCAAGACgACTCcaA

>Bacillus_Fam_324_36_3 Nr. of seq. 3 Alignment length(with gaps) = 36
Alignment score = 0.811728
GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_1:414507-414678
Satlength=172 Nr of Repeats=5 RepeatLength=33 seed=AAGAAACAAG Num.seqs=3
Similarity=0.919192 0 -
AAGAAACAAGAGGAAGCAAAAAAAGCTAGAAGAG--
Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:3533346-3533562
Satlength=217 Nr of Repeats=6 RepeatLength=36 seed=CTCTCTTCTA Num.seqs=6
Similarity=0.871605 0
TAAGAAGCAAGAAGAGGCGAAAAAGCTAGAAGAGAG
Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:4477135-4477387
Satlength=253 Nr of Repeats=7 RepeatLength=36 seed=CTCTCTTCTA Num.seqs=7
Similarity=0.890653 0
TAAGAAACAAGAAGAGGCGAAAAAGCTAGAAGAGAG

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Consensus:

tAAGAAaCAAGAAgAgGCgAAAAAgCTAGAAGAGag

>Bacillus_Fam_325_36_3 Nr. of seq. 3 Alignment length(with gaps) = 36
Alignment score = 0.969136
GCF_000706725.1_ASM70672v1_genomic.fna_1:1338140-1338448 Satlength=309 Nr
of Repeats=5 RepeatLength=36 seed=AATGCAACAA Num.seqs=4
Similarity=0.938272 0
AATGCAACAAGGGATGGGAGGAAACCACCATGCCCC
GCF_001420645.1_ASM142064v1_genomic.fna_39:121221-121545 Satlength=325 Nr
of Repeats=9 RepeatLength=36 seed=ATGCAACAAG Num.seqs=9
Similarity=0.903292 1
AATGCAACAAGGGATGGGAGGAAACCACCANGCCCC
Rev.of_GCF_002019765.1_ASM201976v1_genomic.fna_1:2724974-2725514
Satlength=541 Nr of Repeats=15 RepeatLength=36 seed=CCTTGTTGCA
Num.seqs=15 Similarity=0.918871
12 AATGCAACAAGGGATGGGAGGAAACCACCACGCCCC

Consensus:

AATGCAACAAGGGATGGGAGGAAACCACCAngCCCC

>Bacillus_Fam_326_34_3 Nr. of seq. 3 Alignment length(with gaps) = 35
Alignment score = 0.615873
GCF_000612805.1_FF3_genomic.fna_5:17272-17470 Satlength=199 Nr of
Repeats=6 RepeatLength=33 seed=CGACGAGTAA Num.seqs=6 Similarity=1.000000
0 CGACGAGTAATCGCAGGAGCATA--TGTTTTTTTG
Rev.of_GCF_000429725.1_ASM42972v1_genomic.fna_11:96592-96732
Satlength=141 Nr of Repeats=4 RepeatLength=35 seed=TGCTCCTGCG Num.seqs=4
Similarity=0.974603 21
CGACGAGTAATCGCAGGAGCAAACGGGCTGTGATG
Rev.of_GCF_000429725.1_ASM42972v1_genomic.fna_8:26322-26492 Satlength=171
Nr of Repeats=5 RepeatLength=34 seed=CTGCTCCTGC Num.seqs=5
Similarity=0.898039 22
CGACGAGGAAGCGCAGGAGCAGGC-GGTCTACATG

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Consensus:

CGACGAGtAAtCGCAGGAGCAnacgGtttttnaTG

>Bacillus_Fam_327_25_3 Nr. of seq. 3 Alignment length(with gaps) = 26
Alignment score = 0.846154
GCF_001274775.1_ASM127477v1_genomic.fna_5:147304-147704 Satlength=401 Nr
of Repeats=16 RepeatLength=25 seed=TTGTGCCTGG Num.seqs=16
Similarity=1.000000 0
TTGTGCCTGGCACCTTT-TCCCCTTT
GCF_001274775.1_ASM127477v1_genomic.fna_6:153795-153895 Satlength=101 Nr
of Repeats=4 RepeatLength=25 seed=CCTGGCACCT Num.seqs=4
Similarity=0.911111
5 TTGTACCTGGCACCTTT-TCCCCTTT
Rev.of_GCF_001274775.1_ASM127477v1_genomic.fna_11:335137-335437
Satlength=301 Nr of Repeats=12 RepeatLength=25 seed=AGGTGCCAGG

Num.seqs=12 Similarity=0.862179
14 -TGTGCCTGGCACCTTTCNCCCCTTT

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Consensus:

tTGTgCCTGGCACCTTTtCCCCCTT

>Bacillus_Fam_328_24_3 Nr. of seq. 3 Alignment length(with gaps) = 24
Alignment score = 0.759259
GCF_000161455.1_ASM16145v1_genomic.fna_1:230973-231201 Satlength=229 Nr of
Repeats=4 RepeatLength=24 seed=GAAACCGCCC Num.seqs=3
Similarity=0.925926
0 GAAACCGCCCATGCCCATACCGGG
GCF_000430785.1_ASM43078v1_genomic.fna_57:8024-8408 Satlength=385 Nr of
Repeats=16 RepeatLength=24 seed=CCCATTCCAG Num.seqs=16
Similarity=0.931481
13 GAAACCGCCCATGCCCATTCAGG
GCF_001636315.1_ASM163631v1_genomic.fna_1:5557193-5557289 Satlength=97 Nr
of Repeats=4 RepeatLength=24 seed=GGGTATCCAC Num.seqs=4
Similarity=0.888889 22
GTATCCACCCATGCCCATTGCTGG

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Consensus:

GaAaCCgCCCATGCCCATtcCnGG

>Bacillus_Fam_329_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.661836
GCF_000508325.1_BAVI_1_genomic.fna_8:115910-116014 Satlength=105 Nr of
Repeats=5 RepeatLength=21 seed=TTTACTGGCG Num.seqs=4 Similarity=0.589120
0 TTTACTGGCGGA-ATCCCCGAC-
Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_86:37292-37542 Satlength=251 Nr
of Repeats=11 RepeatLength=21 seed=CGCCAGTAAA Num.seqs=9
Similarity=0.611111 10
TTTACTGGCGGATANCGCC-AC-
GCF_001591665.1_ASM159166v1_genomic.fna_18:66724-66974 Satlength=251 Nr
of Repeats=12 RepeatLength=21 seed=TTTACTGGCG Num.seqs=11
Similarity=0.881097 0
TTTACTGGCGGATA-CNCC-TCT

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Consensus:

TTTACTGGCGGAtAnCnCCaC

>Bacillus_Fam_330_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.642512
GCF_000508325.1_BAVI_1_genomic.fna_48:16287-16371 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TGGCTATTTT Num.seqs=4 Similarity=0.640212
8 GAGGGTTATGGCTATTTT--CT
Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_27:88721-88805
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TAGACAAAAC Num.seqs=4

Similarity=0.600242 14
GAGNGTTTTGTCTATTTTT--AT
Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_15:54241-54325
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TAGCCATAAC Num.seqs=4
Similarity=0.612269 10
GTTATGGCTATTTTT-TNATGGA

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Consensus:

gttnTgtcTaTtTttntGagn

>Bacillus_Fam_331_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.671498
GCF_001591425.1_ASM159142v1_genomic.fna_97:20-272 Satlength=253 Nr of
Repeats=8 RepeatLength=21 seed=TTGGCACAA Num.seqs=5 Similarity=0.822222
19 TGGCACAAAAGCGA-ATC-CGGT
Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_138:7019-7720
Satlength=702 Nr of Repeats=7 RepeatLength=21 seed=CTTTTGCGCC Num.seqs=6
Similarity=0.801010 32
TGGCGCAAAAG-GT-ATCTCGGT
GCF_001591425.1_ASM159142v1_genomic.fna_193:37-142 Satlength=106 Nr of
Repeats=4 RepeatLength=21 seed=ATCTCGGTTG Num.seqs=3 Similarity=0.808081
35 TGGCGCAAAA--GTAATCTCGGT

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Consensus:

GTTGGCgCAAAAgGtATCtCG

>Bacillus_Fam_332_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.690821
GCF_001591665.1_ASM159166v1_genomic.fna_27:91341-91425 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTCGCAAATA Num.seqs=4 Similarity=0.661376
12 AAAACC-CTGA-TATTCGCAAAT
Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_3:0-84 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTGCGAATCT Num.seqs=4 Similarity=0.968254
19 AAAACC-ATCA-GATTCGCAAAT
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_46:16384-16468
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTTATTGCG Num.seqs=4
Similarity=0.607639 24
AAANCCTGTCATTATTCGCAAAT

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Consensus:

TTCGCAAATAAAaCCnTcAtA

>Bacillus_Fam_333_21_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.637681
GCF_001648575.1_ASM164857v1_genomic.fna_59:127044-127915 Satlength=872 Nr
of Repeats=19 RepeatLength=21 seed=TGACGGGATT Num.seqs=12
Similarity=0.566755 0
TGACGGGATTNTCT-TGNGTTG-

Rev.of_GCF_001648575.1_ASM164857v1_genomic.fna_61:125456-126083
Satlength=628 Nr of Repeats=10 RepeatLength=21 seed=AATCCCGTCA
Num.seqs=6 Similarity=0.385470
10 TGACGGGATTATCA-CGTGTTAN
GCF_001648575.1_ASM164857v1_genomic.fna_3:22935-23103 Satlength=169 Nr of
Repeats=5 RepeatLength=21 seed=TGACGGGATT Num.seqs=4 Similarity=0.391865
0 TGACGGGATTTTCTCCGANTTA-

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Consensus:

TGACGGGATTnTctcGngTTa

>Bacillus_Fam_334_23_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.647343
GCF_001484965.1_ASM148496v1_genomic.fna_5:31017-31101 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TCATACCGAC Num.seqs=4 Similarity=0.737374
0 TC-ATACCGACAAGAGCGAGCGT
GCF_001484965.1_ASM148496v1_genomic.fna_5:26815-26983 Satlength=169 Nr of
Repeats=8 RepeatLength=21 seed=CGGACAAGAG Num.seqs=8 Similarity=0.714286
6 TCNATACGGACAAGAGCGAGAGC
Rev.of_GCF_001484965.1_ASM148496v1_genomic.fna_11:871-997 Satlength=127
Nr of Repeats=6 RepeatLength=21 seed=TGTCCGATTG Num.seqs=6
Similarity=0.755556 11
TCAAT-CGGACAGGAGGNAGCGC

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Consensus:

TCnATaCgGACAaGAGcgAGcGc

>Bacillus_Fam_335_23_3 Nr. of seq. 3 Alignment length(with gaps) = 23
Alignment score = 0.743961
GCF_000612665.1_FF4_genomic.fna_55:18802-18886 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TATTTGCGAA Num.seqs=4 Similarity=0.552083
0 TATTTGCGAATTTCTTGCTNTT
Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_24:33836-33920
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATTCGCAAAT Num.seqs=4
Similarity=0.570602 11
TATTTGCGAATTACCTGGCNTTT
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_15:12666-12750
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTGCGAAATA Num.seqs=4
Similarity=0.469017 10
TATTTGCGAATTACNGNGNNTTT

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Consensus:

TATTTGCGAATTaCctnGcntTT

>Bacillus_Fam_336_20_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.676768
GCF_000008505.1_ASM850v1_genomic.fna_1:4488701-4488841 Satlength=141 Nr
of Repeats=7 RepeatLength=20 seed=TATATCGGCG Num.seqs=7

Similarity=0.662887
0 TATATCGGCGA-TTC-TCCATT
GCF_000007845.1_ASM784v1_genomic.fna_1:4493623-4493703 Satlength=81 Nr of
Repeats=4 RepeatLength=20 seed=TATATCGGCG Num.seqs=4 Similarity=0.567460
0 TATATCGGCGACATC-TCGATT
GCF_001636315.1_ASM163631v1_genomic.fna_1:11705-11788 Satlength=84 Nr of
Repeats=4 RepeatLength=21 seed=TTTATCGGCG Num.seqs=3 Similarity=0.504630
19 T-TATCGGCGA-TTCNTCGANT

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Consensus:

TaTATCGGCGAtTCTCgAtT

>Bacillus_Fam_337_20_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.651515

GCF_000285535.1_ASM28553v1_genomic.fna_2:498937-499757 Satlength=821 Nr
of Repeats=30 RepeatLength=20 seed=GACGCAAATA Num.seqs=19
Similarity=0.625341

0

GACGCAAAAAACCTNGT--GGN

Rev.of_GCF_000285535.1_ASM28553v1_genomic.fna_6:20567-21714
Satlength=1148 Nr of Repeats=52 RepeatLength=20 seed=TTTTTGCGTC
Num.seqs=41 Similarity=0.672416

10 GACGCAAAAAANCTCGGT--GGA

Rev.of_GCF_000285535.1_ASM28553v1_genomic.fna_2:814688-815514
Satlength=827 Nr of Repeats=13 RepeatLength=20 seed=TTTTTGCGTC
Num.seqs=8 Similarity=0.607143

10 GACGCAAAAAANNTTGGTCAGGA

* * * * *

Consensus:

GACGCAAAAAnccttgGTGGa

>Bacillus_Fam_338_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.732323

GCF_000401235.1_BacNeaAAU1_genomic.fna_89:3-145 Satlength=143 Nr of
Repeats=7 RepeatLength=20 seed=ATCAGCCAAA Num.seqs=5 Similarity=0.880000

0 ATCAGCCAAAGCAGCTG-G-AT

GCF_000401235.1_BacNeaAAU1_genomic.fna_88:17091-17236 Satlength=146 Nr of
Repeats=7 RepeatLength=21 seed=ATCAGCCAAA Num.seqs=5 Similarity=0.688889

0 ATCAGCCAAAGCAGNTGNG-AT

Rev.of_GCF_001591585.1_ASM159158v1_genomic.fna_21:35910-36015
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TTTGGCTGAT Num.seqs=5
Similarity=0.671212

10

ATCAGCCAAAGTAG-TGGGTAT

* * * * *

Consensus:

ATCAGCCAAAGcAGnTGnGAT

>Bacillus_Fam_339_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.772727

GCF_001591585.1_ASM159158v1_genomic.fna_12:54775-55019 Satlength=245 Nr
of Repeats=12 RepeatLength=20 seed=TTGGCTGAT Num.seqs=8
Similarity=0.681159
0 -TTGGCTGATTTCTCCTTCCG-
GCF_001591585.1_ASM159158v1_genomic.fna_3:245600-245705 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=TTTGGCTGAT Num.seqs=5
Similarity=0.629167
0 TTTGGCTGATTTCTCC-TCCGC
GCF_001591585.1_ASM159158v1_genomic.fna_25:28599-28911 Satlength=313 Nr
of Repeats=15 RepeatLength=21 seed=TTGGCTGATA Num.seqs=13
Similarity=0.736264
TTTGGCTGATTTCCCC-TCCAC

1

***** ** **

Consensus:

tTTGGCTGATTTCTCCTCCgc

>Bacillus_Fam_340_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.616162
GCF_001877785.1_PlanoSAMM_genomic.fna_106:177497-177577 Satlength=81 Nr
of Repeats=4 RepeatLength=20 seed=AATGGATCAT Num.seqs=4
Similarity=0.755556
0 AATGGATCATAAA-TCTCAA-
GCF_001315085.1_ASM131508v1_genomic.fna_1:3481-3565 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=GGATCATAAA Num.seqs=4 Similarity=0.458333
3 GTTGGATCATAAA-TCCGCAAT
GCF_001315085.1_ASM131508v1_genomic.fna_3:99320-99404 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=GGATCATAAA Num.seqs=4 Similarity=0.518519
3 TCTGGATCATAAATTATCNAAT

***** * **

Consensus:

nnTGGATCATAAATctccAAt

>Bacillus_Fam_341_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.727273
GCF_000025805.1_ASM2580v1_genomic.fna_1:339971-340130 Satlength=160 Nr of
Repeats=5 RepeatLength=21 seed=ACTCCTATAA Num.seqs=3 Similarity=0.703704
0 ACTCCTATAATAAAAANNA-TA
Rev.of_GCF_000225265.1_ASM22526v1_genomic.fna_1:4636885-4637044
Satlength=160 Nr of Repeats=6 RepeatLength=21 seed=TTATTATAGG Num.seqs=4
Similarity=0.592172 13
ACTCCTATAATAAAGACGG-TA
Rev.of_GCF_001591565.1_ASM159156v1_genomic.fna_136:5321-5468
Satlength=148 Nr of Repeats=4 RepeatLength=21 seed=TTTATTATAG Num.seqs=3
Similarity=0.585859 13
-CTCCTATAATAAAATGANTA

***** * **

Consensus:

aCTCCTATAATAAAaAngaTA

>Bacillus_Fam_342_22_3 Nr. of seq. 3 Alignment length(with gaps) = 22
 Alignment score = 0.636364
 GCF_000307875.1_BABA1.0_genomic.fna_55:48119-48266 Satlength=148 Nr of
 Repeats=7 RepeatLength=21 seed=TTTGGCGGAA Num.seqs=7 Similarity=0.547619
 0 TTTGGCGGAATTACCANTCNA-
 Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_36:99463-99691
 Satlength=229 Nr of Repeats=10 RepeatLength=21 seed=ATTCCGCCAA
 Num.seqs=9 Similarity=0.427298
 11 TTTGGCGGAATT-CCAANNAAG
 Rev.of_GCF_001591445.1_ASM159144v1_genomic.fna_22:36726-36903
 Satlength=178 Nr of Repeats=6 RepeatLength=21 seed=ATTCCGCCAA Num.seqs=5
 Similarity=0.479710 11
 TTTGGCGGAATNNCTNNTNAAG

***** * *
 Consensus:

TTTGGCGGAATtnCcantnaAg

>Bacillus_Fam_343_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
 Alignment score = 0.737374
 GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:292889-293098
 Satlength=210 Nr of Repeats=9 RepeatLength=21 seed=ATACGGGAGT Num.seqs=8
 Similarity=0.638975 0
 ATACGAGAGTAATC-CACTCCT
 GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_16:9832-10553
 Satlength=722 Nr of Repeats=28 RepeatLength=21 seed=TTTACGAGAG
 Num.seqs=21 Similarity=0.773243
 19 -TACGAGAGTAANCGCACTCTT
 GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_33:58692-58944
 Satlength=253 Nr of Repeats=12 RepeatLength=21 seed=TTACGGGAGT
 Num.seqs=12 Similarity=0.844156
 20 -TACGGGAGTAACCGCACTCGT

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 Consensus:

TACGaGAGTAAnCgCACTCnT

>Bacillus_Fam_344_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
 Alignment score = 0.747475
 GCF_001484965.1_ASM148496v1_genomic.fna_1:76098-76366 Satlength=269 Nr of
 Repeats=13 RepeatLength=21 seed=CTTGAGCGGT Num.seqs=9
 Similarity=0.771886
 0 CTTGAGCGGTATCTCCCTCN-
 Rev.of_GCF_001484965.1_ASM148496v1_genomic.fna_32:15969-16073
 Satlength=105 Nr of Repeats=5 RepeatLength=21 seed=TACCGCTCAA Num.seqs=4
 Similarity=0.773990 11
 CTTGAGCGGTAT-TCTCCTCCG
 GCF_001484965.1_ASM148496v1_genomic.fna_37:19197-19446 Satlength=250 Nr
 of Repeats=12 RepeatLength=21 seed=CTTGAGCGGT Num.seqs=9
 Similarity=0.700176
 21 CTTGAGCGGTAT-TCNGCTCCT

***** ** ***

Consensus:

CTTGAGCGGTATTcncCTCcn

>Bacillus_Fam_345_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.727273

GCF_001578185.1_ASM157818v1_genomic.fna_1:3660606-3660924 Satlength=319
Nr of Repeats=13 RepeatLength=21 seed=ATGAACTGCT Num.seqs=8
Similarity=0.952381 0

ATGAACTGCTGCT-TTCGTCTG

GCF_002019665.1_ASM201966v1_genomic.fna_1:3758998-3759208 Satlength=211
Nr of Repeats=10 RepeatLength=21 seed=CTATTCGTCG Num.seqs=10
Similarity=0.957672 10

-TTAACCACTGCTATTTCGTCCG

GCF_002019665.1_ASM201966v1_genomic.fna_1:3759021-3759394 Satlength=374
Nr of Repeats=18 RepeatLength=21 seed=ATTCGTCCGGT Num.seqs=13
Similarity=0.766900 12

-TTAACCACTGCTATTTCGTCCG

* *** ***** *

Consensus:

TtAACCaCTGCTaTTCGTcGg

>Bacillus_Fam_346_21_3 Nr. of seq. 3 Alignment length(with gaps) = 22
Alignment score = 0.631313

GCF_900156865.1_PRJEB18960_genomic.fna_3:2989497-2989758 Satlength=262 Nr
of Repeats=8 RepeatLength=21 seed=TGTCCCATAT Num.seqs=5
Similarity=0.533333 0

TGTCCCATATAATNGAAGTTN-

Rev.of_GCF_900156865.1_PRJEB18960_genomic.fna_3:3020484-3021148

Satlength=665 Nr of Repeats=13 RepeatLength=21 seed=TTTATGGGAC

Num.seqs=10 Similarity=0.606280

11 TGTCCCATAAANTCCAAGTAN-

Rev.of_GCF_900156865.1_PRJEB18960_genomic.fna_3:3235322-3235665

Satlength=344 Nr of Repeats=9 RepeatLength=21 seed=TTTATGGGAC Num.seqs=7

Similarity=0.541667 11

TGTCCCATATAATCGAATTNTN

***** * * ** *

Consensus:

TGTCCCATAnAaTcgAAgTnn

>Bacillus_Fam_347_18_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.767196

GCF_000430785.1_ASM43078v1_genomic.fna_5:28845-28989 Satlength=145 Nr of
Repeats=8 RepeatLength=18 seed=CCAGGAGCAG Num.seqs=8 Similarity=0.941799
0 CCAGGAGCAGGCTTTGGC---

GCF_000430785.1_ASM43078v1_genomic.fna_5:28846-29137 Satlength=292 Nr of
Repeats=9 RepeatLength=18 seed=CAGGAGCAGG Num.seqs=8 Similarity=0.941799

1 CCAGGAGCAGGCTTTGGC---

GCF_001636345.1_ASM163634v1_genomic.fna_1:1975200-1975335 Satlength=136
Nr of Repeats=5 RepeatLength=21 seed=CAGGACCAGG Num.seqs=4
Similarity=0.788360 1
CCAGGACCAGGNTTTGGCACT

***** *****

Consensus:

CCAGGAgCAGGcTTTGGC

>Bacillus_Fam_348_20_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.708995
GCF_001273755.1_ASM127375v1_genomic.fna_17:4571297-4571397 Satlength=101
Nr of Repeats=4 RepeatLength=20 seed=GTAGGACGAA Num.seqs=3
Similarity=0.717172 0
GTAGGACGAATTATTC-GCGT
Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:4465368-4465568
Satlength=201 Nr of Repeats=6 RepeatLength=20 seed=GCAAATATTT Num.seqs=4
Similarity=0.866667 18
GTAGGTCGAAATATTT-GCGT
GCF_001578185.1_ASM157818v1_genomic.fna_1:3658103-3658186 Satlength=84 Nr
of Repeats=4 RepeatLength=21 seed=AGGACGAATT Num.seqs=3
Similarity=0.788360 2
GAAGGACGAATTATTTGGTGT

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Consensus:

GtAGGaCGAAtTATTTGcGT

>Bacillus_Fam_349_20_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.687831
GCF_001439915.1_ASM143991v1_genomic.fna_84:184831-184911 Satlength=81 Nr
of Repeats=4 RepeatLength=20 seed=ACTGTCACTA Num.seqs=4
Similarity=0.646825
0 ACTGTCACT-ATCCGCAAAAT
GCF_001439915.1_ASM143991v1_genomic.fna_124:109637-109717 Satlength=81 Nr
of Repeats=4 RepeatLength=20 seed=TACTGTCACT Num.seqs=4
Similarity=0.678571 19
ACTGTCACT-ATTCCNAAAAT
Rev.of_GCF_900156865.1_PRJEB18960_genomic.fna_3:2916495-2916575
Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=AGTGGCAGTA Num.seqs=4
Similarity=0.629630 9
ACTGCCACTAATNTCTAAAAT

**** *****

Consensus:

ACTGtCACTATnccnAAAAT

>Bacillus_Fam_350_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.687831

GCF_001591425.1_ASM159142v1_genomic.fna_4:87634-87736 Satlength=103 Nr of Repeats=5 RepeatLength=20 seed=TTTATTTGCG Num.seqs=3 Similarity=0.688889
0 TTTATTTGCGATAA-TACGCC
GCF_001591425.1_ASM159142v1_genomic.fna_176:0-79 Satlength=80 Nr of Repeats=4 RepeatLength=20 seed=TTTATTTGCG Num.seqs=4 Similarity=1.000000
0 TTTATTTGCGATAACTACGT-
Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_108:14449-14552
Satlength=104 Nr of Repeats=5 RepeatLength=21 seed=CGCAAATAAG Num.seqs=3
Similarity=0.915344 10
CTTATTTGCGATACCTTCATC

***** * *

Consensus:

tTTATTTGCGATAAcTaCgtc

>Bacillus_Fam_351_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.957672
GCF_000008505.1_ASM850v1_genomic.fna_1:3003849-3004059 Satlength=211 Nr of Repeats=10 RepeatLength=21 seed=GCCAACCACC Num.seqs=10
Similarity=0.887125 0
GCCAACCACCGTGTCCGCCTT
GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_1:1982219-1982366
Satlength=148 Nr of Repeats=7 RepeatLength=21 seed=GCCAACCACC Num.seqs=7
Similarity=0.873016 0
GCCAACCACCGTGTCCGCCTT
Rev.of_GCF_001645555.1_ASM164555v1_genomic.fna_51:17837-18077
Satlength=241 Nr of Repeats=11 RepeatLength=21 seed=GGTGGTTGGC
Num.seqs=10 Similarity=0.815168
10 GCCAACCACCGTGTCCACCTT

***** ****

Consensus:

GCCAACCACCGTGTCCgCCTT

>Bacillus_Fam_352_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.788360
GCF_000025825.1_ASM2582v1_genomic.fna_1:1391429-1391846 Satlength=418 Nr of Repeats=24 RepeatLength=21 seed=AGAACGGCGA Num.seqs=15
Similarity=0.824641 0
AGAACGGCGAGTACCGCGGGT
Rev.of_GCF_000225265.1_ASM22526v1_genomic.fna_1:3576340-3576466
Satlength=127 Nr of Repeats=5 RepeatLength=21 seed=CGTTCTACTC Num.seqs=4
Similarity=0.894180 6
AGAACGACGAGACGGCGAGT
GCF_000956595.1_ASM95659v1_genomic.fna_23:54484-54736 Satlength=253 Nr of Repeats=11 RepeatLength=21 seed=GAGAGCGGCG Num.seqs=10
Similarity=0.952028
8 AGAACGGCGAGAGCGGCGAGT

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

Consensus:

AGAACGgCGAGagCgGCGaGT

>Bacillus_Fam_353_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.661376
GCF_000813125.1_ASM81312v1_genomic.fna_62:25438-25563 Satlength=126 Nr of
Repeats=5 RepeatLength=21 seed=ATTCCGCGAA Num.seqs=4 Similarity=0.513228
0 ATTCCGCGAAAACCGAGCGGA
Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_86:16754-16838 Satlength=85
Nr of Repeats=4 RepeatLength=21 seed=TTTCGCGGAAT Num.seqs=4
Similarity=0.452899 10
ATTCCGCGAAATCTGAGNTTA
Rev.of_GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_19:24896-25042
Satlength=147 Nr of Repeats=6 RepeatLength=21 seed=TTTCGCGGGA Num.seqs=5
Similarity=0.576389 11 ATCCCGCGAAANNAGAGTNGA

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Consensus:

ATtCCGCGAAAncnGAGnngA

>Bacillus_Fam_354_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.756614
GCF_000948175.1_BFA_2_A_genomic.fna_17:13637-13721 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=AACCGAGAGAGA Num.seqs=4 Similarity=0.591435
0 AACCGAGAGAATAAGGTCNGA
Rev.of_GCF_000948175.1_BFA_2_A_genomic.fna_166:2351-2477 Satlength=127 Nr
of Repeats=6 RepeatLength=21 seed=TCTCTCGGTT Num.seqs=6
Similarity=0.708081 10
AACCGAGAGATTAAGTGCTGA
Rev.of_GCF_000948175.1_BFA_2_A_genomic.fna_190:1516-1684 Satlength=169 Nr
of Repeats=8 RepeatLength=21 seed=TCTCTCGGTT Num.seqs=8
Similarity=0.793651 10
AACCGAGAGATTAATGGCTGG

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

AACCGAGAGAtTAaggGcTga

>Bacillus_Fam_355_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21
Alignment score = 0.788360
GCF_001484965.1_ASM148496v1_genomic.fna_6:66041-66125 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=GATGTGAGAG Num.seqs=4 Similarity=0.765152
0 GATGTGAGAGAGAAGAGCGCG
Rev.of_GCF_001484965.1_ASM148496v1_genomic.fna_16:33130-33410
Satlength=281 Nr of Repeats=10 RepeatLength=21 seed=TCTCTCGCAT
Num.seqs=6 Similarity=0.847619
11 GATGCGAGAGAGAAGAGCTCG
GCF_001484965.1_ASM148496v1_genomic.fna_26:28029-28279 Satlength=251 Nr
of Repeats=10 RepeatLength=21 seed=GGATGTGAGC Num.seqs=7
Similarity=0.848828
20 GATGTGAGCAAGAAGGGCGCG

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Consensus:

GATGtGAGagAGAAGaGCgCG

>Bacillus_Fam_356_21_3 Nr. of seq. 3 Alignment length(with gaps) = 21

Alignment score = 0.671958

GCF_001591445.1_ASM159144v1_genomic.fna_22:68731-68836 Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=ATTCCGCCAA Num.seqs=5

Similarity=0.476812

0 ATTCCGCCAANTTCGNNNTGN

GCF_001591445.1_ASM159144v1_genomic.fna_33:29-282 Satlength=254 Nr of

Repeats=9 RepeatLength=21 seed=ATTCCGCCAA Num.seqs=8 Similarity=0.493271

0 ATTCCGCCAACTTNGGANNNGN

Rev.of_GCF_001591445.1_ASM159144v1_genomic.fna_32:27469-27574

Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=5

Similarity=0.454167

10

ATTCCGCCAACTNTGGAAGNN

***** * ** *

Consensus:

ATTCCGCCAAcTtnGGanngN

>Bacillus_Fam_357_20_3 Nr. of seq. 3 Alignment length(with gaps) = 20

Alignment score = 0.711111

GCF_001439915.1_ASM143991v1_genomic.fna_105:322815-322955 Satlength=141

Nr of Repeats=7 RepeatLength=20 seed=GACGCAAATA Num.seqs=7

Similarity=0.525132

0

GACGCAAATATCGTGAAN--

GCF_001439915.1_ASM143991v1_genomic.fna_83:505700-505820 Satlength=121 Nr of

Repeats=6 RepeatLength=20 seed=ACGCAAATAT Num.seqs=6

Similarity=0.600529

1

GACGCAAATATTGTGAAACT

GCF_001877785.1_PlanoSAMM_genomic.fna_117:26443-26710 Satlength=268 Nr of

Repeats=5 RepeatLength=20 seed=GGCGCAATTA Num.seqs=3 Similarity=0.600000

20 GGCGCAATTATTATGAAACT

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

Consensus:

GaCGCAAaTATtgTGAAact

>Bacillus_Fam_358_20_3 Nr. of seq. 3 Alignment length(with gaps) = 20

Alignment score = 0.877778

GCF_000374565.1_ASM37456v1_genomic.fna_5:154921-155692 Satlength=772 Nr of

Repeats=32 RepeatLength=20 seed=CTCGTATAAA Num.seqs=21

Similarity=0.707937

0

CTCGTATAAAAGCTNCAACT

Rev.of_GCF_000374565.1_ASM37456v1_genomic.fna_7:0-79 Satlength=80 Nr of

Repeats=4 RepeatLength=20 seed=TATGTGAGTT Num.seqs=4 Similarity=1.000000

6 CACATATAAAAGCTCCAAC

GCF_000374565.1_ASM37456v1_genomic.fna_33:0-79 Satlength=80 Nr of
Repeats=4 RepeatLength=20 seed=TAAAAGCTCC Num.seqs=4 Similarity=1.000000
6 CACATATAAAAAGCTCCAAC

* * ***** *

Consensus:

CaCaTATAAAAAGCTcCAACT

>Bacillus_Fam_359_20_3 Nr. of seq. 3 Alignment length(with gaps) = 20
Alignment score = 0.788889
GCF_000612665.1_FF4_genomic.fna_33:10627-10708 Satlength=82 Nr of
Repeats=4 RepeatLength=20 seed=TATCGGGAAA Num.seqs=3 Similarity=0.629630
0 TATCGGGAAAANATTNAATA
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_151:505712-505793
Satlength=82 Nr of Repeats=4 RepeatLength=20 seed=TCCTGATAT Num.seqs=3
Similarity=0.644444 9
TATCAGGAAAAATTTCAATA
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_153:106295-106375
Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=CTGATATATT Num.seqs=4
Similarity=0.731481 26
TATCAGGAAAAATNAAATA

**** ***** *

Consensus:

TATCaGGAAAAaaTtnAATA

>Bacillus_Fam_360_18_3 Nr. of seq. 3 Alignment length(with gaps) = 18
Alignment score = 0.703704
GCF_000175075.1_ASM17507v1_genomic.fna_6:61019-61091 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=GGCGGTCTCTG Num.seqs=4 Similarity=0.962963
0 GGCGGTCTCTGGCTTCGGT
GCF_002019665.1_ASM201966v1_genomic.fna_1:3587353-3587695 Satlength=343
Nr of Repeats=19 RepeatLength=18 seed=GGTGGACCAG Num.seqs=19
Similarity=0.984405 0
GGTGGACCAGGTTCGGT
GCF_001648575.1_ASM164857v1_genomic.fna_62:119312-119492 Satlength=181 Nr
of Repeats=10 RepeatLength=18 seed=TTCTGGTGGTG Num.seqs=10
Similarity=0.795885 12
GGTGCACCGGGATTTCGGT

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

Consensus:

GGtGgaCCnGGnTTCGGT

>Bacillus_Fam_361_18_3 Nr. of seq. 3 Alignment length(with gaps) = 18
Alignment score = 0.746914
GCF_001439635.1_ASM143963v1_genomic.fna_162:551140-551212 Satlength=73 Nr
of Repeats=4 RepeatLength=18 seed=TCAGCAGTAG Num.seqs=4
Similarity=0.802469 0
TCAGCAGTAGAATCAGAA

Rev.of_GCF_001439635.1_ASM143963v1_genomic.fna_174:69602-72152
Satlength=2551 Nr of Repeats=124 RepeatLength=18 seed=CTACTGCTGA
Num.seqs=113 Similarity=0.785902
10 TCAGCAGTAGAGTCNGCG
Rev.of_GCF_001439635.1_ASM143963v1_genomic.fna_174:69602-72528
Satlength=2927 Nr of Repeats=142 RepeatLength=18 seed=CTACTGCTGA
Num.seqs=129 Similarity=0.788123
10 TCAGCAGTAGCGTCNGCG

***** ** *

Consensus:

TCAGCAGTAGagTCnGcg

>Bacillus_Fam_362_18_3 Nr. of seq. 3 Alignment length(with gaps) = 18
Alignment score = 0.679012
GCF_002019595.1_ASM201959v1_genomic.fna_1:3913094-3913256 Satlength=163
Nr of Repeats=9 RepeatLength=18 seed=TGCTCATGAT Num.seqs=9
Similarity=0.759259 0
TGCTCATGATGGTGGTCA
GCF_002019635.1_ASM201963v1_genomic.fna_2:1628719-1628809 Satlength=91 Nr
of Repeats=5 RepeatLength=18 seed=TGCTCATGAT Num.seqs=5
Similarity=0.866667 0
TGCTCATGATGATGTTCA
GCF_002019645.1_ASM201964v1_genomic.fna_1:4893349-4893781 Satlength=433
Nr of Repeats=24 RepeatLength=18 seed=ATGTGAATGA Num.seqs=24
Similarity=0.927805 17
TGTGAATGATCGTGATCA

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

Consensus:

TGctcATGATggTGnTCA

>Bacillus_Fam_363_16_3 Nr. of seq. 3 Alignment length(with gaps) = 16
Alignment score = 0.722222
GCF_000177235.2_ASM17723v2_genomic.fna_1:1028903-1029101 Satlength=199 Nr
of Repeats=5 RepeatLength=16 seed=AACCCGGGTT Num.seqs=3
Similarity=0.888889 0
AACCCGGGTTAAAGCG
GCF_000177235.2_ASM17723v2_genomic.fna_1:1630177-1630375 Satlength=199 Nr
of Repeats=5 RepeatLength=16 seed=GAACCCGGGT Num.seqs=3
Similarity=0.944444 15
AACCCGGGTTAGTGGG
Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:3834979-3835177
Satlength=199 Nr of Repeats=5 RepeatLength=16 seed=GAACCCGGGT Num.seqs=3
Similarity=0.888889 11
AACCCGGGTTCAAGGT

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Consensus:

AACCCGGGTTaaaGgg

>Bacillus_Fam_364_15_3 Nr. of seq. 3 Alignment length(with gaps) = 15
Alignment score = 0.762963
GCF_000307875.1_BABA1.0_genomic.fna_140:27298-27463 Satlength=166 Nr of
Repeats=11 RepeatLength=15 seed=GTATTTCTTC Num.seqs=11
Similarity=0.844849
0 GTATTTCTTCTTGAG
GCF_000706725.1_ASM70672v1_genomic.fna_1:3260718-3261542 Satlength=825 Nr
of Repeats=4 RepeatLength=15 seed=CTTCTTTTGG Num.seqs=3
Similarity=1.000000 6
GTTTTTCTTCTTTG
GCF_001591465.1_ASM159146v1_genomic.fna_27:2859-2976 Satlength=118 Nr of
Repeats=7 RepeatLength=15 seed=GGTTTTTCTT Num.seqs=6 Similarity=0.774815
14 GTTTTTCTTCCTTAG

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Consensus:

GTtTTTCTTCTtTaG

>Bacillus_Fam_365_15_3 Nr. of seq. 3 Alignment length(with gaps) = 15
Alignment score = 0.837037
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_28:32586-32916 Satlength=331 Nr of Repeats=22
RepeatLength=15 seed=TCTGTTTTTT Num.seqs=22 Similarity=0.810651 0
TCTGTTTTTTCTACN
GCF_000831065.1_ASM83106v1_genomic.fna_1:4247809-4248064 Satlength=256 Nr
of Repeats=17 RepeatLength=15 seed=TCTGGTTTTTT Num.seqs=17
Similarity=0.926797 0
TCTGGTTTTTTCTACT
Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:1426778-1426853
Satlength=76 Nr of Repeats=5 RepeatLength=15 seed=CCAGAAGTAG Num.seqs=5
Similarity=0.893333 5
TCTGGTTTCTCTACT

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Consensus:

TCTGgTTTtTCTACT

>Bacillus_Fam_366_15_3 Nr. of seq. 3 Alignment length(with gaps) = 15
Alignment score = 0.755556
GCF_000706725.1_ASM70672v1_genomic.fna_1:1313522-1313585 Satlength=64 Nr
of Repeats=4 RepeatLength=15 seed=TCTTCATCAG Num.seqs=3
Similarity=0.881481
0 TCTTCATCAGTTGTG
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_16:18981-19722
Satlength=742 Nr of Repeats=28 RepeatLength=15 seed=CTGAAGAAGA
Num.seqs=23 Similarity=0.787879
10 TCTTCTTCAGTNACG
Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_16:18981-20088
Satlength=1108 Nr of Repeats=33 RepeatLength=15 seed=CTGAAGAAGA
Num.seqs=23 Similarity=0.787879
10 TCTTCTTCAGTNACG

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Consensus:

TCTTCTTCAGTnacG

>Bacillus_Fam_367_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12

Alignment score = 0.675926

GCF_000832605.1_ASM83260v1_genomic.fna_1:4152867-4152911 Satlength=45 Nr

of Repeats=4 RepeatLength=11 seed=TCCTTTGTTA Num.seqs=4

Similarity=1.000000

0 TCCTTTGTAT-

Rev.of_GCF_000331575.1_ASM33157v1_genomic.fna_1:1646263-1646335

Satlength=73 Nr of Repeats=6 RepeatLength=12 seed=TAAGAAAATA Num.seqs=6

Similarity=0.940741

6

TTCTTAGTTATT

GCF_001274935.1_ASM127493v1_genomic.fna_42:123528-124032 Satlength=505 Nr

of Repeats=4 RepeatLength=12 seed=TTTACTTTGT Num.seqs=3

Similarity=1.000000

10

TACTTTGTCATT

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Consensus:

TnCTTtGTtAtT

>Bacillus_Fam_368_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12

Alignment score = 0.666667

GCF_000007825.1_ASM782v1_genomic.fna_1:4742290-4742338 Satlength=49 Nr of

Repeats=4 RepeatLength=12 seed=ATTGAAAAAG Num.seqs=4 Similarity=0.944444

0 ATTGAAAAAGGC

GCF_000007845.1_ASM784v1_genomic.fna_1:4598687-4598747 Satlength=61 Nr of

Repeats=5 RepeatLength=12 seed=AAGGTATAGA Num.seqs=5 Similarity=0.933333

7 ATAGAACAAGGT

Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_7:48950-49010 Satlength=61

Nr of Repeats=4 RepeatLength=12 seed=CCTTCTTTTA Num.seqs=3

Similarity=0.650794

11

ATAAAAGAAGGT

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Consensus:

ATagAAnAAGGt

>Bacillus_Fam_369_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12

Alignment score = 0.777778

GCF_000196735.1_ASM19673v1_genomic.fna_1:2209405-2209513 Satlength=109 Nr

of Repeats=9 RepeatLength=12 seed=GCTGCTGCAA Num.seqs=9

Similarity=0.944444

0

GCTGCTGCAACG

GCF_000204275.1_ASM20427v1_genomic.fna_1:2293892-2294000 Satlength=109 Nr

of Repeats=9 RepeatLength=12 seed=GCTGCTGCAA Num.seqs=9

Similarity=0.944444

0

GCTGCTGCAACG

GCF_000321185.1_ASM32118v1_genomic.fna_45:7876-8053 Satlength=178 Nr of Repeats=8 RepeatLength=12 seed=CTACTGCTGC Num.seqs=5 Similarity=0.911111
7 GCTGCTACTACT

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Consensus:

GCTGCTgCaACg

>Bacillus_Fam_370_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
Alignment score = 0.888889

GCF_000401235.1_BacNeaAAU1_genomic.fna_107:6849-6933 Satlength=85 Nr of Repeats=6 RepeatLength=12 seed=CCAGGAGAAG Num.seqs=5 Similarity=0.955556
0 CCAGGAGAAGAA

Rev.of_GCF_001648575.1_ASM164857v1_genomic.fna_60:146867-146939
Satlength=73 Nr of Repeats=6 RepeatLength=12 seed=GGTTCTTCAC Num.seqs=6
Similarity=0.881481 2

CCAGGTGAAGAA

Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:4130554-4130638
Satlength=85 Nr of Repeats=7 RepeatLength=12 seed=CCTGGTTCTT Num.seqs=7
Similarity=0.873016 5

CCAGGCGAAGAA

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Consensus:

CCAGGnGAAGAA

>Bacillus_Fam_371_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
Alignment score = 0.777778

GCF_000615945.1_ASM61594v1_genomic.fna_89:34464-35479 Satlength=1016 Nr of Repeats=5 RepeatLength=12 seed=CACCAACACC Num.seqs=3
Similarity=1.000000

0 CACCAACACCAA

Rev.of_GCF_001307105.1_ASM130710v1_genomic.fna_12:24340-24400
Satlength=61 Nr of Repeats=5 RepeatLength=12 seed=TGTTGGTGCT Num.seqs=5
Similarity=1.000000 2

CAACAGCACCAA

GCF_002019645.1_ASM201964v1_genomic.fna_1:657555-657687 Satlength=133 Nr of Repeats=11 RepeatLength=12 seed=GCACCGACAC Num.seqs=11
Similarity=0.963636 5

CACCAGCACCGA

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Consensus:

CACcAgCACCaA

>Bacillus_Fam_372_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
Alignment score = 1.000000

GCF_001273755.1_ASM127375v1_genomic.fna_17:544037-544637 Satlength=601 Nr of Repeats=50 RepeatLength=12 seed=CCGTAACCGC Num.seqs=50
Similarity=1.000000 0

CCGTAACCGCCG

GCF_001273755.1_ASM127375v1_genomic.fna_17:1499377-1499425 Satlength=49
Nr of Repeats=4 RepeatLength=12 seed=CCGTAACCGC Num.seqs=4
Similarity=1.000000 0
CCGTAACCGCCG
GCF_001584325.1_ASM158432v1_genomic.fna_41:69109-69169 Satlength=61 Nr of
Repeats=5 RepeatLength=12 seed=CCGTAACCGC Num.seqs=5 Similarity=1.000000
0 CCGTAACCGCCG

Consensus:

CCGTAACCGCCG

>Bacillus_Fam_373_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
Alignment score = 0.777778
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:1155105-1155231
Satlength=127 Nr of Repeats=8 RepeatLength=12 seed=TGGCCCTGAC Num.seqs=6
Similarity=0.844444 0
TGGCCCTGACCT
GCF_001591425.1_ASM159142v1_genomic.fna_5:37834-37894 Satlength=61 Nr of
Repeats=4 RepeatLength=12 seed=CCTTGCCCTT Num.seqs=3 Similarity=0.925926
3 TGACCTTGCCCT
GCF_001591805.1_ASM159180v1_genomic.fna_7:139777-139831 Satlength=55 Nr
of Repeats=4 RepeatLength=12 seed=TTGACCTTGA Num.seqs=3
Similarity=0.777778
5 TGACCTTGACCT

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Consensus:

TGACCTTGACCT

>Bacillus_Fam_374_12_3 Nr. of seq. 3 Alignment length(with gaps) = 12
Alignment score = 0.777778
GCF_001591465.1_ASM159146v1_genomic.fna_69:93-309 Satlength=217 Nr of
Repeats=17 RepeatLength=12 seed=GAAGCAGAAG Num.seqs=15
Similarity=0.835979
0 GAAGCAGAAGCA
Rev.of_GCF_001591465.1_ASM159146v1_genomic.fna_75:8-188 Satlength=181 Nr
of Repeats=13 RepeatLength=12 seed=TCTGCTTCTG Num.seqs=9
Similarity=0.824074 2
GAAGCAGAAGCA
Rev.of_GCF_001654695.1_ASM165469v1_genomic.fna_3:76041-76089 Satlength=49
Nr of Repeats=4 RepeatLength=12 seed=TTCTGATTCA Num.seqs=4
Similarity=1.000000 3
GAAACTGAATCA

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Consensus:

GAAgCaGAAgCA

>Bacillus_Fam_375_240_2 Nr. of seq. 2 Alignment length(with gaps) = 240
Alignment score = 0.920833

GCF_001645705.1_ASM164570v1_genomic.fna_61:170578-171538 Satlength=961 Nr of Repeats=4 RepeatLength=240 seed=GGTTGGGCGA Num.seqs=4
Similarity=0.727375 0

GGTTGGGCGAAAGTGAATGTAAATGGGAAAACAGGATATGTAAGTAGTCAGTATTTAACAGGCAAGACGAACA
CAGCCCCANCAAAAACCATCTACATCCACACCAGCAAAGACGGAAACAAAATATGTATCTGTAACTCAGGTTC
TATTTTGAATCTACGCAGTAGTGCCAGTACAAGTGCATCAATAATCGGGAACCTATCAAATGGCACAGCGGTA
ACGGTTCAATCAGATTCCAAA

GCF_001645705.1_ASM164570v1_genomic.fna_61:170794-172355 Satlength=1562
Nr of Repeats=7 RepeatLength=240 seed=GTAACGGTTC Num.seqs=6
Similarity=0.815768 216

GGTTGGGCGAAAGTGAAGTGTAAATGGGAAAACAGGGTATGTAAGTAGTCAATATTTAACAGGCAAGACGAACA
CAGCCCCATCAAAAACCGTCAACATCCACACCAGCAAAGACGGAAACAAAATATGTATCTGTAACTCAGGTTC
TANTTTGAATCTACGCAGTAGTGCNAGTACAAGTGCTTCGATAATCGGGAGCCTAACAAATGGCACAGCAGTA
ACGGTTCAATCAGATTCCAAT

Consensus:

GGTTGGGCGAAAGTGAaTGTAATGGGAAAACAGGaTATGTAAGTAGTCAaTATTTAACAGGCAAGACGAACA
CAGCCCCAtCAAAACCaTcACATCCACACCAGCAAAGACGGAAACAAAATATGTATCTGTAACTCAGGTTC
TAtTTTGAATCTACGCAGTAGTGCCaAGTACAAGTGCaTcATAATCGGGAaCcTAAcAAATGGCACAGCaGTA
ACGGTTCAATCAGATTCCAAa

>Bacillus_Fam_376_210_2 Nr. of seq. 2 Alignment length(with gaps) = 210
Alignment score = 0.853968
GCF_000612625.1_JCE_genomic.fna_21:59255-61145 Satlength=1891 Nr of
Repeats=8 RepeatLength=210 seed=GGCTGGTACA Num.seqs=7
Similarity=0.674093
0

GGCTGGTACAGTGATGAAGCACGAACGAATTTGTACGATTTTAATGAGCCAGTNAAAGCAGCGACAAAGTTGT
ATGCGAAATGGACNCATAATCAATATGAAGTCAATTTTGATACNAATGGCGGCAGTNANATTGCTTCGAAAA
TGTGAANTACAATGAAAAAGCAANGAAGCCANNNGNACCAACGAAAGAAGGTACACCTTCGCN

GCF_000612625.1_JCE_genomic.fna_21:59327-62057 Satlength=2731 Nr of
Repeats=13 RepeatLength=210 seed=TATGCGAAAT Num.seqs=13
Similarity=0.617769

72
GGCTGGTACAGTGATGAAGCACTAACGAATTTGTACGATTTTGANGNGCCAGTNAAAGCAGCNANGANNTTGT
ATGCGAAATGGACCCATAATCAATATGAAGTAAGTTTGTGATACNAATGGCGGNAGTNANGTTGCTTCTGAAAA
TGTGAANTACAATGAAAAAGCNANGAAGCCAGNAGTACCAACGAAAGAAGGCTACACCTTCGCN

Consensus:

GGCTGGTACAGTGATGAAGCACgAACGAATTTGTACGATTTTATaAtGaGCCAGTNAAAGCAGCgAcaAagTTGT
ATGCGAAATGGACcCATAATCAATATGAAGTAaAaTTTTGATACNAATGGCGGcAGTNANaTTGCTTCgAAAA
TGTGAANTACAATGAAAAAGCaANGAAGCCAgNaGtACCAACGAAAGAAGGcTACACCTTCGCN

>Bacillus_Fam_377_200_2 Nr. of seq. 2 Alignment length(with gaps) = 200
Alignment score = 0.746667
GCF_001591665.1_ASM159166v1_genomic.fna_21:41016-42003 Satlength=988 Nr
of Repeats=5 RepeatLength=198 seed=ATTGATAAAA Num.seqs=4
Similarity=0.606986
0
ATTGATAAAACAGCTCCAGTCGTAACCTGGTGTAGAAACAAACGGTCTTTACAATAATGATGTAAACAGTTTCA
TTTAATGAAGGAACAGCGACATTAAATGGTAAAGCAGTGAAAACCTGGAACAGTAGTTAAAACAA-
ATGGAACCTTACACAGTAGTGGTAACAGATGCAGCAGGAAACAAAACAACCTGTGAAGTTCACG
GCF_001591665.1_ASM159166v1_genomic.fna_21:46294-47278 Satlength=985 Nr
of Repeats=5 RepeatLength=198 seed=ATTGATAAAA Num.seqs=3
Similarity=0.493290
0 ATTGATAAAACNGCTCCAGTNGTAAGTGGAGTTA-
AAAAACNACGGCCTNTACAATCAAGATGTGACANTTTCNTTTAATGAAGGAACNGCNACATTAAATGGTAANGA
ANTTNCATCTGGTACAGCAGTTAANCCAAGANGANNCTATACANTAGTGGTAACCGACGCAGCAGGNAATAA
AACCACNGTTAAGTTCACN

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Consensus:

ATTGATAAAACaGCTCCAGTcGTAAcTGGaGTTAgAAaACaACGGcCTtTACAATaAaGATGTaACAgTTTCa
TTTAATGAAGGAACaGCgACATTAAATGGTAAaGaAgTgaaAaCTGGaACAGcAGTTAAaaCAAgAtGGAacc
TAcACAgTAGTGGTAACaGAcGCAGCAGGaAAcAAAACaActGtGAAAGTTCACg

>Bacillus_Fam_378_154_2 Nr. of seq. 2 Alignment length(with gaps) = 154
Alignment score = 0.696970
GCF_000177235.2_ASM17723v2_genomic.fna_1:694972-695711 Satlength=740 Nr
of Repeats=5 RepeatLength=145 seed=ACATGTGGCA Num.seqs=3
Similarity=0.993870
0 ACATGTGGCATCATTTCTTTACCGCTTCTAAGAAAAACGAAAACTCG-TT---T---
TTCGTTTTTCAT-AAAAGATATGAGAGT-
ATAAAATATGGCGGTGGAAATGAAGCCACGCGTAGTAGTGAGAAGAGCACTCACTACTACTTTAAAA
Rev.of_GCF_000177235.2_ASM17723v2_genomic.fna_1:2996165-2996769
Satlength=605 Nr of Repeats=4 RepeatLength=151 seed=CTAAAAACGA
Num.seqs=4 Similarity=0.986755

69
ACATGTGGCATCACTTCTTACCgCTTCTAAGAAAAACCTAAAAACGAGCTTCACTAAGCTCGTTTTTAGTCTA
TTCATAAGA-AGTGCTAAAA-A-
GGCGGTGGAAAGTGATGCCACGCGTAGTAGAGAGAAGAGCACTCACTACTACTTTAAAG

Consensus:

ACATGTGGCATCACTTCTTcACCGCTTCTAAGAAAAaCgAAAAACgAGcTTcacTaagcTCGTTTTTaaTcaA
aacATAaGAgAGTgaTAAAAAtAtGGCGGTGGAAaTGAaGCCACGCGTAGTAGaGAGAAGAGCACTCACTACTA
CTTTAAAAa

>Bacillus_Fam_379_153_2 Nr. of seq. 2 Alignment length(with gaps) = 153
Alignment score = 0.644880

GCF_900111815.1_PRJEB17078_genomic.fna_1:368570-369663 Satlength=1094 Nr
of Repeats=8 RepeatLength=150 seed=GATAAGTCAA Num.seqs=7
Similarity=0.990688 0

GATAAGTCAACATCGATTTCGCTATCGCTCATCGTGTTTCCTTTATCTCGAT-
CGAAACCTCCAGGCCGTACAGCGCTAAACGGGCGCTCCGCTTTTCTATTGTCCAGCTTCAGCGCCCA-
GCGCTTATCGTCCTTCGGCTTTCTC-CCTAC
Rev.of_GCF_000171615.1_ASM17161v1_genomic.fna_137:4281-4859 Satlength=579
Nr of Repeats=4 RepeatLength=152 seed=AAGAAAAGCG Num.seqs=3
Similarity=0.740977 101
AATAAGTCAACATCGAATCGCTGACGCTCTTCGTGTTTCCTTTATTTTGATGCCAAGCCCTCCAATCCATACG
CCCCTAAACAGTCGGCTCCGCTTTTCT-
TTGTCCAGCTCCGCCTCCTAGGGGCTAATGGATTTNCGGTCTTGTCACCTTC

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Consensus:

aATAAGTCAACATCGAaTCGCTaaCGCTCaTCGTGTTTCCTTTATcTcGATgCcAAaCCCTCCAagCCaTACa
cCcCTAAAcAgGcGccTCCGCTTTTCTaTTGTCCAGCTcCacCgCCcAgGcGCTaATcGaccTtCGGccTtCt
CaCCTaC

>Bacillus_Fam_380_148_2 Nr. of seq. 2 Alignment length(with gaps) = 148
Alignment score = 0.718468
GCF_000832605.1_ASM83260v1_genomic.fna_1:988424-988982 Satlength=559 Nr
of Repeats=4 RepeatLength=147 seed=TAGATGAGGC Num.seqs=3
Similarity=0.724087
0

TAGATGAGGCGACAAAAGAAAAAGCGAAGTCCATTTTTGAGCAAGAAAAGTCCGGAACATTAACCTCGTGAGCA
AGCAAAAGAGAAATTGAAAGAACTAGGCGTGAAATTCCCAGAGAAAGGG-
AAGCACGGTGATATGTTTCGCGAATT
GCF_001645555.1_ASM164555v1_genomic.fna_23:264674-265262 Satlength=589 Nr
of Repeats=4 RepeatLength=147 seed=AAAGAAAAAG Num.seqs=4
Similarity=0.756006 14
TAGACGAAGCAACAAAAGAAAAGCGAATCAATCTTAGAACAAGAAAATCCGGCAAACTAACACGTGAACA
AGCAAAAGAAGAATTAAACAAAGCTAGGTGTGAAATTCCCGAGAGAAAGGNTAAGCATGAAGACATGTTTGCTAA
CT

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Consensus:

TAGAcGAaGCaACAAAAGAAAAAGCGAAaTCaATcTTaGAaCAAGAAAAaTCCGGaAaAcTAACaCGTGAaCA
AGCAAAAGAaaAATTaAaAaAaCTAGGcGTGAAATTCCCAGAGAAAGGgtAAGCAcGaaGAcATGTTcGCgAA
cT

>Bacillus_Fam_381_145_2 Nr. of seq. 2 Alignment length(with gaps) = 145
Alignment score = 0.671264
GCF_001591825.1_ASM159182v1_genomic.fna_6:118986-119562 Satlength=577 Nr
of Repeats=4 RepeatLength=144 seed=CCACCATTTA Num.seqs=4
Similarity=0.524024 0
CCACCATTTATGCCACAGATTATCGTTGTTTCCACGGACAAAGGTATCGATCCGATTGGCTCCCCATGATAAG
GCAGCCGG-AGAACCCTTCAACCCACGCCGCGGAGCTCCAAGGTCCTCCCACTCACTCCAGCTTGAACCGTC

GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_4:152867-153443
Satlength=577 Nr of Repeats=4 RepeatLength=144 seed=ACCATTTATG
Num.seqs=4 Similarity=0.507358 2
CCACCATTATGCCACATCTGGTCGTTGTCTCCNCTGACAAATGTATCAATGCGGTTTCGNCCCCATGATAAA
GCTCCCGGTGGATCCCTNGAAACCGCCGCGGGTGCCCCGAGATCTTCCCAATCGCTCCAGCGCGAACCATC

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Consensus:

CCACCATTATGCCACAgATgaTCGTTGTtTCCaCgGACAAAgGTATCaATcCGaTTcGccCCCCATGATAAA
GCacCCGGTaGAaCCCTtcAAaCCaCccCGCGGaGcCCaAGaTCcTCCCAaTCaCTCCAGCGcGAACCATC

>Bacillus_Fam_382_140_2 Nr. of seq. 2 Alignment length(with gaps) = 140
Alignment score = 0.814286
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_46:1002-1551
Satlength=550 Nr of Repeats=4 RepeatLength=139 seed=ATCGTCCGAA
Num.seqs=3 Similarity=1.000000 0
ATCGTCCGAAACTATATAACGCCGCGGGGTGGAGCAACGAGCAATGCATCAGTGAAAAAGCAACGAGTTGTC
TCGACGCATAAGCAGCGGAGTAAAGCAGGAAGAGGAAGAGACAGTCAAAGGACATCGAAGC-AGAGC
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_19:46687-47426
Satlength=740 Nr of Repeats=6 RepeatLength=140 seed=AAGGACGTCTG
Num.seqs=4 Similarity=0.972813 120
ATCGTCCGTAAACTTTAAACGTCGCGGGGTGGAGCAACGAGCGAAGCATCATTGAAAAACAGCGAGTTGTC
TCGACGCATTCGCATCGAAGCGAAGCAAGAAGAGGAAGAGACAGTCAAAGGACGTCTGAAGCAAAAGC

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Consensus:

ATCGTCCGaAAACTaTAaAACGcCGCGGGGTGGAGCAACGAGCaAaGCATCAGtGAAAAaCAaCGAGTTGTC
TCGACGCATaaGCAgCGaAGcaAAGCAaGAAGAGGAAGAGACAGTCAAAGGACaTCGAAGCaAaAGC

>Bacillus_Fam_383_138_2 Nr. of seq. 2 Alignment length(with gaps) = 138
Alignment score = 0.990338
GCF_001517115.1_ASM151711v1_genomic.fna_1:286089-286917 Satlength=829 Nr
of Repeats=6 RepeatLength=138 seed=GTTGTCTCGG Num.seqs=6
Similarity=0.875040 0
GTTGTCTCGGAAGCGAGGCTTCGTGAAGAGCAGGAAAATGAAGAGGAAGAAGCTGAGCGGTCTAGCGCCATTGG
CTTTAAAAGCAGAGGAAAGCGGCGGTATAAAAGCAGAAGAAGCGCCAGCTGAGCCGCCAGAGCTT
GCF_001517135.1_ASM151713v1_genomic.fna_26:157017-157839 Satlength=823 Nr
of Repeats=6 RepeatLength=138 seed=GGCTTCGTGA Num.seqs=5
Similarity=0.884058 16
GTTGTCTCGGAAGCGAGGCTTCGTGAAGAGCAGGAAAATGAAGAGGAAGAAGCTGAGCGGTCTAGCGCCATTGG
CTTTAAAAGCAGAGGAAAGCGGCGGTATAAAAGCAGAAGAAGCGCCAGCTGAGCCGCCGAGCTT

Consensus:

GTTGTCTCGGAAGCGAGGCTTCGTGAAGAGCAGGAAAAATGAAGAGGAAGAAGCTGAGCGGTCAGCGCCATTGG
CTTTAAAAGCAGAGGAAAGCGGCGGTATAAAAGCAGAAGAAGCGCCAGCTGAGCCGCCaGAGCTT

>Bacillus_Fam_384_128_2 Nr. of seq. 2 Alignment length(with gaps) = 128
Alignment score = 0.695312

GCF_001877785.1_PlanoSAMM_genomic.fna_85:203375-204000 Satlength=626 Nr
of Repeats=5 RepeatLength=125 seed=AGCTCGAGGT Num.seqs=5
Similarity=0.978667

0 AGCTCGAGGTCATAAGCTAACTTACCAAAAAGGCCAAGAGCGCCTTTCCGGTAAGT--
TCATCTTATGCTTGTGCTCCTGAGCGAGCCGCTCCGCTTTTCT-GTTGTCCAGCTACGGCGGCTAGG
GCF_001274775.1_ASM127477v1_genomic.fna_3:67013-67766 Satlength=754 Nr of
Repeats=6 RepeatLength=126 seed=CTTATGCTTG Num.seqs=4
Similarity=0.741602
62 CCCTCGAGGTCATAAGCCAAAAACCCCAAAAAGGCCAAAGAAGCGCCTTTCCGG-
GAGTCTTCGTCTTATGCTTGTGCTCCTCAGAGCAACCCNCCTCCGCTTTTCTACATGTCCAGCTCCGGCGCGTT
GA

Consensus:

acCTCGAGGTCATAAGCcAAAaacaCCAAAAGGCaAAGaACGCCTTTCCGGtaAGTctTCaTCTTATGCTTG
TCGcCcCaGAGCaAcCCgCCTCCGCTTTTCTacaTGTCCAGCTaCGGCGccTaGa

>Bacillus_Fam_385_127_2 Nr. of seq. 2 Alignment length(with gaps) = 127
Alignment score = 0.616798

GCF_000812025.2_ASM81202v2_genomic.fna_49:98712-99319 Satlength=608 Nr of
Repeats=5 RepeatLength=121 seed=TTGCTTTTC Num.seqs=3
Similarity=0.963269

0 TTGCTTTTCTCTTGTCCAGCTGCAGCGC-CTTGCTCCTCG-
GGTCAAATAACCTTCCTCCATGAAGCCAAAGAGCGG-CTTCTTG-GC-
GGAAGAACATTTGCCGGTCGGAGCAGAACAGGCG-CT
Rev.of_GCF_002019605.1_ASM201960v1_genomic.fna_1:2798720-2799338
Satlength=619 Nr of Repeats=5 RepeatLength=124 seed=AAGAAAAGCG
Num.seqs=3 Similarity=0.863799
12 TCCGCTTTTCT-TTGTCTAGCTGCAG-
GCTCTAGCCCTCGAGGTTAAATAACCTACCTGAAAAAAGTCAAAAAGCGGACTT-
TTGTTcAGTCAGAACATTTACTTGTCGGGGCTGACCAAGAGCCT

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Consensus:

TcCGCTTTTCTcTTGTCCaGCTGCAGcGCTcTaGCcCCTCGaGGTcAAATAACCTaCCTcaAaaAAGcCAAAa
AGCGGaCTTcTTGtgCaGgaAGAACATTTaCcgGTCGgaGCaGAaCAaGaGcCT

>Bacillus_Fam_386_127_2 Nr. of seq. 2 Alignment length(with gaps) = 127
Alignment score = 0.619423

GCF_000812025.2_ASM81202v2_genomic.fna_36:56533-57148 Satlength=616 Nr of
Repeats=5 RepeatLength=123 seed=AGCTAGACAA Num.seqs=5
Similarity=0.666929

0 -AGCTAGACA-A-C-

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Consensus:

GTTCGTTTCGCTTCTTCTTGGTCCATTTGCCCCGGCAACGCCTCGGTTCCACTCATTACCTCTGCCTCTTCAAT
CTCTGGTTCCCCGCGTCCATACC

>Bacillus_Fam_389_84_2 Nr. of seq. 2 Alignment length(with gaps) = 84
Alignment score = 0.603175
GCF_000429725.1_ASM42972v1_genomic.fna_2:377721-378441 Satlength=721 Nr
of Repeats=5 RepeatLength=83 seed=TGGCGAGCTT Num.seqs=3
Similarity=0.828648
0 TGGCGAGCTTTCCGCT-
CGGGGCGTCGCGTTTCGTCCCGTACCTCGACGTACCTCTCGCCTCCAGTGGCGAGGCGGTCCCCATG
Rev.of_GCF_000429725.1_ASM42972v1_genomic.fna_25:9598-10275 Satlength=678
Nr of Repeats=5 RepeatLength=84 seed=CTCGCCAAAC Num.seqs=3
Similarity=0.813953 7
TGGCGAGGTTGGGGCNGCGAGTCGACGAGGTTGGGAGCATACCTCGACGTACCTCTNCCTTCCAGTGGCGAGG
TAGCGACCGTT

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Consensus:

TGGCGAGcTTgccGctgCGaGgCGaCGaGGTTcGgacCaTACCTCGACGTACCTCTccCcTCCAGTGGCGAGG
caGccaCCaTg

>Bacillus_Fam_390_84_2 Nr. of seq. 2 Alignment length(with gaps) = 84
Alignment score = 0.904762
GCF_000496285.1_ASM49628v1_genomic.fna_1:3671784-3672105 Satlength=322 Nr
of Repeats=4 RepeatLength=84 seed=GGAAAAGTAA Num.seqs=3
Similarity=0.904762 0
GGAAAAGTAACAGCAGGTTTAAATACGTAAATGGCAAAACGGGTGAGATGCAGACTGGTATAGGGAAATTAG
TAGACGGTTCA
Rev.of_GCF_000775975.1_ASM77597v1_genomic.fna_1:3704249-3704585
Satlength=337 Nr of Repeats=4 RepeatLength=84 seed=TTTGCTATTT Num.seqs=4
Similarity=0.846561 39
GGAAAAGTAACAGCTGGTTTAAATACGTAAATAGCAAAACAGGTGAGATGCAGACTGGTATAGGGAAATTAG
TAGATGGGTCT

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Consensus:

GGAAAAGTAACAGCaGGTTTAAATACGTAAATaGCAAAACaGGTGAGATGCAGACTGGTATAGGGAAATTAG
TAGAcGGgTCa

>Bacillus_Fam_391_78_2 Nr. of seq. 2 Alignment length(with gaps) = 78
Alignment score = 0.914530
GCF_000245335.1_ASM24533v1_genomic.fna_3:543340-543808 Satlength=469 Nr
of Repeats=6 RepeatLength=78 seed=GAAGATCTTG Num.seqs=6
Similarity=0.949858
0
GAAGATCTTGGTGACCGATATGATTTGGAAGAACTTTTGAATCTGATGAACGATCATATGTTGACGATTGAT
AATCT

GCF_001517115.1_ASM151711v1_genomic.fna_24:533324-533636 Satlength=313 Nr
of Repeats=4 RepeatLength=78 seed=CTGAAGATCT Num.seqs=4
Similarity=0.900285 76
GAAGATCTTGATGACCGATATGATTTGGACGAACTTTTGGTGTCTGATGAACGATCATATTTTGACGATTGAT
AATCT

Consensus:

GAAGATCTTGaTGACCGATATGATTTGGAaGAACTTTTGaTCTGATGAACGATCATATgTTGACGATTGAT
AATCT

>Bacillus_Fam_392_75_2 Nr. of seq. 2 Alignment length(with gaps) = 75
Alignment score = 0.951111
GCF_000217835.1_ASM21783v1_genomic.fna_1:1910042-1910492 Satlength=451 Nr
of Repeats=6 RepeatLength=75 seed=CTTTCCGCCA Num.seqs=6
Similarity=0.732148 0
CTTTCCGCCAACGATGCCGACTCATTTTTACCAGAAACTCCGGNTCGGCCTGCCATTTCATCCTGCGCCACTC
CA
GCF_000832905.1_ASM83290v1_genomic.fna_1:924148-924448 Satlength=301 Nr
of Repeats=4 RepeatLength=75 seed=CTTTCCGCCA Num.seqs=4
Similarity=0.694815
0
CTTTCCGCCAACGATGCCGACTCATTTTTACCAGAAACTCCGGNTCGGCCTGCCATTTCATCCTGCACCACTC
CA

Consensus:

CTTTCCGCCAACGATGCCGACTCATTTTTACCAGaAAACTCCGGNTCGGCCTGCCATTTCATCCTGCaCCACTC
CA

>Bacillus_Fam_393_74_2 Nr. of seq. 2 Alignment length(with gaps) = 74
Alignment score = 0.689189
GCF_000299035.1_ASM29903v1_genomic.fna_4:316574-316862 Satlength=289 Nr
of Repeats=4 RepeatLength=72 seed=TTCTGCTGCT Num.seqs=4
Similarity=0.969136
0
TTCTGCTGCTTGTCTTCTGTTTGGCTGTTTGTTCCTTTTCATCAGCAGAACCATTGTTGATTCTCTTCC-
-
GCF_000712615.1_ASM71261v1_genomic.fna_2:364691-365123 Satlength=433 Nr
of Repeats=6 RepeatLength=72 seed=TCTTTTGAC Num.seqs=6
Similarity=0.987654
67 TTGACCT--
TTGTCAATCAGTTTTACTGTTTGTGCTTTTTCCTCAGTAGAACCGTTCGTTGATTCTCTTCTTT

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Consensus:

TTcacCTgcTTGTcATCaGTTTgaCTGTTTGTGcCTTTTCaTCAGcAGAACCATTcGTTGATTCTCTTCct
t

>Bacillus_Fam_394_67_2 Nr. of seq. 2 Alignment length(with gaps) = 67
Alignment score = 0.611940
GCF_000787375.1_ASM78737v1_genomic.fna_58:8-403 Satlength=396 Nr of
Repeats=6 RepeatLength=66 seed=GTCATATCTC Num.seqs=5 Similarity=0.538889
0 GTCATATCTCCATCTAATCCGTTGCTGTGATATGATATNAAT--C-GTNTATTTCTGNATNNGNTAT
Rev.of_BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:420902-424028
Satlength=3127 Nr of Repeats=37 RepeatLength=66 seed=TCACAGCAAC
Num.seqs=34 Similarity=0.260606
30 GTCATATCTCCATCTATTCCGTTGCTGTGATATGAT-NNAATGNCNNTATCNNNCNNTATNCNTNAN

Consensus:

GTCATATCTCCATCTAaTCCGTTGCTGTGATATGATatNAATgnCngTaTatttCtgtATNcgttAt

>Bacillus_Fam_395_66_2 Nr. of seq. 2 Alignment length(with gaps) = 66
Alignment score = 0.626263
GCF_000712595.1_ASM71259v1_genomic.fna_18:68568-69048 Satlength=481 Nr of
Repeats=8 RepeatLength=60 seed=TGGTACTACT Num.seqs=8 Similarity=0.619243
0 TGGTACTACTT---GAATNA--TAGCGGTGCAATGCAAACAGGTTGGTTGTATGACGATGNAAC
GCF_000161455.1_ASM16145v1_genomic.fna_1:1154071-1154599 Satlength=529 Nr
of Repeats=10 RepeatLength=66 seed=TGAAAACAGG Num.seqs=6
Similarity=0.797678 34
TGGTATTACTTGGATGAAGCAGCTAGCGGAGCAATGAAAACAGGTTGGTTGAAATACGGAGAAAAT

Consensus:

TGGTAcTACTTggatGAAGcAgcTAGCGGaGCAATGaAAACAGGTTGGTTGaAagACGaaGaAAAc

>Bacillus_Fam_396_62_2 Nr. of seq. 2 Alignment length(with gaps) = 62
Alignment score = 0.618280
GCF_000712595.1_ASM71259v1_genomic.fna_8:140638-141178 Satlength=541 Nr
of Repeats=9 RepeatLength=60 seed=GGTGTAATGC Num.seqs=9
Similarity=0.730747
0 GGTGTAATGCAAACAGGTTGGCACAAAGAT-GG-AGGAAGTTGGTACTACTTTGGCNCAAAC
Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:343119-343839
Satlength=721 Nr of Repeats=8 RepeatLength=60 seed=CCAGCCGGTT Num.seqs=7
Similarity=0.904762 21
GGTGTAATGCAAACCGGCTGGGA-AAAGATCGGCAGCAAG-AAGTATTACTTCGACAAAAAT

Consensus:

GGTGTAATGCAAACaGGcTGGcAcAAAGATcGGcAGcAAGtaaGTAcTACTTcGaCaaAAAc

>Bacillus_Fam_397_61_2 Nr. of seq. 2 Alignment length(with gaps) = 61
Alignment score = 0.661202
GCF_001591805.1_ASM159180v1_genomic.fna_17:178840-179140 Satlength=301 Nr
of Repeats=4 RepeatLength=60 seed=TGGTGCGATG Num.seqs=3
Similarity=0.589065 0
TGGTGCGATGAAAACNGGCTGGGT-TAAACCTGGCTCCACTTGGTATTACTTAGATAAAAG
GCF_001591805.1_ASM159180v1_genomic.fna_46:18986-19349 Satlength=364 Nr
of Repeats=5 RepeatLength=60 seed=TGGTATTACT Num.seqs=3

Similarity=0.608379

40 TGGTGCGATGAAGACNGGTTGGTTNTTAA-CTGGTGNGAAATGGTATTACTTAGAAAAAA

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Consensus:

TGGTGCGATGAAaACNGGcTGGgTnTaAAcCTGGcgccAaaTGGTATTACTTAGAaAAAAa

>Bacillus_Fam_398_60_2 Nr. of seq. 2 Alignment length(with gaps) = 60

Alignment score = 0.911111

GCF_000508325.1_BAVI_1_genomic.fna_45:24041-24284 Satlength=244 Nr of Repeats=4 RepeatLength=60 seed=AAATGGTACT Num.seqs=3 Similarity=0.573477

0 AAATGGTACTATCTTAACGCAAACGGCGACATGGCAACAGGCTGGAAGCTGGTTAGCGGA

GCF_001591805.1_ASM159180v1_genomic.fna_13:17036-17279 Satlength=244 Nr of Repeats=4 RepeatLength=60 seed=AAATGGTACT Num.seqs=3 Similarity=0.585185

0 AAATGGTACTACCTTAACGCAAACGGCGAAATGGCAACAGGCTGGAACTGGTTAGCGGC

Consensus:

AAATGGTACTAcCTTAACGCAAACGGCGAaATGGCAACAGGCTGGAAaCTGGTTAGCGGa

>Bacillus_Fam_399_60_2 Nr. of seq. 2 Alignment length(with gaps) = 60

Alignment score = 0.811111

GCF_000508325.1_BAVI_1_genomic.fna_65:18797-19643 Satlength=847 Nr of Repeats=6 RepeatLength=60 seed=AAATGGTACT Num.seqs=4 Similarity=0.637978

0 AAATGGTACTACCTCCAAGCTGACGGCGCNATGAAAACCGGCTGGCTTAGCACAAATAAC

Rev.of GCF_001591805.1_ASM159180v1_genomic.fna_18:13670-14516

Satlength=847 Nr of Repeats=4 RepeatLength=60 seed=AGTACCATTT Num.seqs=3

Similarity=0.683060

10

AAATGGTACTTCCTNCAGGCTGATGGTTCNATGAAAACCGGCTGGCTGAGCACAAACAAC

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Consensus:

AAATGGTACTaCCTcCAaGCTGAcGGcgCNATGAAAACCGGCTGGCTgAGCACAAaAAC

>Bacillus_Fam_400_60_2 Nr. of seq. 2 Alignment length(with gaps) = 60

Alignment score = 0.716667

GCF_000712595.1_ASM71259v1_genomic.fna_1:423888-424608 Satlength=721 Nr of Repeats=12 RepeatLength=60 seed=TATTCATGTA Num.seqs=12

Similarity=0.898990

0

TATTCATGTAATACCATTTCCTCCGAATTCTANCCAGCCTGTTTGCATTACTCCGGAAC

GCF_000712595.1_ASM71259v1_genomic.fna_21:53926-54706 Satlength=781 Nr of Repeats=13 RepeatLength=60 seed=TAATACCACT Num.seqs=13

Similarity=0.900570

8 TATTTAAGTAATACCACTTACCCCAACAGATAACCAGCCTGTTTGCATTTCTCCTGAAC

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Consensus:

TATTCaAaGTAATACCAcTTaCCcCaAaagaTAaCCAGCCTGTTTGCATTaCTCCgGAAC

>Bacillus_Fam_401_60_2 Nr. of seq. 2 Alignment length(with gaps) = 60
Alignment score = 0.688889
GCF_002019645.1_ASM201964v1_genomic.fna_1:5253347-5253767 Satlength=421
Nr of Repeats=7 RepeatLength=60 seed=CCTGGTAGTG Num.seqs=7
Similarity=0.912169 0
CCTGGTAGTGACCTTCGAAATTCGGTGGGTATGGTTGGTCCACTCTCCACCGTTTGGA
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_12:81185-81485
Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=CTCCTCCATT Num.seqs=5
Similarity=0.964444 46
CCTGGTAATGGGCCCTCAAAATTCGGTGGATATGGGAAATCCAACCTCCTCCATTTGGG

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Consensus:

CCTGGTAaTGGaCCcTCaAAATTCGGTGGaTATGGgaaaTTCCAacCTCCaCCaTTTGGA

>Bacillus_Fam_402_57_2 Nr. of seq. 2 Alignment length(with gaps) = 57
Alignment score = 0.625731
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_2:649324-649688
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GGCTTCATGA Num.seqs=7
Similarity=0.749326 0 -
GGCTTCATGAAGC-NTTCATGGCGACC-TTTTC--CCGGCTTCCTTCTGTTTTTG
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_6:279533-280000
Satlength=468 Nr of Repeats=9 RepeatLength=52 seed=CATGGCGACC Num.seqs=8
Similarity=0.767196 18
CGGCTTCATGAAGCACTNCATGGCGACCGTTTTTCAGCC--CTACTCNTCGATTTTTT-

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Consensus:

cGGCTTCATGAAGCacTtCATGGCGACCgTTTTTCagCCggCTaCcCtTCgaTTTTTg

>Bacillus_Fam_403_57_2 Nr. of seq. 2 Alignment length(with gaps) = 57
Alignment score = 0.605263
GCF_900156875.1_PRJEB18969_genomic.fna_10:1559594-1559802 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=AGATGAAGAC Num.seqs=4
Similarity=0.790598 0
AGATGAAGACCG-TTTATGTACCGGA---AGGCTTGAGGAAAGGTTTTTCATAGC-AG
Rev.of_GCF_900156875.1_PRJEB18969_genomic.fna_11:1462191-1462503
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=CGGTCTTCAT Num.seqs=6
Similarity=0.825786 11 -
GATGAAGACCGCTTTA-GCATTGGATCCA-GC-AGAGGAAAGGTTCTCATAGCGAG

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Consensus:

aGATGAAGACCGcTTTAtGcAccGGAtccAgGCTaGAGGAAAGGTTcTCATAGCgAG

>Bacillus_Fam_404_57_2 Nr. of seq. 2 Alignment length(with gaps) = 57
Alignment score = 0.684211
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_26:134607-134815
Satlength=209 Nr of Repeats=4 RepeatLength=53 seed=AGGAAGAAAG Num.seqs=3

Similarity=0.882600 68 AGTGGGAAGAGTCTG----
AGGAAGAAAGGTCACCAACAAGGCCCATTGGTGCCCAA
Rev.of_GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_36:66229-66446
Satlength=218 Nr of Repeats=4 RepeatLength=53 seed=ATTGGTGACC Num.seqs=3
Similarity=0.773663 87 AGT---AAGTGT-
TGCTAGAACAAAGAAAGGTCACCAATAAGGCTCATTGGTGCCCAA

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Consensus:

AacAAGAAAGGTCACCAAcAAGGCcCATTGGTGCCCAAAGTgggAAGaGTcTGctag

>Bacillus_Fam_405_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.636905
GCF_000175075.1_ASM17507v1_genomic.fna_2:12013-12273 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=ATGAAGACCT Num.seqs=5 Similarity=0.897436
0 ATGAAGACCTGTCCATGGCGGAA---AAGTTGGAAGAGATGTCTTCATAAGGTGG
GCF_900156865.1_PRJEB18960_genomic.fna_3:551238-551654 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=ATGAAGACCT Num.seqs=8
Similarity=0.723270
0 ATGAAGACCTG--AANGGAGGAATTTGTAGTAGGAAGAG--GTCATCATAAGGTGG

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Consensus:

ATGAAGACCTGtcaAtGGaGGAAtttgaAGTaGGAAGAGatGTCaTCATAAGGTGG

>Bacillus_Fam_406_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.622024
GCF_000175075.1_ASM17507v1_genomic.fna_4:76487-76903 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=TCTCTGTTAC Num.seqs=8 Similarity=0.834249
0 TCTCTGTTACCGTTTTTCCTGTTT--GAATCGCAGTTCGGGCACTGAGACCGCC-
Rev.of_GCF_000175075.1_ASM17507v1_genomic.fna_32:624889-625097
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GTCTCTGTGC Num.seqs=4
Similarity=0.868973 48
TCTCTCTTACCG-TTTTCCTTTTTCCCGAA--GTCTTTCGGGCACAGAGA-CGCCT

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Consensus:

TCTCTcTTACCGtTTTTCTGtTTTcccGAAtcGcagTTCGGGCACaGAGAcCGCct

>Bacillus_Fam_407_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.601190
GCF_001636345.1_ASM163634v1_genomic.fna_1:2699397-2699657 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=GTTCCTTCA Num.seqs=5
Similarity=0.744654 0
GTTCCTTCAAGGCTC--CCTTTTCTCTGCTGACGGGCACTTTC-GC-CACAACTTA
Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:1077933-1078141
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AAGTGCCCGT Num.seqs=4
Similarity=0.485867 39
GTTCCTTCA-GCTCTGAGTTTTCNCT-CTGACGGGCACTTCCTGCTNNCACTTTA

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Consensus:

GTTCCCGTCAGGCTCtgacTTTTCTgCTGACGGGCACTTcCtGctcaCAacTTA

>Bacillus_Fam_408_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.669643
GCF_002019645.1_ASM201964v1_genomic.fna_1:3948839-3949826 Satlength=988
Nr of Repeats=19 RepeatLength=52 seed=ACTTCGGACA Num.seqs=18
Similarity=0.865091 86
TTGTTTTAGAGC---AAAGCTGTCTGAACTCTGGCCT-ACTTCGGACAGCTTTAGC
GCF_002019645.1_ASM201964v1_genomic.fna_1:4298062-4299581 Satlength=1520
Nr of Repeats=20 RepeatLength=52 seed=CTCTCTTCGG Num.seqs=18
Similarity=0.844469 136
-TCTTTCAG-GCTTCAAAGCTGTCTGAAC-CTGGACTCTCTTCGGACAGCTTTGGC

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Consensus:

aCTTCGGACAGCTTTaGctTcTTTcAGaGcttcAAAGCTGTCTGAACTCTGGaCTc

>Bacillus_Fam_409_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.625000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_16:18479-18947
Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=TTTGTTCAT Num.seqs=9
Similarity=0.798567 0 TTTGTTCATAGACAG-
CTTCTATCGGACAACTCTAT-GATNC--GCCTATCCGT
Rev.of_GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_25:10104-10364
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AATAGAGGTC Num.seqs=5
Similarity=0.825641 24 TTTGTTCATAGA-
AGACCTCTATTGGACAAA--CTATCGATTCAAG-CTATGTGT

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Consensus:

TTTGTTCATAGAcAGaCcTCTATcGGACAAActCTATcGATtCaaGcCTATccGT

>Bacillus_Fam_410_56_2 Nr. of seq. 2 Alignment length(with gaps) = 56
Alignment score = 0.601190
GCF_000181495.1_ASM18149v1_genomic.fna_164:6846-7219 Satlength=374 Nr of
Repeats=7 RepeatLength=53 seed=TTTAGAGGTT Num.seqs=5 Similarity=0.816364
0 TTTAGAGGTTGCCGATTGAAGGTCGTG-GAGGAATC-GAGGTAGTCAAAGAG-GCC
GCF_000181495.1_ASM18149v1_genomic.fna_186:321552-322293 Satlength=742 Nr
of Repeats=14 RepeatLength=53 seed=GGTTGTGCGAT Num.seqs=13
Similarity=0.775087 5
TAT-GGGGTTGTGCGATTGGNTGT-TTGAGAGGAATCGGTGGT-GTCAAAGAGAGCC

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Consensus:

TaTaGaGGTTGcCGATTGaagGTcgTgaGAGGAATCgGaGGTaGTCAAAGAGaGCC

>Bacillus_Fam_411_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
 Alignment score = 0.654545
 GCF_000181495.1_ASM18149v1_genomic.fna_57:492-700 Satlength=209 Nr of
 Repeats=4 RepeatLength=52 seed=CTCAAGACAC Num.seqs=4 Similarity=0.743187
 0 CTCAAGACACTTTCCTCGGC--ATTTTACCCGGTTTATGTCCTTGAGA-ACCTCC
 Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_186:148691-149003
 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TCTCAAGGAC Num.seqs=6
 Similarity=0.745912 46
 NTCAAGACACTTT--TGAGCTAATTTTATCCTGTTCATGTCCTTGAGACTCTTCC

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Consensus:

cTCAAGACACTTTcTcaGCTaATTTTAcCCgGTTcATGTCCTTGAGAcAcTCC

>Bacillus_Fam_412_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
 Alignment score = 0.624242
 GCF_000285535.1_ASM28553v1_genomic.fna_3:66531-66842 Satlength=312 Nr of
 Repeats=6 RepeatLength=52 seed=CTTCATCAAC Num.seqs=5 Similarity=0.858974
 0 CTTCATCAACC-CGATGAAGGACTTTCAGCGA-CACT-TCCGCTGCATTGCGA
 GCF_000285535.1_ASM28553v1_genomic.fna_3:178754-178962 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=ATGAAGGACT Num.seqs=4
 Similarity=0.497428
 14 CTTCATCAGCCTCGATGAAGGACTTTCC-CCTAGTAATCTAC-CTCCATTGCGA

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Consensus:

CTTCATCAaCCtCGATGAAGGACTTTCcAcCgAgcAaTcTaCgCTcCATTCGaGA

>Bacillus_Fam_413_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
 Alignment score = 0.633333
 GCF_000294775.2_ASM29477v2_genomic.fna_1:2273821-2274185 Satlength=365 Nr
 of Repeats=7 RepeatLength=52 seed=CTCAAAAAAT Num.seqs=7
 Similarity=0.943834 0
 CTCAAAAAATGGGAGCTAATCGAAATGAATAACGACGAAAAAGAAACCTCTA--
 Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:2924329-2925107
 Satlength=779 Nr of Repeats=15 RepeatLength=52 seed=TTTTCGTCGT
 Num.seqs=13 Similarity=0.847469
 41 CATAAGAAATGGTAGTTAATCGTAATGAATAACGACGAAAAAG---GCTGTGCNC

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Consensus:

CacAAaAAATGGgAGcTAATCGaAATGAATAACGACGAAAAAGaaacCTcTacnc

>Bacillus_Fam_414_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
 Alignment score = 0.639394
 GCF_000307875.1_BABA1.0_genomic.fna_114:62513-62721 Satlength=209 Nr of
 Repeats=4 RepeatLength=52 seed=TTTTGTCTTT Num.seqs=4 Similarity=0.897436
 0 TTTTGTCTTTAATAAGGGTCTTAAAGAC--ATTTCAGCGAAAGGAACATGCA-
 Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_52:7926-8342 Satlength=417
 Nr of Repeats=8 RepeatLength=52 seed=CCCTTATTAA Num.seqs=8

Similarity=0.879155

18

TTTTGTCTTTAATAAGGGCTCTTAAAGACAAAAATGCAG-GAAA-G-CCATGGGG

Consensus:

TTTTGTCTTTAATAAGGGcTCTTAAAGACaaAaaTcCAGcGAAAgGaaCATGcag

>Bacillus_Fam_415_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55

Alignment score = 0.642424

GCF_000508325.1_BAVI_1_genomic.fna_45:30780-31040 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTCATAAAGC Num.seqs=5 Similarity=0.851282

0 TTCATAAAGCCCG-CGCCAGAGGAAAAAAG--GTCAAAGCGGTCAATAAGAGAGG

Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_7:179457-179715

Satlength=259 Nr of Repeats=5 RepeatLength=52 seed=GGGCTTTATG Num.seqs=3 Similarity=0.786325 12

TTCATAAAGCCCGTNGAC-GCNGAAAAAGCCGNC-CA-CGGTCAATAAGAGCGG

Consensus:

TTCATAAAGCCCGtcGaCaGagGAAAAAGccGtCaaAgCGGTCAATAAGAGaGG

>Bacillus_Fam_416_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55

Alignment score = 0.624242

GCF_000621445.1_ASM62144v1_genomic.fna_2:234605-234813 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TTTGTCTAAT Num.seqs=4

Similarity=0.847737

0 TTTGTCTAATAGAGCCTTTCTATTGGACACTTTTCTCCGATT-TTGCAC-T-CGT

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_73:46396-46657

Satlength=262 Nr of Repeats=5 RepeatLength=52 seed=CGGGAAAGAA Num.seqs=4 Similarity=0.738470 47

TTTGTCCGATAGAGCCTTTCTATCGGACA--TTT-TCCGCTTCTTTCCCGTCCCT

Consensus:

TTTGTCCaATAGAGCCTTTCTATcGGACActTTTcTCCGaTTcTTgCaCgTcCcT

>Bacillus_Fam_417_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55

Alignment score = 0.636364

GCF_000709935.2_ASM70993v2_genomic.fna_1:279198-279562 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=AATTGCTCCA Num.seqs=7

Similarity=0.831387

0 AATTGCTCCAGCTGATTTATAGGGAACCATAATTG---CTTTTTGATACCCATA

Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_2:135718-136030

Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GGGAAGCAAA Num.seqs=4 Similarity=0.736625 50

ATTTGCTCCGTCTGATTTATGAGGTACCAT-TTTGACGCTTTTGTCTTCCCTATA

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Consensus:

AaATTGCTCCagCTGATTTATaaGGaACCATAaTTGacgCTTTTTGaTaCCcATA

>Bacillus_Fam_418_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.624242
GCF_000986785.1_ASM98678v1_genomic.fna_1:69648-69960 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=CCTCCATTCG Num.seqs=6 Similarity=0.831447
0 CCTCCATTCGGA CTC-GAGACACCGCTTTC-CTC-CTCGGCCTGTCCGAATCAGA
Rev.of_GCF_001591645.1_ASM159164v1_genomic.fna_5:52435-52699
Satlength=265 Nr of Repeats=5 RepeatLength=53 seed=TCGGACAGC Num.seqs=4
Similarity=0.878407 48
CCTTCATTCGGA CTCAGA-AGATCACTTGCTCTCGCTTTG-CTGTCCGAATCAGT

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Consensus:

CCTcCATTCGGA CTCaGaAcAcCaCTTgCtCTCgCTcgGcCTGTCCGAATCAGa

>Bacillus_Fam_419_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.669697
GCF_001420715.1_ASM142071v1_genomic.fna_22:613446-613812 Satlength=367 Nr
of Repeats=7 RepeatLength=52 seed=TTCAAAAGAC Num.seqs=5
Similarity=0.861538 0
TTCAAAAGACCAAGAGGAAGGAAAAATCAG--GTGCGATGGTCTTTAT-NGGGA
Rev.of_GCF_001420715.1_ASM142071v1_genomic.fna_22:3743530-3743790
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TCCTCTTGGT Num.seqs=5
Similarity=0.866667 17 -
TCAAAAGACCAAGAGGAAGG-AAAACCGGAAG-CGAGATGTCCTTTATAAGGGT

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Consensus:

tTCAAAAGACCAAGAGGAAGGaAAAAcCaGaaGtCGAGATGgcCTTTATaaGGGa

>Bacillus_Fam_420_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.627273
GCF_001420715.1_ASM142071v1_genomic.fna_22:733261-733781 Satlength=521 Nr
of Repeats=10 RepeatLength=52 seed=GGTAACAATA Num.seqs=10
Similarity=0.930484 0
GGTAACAATAGAAGGAGTATCGTGCCCGAAATCAAGCCCG-AAGAAGG-AATAT-
Rev.of_GCF_001420715.1_ASM142071v1_genomic.fna_22:2607422-2607686
Satlength=265 Nr of Repeats=5 RepeatLength=52 seed=TATTGTTACC Num.seqs=3
Similarity=0.897436 10
GGTAACAATAGTCCAAGTATTGTGCCCGAAATCAAG--GTAAGCAGGCAAAAAC

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Consensus:

GGTAACAATAGaacaAGTATcGTGCCCGAAATCAAGcccGtAAGaAGGcAAaAac

>Bacillus_Fam_421_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.630303
GCF_001439915.1_ASM143991v1_genomic.fna_83:102373-102576 Satlength=204 Nr
of Repeats=4 RepeatLength=52 seed=GGTTATGAAG Num.seqs=3
Similarity=0.794872 0
GGTTATGAAGGAC--ATTCCGAAGAGAGAACNNCGACGAACAGTCCTTCATCGA

Rev.of_GCF_001636425.1_ASM163642v1_genomic.fna_1:2411742-2412106
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=ATGAAGGACT Num.seqs=7
Similarity=0.880342 49
GGGGATGAAGGACGAAAGGACGAGGAGAGAA--GCGA-GAAAAGTCCTTCATCGA

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Consensus:

GGggATGAAGGACgaaAggaCGAaGAGAGAAcngCGAcGAAaAGTCCTTCATCGA

>Bacillus_Fam_422_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.624242
GCF_001439915.1_ASM143991v1_genomic.fna_122:173650-173910 Satlength=261
Nr of Repeats=4 RepeatLength=52 seed=TTTCGGACTC Num.seqs=3
Similarity=0.811966 0
TTTCGGACTCATCA--TTTCGAAA-TATGCTCGCGGCTGTCCGAATCAAGCGCTC
Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_124:121562-121979
Satlength=418 Nr of Repeats=8 RepeatLength=52 seed=CCTTGATTTCG Num.seqs=7
Similarity=0.800977 48
TTTCGGACTCAACAGGCTAAAAAGTATGCACTC--TGTCCGAATCAAGGGCTC

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Consensus:

TTTCGGACTCAaCAggcTaaaAAAgTATGCaCgCggcTGTCCGAATCAAGcGCTC

>Bacillus_Fam_423_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.651515
GCF_001591945.1_ASM159194v1_genomic.fna_9:103168-103374 Satlength=207 Nr
of Repeats=4 RepeatLength=52 seed=TTTGTCTTTT Num.seqs=3
Similarity=0.880342
0 TTTGTCTTTTAGCACGCT-TCTCTCGGACATCTTCTCCCT-TTTCTTCCCCAC-
GCF_001591945.1_ASM159194v1_genomic.fna_9:110417-110677 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TCCTTTAGAC Num.seqs=5
Similarity=0.835897
4 TCTGTCTTTTAG-ACGCTCTCTCTTAGACA-CTT-CTCCCTGATTCTCACCCACT

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Consensus:

TcTGTCTTTTAGcACGCTcTCTCTcaGACAtCTTcCTCCCTgaTTCTcaCCCACT

>Bacillus_Fam_424_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.612121
GCF_001636315.1_ASM163631v1_genomic.fna_1:1916684-1916892 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=ACCTTTTTCa Num.seqs=4
Similarity=0.846154 0
ACC---TTTTTCATAGAGTTCCCTCTTTTTTCGGGCAATGCAACCCACTCTCATTT
GCF_001636315.1_ASM163631v1_genomic.fna_1:972743-973108 Satlength=366 Nr
of Repeats=7 RepeatLength=52 seed=CAATGCAACC Num.seqs=6
Similarity=0.733333
33 ACCGAAAATATCA-ATCTTTTCTCTTTTTTCGGGCAATGCAACCCCTTCCATTA

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Consensus:

ACCgaaaaTaTCAtAgagTTcCCTCTTTTTTCGGGCAATGCAACCCaCTccCATTa

>Bacillus_Fam_425_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.603030
GCF_001636315.1_ASM163631v1_genomic.fna_1:2344320-2344632 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=GATGAAGGAC Num.seqs=6
Similarity=0.933333 0
GATGAAGGACATTTTG-CATGGGAACCTGCTTCG-TTTGGTCTTCATC-ACGCC
GCF_001636425.1_ASM163642v1_genomic.fna_1:2956434-2957110 Satlength=677
Nr of Repeats=13 RepeatLength=52 seed=AAGGGCTTCA Num.seqs=13
Similarity=0.827447 34
-ATGAAGGACTTTTCGCCAT-GG-AACCAACCTCGATAAGGGCTTCATCGACGCC

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Consensus:

gATGAAGGACaTTTcGcCATgGGaAACCaCcTCGaTaaGGgCTTCATCgACGCC

>Bacillus_Fam_426_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.657576
GCF_001636345.1_ASM163634v1_genomic.fna_1:388884-389144 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GAAACAGGAC Num.seqs=5
Similarity=0.820126
0 GAAACAGGACANTAAACCCAGTAAGTGGAAAATAGAGAGACG-G-AAA-GAGCG
Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:2655784-2656044
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTTCTCTCAT Num.seqs=5
Similarity=0.841026 3 -
AAACAGGACANGAAACCCAGTAACTGGTAAAT-G-GAGTCGTGTAAATGAGAG

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Consensus:

gAAACAGGACANgAAACCCAGTAActGGaAAATaGaGAGaCGtGtAAAtGAGaG

>Bacillus_Fam_427_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.690909
GCF_002019605.1_ASM201960v1_genomic.fna_1:4272331-4272850 Satlength=520
Nr of Repeats=10 RepeatLength=52 seed=AACGAGCAGG Num.seqs=9
Similarity=0.846154 28
GGTAACTATGAAGCGTTCATGATGCCCGAACGAGCAGGAGAAGAAA---GAAAC
GCF_002019605.1_ASM201960v1_genomic.fna_1:4387305-4388137 Satlength=833
Nr of Repeats=16 RepeatLength=52 seed=CGAGAGAAGA Num.seqs=16
Similarity=0.917949 28
GGTAACTATAGAGCGTTCATAATGCCCG--CGAG-AGAAGAAAAAATGAGAGAAC

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Consensus:

aaCGAGcAGaAGAAaAAAtgaGAaAACGGTAACTATaaAGCGTTCATaATGCCCG

>Bacillus_Fam_428_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.636364

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Consensus:

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>Bacillus_Fam_429_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.660606
GCF_001315165.1_ASM131516v1_genomic.fna_30:29786-29998 Satlength=213 Nr
of Repeats=4 RepeatLength=53 seed=CCCTTATGCG Num.seqs=4
Similarity=0.882600
0      CCCTTATGC-GAGGAAATGTCATCTATAAGGGTACAATTA-AGAGCGAATCATA
GCF_001315165.1_ASM131516v1_genomic.fna_78:17736-17948 Satlength=213 Nr
of Repeats=4 RepeatLength=53 seed=AATCGTACCC Num.seqs=4
Similarity=0.878407
46     CCCTTATGCAGGGTAACCGGTC-CCTATAAGGGTACAATTAGGGAG-GAATCGTA
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CCCTTATGCaGaGgAAaagGTCacCTATAAGGGTACAATTAgagAGGcGAATCaTA

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>Bacillus_Fam_430_55_2 Nr. of seq. 2 Alignment length(with gaps) = 55
Alignment score = 0.660606
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_22:99833-100097
Satlength=265 Nr of Repeats=5 RepeatLength=53 seed=ATTGGTGACC Num.seqs=4
Similarity=0.920335 1 CATTGGTGACCTTTCTTCAAC-
TTCACCCACCTAGATAGGGCACCAAT-AGCCTT
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_22:209996-210208
Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=ATTGGTGACC Num.seqs=4
Similarity=0.756173 1
CATTGGTGACCTTTCTTCTCTTTTCATCTACC-ACTTAGGGCACCAATCAACC-C
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Consensus:

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>Bacillus_Fam_431_54_2  Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.669753
GCF_000171615.1_ASM17161v1_genomic.fna_74:41439-41699 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=GCGCGGTGCA Num.seqs=5 Similarity=0.912821
0      GCGCGGTGCAGAAAAGAGGAG-AAGGAAGAGAGAACAGCCCCGCGCGAGCCG-G
Rev.of_GCF_000171615.1_ASM17161v1_genomic.fna_128:4002-4209 Satlength=208
Nr of Repeats=4 RepeatLength=52 seed=GCTCTTCTCC Num.seqs=3
```

37

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gCGCGGTGCagaAAAGAGGAGaAAaGAAGaGAGAAcAGCaCCGCGCGaGccGaG

Alignment score = 0.743827

0 AATGAAGACACCTCTC-CTCCTAATTTACCTCACTCACGTCTTCATACC-TCG

Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=ATGTCTTCAT Num.seqs=8

ATGAAGACATCTCTCACTCC-ATTTTCACCTCACGGACGTCTTCATACCGTCT

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aATGAAGACAcCTCTCaCTCtAaTTTCACCTCACgcACGTCTTCATACCgTCg

Alignment score = 0.629630

Similarity=0.865690

Rev.of GCF 000175075.1 ASM17507v1 genomic.fna 31:202656-202864

Similarity=0.893162

GG-AAACATTGTCCTCGTAGG-GTGTCAATGAAGCCCTGAGCCGATGAAAAAGA

GGtaAACATTGTCCTCGTAGGaGTGt cAATGAaGCCcTcaaCCGaTGaAAAAGa

Alignment score = 0.771605

Similarity=0.816872

GCF_000177235.2_ASM17723v2_genomic.fna 1:4577046-4578346 Satlength=1301

Similarity=0.816154

TCTTACCTTCACACTATTTTATTTCGCTCAAGGGCAGATGG--GACNGCGCCA

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Consensus :

TCTTACCTTCACACTaTTTTTTaTTcGCTCAAGGGCAGATGGcaGACtqCqCCA

>Bacillus_Fam_435_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
 Alignment score = 0.654321
 GCF_000177235.2_ASM17723v2_genomic.fna_1:4033931-4034762 Satlength=832 Nr
 of Repeats=17 RepeatLength=52 seed=TTTCCTTTCT Num.seqs=14
 Similarity=0.882784 3
 GGCTTTCCTTTCT-ATGCACTTTTCATCCTTAGAAAGGAATACTA-ACTCCTCT
 GCF_000177235.2_ASM17723v2_genomic.fna_1:4080458-4081081 Satlength=624 Nr
 of Repeats=12 RepeatLength=52 seed=AAAGGAATGC Num.seqs=11
 Similarity=0.865734 32
 CGCTTTCCTTTCTAACGCTCGTTTC-TCTTCAGAAAGGAATGCTAGACTCGT-T

 Consensus:

TTTCCTTTCTaAcGCaCgTTTCaTCcTcAGAAAGGAATaCTAgACTCcTcTcGC

>Bacillus_Fam_436_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
 Alignment score = 0.617284
 GCF_000181495.1_ASM18149v1_genomic.fna_177:12081-12289 Satlength=209 Nr
 of Repeats=4 RepeatLength=52 seed=TTCATAAGAC Num.seqs=4
 Similarity=0.846154
 0 TTCAT-AAGACCAAACTAAGGTGGAAATGCAG-TTAGGGTGTCTCATGAACGC
 Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_156:9142-9350 Satlength=209
 Nr of Repeats=4 RepeatLength=52 seed=TCTTTTGGC Num.seqs=4
 Similarity=0.849057 18
 TTCATGGAG-CCAAAAAGAGAGTGGATTTCAAGATTAGGGTGTCTCATGAAAGG

 Consensus:

TTCATgAAGaCCAAAAagAaaGTGGAaaTcaAGaTTAGGGTGTCTCATGAAaGc

>Bacillus_Fam_437_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
 Alignment score = 0.635802
 GCF_000181495.1_ASM18149v1_genomic.fna_177:51711-52127 Satlength=417 Nr
 of Repeats=8 RepeatLength=52 seed=GTTAGACCT Num.seqs=8
 Similarity=0.792677
 0 GTTAGACCTGTGGAATTGAAGAAAAAGA-AATCGGCCGTGTAAAA-AGGTTG
 GCF_000181495.1_ASM18149v1_genomic.fna_186:402271-402635 Satlength=365 Nr
 of Repeats=7 RepeatLength=52 seed=AAGAGAATCG Num.seqs=7
 Similarity=0.820305 25
 TTTGGACCCGGTGAATCCNA-AAAGAAGAGAATCGACCGGGTTAAAGAGG-TG

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 Consensus:

gTTaGACCCgGTGGAATccaAgAAAaAAGAgAATCGaCCGgGTTAAAgAGGtTG

>Bacillus_Fam_438_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
 Alignment score = 0.635802
 GCF_000242895.2_ASM24289v3_genomic.fna_1:1675220-1675480 Satlength=261 Nr
 of Repeats=5 RepeatLength=52 seed=AAAAAGTGTG Num.seqs=5

Similarity=0.902564	0
AAAAAGTGTGGAG-CGGTAACTGAAACAAG-GAAGTAGTGACCAAAGAGGGTGG	
GCF_000242895.2_ASM24289v3_genomic.fna_1:1925605-1925915	Satlength=311
of Repeats=6 RepeatLength=52 seed=CGGTCACTAA Num.seqs=5	
Similarity=0.757862	14
AAAAAGNACCCAGNCGGTCACT-AAACCAGTGAAGTAGTGACCAAAGAGAG-GA	

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Consensus:

AAAAAGtaccAGnCGGTaACTgAAACaAGtGAAGTAGTGACCAAGAGaGtGa

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>Bacillus_Fam_439_54_2  Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.611111
GCF_000311725.1_ASM31172v1_genomic.fna_2:554922-555286 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=TGTC CGAATC Num.seqs=7
Similarity=0.875458
0      TGTCCGAATC-CAGCTATTATTCGGACTCCTTCTTTGTTTTTCGCTCCAC-TC
Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_116:114146-114724
Satlength=579 Nr of Repeats=10 RepeatLength=52 seed=GGTGTGATTC
Num.seqs=6 Similarity=0.815385
15     TGTCCGAATCACACCTACT-TTCAGACTCNACCTTCGCTTTTCCGC-CAACATC
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Consensus:

TGTCCGAATCaCAcCTAcTaTTCaGACTCcacCTTcGcTTTTcCGCtCaACaTC

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>Bacillus_Fam_440_54_2  Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.660494
GCF_000331575.1_ASM33157v1_genomic.fna_1:1524595-1525167 Satlength=573 Nr
of Repeats=11 RepeatLength=52 seed=TTTTCTGTCC Num.seqs=11
Similarity=0.902564 0
TTTTCTGTCCGAACTTGGCCTCAGTTCGGACTCAATTTTAGCTTTTGCTGCG--
Rev.of_GCF_000331575.1_ASM33157v1_genomic.fna_4:27225-27953 Satlength=729
Nr of Repeats=14 RepeatLength=52 seed=GACAGGAAAT Num.seqs=14
Similarity=0.915187 9
TTTCCTGTCCGAACTGGGGCTGAGTTCGGACACGA-TTtagCAGTT-CTGGGGA
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Consensus:

TTTcCTGTCCGAACtGgGcCTcAGTTCGGACaCaAtTTTAGCagTTgCTGcGga

```
>Bacillus_Fam_441_54_2  Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.626543
GCF_000374345.1_ASM37434v1_genomic.fna_8:71233-71545 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=AGAAAATATC Num.seqs=6 Similarity=0.796581
0      AGAAAATATCGGGCCGGAATGGCGTTCATAGGGNAAATGAAAGCTATTTTG-G-
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_18:16790-17225
Satlength=436 Nr of Repeats=6 RepeatLength=52 seed=TGGCTTTCAT Num.seqs=4
Similarity=0.591919
AG-AAATAGCAGG-GGGAATGGCGTTCATTTGGGTGATGAAAGCCATCTTGAGA
44
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Consensus:

AGaAAATAgCaGGccGGAATGGCGTTCATagGGgaaATGAAAGCcATcTTGaGa

>Bacillus_Fam_442_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.617284
GCF_000374345.1_ASM37434v1_genomic.fna_16:99-567 Satlength=469 Nr of
Repeats=9 RepeatLength=52 seed=GCGTTCATCC Num.seqs=9 Similarity=0.717680
0 GCGTTCATCCCGCTNATGAACGTCATTACAANTCAANTTTTGCA-CC-GGGATG
Rev.of_GCF_000374345.1_ASM37434v1_genomic.fna_74:7594-7802 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=GGGGATGAAC Num.seqs=4
Similarity=0.790598 12
GCGTTCATCCCCCTTATGAACGCCATCTC-GTTCAA-TTTTCCATCCTGTGATA

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Consensus:

GCGTTCATCCCCCTtATGAACGcCATcaCaatTCAAnTTTTcCATCctGgGATa

>Bacillus_Fam_443_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.641975
GCF_000401235.1_BacNeaAAU1_genomic.fna_108:2225-2531 Satlength=307 Nr of
Repeats=4 RepeatLength=52 seed=AGGTAACAGAG Num.seqs=3 Similarity=0.775681
0 AGGTAACAGAGAGAACTGCTCAGTGACCGT-TGCA-GCAAAGGAAAGGAGGAAA
GCF_000401235.1_BacNeaAAU1_genomic.fna_276:14688-14894 Satlength=207 Nr
of Repeats=4 RepeatLength=52 seed=GAAAAACAAA Num.seqs=3
Similarity=0.914530
36 AGGTAACAGAGAGGGCTCCTCAGTGCCCGTAAGCACGAAAAACAAA--AGCAAA

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Consensus:

AGGTAACAGAGAGaAcTcCTCAGTGaCCGTaaGCACGaAAAacAAAggAGcAAA

>Bacillus_Fam_444_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.654321
GCF_000430765.1_ASM43076v1_genomic.fna_6:269287-269548 Satlength=262 Nr
of Repeats=5 RepeatLength=52 seed=CACTTCGGAC Num.seqs=4
Similarity=0.871795
0 CACTTCGGACAGATTGCGGACCCTGGT--CTCAAAAGCTGTCCGAACTCAGATC
GCF_002019645.1_ASM201964v1_genomic.fna_1:4520185-4521327 Satlength=1143
Nr of Repeats=22 RepeatLength=52 seed=GTTCGGACAG Num.seqs=20
Similarity=0.812551 2
AAGTTCGGACAGCTT--GGACCCCAATAGATCAAAAGCTGTCCGAACTCAGAGC

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Consensus:

aAcTTCGGACAGaTTgcGGACCCcaaTagaTCAAAAGCTGTCCGAaCTCAGAgC

>Bacillus_Fam_445_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.694444

GCF_000508325.1_BAVI_1_genomic.fna_12:41249-41457 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AAAAAAGAAG Num.seqs=4 Similarity=0.910256
0 AAAAAAGAAGGAGACGGGCACTGTGGAG-GGTTTCAGAGTGCCCGTGGGAGCTG-
Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_10:78357-78669
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TTACACGGGCA Num.seqs=6
Similarity=0.852991 47
AAAAAGCGGGAGTCGGTCACT-TAGAGAGGTTTCATAGTGCCCGT-GAAGCTGA

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Consensus:

AAAAAAGaaGGAGaCGGgCACTgTaGAGaGGTTCAgAGTGCCCGTgGaAGCTGa

>Bacillus_Fam_446_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.604938
GCF_000708755.2_ASM70875v2_genomic.fna_7:27921-28441 Satlength=521 Nr of Repeats=9 RepeatLength=52 seed=TTGACCCTTC Num.seqs=8 Similarity=0.814103
0 TTGACCCTTCAGCTCTNT--TGGTTTGCTCTGAAGAGTCATATGCNATCCTGTT
GCF_000709935.2_ASM70993v2_genomic.fna_4:144384-144644 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GAAGGGTCAT Num.seqs=5
Similarity=0.730818
29 TAGACCCTTCAGAT-TATGCTGGTCT-CCGTGAAGGGTCATATGTGCTCCCGTT

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Consensus:

TaGACCCTTCAGaTcTaTgcTGGTcTgCccTGAAGaGTCATATGcgaTCCcGTT

>Bacillus_Fam_447_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.629630
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_41:274960-275582
Satlength=623 Nr of Repeats=12 RepeatLength=52 seed=GTCTATGAGC
Num.seqs=11 Similarity=0.849285 0
GTCTATGAGCCCCGAAAA-AGCAGAAACCCCGTAAAAAGCGGTTC-ATAGAAATG
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_43:179773-180164
Satlength=392 Nr of Repeats=8 RepeatLength=52 seed=CGTCTATGAA Num.seqs=7
Similarity=0.941392 51
GTCTATGAACCCAAAAATAAC-GAAATTCCGCAAAAA-CGGTCCTATAGAACTC

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Consensus:

GTCTATGAaCCCaAAAAAtAaCaGAAAccCCGcAAAAAgCGGTcCtATAGAAaTc

>Bacillus_Fam_448_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.620370
GCF_000759675.1_ASM75967v1_genomic.fna_159:74142-74454 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TTTGGTTCCC Num.seqs=6
Similarity=0.748971
0 TTTGGTTCCCTT-TATCGTTGAAAAGGTGAGTTCTTGGGAATCAAAAGAGAGT-
GCF_000759675.1_ASM75967v1_genomic.fna_170:98-669 Satlength=572 Nr of Repeats=11 RepeatLength=52 seed=AGGGGAATCAA Num.seqs=10
Similarity=0.895157
34 TTGGGTTCCCTTCAAAGGGAAAAAGCTGAGTT-GAGGGGAATCAAAAG-GAGTC

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Consensus:

TTgGGTTCCTTcaAacGgaaAAAAGcTGAGTTcgaGGGAATCAAAAGaGAGTc

>Bacillus_Fam_449_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54

Alignment score = 0.654321

GCF_000787375.1_ASM78737v1_genomic.fna_2:246377-246585 Satlength=209 Nr

of Repeats=4 RepeatLength=52 seed=TACTCTTCTC Num.seqs=4

Similarity=0.884615

0 TACTCTTCTCTCAATCTCT-TTTTCGGGCGACCATCCTTCC-CTTTGACTACCG

GCF_000787375.1_ASM78737v1_genomic.fna_76:11-375 Satlength=365 Nr of

Repeats=7 RepeatLength=52 seed=CTACCGTAAT Num.seqs=7 Similarity=0.860806

46 TAATCCTCT-TCAGGCTCTCTTTTCGGG-TTCCAACCTCCTCTTTGGCTACCG

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Consensus:

TAATCcTCTcTCAagCTCTcTTTTCGGGcgaCCAaCCTTCctCTTTGaCTACCG

>Bacillus_Fam_450_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54

Alignment score = 0.654321

GCF_000813125.1_ASM81312v1_genomic.fna_8:49357-49722 Satlength=366 Nr of

Repeats=7 RepeatLength=52 seed=GGGGGACTTC Num.seqs=6 Similarity=0.875214

0 GGGGGACTTCGGACAAATT-CTG-CTCTTCCATCAGCTGTTTGTCCGAACCTG

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_57:52500-52812

Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GTTCGGACAA Num.seqs=4

Similarity=0.668724

49

GGGTGACTTCGGACAAATTGAAGCCTC-TCCGGC-GATTCTTTGTCCGAACCTG

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Consensus:

GGGgGACTTCGGACAAATTgaaGcCTcTCCagCaGaTgcTTTGTCCGAACCTG

>Bacillus_Fam_451_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54

Alignment score = 0.669753

GCF_000813125.1_ASM81312v1_genomic.fna_12:28-289 Satlength=262 Nr of

Repeats=5 RepeatLength=52 seed=TGGAAATGTC Num.seqs=4 Similarity=0.846154

0 TGGAAATGTCTGAAGTAGCCCCAGGTTTCGGCCAAAACAAC--CACTGGGATCGC

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_141:38715-39390

Satlength=676 Nr of Repeats=11 RepeatLength=52 seed=ACTTCAGACA

Num.seqs=8 Similarity=0.728938

15 -GGAAATGTCTGAAGTAGCCNCAGGTTTCAGCCAAAATACCGTCA-TAGNCACGA

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Consensus:

tGGAAATGTCTGAAGTAGCCcCAGGTTCaGCCAAAaAaCgtCAcTaGgaaCGa

>Bacillus_Fam_452_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54

Alignment score = 0.611111

GCF_000934845.1_ASM93484v1_genomic.fna_40:14255-14619 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=AAACACCAGT Num.seqs=7 Similarity=0.798443
0 AAACACCAGTAACT-GGGAAAACAGTACACCAATAAGCCG-ATTGGAGCACTA
Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_37:21000-21475
Satlength=476 Nr of Repeats=9 RepeatLength=53 seed=GCACCAATAC Num.seqs=7
Similarity=0.824221 49
AAAAACCAGAAATTAGGNAATNAGGTCACCAAT-GAGCCGTATTGGTGCNCGA

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Consensus:

AAAaACCAGaAAcTaGGgAAAacAGgaCACCAATaaAGCCGtATTGGaGCaCgA

>Bacillus_Fam_453_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.648148
GCF_000986785.1_ASM98678v1_genomic.fna_2:121115-121636 Satlength=522 Nr of Repeats=10 RepeatLength=52 seed=ATCAGTGACC Num.seqs=9
Similarity=0.800570
0 ATCAGTGACC--TTTTCGGAGCTGGCCTGCTCATTTTGGGCACTGACAGCCTCT
Rev.of_GCF_000986785.1_ASM98678v1_genomic.fna_22:27488-27748
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TGTCAGTACC Num.seqs=5
Similarity=0.830818 46
CTCAG-GACCACTTTTTGGAG-GGGNCGGCTCATTTTGGGTACTGACAGCGCAT

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Consensus:

aTCAGtGACCacTTTTcGGAGcgGGcCgGCTCATTTTGGGcACTGACAGCccaT

>Bacillus_Fam_454_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.663580
GCF_000986785.1_ASM98678v1_genomic.fna_5:231430-232157 Satlength=728 Nr of Repeats=14 RepeatLength=52 seed=TGTCAGTGCC Num.seqs=13
Similarity=0.751820 0
TGTCAGTGCCGTGTTTTTGTNGTGAGGA-NGTTTTTGGGTACTGAGGNGAGT-
Rev.of_GCF_000986785.1_ASM98678v1_genomic.fna_33:21710-22022
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GGCACTGACA Num.seqs=6
Similarity=0.745912 10
TGTCAGTGCCCGTTTTTTCGAG-GGGGAGCGAGTTTTTGGGTACTGAGGGG-GTC

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Consensus:

TGTCAGTGCCcGTTTTTTCgaGtGaGGAgcGagTTTTGGGTACTGAGGgGaGTc

>Bacillus_Fam_455_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.617284
GCF_001315085.1_ASM131508v1_genomic.fna_43:21365-21625 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AACCAAAAGA Num.seqs=5
Similarity=0.794872
0 AACCAAAA-GAACGTGTG-GAGCAGAGGAAAAAGGTCATCATAAGGTCGATGAG
GCF_001315085.1_ASM131508v1_genomic.fna_73:11538-11746 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AAACCAAGCT Num.seqs=4

Similarity=0.801363

5 GCCCAAAACCAAGCTGAGCGAGCACA--AAAAAGGTCATCATAAAGCCGATGAA

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Consensus:

aaCCAAAAccAAcCTGaGcGAGCAcAggAAAAAGGTCATCATAAaGcCGATGAa

>Bacillus_Fam_456_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54

Alignment score = 0.604938

GCF_001420595.1_ASM142059v1_genomic.fna_11:518620-519088 Satlength=469 Nr

of Repeats=9 RepeatLength=52 seed=GGTAACCAAA Num.seqs=9

Similarity=0.764245

0

GGTAACCAAAAGGNAAGCAT-TGGTGCCCGTAAACGAGGAAAAATAG-CGTTCCAC

Rev.of GCF_001591445.1_ASM159144v1_genomic.fna_2:21009-21217

Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TCACGGGCAT Num.seqs=4

Similarity=0.816239

31

GGTAACCATAGG-AAGCGTATGATGCCCGTGAAGGTTGAAAA-AGTGGATCAAC

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Consensus:

GGTAACCAaAGGnAAGCaTaTGaTGCCCGTaAAcGagGAAAAAtAGtcGaTCaAC

>Bacillus_Fam_457_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54

Alignment score = 0.632716

GCF_001420595.1_ASM142059v1_genomic.fna_11:2718654-2718914 Satlength=261

Nr of Repeats=5 RepeatLength=52 seed=TCTTGTTACC Num.seqs=5

Similarity=0.912821

0

TCTTGTTACCGTGAACCTCACT-TTTTCTGCTTTCAGGGGTACATGACACA-CAC

GCF_001420595.1_ASM142059v1_genomic.fna_11:4652534-4652852 Satlength=319

Nr of Repeats=6 RepeatLength=53 seed=TCTTGTTACC Num.seqs=6

Similarity=0.902725

0

TCTTGTTACCGCGAACACTCTCTTTTCTACTTTCTTGGGCACATGTGGCATCT-

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Consensus:

TCTTGTTACCGcGAACaCaCTcTTTTCTaCTTTCagGGGcACATGacaCAcCac

>Bacillus_Fam_458_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54

Alignment score = 0.635802

GCF_001420715.1_ASM142071v1_genomic.fna_22:875387-875647 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=5

Similarity=0.546667

0

TGTCCTTCATAG-TGNTAATGAAGGACAAGTTNGAAGGAAA-AATAAGTACAGA

GCF_001420715.1_ASM142071v1_genomic.fna_22:1038345-1038761 Satlength=417

Nr of Repeats=8 RepeatLength=52 seed=ATGAAGGACA Num.seqs=8

Similarity=0.602293

18

TGTCCTTCATAGACGgTNATGAAGGACAAATTCGNAAAAAAGAATAGGCAANGC

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Consensus:

TGTCCTTCATAGacGgTaATGAAGGACAAaTTcGaAaaAAAgAATAaGcAaaGa

>Bacillus_Fam_459_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.722222
GCF_001591445.1_ASM159144v1_genomic.fna_1:86829-87037 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=CTCTATGTTA Num.seqs=4 Similarity=0.846154
0 CTCTATGTTACCGTCAACCGCTTTTTTCTT-GCTCCACGGTCACTTA-AAGCCT
GCF_001591445.1_ASM159144v1_genomic.fna_74:6946-7154 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TATGTTACCG Num.seqs=4 Similarity=0.615421
3 CTTTATGTTACCGTACACTTC-TTTTTCTTCNCTGCACGGTCACTTAGAAGCCT

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Consensus:

CTcTATGTTACCGTaaACcgCtTTTTTCTTcgCTcCACGGTCACTTAgaAAGCCT

>Bacillus_Fam_460_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.608025
GCF_001591485.1_ASM159148v1_genomic.fna_6:19015-20109 Satlength=1095 Nr
of Repeats=20 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=12
Similarity=0.790210 0
TGTCCTTCATTCCTGATGAAGGACATTTTTCTCACGA--CACAACCATGGTA
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:3151872-3152287
Satlength=416 Nr of Repeats=8 RepeatLength=52 seed=AAATGGTCTT Num.seqs=7
Similarity=0.843712 29 -
GGCCTTCATTCGCTTATGAA-GACCATTTTCACTCGAGCCACAACCTTTTTT

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Consensus:

tGgCCTTCATTCCaCTgATGAAGGACaaTTTTCaCaCGAgcCACAACCaTggTa

>Bacillus_Fam_461_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.617284
GCF_001591585.1_ASM159158v1_genomic.fna_16:64946-65206 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TCTCTCACTT Num.seqs=5
Similarity=0.948718
16 CCA-CTTTTTCCTTTCCT-CTCTCACTTTTCGGCTTTCATCAANCTCCTGTACA
GCF_001591585.1_ASM159158v1_genomic.fna_21:8882-9244 Satlength=363 Nr of
Repeats=7 RepeatLength=52 seed=GCTCTCCTTT Num.seqs=5 Similarity=0.892308
17 CCATCTTTCT-CTTCCCTGCTCTC-TTTTTGGTTTTCATCANC GTTATGAACA

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Consensus:

TgCTCTCaCTTTTcGGcTTTCATCAaccTcaTGaACACCAcCTTTcTcCTTcCC

>Bacillus_Fam_462_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.608025
GCF_001591645.1_ASM159164v1_genomic.fna_1:794104-794312 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=AACGTTCTTC Num.seqs=4
Similarity=0.830713
0 AACGTTCTTCATCCGGCTTATGAAAGACGTTACGGAGCGATTTACTTGA--GCA

GCF_001591645.1_ASM159164v1_genomic.fna_4:234973-235232 Satlength=260 Nr
of Repeats=5 RepeatLength=52 seed=TGATTGAAAC Num.seqs=4
Similarity=0.718254
44 -ACGTTCTTCATCAGGAGGATGAAAGACGTTAGGGTGTGA-ATAAATGATTGAA

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Consensus:

aACGTTCTTCATCaGGaggATGAAAGACGTTAcGGaGcGAtaTAaaTGAttGaA

>Bacillus_Fam_463_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.709877
GCF_001591665.1_ASM159166v1_genomic.fna_35:21709-21917 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=ATCGAAGTAG Num.seqs=4
Similarity=0.807692
0 ATCGAAGTAGACAG-ATTCTACTTCAACTTTCTAG-TCTAAAATCCAGGGAAAC
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_68:10391-10651
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CTTCTACTTC Num.seqs=5
Similarity=0.828205 13
GTCGAAGTAGA-AGTGCTCTACTTCAACATTCANGCTC-AAAATCCAGGGAAAC

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Consensus:

aTCGAAGTAGAcAGtacTCTACTTCAACaTTCaaGcTcTAAAAATCCAGGGAAAC

>Bacillus_Fam_464_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.682099
GCF_001591805.1_ASM159180v1_genomic.fna_10:65143-65350 Satlength=208 Nr
of Repeats=4 RepeatLength=52 seed=TTTTTCCGG Num.seqs=3
Similarity=0.948718
49 TTTCCGGGCGACGGGCACTATGAACCTCTTATAGTGCCCATGAACG-CTC-TTT
Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_16:206404-206612
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AGGTTCATAG Num.seqs=4
Similarity=0.897436 79
TTTCCTGTCCGCGGCACTATGAACCTTTTATAGTGCCC--GTTCGTGTCTTTT

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Consensus:

TTTTTTCCgGgCcaCGGGCACTATGAACCTcTTATAGTGCCCatGaaCGtcTcT

>Bacillus_Fam_465_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.604938
GCF_001636315.1_ASM163631v1_genomic.fna_1:2650478-2651310 Satlength=833
Nr of Repeats=16 RepeatLength=52 seed=TGCTGTCTGA Num.seqs=14
Similarity=0.845590 30
AGTATAGAGAGCAAGTAGAAAGGCGCTAGGTGCTGTCTGAAAAG--GAAAATTG
GCF_001636315.1_ASM163631v1_genomic.fna_1:3094934-3095142 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=CAAGTAGAAG Num.seqs=4
Similarity=0.863248 63
AATTTAGAGATCAAGTAGAAGCCCTCTAGCTGCTGTCT--AAAGTCAAAAATCC

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Consensus:

TGCTGTCTgaAAAGtcaAAAATccAaTaTAGAGAgCAAGTAGAAaccCgCTAGc

>Bacillus_Fam_466_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.703704
GCF_001636315.1_ASM163631v1_genomic.fna_1:3142771-3143187 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=CTATAGGCGA Num.seqs=8
Similarity=0.869963 0
CTATAGGCGACCGAGAG-GCGAGAAAAAAGTGAGGA-GGGTAGCGTATAAGGA
GCF_001636315.1_ASM163631v1_genomic.fna_1:3843104-3843416 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=TAGGCGACCG Num.seqs=6
Similarity=0.844864 3
TTATAGGCGACCGAGAGAGCG-G-AAAAAAGAGATTACGGGTAGCGTAGAAGGG

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Consensus:

cTATAGGCGACCGAGAGaGCGaGaAAAAAAGaGAggAcGGGTAGCGTAgAAGGa

>Bacillus_Fam_467_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.697531
GCF_001636315.1_ASM163631v1_genomic.fna_1:3535170-3535534 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=GTGTGAATTT Num.seqs=7
Similarity=0.894994 17
CCATTGGAAACACTTTGGTTGTAATTTT--CTAGAGTATTGTCTCGGCAATAGCCG
GCF_001636315.1_ASM163631v1_genomic.fna_1:3851718-3851925 Satlength=208
Nr of Repeats=4 RepeatLength=52 seed=CTATTGGAAA Num.seqs=3
Similarity=0.897436 52
CTATTGGAAACACTTTG--TCCAATTTTAACTCAAGTATTGTCTGCCAATACCGG

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Consensus:

gtTccAATTTTaaCTaaAGTATTGTCTGcCAATAcCcGcCATTGGAAACACTTTG

>Bacillus_Fam_468_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.611111
GCF_001636325.1_ASM163632v1_genomic.fna_1:372049-372413 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=ATCGCCCGTT Num.seqs=7
Similarity=0.791255
0 ATCGCCCGTTCTGCTGCGNAAAGNTCCA-CAGAAGGTAGAAGAGAAGCGT-CCTC
Rev.of_GCF_001636325.1_ASM163632v1_genomic.fna_1:2619668-2620033
Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=TTGACCTTC Num.seqs=6
Similarity=0.852991 39
ATCGCCCGTTCTGCTGCTCAAAG-TATAGCAGAAGGTGAATAGAAG-GTGTCTC

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Consensus:

ATCGCCCGTTCTGccGcccAAAGnTacAgCAGAAGGTaGAAGAGAAGcGTgcCTC

>Bacillus_Fam_469_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.623457

GCF_001636335.1_ASM163633v1_genomic.fna_1:484026-484390 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=AAAGTCCATC Num.seqs=7
Similarity=0.904762
0 AAAGTCCATCATAGCGTTGATGATGGACAAAACGCGGTGTGAAAGC--AAATGC
Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:2460494-2460702
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CTTTTTCGT Num.seqs=4
Similarity=0.974359 2
AGAGTCCGTCATCAAGGTGATGATGGACAAAACGTGGTCAGAAAACGGAAAA--

AaAGTCCaTCATaaaGgTGATGATGGACAAAACGcGGTcaGAAAaCggAAAagc

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Consensus:

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>Bacillus_Fam_471_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.604938
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_19:74323-74582
Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=GTTTTGTCTA Num.seqs=4
Similarity=0.846154 0 GTTTTGTCTAATAGGAGCGC-
T-CTATCGGACAACTAAGCTCTCTGGCCTCCT
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_20:569803-570062
Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=GTTTTGTCTG Num.seqs=4
Similarity=0.807692 0 GTTTTGTCTGATA-GA-
CGCTTCCTATTAGACAACTCTCCTCCCGAGACCACCT
```

GT TTTGTCTaATAgGAqCGCtTcCTATcaGACAAACTaacCTCcCaGaCCaCCT

Similarity=0.923077 0 GCCGCTTC-CAAGGCT-
GTTTCGAACACGATTAGCTTCTATTCGTTAACGTTCA
Rev.of_GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_42:756073-756385
Satlength=313 Nr of Repeats=5 RepeatLength=52 seed=CGAAAGTAGT Num.seqs=4
Similarity=0.931624 21 GCGGCTTCTCAA--
CTACTTTCGATCACGATTAGCTCCTTTTCTTTTACGTACA

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Consensus:

GCcGCTTcCAAggCTacTTTCGAaCACGATTAGCTcCTaTTCgTTaACGTaCA

>Bacillus_Fam_473_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.654321
GCF_000181495.1_ASM18149v1_genomic.fna_106:8005-8522 Satlength=518 Nr of
Repeats=8 RepeatLength=53 seed=TCGAAAAGAA Num.seqs=5 Similarity=0.939623
0 TCGAAAAGAAGCTAAACGATCCAATGAGAAGGGGAAACCGAGTGGATGTAGG-G
GCF_000181495.1_ASM18149v1_genomic.fna_107:1831-2096 Satlength=266 Nr of
Repeats=5 RepeatLength=53 seed=TGAAAAAGAG Num.seqs=5 Similarity=0.899371
0 T-GAAAAAGAGGTAACCGCCCCAACGAGAAAGGGAAACCAAGCGGATGTTGGTG

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Consensus:

TcGAAAAaaAGcTAAaCGacCCAAcGAGAAaGGGAAACCaAGcGGATGTaGGtG

>Bacillus_Fam_474_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.635802
GCF_000181495.1_ASM18149v1_genomic.fna_139:7643-8120 Satlength=478 Nr of
Repeats=9 RepeatLength=53 seed=TGAAATGATG Num.seqs=9 Similarity=0.769818
0 TGAAATGATGTCCGCGCCTGGC-GAGCGCATGACATCATTATGAAGTTCGTNA
Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_186:108256-108627
Satlength=372 Nr of Repeats=7 RepeatLength=53 seed=GCGGTACATC Num.seqs=7
Similarity=0.828691 16
TGCAATGATGTACCGCG-CTGACTGTGCGCATGGCATCATTTTGTGATTCCTGT

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Consensus:

TGaAATGATGTaCCGCGcCTGaCtGaGCGCATGaCATCATTaTGaaaTTCcTga

>Bacillus_Fam_475_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.709877
GCF_000181495.1_ASM18149v1_genomic.fna_170:14885-15361 Satlength=477 Nr
of Repeats=8 RepeatLength=53 seed=ATGTTGGTCT Num.seqs=5
Similarity=0.738272
0 ATGTTGGTCTGATTAGGATGTTTTAGNCCAATGAGACTCAATATTC-AAGGAG
GCF_000181495.1_ASM18149v1_genomic.fna_183:28650-29233 Satlength=584 Nr
of Repeats=10 RepeatLength=53 seed=GAGCTAATCA Num.seqs=9
Similarity=0.796296
16 ATGTTGGTCTGTTTAGGAGCTAATCAGGCCAGTGAGATTCAATTTTCGAAGG-G

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Consensus:

ATGTTGGTCTGaTTAGGAgcTaaTCAGgCCAAaTGAGAcTCAATaTTCgAAGGaG

>Bacillus_Fam_476_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.827160
GCF_000708755.2_ASM70875v2_genomic.fna_1:195812-196130 Satlength=319 Nr
of Repeats=6 RepeatLength=53 seed=TTATCGGCTT Num.seqs=6
Similarity=0.755556

0 TTATCGGCTTGATTAGAACCATCAA-GGAAAGGAAGAAGCATGCTTGAGGGTAC
GCF_000709935.2_ASM70993v2_genomic.fna_1:196645-196910 Satlength=266 Nr
of Repeats=5 RepeatLength=53 seed=TGATTAGAAC Num.seqs=5
Similarity=0.861635

9 TTATCGGCGTGATTAGAACCACCAAGGGACAGG-AGAAGCATGCTTGAGGGTAT

Consensus:

TTATCGGCgTGATTAGAACCACCAAgGGAaAGGaAGAAGCATGCTTGAGGGTAc

>Bacillus_Fam_477_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.913580
GCF_000708755.2_ASM70875v2_genomic.fna_6:313159-313635 Satlength=477 Nr
of Repeats=9 RepeatLength=53 seed=GACTTGTGGC Num.seqs=8
Similarity=0.765983

0 GACTTGTGGCACCACCTAGGCGGAGTGATACCACTTTTCACTCTTCCA-CCACCG
GCF_000709935.2_ASM70993v2_genomic.fna_5:520546-520916 Satlength=371 Nr
of Repeats=7 RepeatLength=53 seed=TGTGGCACCA Num.seqs=6
Similarity=0.747325

4 GACTTGTGGCACCACCTAGGCGGAGTGACCACTTTTCACTCTTCCANCCATCG

Consensus:

GACTTGTGGCACCACCTAGGCGGAGTGAcACCACTTTTCACTCTTCCAnCCAcCG

>Bacillus_Fam_478_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.669753
GCF_001420715.1_ASM142071v1_genomic.fna_22:1363621-1363829 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=ATGAAGGACA Num.seqs=4
Similarity=0.570988 40

TGAAGCAAGAGAAAGA-AGGAAGTGTCTTCACAAAGGTTGATGAAGGACAAAA
Rev.of_GCF_001591485.1_ASM159148v1_genomic.fna_34:25092-25304
Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=CCCTTCATGA Num.seqs=4
Similarity=0.907757 91
CTAAGGAAGAGAAGGATAAAAATTGTCCTTCATGAAGGGTA-TGAAGGACAAAA

Consensus:

aTGAAGGACAAAAcgaAGcAAGAGAAaGAtAaaAAgTGTCTTCaAAGGgTa

>Bacillus_Fam_479_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.657407

GCF_001439915.1_ASM143991v1_genomic.fna_83:403240-403615 Satlength=376 Nr of Repeats=8 RepeatLength=53 seed=CAATTTGGAG Num.seqs=5
Similarity=0.851852 0
CAATTTGGAGGTCCACCATATTTCCAATAATTAGGAGAATGGTGCCCCCTCGAAN-
GCF_001439915.1_ASM143991v1_genomic.fna_84:151113-151792 Satlength=680 Nr of Repeats=13 RepeatLength=53 seed=GAAGGTCACCT Num.seqs=11
Similarity=0.830303 6
NGTTTTGAAGGT-CACTATATACCAGTAATTAGGAGAATAGTGCCACTCCATTT

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Consensus:

caaTTTGaAGGTcCACcATATaCCAaTAATTAGGAGAATaGTGCCaCTCcAatt

>Bacillus_Fam_480_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.790123
GCF_002019605.1_ASM201960v1_genomic.fna_1:3068298-3068510 Satlength=213
Nr of Repeats=4 RepeatLength=53 seed=TCATAGTGAC Num.seqs=4
Similarity=0.844864 0
TCATAGTGACCGTCCGAGCAGGAAACCAGGTGAGAGCGGTCACTAT-CAAGAGC
GCF_002019605.1_ASM201960v1_genomic.fna_1:3905986-3906776 Satlength=791
Nr of Repeats=15 RepeatLength=53 seed=GCTCATAGTG Num.seqs=10
Similarity=0.746296 52
TCATAGTGCCCATCCGAGAAGGAAATCAGGTGAGTACGGTCACTATGAAAGAGC

Consensus:

TCATAGTGaCCaTCCGAGaAGGAAAcCAGGTGAGaaCGGTCACTATgaAAGAGC

>Bacillus_Fam_481_54_2 Nr. of seq. 2 Alignment length(with gaps) = 54
Alignment score = 0.882716
GCF_001887185.1_ASM188718v1_genomic.fna_148:138342-138666 Satlength=325
Nr of Repeats=6 RepeatLength=54 seed=TATAACAAAT Num.seqs=4
Similarity=0.868313 0
TATAACAAATATAGTAGCAGAACGAGGAATCGTATCCCCAGCACCAGTAAATAG
GCF_002009555.1_ASM200955v1_genomic.fna_427:1374-1752 Satlength=379 Nr of Repeats=7 RepeatLength=54 seed=GCACCAGTAA Num.seqs=7 Similarity=0.891828
40 TATAACAAATGTAGTAGCGGAGCGAGGAATCGTGTCNCCAGCACCAGTAAATAG

Consensus:

TATAACAAATaTAGTAGCaGAaCGAGGAATCGTaTCCcCAGCACCAGTAAATAG

>Bacillus_Fam_482_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
GCF_000181495.1_ASM18149v1_genomic.fna_116:6074-6381 Satlength=308 Nr of Repeats=6 RepeatLength=51 seed=AGGACGATAA Num.seqs=5 Similarity=0.900654
0 AGGACGATAAAATAAG-AAAATTAAAATTAAAGTACTATAGAGAGGTTT-TAA
GCF_000181495.1_ASM18149v1_genomic.fna_182:70379-70940 Satlength=562 Nr of Repeats=11 RepeatLength=51 seed=GAAATTAAAG Num.seqs=9
Similarity=0.963689
22 AGGAC-ATTAAAAAAGCAAAAGCGAAATTAAAGTCCTATA-AAAGGTTTCTAA

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Consensus:

AGGACgATaAAAAaAGcAAAAgcaAAATTAAAGTaCTATAgAaAGGTTTcTAA

>Bacillus_Fam_483_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.676101

GCF_000181495.1_ASM18149v1_genomic.fna_183:116608-117220 Satlength=613 Nr

of Repeats=12 RepeatLength=51 seed=AAACTCCAAA Num.seqs=10

Similarity=0.941903

0

AAACTCCAAATTATCGTCCTTTAAAACGGC-TCTATAAGACATTAAT-TACTC

Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_186:301034-301853

Satlength=820 Nr of Repeats=16 RepeatLength=51 seed=TTTAAAGGAC

Num.seqs=11 Similarity=0.656718

24 -CACCCCAANTTATCGTCCTTT-AAAGGGCTTCTATAGGACGTTAATCTCCTN

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Consensus:

aaACcCCAAaTTATCGTCCTTTaAAAcGGCtTCTATAaGACaTTAATcTaCTc

>Bacillus_Fam_484_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.625786

GCF_000292245.2_ASM29224v2_genomic.fna_23:12860-13115 Satlength=256 Nr of

Repeats=5 RepeatLength=51 seed=TTCATTACCT Num.seqs=5 Similarity=0.755128

0 TTCATTACCTATTCCTGACTATTCGCACCTTAATTTTGCA--TTCGCCGTGGT

GCF_000292245.2_ASM29224v2_genomic.fna_87:12883-13293 Satlength=411 Nr of

Repeats=8 RepeatLength=51 seed=CTTTTTTCAT Num.seqs=6 Similarity=0.904139

45 -TCATTACTTATCCTTTGTTATTTCGCACCTTAATTTGGCACGTTC-CCTTTTT

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Consensus:

tTCATTACcTATcCcTgacTATTCGCACCTTAATTTgGCacgTTCgCCgTggT

>Bacillus_Fam_485_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.685535

GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:92768-93125

Satlength=358 Nr of Repeats=7 RepeatLength=51 seed=TTTTTGTTCCA Num.seqs=7

Similarity=0.915344

0 T-

TTTTTGTTCCAATAGACCGCTGCTATCGGACAACCTT-TTTCGAAAACAGGCT

GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_22:525505-525906

Satlength=402 Nr of Repeats=8 RepeatLength=52 seed=GTTTTGTCCA Num.seqs=6

Similarity=0.831687

1

TGTTTTGTCCAATAGACCGCCCTATCGAACAAATTCTTTCCCAGAC-CGCT

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Consensus:

TgTTTTGTCCAATAGACCGCccCTATCGaACAAaTTcTTTCCcaAaACacGCT

>Bacillus_Fam_486_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.635220
GCF_001636335.1_ASM163633v1_genomic.fna_1:554579-554937 Satlength=359 Nr
of Repeats=7 RepeatLength=51 seed=AAAAAGGAGT Num.seqs=6
Similarity=0.877996
0 AAAAAGGAGTGAAGTAAAAATAGGTAGTTAAG--AGGCGTTTAAACTCCCGA
Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_1:1522005-1522515
Satlength=511 Nr of Repeats=10 RepeatLength=51 seed=GGGCGTTATA
Num.seqs=10 Similarity=0.911111
49 AAATCGGAGAATCAGAAAAATTGGTAGTTAAGCCA-GC-TTTATAACGCCCGA

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Consensus:

AAAAaGGAGaaaCaGAAAAATaGGTAGTTAAGccAgGCgTTTAaAACgCCCGA

>Bacillus_Fam_487_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.679245
GCF_000169195.2_ASM16919v2_genomic.fna_1:334661-335181 Satlength=521 Nr
of Repeats=9 RepeatLength=52 seed=TGAAGGACAT Num.seqs=8
Similarity=0.706570
0 TGAAGGACATTTTAATG-GTTCGTGGCTCGCGTTTTGTCCTTCATTANCCCGA
GCF_001636335.1_ASM163633v1_genomic.fna_1:3219373-3219737 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=ACTTTTGTGAC Num.seqs=7
Similarity=0.936508
TGAAGGACTTTTTGACGTGCCCCCTTGCTC-CGCTTTGTCCTTCATTACCCGA

6

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Consensus:

TGAAGGACaTTTTaAcGtGccCcTgGCTCgCGcTTTGTCTTCATTaaCCCGA

>Bacillus_Fam_488_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.613208
GCF_000169195.2_ASM16919v2_genomic.fna_1:636213-636421 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GTTCCTTAAC Num.seqs=4
Similarity=0.806080
0 GTTCCTTAACGTAGAACCACTCTATGTGAAGTTATGACCGGATTTTTCGTCT-
GCF_000169195.2_ASM16919v2_genomic.fna_1:1145839-1146151 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=TCTATGTTAA Num.seqs=6
Similarity=0.768485
CTTCCTTAACGTAGAGCCTCTCTATGTTAAGATA-CACGGCAGATTTTCAGCTG

20

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Consensus:

cTTCCTTAACGTAGAAcCaCTCTATGTgAAcaTAtcACcGcAgaTTTCagCTg

>Bacillus_Fam_489_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.628931
GCF_000169195.2_ASM16919v2_genomic.fna_1:2292482-2293472 Satlength=991 Nr
of Repeats=19 RepeatLength=52 seed=AATGTCTTTT Num.seqs=18
Similarity=0.800551
AATGTCTTTTACAANGGCTCAAAGGACAAAAG-GGTGCACGTTGCCGGTTGA

0

GCF_000217835.1_ASM21783v1_genomic.fna_1:954299-954610 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=AAAAGACAAA Num.seqs=5 Similarity=0.805128

21 ACTGTCTTTTACAACGGTTCAAAAAGACAAAAGCGTTCCAGCTTTCC-ACCGA

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Consensus:

AaTGTCTTTTACAACGGcTCAAAAaGACAAAAGcGgTcCAccTTgCCgaccGA

>Bacillus_Fam_490_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.622642

GCF_000175075.1_ASM17507v1_genomic.fna_5:15548-15860 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GTCAGAGAGG Num.seqs=6 Similarity=0.822428

0 GTCAGAGAGGTCTTGATAGCGGTTATGAGGACATCTG-TTGGTGAGAAATGAG

GCF_000175075.1_ASM17507v1_genomic.fna_33:121241-121605 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TTATGAAGAC Num.seqs=7 Similarity=0.838828

21 G-GAGAGAGGTCTTCATCGCACTTATGAAGACGTCAGTTTGGAGAGAAAGGCC

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Consensus:

GtcAGAGAGGTCTTcATaGCacTTATGAaGACaTCaGtTTGGaGAGAAAgGac

>Bacillus_Fam_491_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.672956

GCF_000175075.1_ASM17507v1_genomic.fna_29:40755-41014 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=TCTCTGTTAC Num.seqs=4 Similarity=0.948718

41 G-AACGCCATTGTTTTTCGGGGCTTCGGGCTTTGAGACGCCCTCTCTGTTACC

GCF_000175075.1_ASM17507v1_genomic.fna_29:166890-167254 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=CTCTCTGTTA Num.seqs=7 Similarity=0.794872

92 GTTCCCTGCTGTTGCTCGGCG-TTCGGGCTTTGAGAGGCCCTCTCTGTTACC

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Consensus:

TCTCTGTTACCGtaaCcCcacTGTTgcTCGGcGcTTCGGGCTTTGAGAcGCCC

>Bacillus_Fam_492_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.638365

GCF_000175075.1_ASM17507v1_genomic.fna_32:50201-50513 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=TTCGGTCAAA Num.seqs=6 Similarity=0.829060

0 TTCGGTCAAATAGAAGGGCTCTATACGCCCGAAGCGGAAGTGAGACTGGGAG-

GCF_000175075.1_ASM17507v1_genomic.fna_34:151816-152128 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GAGCTTCGGT Num.seqs=6 Similarity=0.837607

48 TTCGGTCGTATAGAAGGGCTCTATAAGCCTAAAGAGCAACT-ATAGCCGGAGC

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Consensus:

TTCGGTCAaATAGAAGGGCTCTATAaGCCcaAAGaGcAAcTgAgAcccGGAGc

>Bacillus_Fam_493_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.660377
GCF_000175075.1_ASM17507v1_genomic.fna_32:253955-254216 Satlength=262 Nr of Repeats=5 RepeatLength=52 seed=ATGAAGACAT Num.seqs=4
Similarity=0.901709
0 ATGAAGACATCAGTAGCG-TGAAAACCGGTAGAGAGAGGTCTTGAGAAGAGGC
GCF_000175075.1_ASM17507v1_genomic.fna_36:46227-46487 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AGAGAGGTCT Num.seqs=5 Similarity=0.823077
31 ATGAAGACATCTGTTGNNCTAATCACAGCT-GAGAGAGGTCTTGAGAAGTGA

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Consensus:

ATGAAGACATCaGTaGcgcTaAaaACaGcTaGAGAGAGGTCTTGAGAAGaGGa

>Bacillus_Fam_494_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.660377
GCF_000175075.1_ASM17507v1_genomic.fna_36:67347-67919 Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=AGCGAATGAA Num.seqs=11
Similarity=0.862471
0 AGCGAATGAAGACATCAGTGAAGCAGGAAAC-GAGNNAGAGAAGTCTTCATGA
GCF_000175075.1_ASM17507v1_genomic.fna_43:58907-59115 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GTTATGAAGA Num.seqs=4 Similarity=0.901709
2 AGGTTATGAAGACATGAGTG-ACCGGAATCTGAGTGAGAGATGTCTTCATGG

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Consensus:

AGcgaATGAAGACATcAGTGaAcCaGGAAaCtGAGtgAGAGAAgTCTTCATGa

>Bacillus_Fam_495_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.647799
GCF_000175075.1_ASM17507v1_genomic.fna_47:55295-55555 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GGGTCCCTCAT Num.seqs=5 Similarity=0.835897
0 GGGTCCTCATAAGGCTGATGAAGACATGAGTTGGTT-GAATTTGTGCGAGAG
Rev.of_GCF_900156865.1_PRJEB18960_genomic.fna_3:2588481-2588898
Satlength=418 Nr of Repeats=8 RepeatLength=52 seed=TCAGGTCTTC Num.seqs=7
Similarity=0.874237 29
AGGTTCCTCATAAGTGTTATGAAGACCTGAG-TGGTTGGGATATTATTCGAAAG

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Consensus:

aGGTcCTCATAAGgcTgATGAAGACaTGAGtTGGTTgGaATaTTaTgCGAAaAG

>Bacillus_Fam_496_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.713836
GCF_000177235.2_ASM17723v2_genomic.fna_1:3849630-3849838 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GCTATTTTAG Num.seqs=4
Similarity=0.943920 0
GCTATTTTAGTTTGCTGCCCTTTCTTATGCTGTTCCCTTACTTTGAATGGGCT-
GCF_000177235.2_ASM17723v2_genomic.fna_1:3977361-3977881 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=CACCTTACAA Num.seqs=10

36

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CGaGaAcGcAaGAAAAAGaGAAAaaaCGGTAAcTAGTaGAGGCGaCTAaTGCC

>Bacillus_Fam_500_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.823899
GCF_000612665.1_FF4_genomic.fna_66:68659-68921 Satlength=263 Nr of
Repeats=5 RepeatLength=52 seed=GTCACGTAGA Num.seqs=4 Similarity=0.893606
0 GTCACGTAGAGCCTGTCTACGTTACCCAAATCTAG-TCTTTTCAATGTTTACG
GCF_000612665.1_FF4_genomic.fna_72:16126-16334 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TACGTTACCC Num.seqs=4 Similarity=1.000000
17 GTCACGTAGAGGCTGTCTACGTTACCCATATCCAGCTC-TTTCATGTTTTTCG

Consensus:

GTCACGTAGAGcCTGTCTACGTTACCCAAATCcAGcTcTtTTTCAATGTTTaCG

>Bacillus_Fam_501_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.757862
GCF_000708755.2_ASM70875v2_genomic.fna_22:103405-103718 Satlength=314 Nr
of Repeats=6 RepeatLength=52 seed=AATAGAACCA Num.seqs=5
Similarity=0.704321
0 AATAGAACCATCAAAACCGAAAATGAGCAGCTTGATGGCNCTAANCAGGCNG-
GCF_000709935.2_ASM70993v2_genomic.fna_24:214095-214304 Satlength=210 Nr
of Repeats=4 RepeatLength=52 seed=AATAGAACCA Num.seqs=3
Similarity=0.708595
0 AATAGAACCATCAAAANCGTGAATCAAAAGCTTGATGGCNCTAAACAGGC-GT

Consensus:

AATAGAACCATCAAAAcCGaaAATcAaaAGCTTGATGGCNCTAAaCAGGCnGt

>Bacillus_Fam_502_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.710692
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_41:44624-45040
Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=TCTATGAGCC Num.seqs=8
Similarity=0.856151 0
TCTATGAGCCCGAAAATCAGGTG-AAGGATCAAAAATGGGTTTCATAGACCGAA
Rev.of_GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_24:138370-
138786 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=GGGATCATAG
Num.seqs=8 Similarity=0.711310 11
TCTATGATCCCAAAATTCGAGTGNAAGAGCAAAAATGGTTGATAGAACGAA

Consensus:

TCTATGAgCCCaAAAATCaaGTGnAAaGAgCAAAAATgGGTTcATAGAAcCGAA

>Bacillus_Fam_503_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
GCF_000813125.1_ASM81312v1_genomic.fna_15:34784-35096 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=TGACAGCTTT Num.seqs=6 Similarity=0.786325
0 TGACAGCTTTTCTGGTGAATGA-GCCAAAGCTGTCATGATTCCTCCGTTATTC
GCF_000813125.1_ASM81312v1_genomic.fna_130:47-256 Satlength=210 Nr of
Repeats=4 RepeatLength=52 seed=TGTCATGATT Num.seqs=3 Similarity=0.914530
30 TGACAGGTTTGATGATG-CTGAGGACAAAGCTGTCATGATTACACAGTTATTT

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Consensus:

TGACAGcTTTgATGaTGaaTGAGaCAAAGCTGTCATGATTaCaCaGTTATTc

>Bacillus_Fam_504_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.679245

GCF_000813125.1_ASM81312v1_genomic.fna_25:31-239 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GCTTTTCTTG Num.seqs=4 Similarity=0.805556

0 GC-TTTTCTTGACAGCTTTGGCCCCGTATCCTTGAAACCTGTCACAATAACTA

GCF_001315165.1_ASM131516v1_genomic.fna_8:68848-69212 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GAATCTTGAC Num.seqs=7 Similarity=0.847375

3 NCGGAATCTTGACAGCTTTGGCCCCGGATCCAGAAAAGCTGTCACAAAAC-A

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Consensus:

gCggaaTCTTGACAGCTTTGGCCCCgATCCagaAAAcCTGTCACAAaAACTa

>Bacillus_Fam_505_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.723270

GCF_000813125.1_ASM81312v1_genomic.fna_119:16360-16620 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=ATGACGGACA Num.seqs=5

Similarity=0.844025

0 ATGACGGACACTTTTCCTCTCAA-TCTCGCTCTTTCTGTCCGTCATCACGTCT

Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_3:68869-69077

Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TGTCGGTCAT Num.seqs=4

Similarity=0.867521

10

ATGACGGACACTTTTCTCTCAATTATCG-AATTTCTGTCCGTCATCGGGGTT

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Consensus:

ATGACGGACACTTTTCcTCTCAAtTaTCGcaaTTTCTGTCCGTCATCacGgcT

>Bacillus_Fam_506_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.622642

GCF_000813125.1_ASM81312v1_genomic.fna_122:25239-25553 Satlength=315 Nr of Repeats=5 RepeatLength=52 seed=GACATTTCCCT Num.seqs=4

Similarity=0.841880

0 GACATTTCCCTGGGATTCTG-CCCCCTGTTGGCCGATAGACCCCTTCTATCG

Rev.of_GCF_001315165.1_ASM131516v1_genomic.fna_117:8723-8931

Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TCTATCGGAC Num.seqs=4

Similarity=0.785115

40

GACAGAT-TTAGGATATTGTCCTTCTGTTTGTCCGATAGAGCCCTTCTAATG

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Consensus:

GACAGaTccTTaGGATacTgtCCccCTGTTTGgCCGATAGAcCCCTTCTAacG

>Bacillus_Fam_507_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.610063

GCF_000813125.1_ASM81312v1_genomic.fna_134:91815-92127 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=AAAAACAGGG Num.seqs=6
Similarity=0.830769
0 AAAAAACAGGGCACCAATACAGCCTATTGATGACCTAAAT-CTCGAAAATACGA
Rev.of_GCF_001420595.1_ASM142059v1_genomic.fna_11:1279366-1279626
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TAGCGGATTT Num.seqs=5
Similarity=0.753846 2
TAATTC-GGTAACCAATACAGCNTATTGGCGACCTTANTCCTCCAAAATCCGC

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Consensus:

aAAaCaGGGaACCAATACAGCcTATTGacGACCTaAaTcCTCcAAAATaCGa

>Bacillus_Fam_508_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.915094
GCF_000986785.1_ASM98678v1_genomic.fna_11:5-369 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TCTCAGTGCC Num.seqs=7 Similarity=0.799341
0 TCTCAGTGCCCGAAATGTCTCCTGCCACTACAAANAGGTCACCTGACANCTCC-
GCF_000986785.1_ASM98678v1_genomic.fna_16:123816-124024 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AGGGCACTGA Num.seqs=4
Similarity=0.788260
35 TCTCAGTGCCCGAAATGTCTCCTGCCACTACAAACAGGGCACTGACACCTCCT

Consensus:

TCTCAGTGCCCGAAATGTCTCCTGCCACTACAAAcAGGgCACTGACAcCTCct

>Bacillus_Fam_509_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.628931
GCF_001315045.1_ASM131504v1_genomic.fna_27:2070-2330 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TGTCCGAAGA Num.seqs=5 Similarity=0.838462
0 TGTCCGAAGAGAGAGNATCTTCGGACAGGAAGGCGGAACAA-AGCGAAAAGC
GCF_001315045.1_ASM131504v1_genomic.fna_33:22668-22876 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GTTCGGACAG Num.seqs=4
Similarity=0.722222
18 TGTCCGAAGAGAGTGCAAGTTCGGACA-GAAAACCGGGTGAAGAGCTAGAAGG

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Consensus:

TGTCCGAAGAGAGaGcAacTTCGGACAgGAAAcCGGaacAAgAGCgAaAAGc

>Bacillus_Fam_510_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.622642
GCF_001315045.1_ASM131504v1_genomic.fna_43:12-220 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AGTTCGGACA Num.seqs=4 Similarity=0.833333
0 AGTTCGGACAAGA-ATGAGGGGAAGAAGCAGAAAGTTGTCCGAAGAAGGCACA
Rev.of_GCF_001420595.1_ASM142059v1_genomic.fna_11:3566111-3566319
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TCTTGTCCGA Num.seqs=4
Similarity=0.811966 13
AGTTCGGACAAGATTTCACTTGAATAAGC-CAAAGCAGTCCGAAGTGGGCTCA

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Consensus:

AGTTCGGACAAGAtaTcAcggGAAGcAAAGcaGTCCGAAGaaGGCaCA

>Bacillus_Fam_511_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.650943

GCF_001315085.1_ASM131508v1_genomic.fna_1:106214-106474 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=AAAAGGTCAT Num.seqs=5

Similarity=0.828931

0 AAAAGGTCATCATCAAGCTGATGAAGA-CCGAAAGCATCTGGAAAGCTGAGAA

Rev.of_GCF_900156865.1_PRJEB18960_genomic.fna_3:3307735-3308723

Satlength=989 Nr of Repeats=18 RepeatLength=52 seed=CCTCTTTCTT

Num.seqs=17 Similarity=0.808069

5 -AGAGGTCNTCATCAAGGTAATGAAGACCCGAAAGCANGTCCACCGCAAAGAA

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Consensus:

aAaAGGTCaTCATCAAGcTaATGAAGAcCCGAAAGCATcTccAaaGcAaAGAA

>Bacillus_Fam_512_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.628931

GCF_001420595.1_ASM142059v1_genomic.fna_11:4880278-4880695 Satlength=418

Nr of Repeats=8 RepeatLength=52 seed=GACTTCGGAC Num.seqs=7

Similarity=0.776280

GACTTCGGAC-TTGGTTcAGCTTTTTCTTGTACCTGTCTGAACTCGGGTN

GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_19:196185-196445

Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTcAGACAAT Num.seqs=5

Similarity=0.907692

CCTTTTCCTATCACACCTGTCTGAACTTGGATC

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Consensus:

GACTTCaGACaaTcgTTCAGcCTTTTCCTaTcacACCTGTCTGAACTcGGaTc

>Bacillus_Fam_513_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.716981

GCF_001420715.1_ASM142071v1_genomic.fna_24:660131-660443 Satlength=313 Nr

of Repeats=6 RepeatLength=52 seed=GTCCTTCATC Num.seqs=6

Similarity=0.837607

GTCCTTCATCCCTCCGATGAACGACATCTGGAGCTTTTCCTTTTG-CNTTTTT

Rev.of_GCF_001636425.1_ASM163642v1_genomic.fna_1:3965800-3966164

Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GTCCTTCATC Num.seqs=7

Similarity=0.849817

GTCCTTCATCCCNCCGATGAAGGACATCTCANGC-TTCCTCTCGCCCGTTTT

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Consensus:

GTCCTTCATCCCTCCGATGAACGACATCTcaaGCTTTTCCTcTcGcCcGTTTT

>Bacillus_Fam_514_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.663522
GCF_001587375.1_ASM158737v1_genomic.fna_14:64719-64927 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GTTGTTTCAT Num.seqs=4
Similarity=0.935897
0 GTTGTT-TCATCTTCCCGCATCCCTCTGATTGAGCACTTCGCCACTGCTCTC
Rev.of_GCF_001587375.1_ASM158737v1_genomic.fna_105:15709-16177
Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=AGAGATGCGG Num.seqs=9
Similarity=0.864672 24 -
TTCTTCTCATCTTCCCGCATCTCTCGGTTTCGAGCATTTTCGCTGGGGATCCC

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Consensus:

gTTCtTcTCATCTTCCCGCATCcCTCgGaTTCGAGCAcTTCGCcaccgGaTCcC

>Bacillus_Fam_515_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.613208
GCF_001587375.1_ASM158737v1_genomic.fna_44:21063-21635 Satlength=573 Nr
of Repeats=11 RepeatLength=52 seed=CTCCTTATCT Num.seqs=11
Similarity=0.748650 0
CTCCTTATCTTCCCGCATCCGATGCTTGCGGGTAGTTGAGAGGGNGATCTCT-
GCF_001587375.1_ASM158737v1_genomic.fna_146:5307-5722 Satlength=416 Nr of
Repeats=8 RepeatLength=52 seed=TTGCGGGAAC Num.seqs=7 Similarity=0.824498
25 CTCCTCATCTTCCCGTATCCTATCTTTGCGGGAAC TTCATTCGG-GCTTTCTT

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Consensus:

CTCCTcATCTTCCCGcATCCgATccTTGCGGGaAcTTcAgacGGnGaTcTCTt

>Bacillus_Fam_516_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.622642
GCF_001587375.1_ASM158737v1_genomic.fna_83:277-589 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=CGAATGGGAT Num.seqs=6 Similarity=0.810256
0 CGAATGGGATGGATGCGGGAAC TTG-GAGCAAGAGACCCGAGTTGAAGTGCC
GCF_001587375.1_ASM158737v1_genomic.fna_137:57747-58007 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GAAGCGAAGT Num.seqs=5
Similarity=0.830769
39 CGAATCGGCTGGATACGGGAAC TTGATAGTAGGAAAGGTGAAG-CGAAGTGCC

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Consensus:

CGAATcGGaTGATaCGGGAAC TTGagAGcAaGAaAcccGaAGtcGAAGTGCC

>Bacillus_Fam_517_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.647799
GCF_001591645.1_ASM159164v1_genomic.fna_3:242834-243042 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=ATTAGTGGA Num.seqs=4
Similarity=0.776205
0 ATTAGTGGAATCAGTGAAC TAAACGATCATTTAGAACATATG-AATTCCAGAA

GCF_001591645.1_ASM159164v1_genomic.fna_13:94849-95106 Satlength=258 Nr of Repeats=5 RepeatLength=52 seed=TTTAGGACAT Num.seqs=4 Similarity=0.700103

29 ACTAGTGGAATTGGTGAACCTAAGTTNGCCTTTAGGACATGNGTATTTCCAGAA

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Consensus:

AcTAGTGGAATcaGTGAACTAAacgagCaTTTAGaACATatGtAaTTCCAGAA

>Bacillus_Fam_518_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.710692

GCF_001591805.1_ASM159180v1_genomic.fna_9:77461-77667 Satlength=207 Nr of Repeats=4 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=3 Similarity=0.914530

0 TGTCCCTTCATAAGGGAGATGAAGGACATTTATGTTGG-AAAACAAGAGAGATT

Rev.of GCF_001420715.1_ASM142071v1_genomic.fna_24:84088-84296

Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CTTACCAAGA Num.seqs=4

Similarity=0.865828

41

TGTCCTTCATAATGCAGATGAAGGACATTTCTCTTGTAAGTCAGTCGGGATT

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Consensus:

TGTCCTTCATAAgGcAGATGAAGGACATTTaTcTTGGtAAaaCAagaGaGATT

>Bacillus_Fam_519_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.672956

GCF_001636315.1_ASM163631v1_genomic.fna_1:3498555-3498923 Satlength=369

Nr of Repeats=7 RepeatLength=52 seed=GTAACGTAGA Num.seqs=5

Similarity=0.800000

0

GTAACGTAGAGCTCGTCTACGTGCCCCGACCGGA-GTATTTTTTCGCTGTAAGG

GCF_001636315.1_ASM163631v1_genomic.fna_1:3505767-3506235 Satlength=469

Nr of Repeats=8 RepeatLength=52 seed=GGTAACGTAG Num.seqs=7

Similarity=0.834681

51

GTAACGTAGAGCCCGTCTACGTGCCCCGAAGAGATGGA-AATTTAGCAGTTAGG

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Consensus:

GTAACGTAGAGCcCGTCTACGTGCCCCGAacaGAtGgAtaaTTTaGCaGTaAGG

>Bacillus_Fam_520_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53

Alignment score = 0.874214

GCF_001636345.1_ASM163634v1_genomic.fna_1:3361805-3362988 Satlength=1184

Nr of Repeats=15 RepeatLength=52 seed=TTCTTGAAAT Num.seqs=13

Similarity=0.838952

0

TTCTTGAAATCTGTGGCTTCC-CTNCTTTTCGGGAATGACTCGCCTTGGGGGA

GCF_001636345.1_ASM163634v1_genomic.fna_1:3809215-3809682 Satlength=468

Nr of Repeats=9 RepeatLength=52 seed=GGAATGACTC Num.seqs=8

Similarity=0.843407

31

TTCTTGAAATCTGTGGCTTCCGCT-CTTTTCGGGAATGACTCGCCTTGGGTCA

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Consensus:

TTCCTGAAATCTGTGGCTTCCgCTnCTTTTCGGGAATGACTCGCCTTGGGgcA

>Bacillus_Fam_521_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.773585
GCF_001648575.1_ASM164857v1_genomic.fna_58:95837-96675 Satlength=839 Nr
of Repeats=16 RepeatLength=52 seed=CTGTATGACA Num.seqs=13
Similarity=0.879684 0

CTGTATGACACGCATAATCTTGT-TCCATTAGGATTTTCGCGTTTCATTCGTG
GCF_001648575.1_ASM164857v1_genomic.fna_67:84110-84424 Satlength=315 Nr
of Repeats=6 RepeatLength=52 seed=TCATTCGTGC Num.seqs=4
Similarity=0.841880

43 CTGTATGACACGCAAAATCATGTCTCC-TTTGAATGTTTCGCGTCTCATTCGTG

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Consensus:

CTGTATGACACGCAaATCaGTcTCCaTTaGaATgTTCGCGTcTCATTCGTG

>Bacillus_Fam_522_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.672956
GCF_002019605.1_ASM201960v1_genomic.fna_1:4201819-4202236 Satlength=418
Nr of Repeats=8 RepeatLength=52 seed=GGTAACTATG Num.seqs=7
Similarity=0.836777 0

GGTAACTATG-AGGCGTTCATAGTGACCAAAGTGAAGTAGAAAAAGCAAGAAC
GCF_002019605.1_ASM201960v1_genomic.fna_1:4298572-4298988 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=GTGACCGAAC Num.seqs=8
Similarity=0.847985 21

GGTAACTATGAAAGCG-TCATAGTGACCGAACCCAAAGAGAAAAAGCCAAAGC

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Consensus:

GGTAACTATGaAaGCGtTCATAGTGACCaAAcccAAagAGAAAAAGCaAaAaC

>Bacillus_Fam_523_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.751572
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_42:562044-562408
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TGTCCTCAAG Num.seqs=7
Similarity=0.661654 0

TGTCCTCAAGGAGTGTtTATGAGGACAAACTGGGGTTGGAAGCGTAGTCGAA-
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_42:623373-623581
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GGACAAACTC Num.seqs=4
Similarity=0.830189 22

TGTCCTCAAGAAGGGCTTATGAGGACAAACTCGAGTCCGAAGCGTCGGCGAAN

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Consensus:

TGTCCTCAAGaAGgGcTTATGAGGACAAACTcGaGTccGAAGCGTaGgCGAAn

>Bacillus_Fam_524_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.855346
GCF_900156865.1_PRJEB18960_genomic.fna_3:4352895-4353155 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=AGGTCATCAT Num.seqs=5
Similarity=0.727273 0
AGGTCATCATGGAGGTGATGAAGACTC-GAAGCNGTGTGNTTGGTAGNGAAG
GCF_900156865.1_PRJEB18960_genomic.fna_3:4347937-4349809 Satlength=1873
Nr of Repeats=36 RepeatLength=52 seed=GAAGCGGTGT Num.seqs=36
Similarity=0.899571 28
AGGTCATCATGGAGGTGATGAAGACTCTGAAGCGGTGTTGCTTGGATGGGAAG

Consensus:

AGGTCATCATGGAGGTGATGAAGACTCtGAAGCgGTGTTGcTTGGaaGgGAAG

>Bacillus_Fam_525_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 1.000000
GCF_000153365.1_ASM15336v1_genomic.fna_14:139111-139848 Satlength=738 Nr
of Repeats=14 RepeatLength=53 seed=CTCTCTTGAG Num.seqs=9
Similarity=0.849057 0
CTCTCTTGAGTGACTCATATCGGTTCTCTGAGGCACTCTGGGGCGGGGGGTCT
GCF_000473245.1_ASM47324v1_genomic.fna_1:4678509-4679246 Satlength=738 Nr
of Repeats=14 RepeatLength=53 seed=CTCTCTTGAG Num.seqs=9
Similarity=0.849057 0
CTCTCTTGAGTGACTCATATCGGTTCTCTGAGGCACTCTGGGGCGGGGGGTCT

Consensus:

CTCTCTTGAGTGACTCATATCGGTTCTCTGAGGCACTCTGGGGCGGGGGGTCT

>Bacillus_Fam_526_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.974843
GCF_000153365.1_ASM15336v1_genomic.fna_16:253052-253476 Satlength=425 Nr
of Repeats=8 RepeatLength=53 seed=GTACAGAGTG Num.seqs=8
Similarity=0.816799
0 GTACAGAGTGCCCTCAAACGAAGTCTATGAAGCACTCTAAAGATGGAAAGGAGC
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2556644-2557068
Satlength=425 Nr of Repeats=8 RepeatLength=53 seed=CACTCTGTAC Num.seqs=8
Similarity=0.809091 10
GTACAGAGTGCCCTCAAACGAAGTCTATGAAGCACTCTAGAGATGGAAAGGAGC

Consensus:

GTACAGAGTGCCCTCAAACGAAGTCTATGAAGCACTCTAaAGATGGAAAGGAGC

>Bacillus_Fam_527_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.943396
GCF_000153365.1_ASM15336v1_genomic.fna_67:19007-19908 Satlength=902 Nr of
Repeats=17 RepeatLength=53 seed=CATGTATCCA Num.seqs=17
Similarity=0.747950
0 CATGTATCCAGTAGCTTTTTCGGGATACATGACACCNCNTTTTTTTNCTCGGT

AAATAGCATAAGATAAGCAaGGAATCGTACGCTATAATCTcaAGCCAGTGTAC

>Bacillus_Fam_531_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.811321
GCF_000708755.2_ASM70875v2_genomic.fna_2:36778-37043 Satlength=266 Nr of
Repeats=5 RepeatLength=53 seed=TTGGTTCTAAA Num.seqs=5 Similarity=0.861635
0 TGGTTCTAAAGCGCGTTAATAGTGCCATCAAAGGGTTGGGGTTGGNAGNTTGA
GCF_000709935.2_ASM70993v2_genomic.fna_24:75878-76198 Satlength=321 Nr of
Repeats=6 RepeatLength=53 seed=TTGATGGTTC Num.seqs=4 Similarity=0.802935
49 TGGTTCTAAACCGAGTTAATAGTGCCATCAAAGGAGGGGATTGGGAGCTTGA

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Consensus:

TGGTTCTAAAcCGaGTTAATAGTGCCATCAAAGGaggGGGaTTGGgAGcTTGA

>Bacillus_Fam_532_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.880503
GCF_000708755.2_ASM70875v2_genomic.fna_2:902427-902638 Satlength=212 Nr
of Repeats=4 RepeatLength=53 seed=TGTTGCCACT Num.seqs=3
Similarity=0.849057
0 TGTTGCCACTTTACTTCACGCATGGAGCCTGTTTGTGGCGCAACTCACCGGAT
GCF_000709935.2_ASM70993v2_genomic.fna_4:157618-157829 Satlength=212 Nr
of Repeats=4 RepeatLength=53 seed=TGTTTGTGGC Num.seqs=3
Similarity=0.773585
29 TGNTGCCACTTTTCTTCACCCATGAAGCCTGTTTGTGGCGCAACTCACCGGAG

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Consensus:

TGtTGCCACTTTaCTTCACcCATGaAGCCTGTTTGTGGCGCAACTCACCGGAg

>Bacillus_Fam_533_53_2 Nr. of seq. 2 Alignment length(with gaps) = 53
Alignment score = 0.628931
GCF_001439915.1_ASM143991v1_genomic.fna_122:165197-165557 Satlength=361
Nr of Repeats=6 RepeatLength=53 seed=GCGGTACATG Num.seqs=5
Similarity=0.771069 0
GCGGTACATGCTTGGNAGAAATCCGCTTGAGCGTGTAACCGCTAGACCACTCTT
GCF_001439915.1_ASM143991v1_genomic.fna_126:34957-35437 Satlength=481 Nr
of Repeats=9 RepeatLength=53 seed=AAGCGTGTAC Num.seqs=8
Similarity=0.901168
28 GCGGTACACGCTCGCAAAAAATTGCCAAAGCGTGTACCGTAAGACGGTTCTA

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Consensus:

GCGGTACAcGCTcGcaAaAAATcCGCcaaAGCGTGTACCGcaAGACcactCTa

>Bacillus_Fam_534_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.826923
GCF_000169195.2_ASM16919v2_genomic.fna_1:2621330-2621590 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CAAAAGGACA Num.seqs=5

Similarity=0.615789 0
CAAAAGGACAATTCAGGNAGAAACAAAGNGCAAATTGTCCTTTANAG-GGTT
Rev.of_GCF_000217835.1_ASM21783v1_genomic.fna_1:2113071-2113331
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TGTCCTTTTG Num.seqs=5
Similarity=0.648718 10
CAAAAGGACAATTCGGGNAGAGACAAAGAGCAAACGTTCCTTTAGAGNGGTT

Consensus:

CAAAAGGACAATTCaGGNAGAAaCAAAGaGCAAACGTTCCTTTAgAGnGGTT

>Bacillus_Fam_535_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.743590
GCF_000292245.2_ASM29224v2_genomic.fna_25:14121-14376 Satlength=256 Nr of
Repeats=5 RepeatLength=51 seed=TTTTCATTTAC Num.seqs=5 Similarity=0.746296
0 TTTTCATTACCTATTAT-CTGCTATTCGCACCCTAATCTTGGCTTTGCTGGC
GCF_000292245.2_ASM29224v2_genomic.fna_55:71-275 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=GATTTTCATT Num.seqs=4 Similarity=0.860566
49 TTTTCATTACCTATTATGAAGGT-TACGCACCCTAACCTTGGCTTTGCTAGA

Consensus:

TTTTTCATTACCTATTATgaaGcTaTaCGCACCTAAcCTTGGCTTTGCTaGa

>Bacillus_Fam_536_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.602564
GCF_000292245.2_ASM29224v2_genomic.fna_35:14658-15015 Satlength=358 Nr of
Repeats=7 RepeatLength=51 seed=GTAATGAAAT Num.seqs=7 Similarity=0.845627
0 GTAATGAAATTAGNCGACTCACTTGA-TTTCAGTGCCTATTACTCTTTATTG
GCF_000292245.2_ASM29224v2_genomic.fna_111:7118-7883 Satlength=766 Nr of
Repeats=15 RepeatLength=51 seed=GATTGGTAAT Num.seqs=15
Similarity=0.816247
46 GTAATGAAATT-CTCGCTTTTCCTGATTTTCATTACCTATTACTCCNGATTG

Consensus:

GTAATGAAATTactCGacTcaCcTGAtTTTCAGTaCcTATTACTCctgATTG

>Bacillus_Fam_537_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.641026
GCF_000331575.1_ASM33157v1_genomic.fna_1:73323-73782 Satlength=460 Nr of
Repeats=9 RepeatLength=51 seed=TCAGCAAATC Num.seqs=9 Similarity=0.947712
0 TCAGCAAA-TCGCTGAAAAATCCTTTTGTGCTGATAATAAACCGATTTACCA
GCF_000331575.1_ASM33157v1_genomic.fna_1:1667305-1667917 Satlength=613 Nr
of Repeats=12 RepeatLength=51 seed=TTTACTATCA Num.seqs=12
Similarity=0.857794 44
TCACCAAAATTCGCT-CTGCGTCCGTTTTGCTGATGATAAATCGGATTTACTA

Consensus:

TCACCAAAtTCGCTgaaaaaTCCgTTTTGCTGATaATAAAaCcGATTTACcA

>Bacillus_Fam_538_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.692308
GCF_001636335.1_ASM163633v1_genomic.fna_1:405681-405987 Satlength=307 Nr
of Repeats=6 RepeatLength=51 seed=TTAAGAAGGG Num.seqs=6
Similarity=0.893682
0 TTAAGAAGGGTTCAAAACGCCCG-TATTTGTAAAAGAAGGAAAAATTGGTAG
GCF_001636335.1_ASM163633v1_genomic.fna_2:334616-334973 Satlength=358 Nr
of Repeats=7 RepeatLength=51 seed=CGCCCGAAAT Num.seqs=5
Similarity=0.788462
17 CCAAGAAGCGTTCATGACGCCCGAAATTTCAAAAAGAA-GAAAAATCGGTAG

Consensus:

ccAAGAAGcGTTCAaaACGCCCGaaATTTcaAAAAGAAgGAAAAATcGGTAG

>Bacillus_Fam_539_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.698718
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_15:150210-151014
Satlength=805 Nr of Repeats=6 RepeatLength=51 seed=ACTTTTTTCT Num.seqs=5
Similarity=0.850980 0
ACTTTTTTCTGGTGATCTACTCGATTTTGTCTTTCAT-AGCNCGGATGAAAG
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_19:93292-93547
Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=ATGAAAGACT Num.seqs=5
Similarity=0.830065 44
ACTTTTTCCTATTGAACATTTCNATTTTGTCTTCATCAGC-CTCATGAAAG

Consensus:

ACTTTTTCCTagTGAAcTAcTCgATTTTGTCCtTCATcAGCnCgcATGAAAG

>Bacillus_Fam_540_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GCF_000153365.1_ASM15336v1_genomic.fna_9:45356-45772 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=AGAGGGTGTT Num.seqs=8 Similarity=0.840659
0 AGAGGGTGTTAGTGGTAGCGACTAAAGCCGTCTAAGAGAGATTTTGCTAAAC
GCF_000473245.1_ASM47324v1_genomic.fna_1:212820-213236 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=AGAGGGTGTT Num.seqs=8
Similarity=0.840659
0 AGAGGGTGTTAGTGGTAGCGACTAAAGCCGTCTAAGAGAGATTTTGCTAAAC

Consensus:

AGAGGGTGTTAGTGGTAGCGACTAAAGCCGTCTAAGAGAGATTTTGCTAAAC

>Bacillus_Fam_541_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000

GCF_000153365.1_ASM15336v1_genomic.fna_16:445040-445454 Satlength=415 Nr of Repeats=8 RepeatLength=52 seed=AGCCACTATT Num.seqs=6
Similarity=0.823868
0 AGCCACTATTTTCATTTTCTTCAGGATAGTGGTCCCAGCTCCTGTGGCTGG
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:2366668-2367085
Satlength=418 Nr of Repeats=8 RepeatLength=52 seed=AAAATAGTGG Num.seqs=5
Similarity=0.795152 12
AGCCACTATTTTCATTTTCTTCAGGATAGTGGTCCCAGCTCCTGTGGCTGG

Consensus:

AGCCACTATTTTCATTTTCTTCAGGATAGTGGTCCCAGCTCCTGTGGCTGG

>Bacillus_Fam_542_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GCF_000153365.1_ASM15336v1_genomic.fna_60:10538-10746 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GAACCGCTAT Num.seqs=4 Similarity=0.811966
0 GAACCGCTATTTTAGCTTTACACAGAAATAGTGGTCCCAGCGAGCGTGGCTA
GCF_000473245.1_ASM47324v1_genomic.fna_1:2054544-2054752 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GAACCGCTAT Num.seqs=4
Similarity=0.811966 0
GAACCGCTATTTTAGCTTTACACAGAAATAGTGGTCCCAGCGAGCGTGGCTA

Consensus:

GAACCGCTATTTTAGCTTTACACAGAAATAGTGGTCCCAGCGAGCGTGGCTA

>Bacillus_Fam_543_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GCF_000153365.1_ASM15336v1_genomic.fna_74:14504-15024 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=GTCACTCTAA Num.seqs=10
Similarity=0.908832
0 GTCACTCTAACCAAAGAACATAGAATCAGAGTGCCTCAAAAAGAGGATATGA
GCF_000473245.1_ASM47324v1_genomic.fna_1:2071154-2071674 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=GTCACTCTAA Num.seqs=10
Similarity=0.908832 0
GTCACTCTAACCAAAGAACATAGAATCAGAGTGCCTCAAAAAGAGGATATGA

Consensus:

GTCACTCTAACCAAAGAACATAGAATCAGAGTGCCTCAAAAAGAGGATATGA

>Bacillus_Fam_544_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GCF_000153365.1_ASM15336v1_genomic.fna_74:34309-34724 Satlength=416 Nr of Repeats=7 RepeatLength=52 seed=AAATCAGAGG Num.seqs=6 Similarity=0.894017
0 AAATCAGAGGGCCTCAAACGAGCGAAATGGAACCTCTAAACTGAAATAATC
GCF_000473245.1_ASM47324v1_genomic.fna_1:2090960-2091375 Satlength=416 Nr of Repeats=7 RepeatLength=52 seed=AAATCAGAGG Num.seqs=6
Similarity=0.894017 0
AAATCAGAGGGCCTCAAACGAGCGAAATGGAACCTCTAAACTGAAATAATC

Consensus:

AAATCAGAGGGCCTCAAACGAGCGAAATGGAACCTCTAAACTGAAATAATC

>Bacillus_Fam_545_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 0.820513

GCF_000177235.2_ASM17723v2_genomic.fna_1:494305-494982 Satlength=678 Nr

of Repeats=13 RepeatLength=52 seed=ACTCTATTTC Num.seqs=12

Similarity=0.894716

0

ACTCTATTTTCGGACAGAGTTTCTTGTTTAATATTCAACTCTGTCCGATTGCA

GCF_000177235.2_ASM17723v2_genomic.fna_1:4603616-4604344 Satlength=729 Nr

of Repeats=14 RepeatLength=52 seed=ATTGCTTCTC Num.seqs=14

Similarity=0.915187

46

TCTCTTTTTCGGACAGAGTTCCTTGTTTCAATTATTCAACTCTGTCTGATTGCT

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Consensus:

aCTCTaTTTCGGACAGAGTTcCTTGTTcAaTATTCAACTCTGTCCGATTGCa

>Bacillus_Fam_546_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 0.801282

GCF_000177235.2_ASM17723v2_genomic.fna_1:2323006-2323553 Satlength=548 Nr

of Repeats=10 RepeatLength=52 seed=AAGGTCATCA Num.seqs=9

Similarity=0.859687

0

AAGGTCATCATACGAAGTCTATGCTACCCGAAAAATNGAAACCGAGCAGATG

GCF_000177235.2_ASM17723v2_genomic.fna_1:2835835-2836198 Satlength=364 Nr

of Repeats=5 RepeatLength=52 seed=AAGGGCAGCA Num.seqs=3

Similarity=0.880342

0

AAGGGCAGCATACGAAGCCTATGCCTCCCGAAAAAATGAAATCGAGCAGATG

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Consensus:

AAGGgCagCATACGAAGcCTATGCcaCCCGAAAAAatGAAAcCGAGCAGATG

>Bacillus_Fam_547_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 0.878205

GCF_000177235.2_ASM17723v2_genomic.fna_1:4408835-4409251 Satlength=417 Nr

of Repeats=8 RepeatLength=52 seed=CGCTATGATT Num.seqs=8

Similarity=0.869048

0

CGCTATGATTACCTTCAACTCATTTTGGGCTCGTTCTCGGGAAGCATACAAT

GCF_000177235.2_ASM17723v2_genomic.fna_1:4410749-4411009 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=CTATGATTAC Num.seqs=5

Similarity=0.817949

2

CGCTATGATTACCGTCAACTCATTTTGGGCTCNCTCTCGGGAAGCATACACG

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Consensus:

CGCTATGATTACCGTCAACTCATTTTGGGCTCgcTCTCGGGAAGCATACAag

>Bacillus_Fam_548_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.955128
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_4:260068-260380
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GTTCAGACAG Num.seqs=6
Similarity=0.890356 0
GTTCAGACAGGAAGAACGAGAAATAGCCTGTTTGTGTCCGAAGAAGGGGCAG
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:3372157-3372521
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TCTTCGGACA Num.seqs=7
Similarity=0.864469 44
GTTCAGACAGGAAGAACGAGAAATAGNCTGTTTGTGTCCGAAGACGGGGCAG

Consensus:

GTTCAGACAGGAAGAACGAGAAATAGcCTGTTTGTGTCCGAAGaAGGGGCAG

>Bacillus_Fam_549_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.910256
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_5:20059-20318
Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=TGGGAGTTAA Num.seqs=4
Similarity=0.816239 0
TGGGAGTTAACCAAAGGGAATAAAGCCGAAATCCCAGAGCCAGCCAACAAAA
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:2910855-2911062
Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=CTCCCATTTT Num.seqs=3
Similarity=0.811966 6
TGGGAGTTAATCAAANGGAATAAAGNCGAAATCCCAGAGCAAGCCAACAAAA

Consensus:

TGGGAGTTAAcCAAAGGGAATAAAGcCGAAATCCCAGAGCaAGCCAACAAAA

>Bacillus_Fam_550_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_5:39414-39827
Satlength=414 Nr of Repeats=8 RepeatLength=52 seed=GTCGCCATAA Num.seqs=5
Similarity=0.858974 0
GTCGCCATAAGAGGTTTCATGACGACGAAAAATTGGAGGTCCAAGTAAAAACA
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:2898257-2898722
Satlength=466 Nr of Repeats=9 RepeatLength=52 seed=TTATGGCGAC Num.seqs=6
Similarity=0.825641 10
GTCGCCATAAGAGGTTTCATGACGACGAAAAATTGGAGGTCCAAGTAAAAACG

Consensus:

GTCGCCATAAGAGGTTTCATGACGACGAAAAATTGGAGGTCCAAGTAAAAACa

>Bacillus_Fam_551_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.923077
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_5:358104-358520
Satlength=417 Nr of Repeats=7 RepeatLength=52 seed=TTCGGACTCA Num.seqs=6
Similarity=0.822222 0
TTCGGACTCAACGACCATCCGTTTCGCGGTTTTGAGTCCGAACACCAGTCAAC

Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:2554186-2554498
Satlength=313 Nr of Repeats=5 RepeatLength=52 seed=TGAGTCCGAA Num.seqs=4
Similarity=0.747379 10
TTCGGACTCAGCGAGCATCCGTTTCGCGGTTTTGTGTCCGAACACCAGTCAAC

Consensus:

TTCGGACTCAaCGAcCATCCGTTTCGCGGTTTTGaGTCCGAACACCAGTCAAC

>Bacillus_Fam_552_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_6:198141-198401
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CATGAAATAT Num.seqs=5
Similarity=0.816352 0
CATGAAATATGGGAGTTAATTCTAATCATTATCGACCAAACAAGAGATGCCA
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:899649-899960
Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=TAATCCCAT Num.seqs=5
Similarity=0.871795 18
CATGAAATATGGGAGTTAATCCTAATCATTATCGACCAAACAAGAGATGCCA

Consensus:

CATGAAATATGGGAGTTAATcCTAATCATTATCGACCAAACAAGAGATGCCA

>Bacillus_Fam_553_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.948718
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_7:64235-64495
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CACCTTCGGA Num.seqs=5
Similarity=0.844025 0
CACCTTCGGACTCGCTCACGTTGATTTCTCCCTTTCTGTCCGAACCTGCTC
Rev.of_GCF_000294775.2_ASM29477v2_genomic.fna_1:658243-658659
Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=GAGTCCGAAG Num.seqs=8
Similarity=0.829739 13
CACCTTCGGACTCGCTCACGTTGATTTCTCCCTTTCTGTCCGAACCTCCTC

Consensus:

CACCTTCGGACTCGCTCACGTTGATTTCTCCcTTTCTGTCCGAACCTcCTC

>Bacillus_Fam_554_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.897436
GCF_000285535.1_ASM28553v1_genomic.fna_2:1010386-1010802 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=TCCTCTTCAT Num.seqs=8
Similarity=0.735175 0
TCCTCTTCATAAGCCCCGTGAAGAGGAAACGTAACCAAAATCTCATTCTTTT
Rev.of_GCF_000285535.1_ASM28553v1_genomic.fna_45:36-244 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=AAGAGGAAAA Num.seqs=4
Similarity=0.794872
7 TCCTCTTCATAAGCTTCGTGAAGGGGAAACGTAACCAAAATCTCATTCTTTT

Consensus:

TCCTCTTCATAAGCccCGTGAAGaGGAAACGTAACCAAAATCTCATTCcTTT

>Bacillus_Fam_555_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.820513
GCF_000285535.1_ASM28553v1_genomic.fna_3:290400-290816 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=TGAAGAGGAT Num.seqs=8 Similarity=0.851648
0 TGAAGAGGATTACAAGCTTATGTTTCGTCCTTCCTCTTCATCTAGGCTT
GCF_000285535.1_ASM28553v1_genomic.fna_41:8-216 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TGAAGAGGAT Num.seqs=4 Similarity=0.846154
0 TGAAGAGGATTACAGGCTTCAATTCCTCCCACTTTCTCTTCATCTAGGCTA

Consensus:

TGAAGAGGATTACAaGCTTaaATTcTCCCaCTTCTCTTCATCTAGGCTa

>Bacillus_Fam_556_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.692308
GCF_000307875.1_BABA1.0_genomic.fna_34:24055-24262 Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=TGTCCTCAAT Num.seqs=3 Similarity=0.811966
0 TGTCCTCAATAAGGGCTATTGAGGACAAAACCTCGCTGGATAGCAGGAAAAA
GCF_001591665.1_ASM159166v1_genomic.fna_21:148942-149150 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GCTCTTAAAG Num.seqs=4 Similarity=0.846154 14
TGTCTTTAATAAGGGCTCTTAAAGACAAAACCTCCGCGGAAAGCAATCAAAA

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Consensus:

TGTcCTcAATAAGGGCTaTTaAaGACAAAACCTCccCgGGaAGCAagaAAAA

>Bacillus_Fam_557_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.628205
GCF_000311725.1_ASM31172v1_genomic.fna_4:30876-31291 Satlength=416 Nr of Repeats=8 RepeatLength=52 seed=ATTCGGACTC Num.seqs=7 Similarity=0.783550
0 ATTCGGACTCCCTTNCNCCTTTTCCTGCTCGACCTGTCCGAATCCCCTTCT
GCF_000311725.1_ASM31172v1_genomic.fna_6:46056-46316 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TCTATTCGGA Num.seqs=5 Similarity=0.887179
49 ATTCGGACTTACTTATTTGTTTTACAGCTTGGGCTGTCCGAATAGCCCCTCT

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Consensus:

ATTCGGACTcaCTTactccTTTTaCaGCTcGacCTGTCCGAATaCCCCtCT

>Bacillus_Fam_558_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.641026
GCF_000374345.1_ASM37434v1_genomic.fna_5:87235-87443 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GGCTTTTCATC Num.seqs=4 Similarity=0.905983
0 GGCTTTTCATCCCCTTTATGAGCGACCATAACCGATGTGTTTTACCATGGCAGC

GCF_000374345.1_ASM37434v1_genomic.fna_49:17746-17954 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CCTATGTGTT Num.seqs=4 Similarity=0.876068
29 GGCGGTCATTCCCCTTATGAACGACCGTGCTATGTGTTTTTCATTCTCGCG

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Consensus:

GGCggTCATcCCCcTTATGAaCGACCaTaCCgATGTGTTTTaCaaTcgCaCG

>Bacillus_Fam_559_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.666667

GCF_000374345.1_ASM37434v1_genomic.fna_8:79176-79540 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=AATCAAACGG Num.seqs=7 Similarity=0.796047
0 AATCAAACGGTCGCTCATCCCCTTTATGAACGCCGCGCCTGCTGAGTTTTT
GCF_000374345.1_ASM37434v1_genomic.fna_9:12991-13459 Satlength=469 Nr of Repeats=8 RepeatLength=52 seed=TCACACGGTC Num.seqs=7 Similarity=0.789988
2 AATCACACGGTCGATCATTTCCCTTATGAACGACCACGCCGCTGAAAATCC

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Consensus:

AATCAaACGGTCGaTCATccCCcTTATGAACGaCCaCGCCgGCTGAaaaTcc

>Bacillus_Fam_560_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.724359

GCF_000374565.1_ASM37456v1_genomic.fna_1:698811-699383 Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=ATTAGTGACC Num.seqs=11
Similarity=0.762851
ATTAGTGACCGTTATCCGGGATTTTNCCTAAATACGGGTACCTTTTACTGCT
Rev.of_GCF_000374565.1_ASM37456v1_genomic.fna_3:262427-263155
Satlength=729 Nr of Repeats=14 RepeatLength=52 seed=GGTCACTAAT
Num.seqs=14 Similarity=0.765004
10 ATTAGTGACCGAGCTACGGGATTTACCGTAAATACGGGAACCTTTTGCCGCG

0

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Consensus:

ATTAGTGACCGagaTaCGGGATTTacCctAAATACGGGaACCTTTTaCcGCg

>Bacillus_Fam_561_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.615385

GCF_000374565.1_ASM37456v1_genomic.fna_29:5643-6006 Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=TTAGTTACCG Num.seqs=6 Similarity=0.733333
0 TTAGTTACCGTTTTTCGCACTTAAACCCGTATTCGGGCACCTTTCCCCGCGA
Rev.of_GCF_000374565.1_ASM37456v1_genomic.fna_32:3468-3780 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=CCCGAAAAAG Num.seqs=6
Similarity=0.814675
TTAGTGACCGTTTTCCCTCTCGGACGCTTTTTCGGGCACTATTACTCTCGA

37

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Consensus:

TTAGTgACCGgTTTTCCcCaCTcaaACcCgTaTTCGGGCACcaTTaCcCgCGA

>Bacillus_Fam_562_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.910256
GCF_000708755.2_ASM70875v2_genomic.fna_1:24282-24750 Satlength=469 Nr of
Repeats=8 RepeatLength=52 seed=CAGAAAATCA Num.seqs=7 Similarity=0.840049
0 CAGAAAATCAGATTTGATGGCACTGAACATTGAGAATAGNACCACCAACGAA
GCF_000709935.2_ASM70993v2_genomic.fna_1:24497-24861 Satlength=365 Nr of
Repeats=7 RepeatLength=52 seed=GATGGCACTG Num.seqs=7 Similarity=0.796646
15 CAGANAATCAGTTTTGATGGCACTGAACATCGAGAATAGGACCACCAACGAA

Consensus:

CAGAAATCAGaTTTGTATGGCACTGAACATcGAGAATAGgACCACCAACGAA

>Bacillus_Fam_563_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GCF_000708755.2_ASM70875v2_genomic.fna_1:149824-150187 Satlength=364 Nr
of Repeats=7 RepeatLength=52 seed=TGAAAGTGTT Num.seqs=6
Similarity=0.926496
0 TGAAAGTGTTGCTAACCCAGTTTAAGAACAACCTTTTCCGCAGAGCAGAAGGGT
GCF_000709935.2_ASM70993v2_genomic.fna_1:150814-151022 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TTGAAAGTGT Num.seqs=4
Similarity=0.893162
51 TGAAAGTGTTGCTAACCCAGTTTAAGAACAACCTTTTCCGCAGAGCAGAAGGGT

Consensus:

TGAAAGTGTTGCTAACCCAGTTTAAGAACAACCTTTTCCGCAGAGCAGAAGGGT

>Bacillus_Fam_564_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.980769
GCF_000708755.2_ASM70875v2_genomic.fna_1:165249-165509 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TGATGTGAAG Num.seqs=5
Similarity=0.771795
0 TGATGTGAAGGGTTATAAGTAAGTGAGAATTGACCCCTNAGTGCAGCCGTAG
GCF_000709935.2_ASM70993v2_genomic.fna_1:166061-166321 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TGATGTGAAG Num.seqs=5
Similarity=0.771795
0 TGATGTGAAGGGTTATAAGTAAGTGAGAATTGACCCCTNAGTGCAGCCGTAG

Consensus:

TGATGTGAAGGGTTATAAGTAAGTGAGAATTGACCCCTNAGTGCAGCCGTAG

>Bacillus_Fam_565_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
GCF_000708755.2_ASM70875v2_genomic.fna_1:230141-230557 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=GTGAATGAAC Num.seqs=8
Similarity=0.861722
0 GTGAATGAACCCTTCGTACGAAGAATCAGGAGCTGAAGGGTCAAAAGGCGTC
GCF_000709935.2_ASM70993v2_genomic.fna_1:229818-230026 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GTGAATGAAC Num.seqs=4

Similarity=0.858974

0 GTGAATGAACCCTTCATACGAAGAATCAGGAGCTGAAGGGTCAAAAGGCGTC

Consensus:

GTGAATGAACCCTTCaTACGAAGAATCAGGAGCTGAAGGGTCAAAAGGCGTC

>Bacillus_Fam_566_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 1.000000

GCF_000708755.2_ASM70875v2_genomic.fna_2:776717-776977 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=CATGAAGGGT Num.seqs=5

Similarity=0.897436

0 CATGAAGGGTCATATCATGCTCGCTTATGACCACTCAGCTCACCCCTGCCCTG

GCF_000709935.2_ASM70993v2_genomic.fna_4:32363-32675 Satlength=313 Nr of

Repeats=6 RepeatLength=52 seed=GCATGAAGGG Num.seqs=6 Similarity=0.912821

51 CATGAAGGGTCATATCATGCTCGCTTATGACCACTCAGCTCACCCCTGCCCTG

Consensus:

CATGAAGGGTCATATCATGCTCGCTTATGACCACTCAGCTCACCCCTGCCCTG

>Bacillus_Fam_567_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 0.826923

GCF_000708755.2_ASM70875v2_genomic.fna_5:240351-240559 Satlength=209 Nr

of Repeats=4 RepeatLength=52 seed=CAGGTTTAAAG Num.seqs=4

Similarity=0.901709

0 CAGGTTTAAAGAGCACAAACGTGTCTACCCAGCTAAGAGTTTGTGCTGCAAAC

GCF_000709935.2_ASM70993v2_genomic.fna_13:174173-174383 Satlength=211 Nr

of Repeats=4 RepeatLength=52 seed=AGTTTGTGCT Num.seqs=3

Similarity=0.786325

36 AAGGTTTAAAGAGCACTAACGCGTCTTCCCAGANAAGAGTTTGTGCTGCTAAC

Consensus:

aAGGTTTAAAGAGCACaAACGcGTCTaCCCAGatAAGAGTTTGTGCTGCaAAC

>Bacillus_Fam_568_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 0.948718

GCF_000708755.2_ASM70875v2_genomic.fna_6:356690-356898 Satlength=209 Nr

of Repeats=4 RepeatLength=52 seed=TCTTACCCTC Num.seqs=4

Similarity=0.811966

0 TCTTACCCTCCCAAACCGTTATTCGATCTGACAGGGTAAGCAAACCTACGTT

GCF_000709935.2_ASM70993v2_genomic.fna_5:562744-562952 Satlength=209 Nr

of Repeats=4 RepeatLength=52 seed=TCTTACCCTC Num.seqs=4

Similarity=0.803419

0 TCTTACCCTCCCAAACCGTTATTCGATCTGACAGGGCAAGCAAACCTACTTT

Consensus:

TCTTACCCTCCCAAACCGTTATTCGATCTGACAGGGcAAGCAAACCTACgTT

>Bacillus_Fam_569_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.897436
GCF_000708755.2_ASM70875v2_genomic.fna_7:38513-38773 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=AAGTGTCTT Num.seqs=5 Similarity=0.820513
0 AAGTGTCTTAACCTGGGTTAGCAACACAACTTTGTTGATTGTTCACTGGA
GCF_000709935.2_ASM70993v2_genomic.fna_19:41278-41486 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=GGAAAGTGTT Num.seqs=4 Similarity=0.820513
49 AAGTGTCTTAATCTGAGTTAGCAACACAACTCTGTTGATCGTTCACTGGA

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Consensus:

AAGTGTCTTAACCTGaGTTAGCAACACAACTcTGTGATcGTTCACTGGA

>Bacillus_Fam_570_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.794872
GCF_000708755.2_ASM70875v2_genomic.fna_7:121702-121910 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TTGATGGTTC Num.seqs=4
Similarity=0.905983
0 TTGATGGTCTTATAAGCCCGATAAGTACCACCAAACCTCTGATTCCCTTGAA
Rev.of_GCF_000708755.2_ASM70875v2_genomic.fna_22:145264-145525
Satlength=262 Nr of Repeats=5 RepeatLength=52 seed=TAAGAACCAT Num.seqs=4
Similarity=0.747863 13
TTGATGGTCTTATAAGCCCGATAAGTGCCATCAACCTCTGAGTTTTTTGGA

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Consensus:

TTGATGGTCTTATAAGCCCGATAAGTaCCAcCAAACTCTGAgTcccTTGaA

>Bacillus_Fam_571_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.948718
GCF_000708755.2_ASM70875v2_genomic.fna_22:151396-151604 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GAAGGTCACA Num.seqs=4
Similarity=0.846154
0 GAAGGTCACAAAACAGGAAGGAATGTGCCCTTCGTGAAGTGTTCCAAGGTGT
GCF_000709935.2_ASM70993v2_genomic.fna_24:262239-262603 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=GAAGGTCACA Num.seqs=7
Similarity=0.851038
0 GAAGGTCACAAAACGGAAGGAATGTGCCCTTCGTGAAGTGTTCCAAGATGT

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Consensus:

GAAGGTCACAAAACaGGAAGGAATGTGCCCTTCGTGAAGTGTTCCAAGaTGT

>Bacillus_Fam_572_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GCF_000708755.2_ASM70875v2_genomic.fna_22:158758-159018 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GGAAAGTGTT Num.seqs=5
Similarity=0.779487
0 GGAAAGTGTTCTAAAAAGGGTTTAGCAACATTAACCCTGGCTGGAGAAGAGA

GCF_000709935.2_ASM70993v2_genomic.fna_24:269755-270118 Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=GGAAAAGTGTT Num.seqs=6 Similarity=0.832479
0 GGAAAAGTGTTCTAAAAAGGGTTTAGCAACATTAACCCTGGCTGGAGAAGAGA

Consensus:

GGAAAAGTGTTCTAAAAAGGGTTTAGCAACATTAACCCTGGCTGGAGAAGAGA

>Bacillus_Fam_573_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52 Alignment score = 1.000000
GCF_000708755.2_ASM70875v2_genomic.fna_22:241123-241383 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TGAAAAGGTCA Num.seqs=5 Similarity=0.866667
0 TGAAAAGGTCAATAAGCGGAAGGATAAGACCCTTTATCAAAGCTGGTCCGCCG
GCF_000709935.2_ASM70993v2_genomic.fna_24:352189-352449 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TGAAAAGGTCA Num.seqs=5 Similarity=0.866667
0 TGAAAAGGTCAATAAGCGGAAGGATAAGACCCTTTATCAAAGCTGGTCCGCCG

Consensus:

TGAAAAGGTCAATAAGCGGAAGGATAAGACCCTTTATCAAAGCTGGTCCGCCG

>Bacillus_Fam_574_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52 Alignment score = 0.641026
GCF_000787375.1_ASM78737v1_genomic.fna_3:77617-77929 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=CTTTGACTCC Num.seqs=6 Similarity=0.735867
0 CTTTGACTCCCGTTCTCGGGCTTCCTCCAACCTTCGGGTGCCATCCCCTTC
GCF_000787375.1_ASM78737v1_genomic.fna_4:23329-23745 Satlength=417 Nr of Repeats=6 RepeatLength=52 seed=TCTTTCTGCT Num.seqs=4 Similarity=0.863248
13 CTTTGACTACCGGTCTTTCTGCTTCCTCTCGTTTCGGTAGTCAACCCCTTC

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Consensus:

CTTTGACTaCCGgTCTcgcgGCTTCCTCcaacTTTCGGGaGcCAaCCCCCTTC

>Bacillus_Fam_575_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52 Alignment score = 0.910256
GCF_000934845.1_ASM93484v1_genomic.fna_81:9-269 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=AATCTCCACA Num.seqs=5 Similarity=0.815385
0 AATCTCCACATACTGGAAAATCGTAGTCCCAATCAGCCCTATTGGTGCTCCN
Rev.of_GCF_000934845.1_ASM93484v1_genomic.fna_105:32-292 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TATGTGGAGA Num.seqs=5 Similarity=0.762963
AATCTCCACATACTGGTAAATCNTAGTCCCAATAAGCCCTATTGGTGCTCCG

12

Consensus:

AATCTCCACATACTGGaAAATCgTAGTCCCAATaAGCCCTATTGGTGCTCCg

>Bacillus_Fam_576_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
GCF_000986785.1_ASM98678v1_genomic.fna_3:238264-238524 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GGGCCTCCAT Num.seqs=5
Similarity=0.876730
0 GGGCCTCCATCAGGGCGATGGACGACCGTTTATTGCTCAATCTCAGGTTTCA
Rev.of_GCF_000986785.1_ASM98678v1_genomic.fna_6:203684-203891
Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=GATGGAGGCC Num.seqs=3
Similarity=0.880342 11
GGGCCTCCATCGGGCGATGGACGACCGTTTATTGCTCAATCTCAGGTTTCA

Consensus:

GGGCCTCCATCaGGGCGATGGACGACCGTTTATTGCTCAATCTCAGGTTTCA

>Bacillus_Fam_577_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.730769
GCF_000986785.1_ASM98678v1_genomic.fna_9:47447-47966 Satlength=520 Nr of
Repeats=10 RepeatLength=52 seed=TTTTTCTCTC Num.seqs=9
Similarity=0.773235
0 TTTTTCTCTCATTTCNGCTGATTTCCGGTACTGAGGCCGCTGTCAGTACCTC
Rev.of_GCF_000986785.1_ASM98678v1_genomic.fna_31:15669-16293
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=AGAAAAAGAG
Num.seqs=12 Similarity=0.747942
7 TTTTTCTCCNCTCTGCCGATTTCCGGTACTGACACGACCTGTCAGTGACTC

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Consensus:

TTTTTCTCcCacTcTGCcGATTTCCGGTACTGAcCcaCCTGTCAGTaaCTC

>Bacillus_Fam_578_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.666667
GCF_001315085.1_ASM131508v1_genomic.fna_3:24629-24950 Satlength=322 Nr of
Repeats=4 RepeatLength=52 seed=GATGAAGACC Num.seqs=3 Similarity=0.846154
0 GATGAAGACCGGAATGAAGCTTGAGTGAGAGGAAAAAGGTATTCATGAGGTT
Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_122:112785-113045
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GGTCTTCATA Num.seqs=5
Similarity=0.716049 10
TATGAAGACCTGAACGAAGCTTGAGCCTGCCCGAAAAGGTCTTCATCGGGTT

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Consensus:

gATGAAGACCgGAACGAAGCTTGAGccaGaccaAAAAGGTaTTCATcaGGTT

>Bacillus_Fam_579_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.692308
GCF_001375535.1_Bacillus_niamyensis_genomic.fna_6:1820901-1821109
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GCGAGTTCGG Num.seqs=4
Similarity=0.935897 0
GCGAGTTCGGGACGTGAGAGTCGCCATCATGACCCATCAACGCGACTTTTCC

Rev.of_GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3265006-3265630
Satlength=625 Nr of Repeats=12 RepeatLength=52 seed=GCAAAAGTCG
Num.seqs=12 Similarity=0.846154 0
GCGGATTCGGGACATGAGGGACTCCATCATGAACCATTGGCACGACTTTTGC

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Consensus:

GCGaaTTCGGGACaTGAGaGaCcCATCATGAaCCATcaaCaCGACTTTTcC

>Bacillus_Fam_580_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.705128
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2171941-2172148
Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=GGCCCGTTGG Num.seqs=3
Similarity=0.888889 0
GGCCCGTTGGTCTCTTTTTTGACACGAACGGGACATGATAAAGCNTCTCAT
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4192776-4193140
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=TCTCATGTCC Num.seqs=7
Similarity=0.829060 46
GTCCCGTAGGNTCCTTTTTTTTCCGCGAACGGTCCGTGATAAAGCGTCTCAT

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Consensus:

GgCCCGTaGGtTCccTTTTTTGaCaCGAACGGGaCaTGATAAAGCgTCTCAT

>Bacillus_Fam_581_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.653846
GCF_001420715.1_ASM142071v1_genomic.fna_22:1909065-1909431 Satlength=367
Nr of Repeats=7 RepeatLength=52 seed=ATGAAGGACA Num.seqs=5
Similarity=0.853846 0
ATGAAGGACAAGTTACACCAAGACAAAAGCAAAATGTCCTTCATCAAGTGG
Rev.of_GCF_001420715.1_ASM142071v1_genomic.fna_22:3763575-3764043
Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=ATGAAGGACA Num.seqs=9
Similarity=0.763627 45
ATGAAGGCCAAGTGACAGCAAGAAATTACGAANAGTGTCTTCATNAGGTAA

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Consensus:

ATGAAGGaCAAGTgACAcCAAGAAaaaAaGaAaAaTGTCTTCATcAaGTaa

>Bacillus_Fam_582_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.801282
GCF_001420715.1_ASM142071v1_genomic.fna_22:3674885-3675145 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=TGGTCTTTTG Num.seqs=5
Similarity=0.820513 40
NCCTTATAAAGACCATTCGGAACCGGATTCTTCCACCAATTGGTCTTTTGAT
GCF_001420715.1_ASM142071v1_genomic.fna_24:163648-164012 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=TAAAGACCAT Num.seqs=7
Similarity=0.832723 58
ACCTTATAAAGACCATTCGGATTCTTCTCACATTGGGCTTTTGAT

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Consensus:

Consensus:

TGGgCTTTTGATaCCTTATAAAGACCATTcGGAacCGGATTCTTCCaCaaAT

>Bacillus_Fam_583_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.775641
GCF_001439965.1_ASM143996v1_genomic.fna_121:145618-145878 Satlength=261
Nr of Repeats=4 RepeatLength=52 seed=AGTTCCCGAA Num.seqs=3
Similarity=0.794549 0
AGTTCCCGAACCCAGGCAAACTCCCCTTCCAGGGTAATNAATCGTTCACCTTA
Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_550:13876-14084
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CGGGAATAA Num.seqs=4
Similarity=0.722222 8
AGTTCCCGTGCCTAGGCAAAATCCCCTCCAGGGTAATTAATCGGTCACTTT

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Consensus:

AGTTCCCGaaCCcAGGCAAAaTcCCCcTCCAGGGTAATtAATCGgTCACTTa

>Bacillus_Fam_584_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.666667
GCF_001591665.1_ASM159166v1_genomic.fna_18:135261-135572 Satlength=312 Nr
of Repeats=6 RepeatLength=52 seed=TCAGTGCCCG Num.seqs=5
Similarity=0.784615 0
TCAGTGCCCGTGCAGGGTAAAAAACAGGCTTATGGGCACTCAGACAGGTTG
GCF_001591665.1_ASM159166v1_genomic.fna_19:38371-38679 Satlength=309 Nr
of Repeats=6 RepeatLength=52 seed=GGCACTCAGA Num.seqs=4
Similarity=0.830713
35 TCAGTGCCCATGGAGGGGAAAAATGAATGCCACGGGCACTCAGAAAGGTTT

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Consensus:

TCAGTGCCCaTGcAGGGGaAAAAaaaAgGCccAcGGGCACTCAGAAAGGTTg

>Bacillus_Fam_585_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.647436
GCF_001591665.1_ASM159166v1_genomic.fna_57:39088-39504 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=ATGAGGACAG Num.seqs=8
Similarity=0.800366
0 ATGAGGACAGGTTAGGCCCTTGCTTAACGATTTTGTCTCATGAACACCTC
GCF_001591805.1_ASM159180v1_genomic.fna_32:17384-17591 Satlength=208 Nr
of Repeats=4 RepeatLength=52 seed=GTCTCATGA Num.seqs=3
Similarity=0.610063
35 CTGAGGACAATTTAGCTCTTGCTCGNTGAGTTCTGTCTCATGAACGCCCC

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Consensus:

aTGAGGACAagTTaaGCcCTTGCTcaacGAgTTcTGTCTCATGAACaCCcC

>Bacillus_Fam_586_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.717949

GCF_001591805.1_ASM159180v1_genomic.fna_49:24442-24701 Satlength=260 Nr
of Repeats=5 RepeatLength=52 seed=CTATTGGACA Num.seqs=4
Similarity=0.824786
0 CTATTGGACAAAACCCCTTATAAAGCACCCAGAATGTCCATTAGAGCCCTT
Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_80:5111-5317 Satlength=207
Nr of Repeats=4 RepeatLength=52 seed=TTGTCCAATA Num.seqs=3
Similarity=0.880342 11
CTATTGGACAAAACCTCTTTTATAAACCCCTTAAATTGTCCAATAGACCCCTT

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Consensus:

CTATTGGACAAAACcCccTTATAAAcCaCccAaAaTGTCCAaTAGAcCCCTT

>Bacillus_Fam_587_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.717949
GCF_001636315.1_ASM163631v1_genomic.fna_1:1902145-1902509 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=TGTGCACATT Num.seqs=7
Similarity=0.765568 0
TGTGCACATTGAAGCGTTCAATGAACACGAGAGAAAGGAATATCCACATAGA
Rev.of_GCF_001636315.1_ASM163631v1_genomic.fna_1:5398707-5398968
Satlength=262 Nr of Repeats=5 RepeatLength=52 seed=CTTCAATGTG Num.seqs=4
Similarity=0.696581 14
AGTGCACATTGAAGGCTTCAATGAACACGGGAGCAAGGGAAATCATCGAAGA

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Consensus:

aGTGCACATTGAAGccTTCAATGAACACGaGAGaAAGGaAaATCaaCaaAGA

>Bacillus_Fam_588_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.621795
GCF_001636325.1_ASM163632v1_genomic.fna_2:129056-129316 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TTATTCCTCT Num.seqs=5
Similarity=0.941026
0 TTATTCCTCTGAAGAAGAAAGAAATGAGCGGTCTTCCGGTGAATAACCAGAGT
GCF_001636325.1_ASM163632v1_genomic.fna_3:419541-420114 Satlength=574 Nr
of Repeats=11 RepeatLength=52 seed=TTCAGGTGAA Num.seqs=10
Similarity=0.909402 32
TTATTCCTCTGAAGCAGCNCAAAAGCACCTTGTTTCAGGTGAATAACCACGGT

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Consensus:

TTATTCCTCTGAAGaAGaaaaAAaGaaCcgTcTTCaGGTGAATAACCACaGT

>Bacillus_Fam_589_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.641026
GCF_001636335.1_ASM163633v1_genomic.fna_1:413718-414550 Satlength=833 Nr
of Repeats=16 RepeatLength=52 seed=AAGAAAAAGT Num.seqs=16
Similarity=0.861325 28
ATGAAGGACAAAACGCAATGAGCAAAGGAAGAAAAAGTCCATCATAGGGCGA
Rev.of_GCF_002019635.1_ASM201963v1_genomic.fna_2:1603355-1603717
Satlength=363 Nr of Repeats=7 RepeatLength=52 seed=TGAAGGACTT Num.seqs=6

Similarity=0.717695

44

ATGAAAGACAAAAGCCAACCGTCACAGAAGGGAAAAGTCCTTCATAGGGGCA

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Consensus:

AaGaAAAAGTCCaTCATAGGGccAATGAAaGACAAAaccCAAccagCAaAGa

>Bacillus_Fam_590_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 0.698718

GCF_001636335.1_ASM163633v1_genomic.fna_1:1586996-1587464 Satlength=469

Nr of Repeats=9 RepeatLength=52 seed=ATGATGGACT Num.seqs=9

Similarity=0.908832

0

ATGATGGACTTTTCTGGCTTTNCCTGAATCGGTTTTGTCTTCATACCCCTT

Rev.of_GCF_001636335.1_ASM163633v1_genomic.fna_2:265356-265928

Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=ATCATCAAGG

Num.seqs=11 Similarity=0.870862

5 ATGATGGACTTTTTCCGCGTTCCCTCACACGCTTTTGTCTTCAGAACCTTG

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Consensus:

ATGATGGACTTTTcccGCgTTcCCTcAaaCGcTTTTGTCTTCaGaaCCTTg

>Bacillus_Fam_591_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 0.769231

GCF_001636345.1_ASM163634v1_genomic.fna_1:791126-791369 Satlength=244 Nr

of Repeats=4 RepeatLength=52 seed=CTGGATTATA Num.seqs=3

Similarity=0.811966

0 CTGGATTATAGAGGTGTGTTTCGCGCTTTATCGGGACTCCGATTACCAAAAT

Rev.of_GCF_001636345.1_ASM163634v1_genomic.fna_1:2232952-2233471

Satlength=520 Nr of Repeats=10 RepeatLength=52 seed=GAGAAACACA

Num.seqs=8 Similarity=0.748168

24 CTGGATTATAGAGGTGTGTTTCTCGCCGAATTGGGACACTGTTTACCAAATT

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Consensus:

CTGGATTATAGAGGTGTGTTTCgCGCcgaATcGGGACaCcGaTTACCAAAaT

>Bacillus_Fam_592_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52

Alignment score = 0.647436

GCF_001636345.1_ASM163634v1_genomic.fna_1:1139536-1139952 Satlength=417

Nr of Repeats=8 RepeatLength=52 seed=GGAGAAACGA Num.seqs=8

Similarity=0.882784

0

GGAGAAACGAGCCCGAAAAGTCCAGTAAGTGGAAAAAGTGTCTGTAAACA

GCF_001636345.1_ASM163634v1_genomic.fna_1:1221728-1222246 Satlength=519

Nr of Repeats=10 RepeatLength=52 seed=GTATATGGAA Num.seqs=9

Similarity=0.850427

24

GGNTAAACGAGACACAATAGTCCAGTATATGGAAAACAGAGTCGTGATTACG

* *

Consensus:

GGGagAAACGAGaCacAAaAGTCCAGTAaaTGGAAAAaAGaGTCGTGaaaACa

>Bacillus_Fam_593_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.608974
GCF_001636425.1_ASM163642v1_genomic.fna_1:697484-697900 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=TCATGAAGGA Num.seqs=8
Similarity=0.717880
0 TCATGAAGGACGTNTCCCTGGATATAGCAGCTCGAATTGTCCTTCATCACGC
Rev.of_GCF_001636425.1_ASM163642v1_genomic.fna_1:4328531-4328895
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=AAAGTCCTTC Num.seqs=7
Similarity=0.868132 14
TCATGAAGGACTTTTCTCAAGACATCGGACANCCAAAAGTCCTTCATCNCCC

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Consensus:

TCATGAAGGACgTtTCcCaaGAcATaGcAcatCcAAaaGTCCTTCATCaCcC

>Bacillus_Fam_594_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.974359
GCF_001887185.1_ASM188718v1_genomic.fna_162:152517-152725 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=CACATTTTTC Num.seqs=4
Similarity=0.854701 0
CACATTTTCTGCATTTTCGCTCCATTATCTGTTTCAAAACCTCTAGTTGACG
GCF_002009555.1_ASM200955v1_genomic.fna_224:12277-12640 Satlength=364 Nr
of Repeats=7 RepeatLength=52 seed=ACATTTTCT Num.seqs=6
Similarity=0.852991
1 CACATTTTCTGCATTTTCGCTCCATTATCTGTTTCAAAACCTCGAGTTGACG

Consensus:

CACATTTTCTGCATTTTCGCTCCATTATCTGTTTCAAAACCTCgAGTTGACG

>Bacillus_Fam_595_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.929487
GCF_001887185.1_ASM188718v1_genomic.fna_178:71698-72478 Satlength=781 Nr
of Repeats=15 RepeatLength=52 seed=GGGCACCTTT Num.seqs=15
Similarity=0.850305 0
GGGCACCTTTCTCCCTCTTTCGTTACCGCGAAACCGNTTTTTCCTCTCTAGC
Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_534:4610-5026
Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=AAAGGTGCCC Num.seqs=8
Similarity=0.880952 10
GGGCACCTTTCTCCCTCTTTCGTTACCGCGAAACCGCTTTTTCCTCTCGGGC

Consensus:

GGGCACCTTTCTCCCTCTTTCGTTACCGCGAAACCGcTTTTTCCTCTCgAGC

>Bacillus_Fam_596_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.794872

GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_16:433491-433753
Satlength=263 Nr of Repeats=5 RepeatLength=52 seed=CTTCAATGTT Num.seqs=3
Similarity=0.914530 0
CTTCAATGTTACCGTTTCTATGATTTCAATAACTTTTTGGTCACATTGAGCT
Rev.of_GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_34:7995-8202
Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=CAGAGAAACG Num.seqs=3
Similarity=0.948718 22
CTTCAATGTGACCGTTTCTCTGATTTTACTTGCGTTTTGGTCACATTGAGCC

Consensus:

CTTCAATGTgACCGTTTCTaTGATTTcAaTaaCgTTTTGGTCACATTGAGCc

>Bacillus_Fam_597_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 0.955128
GCF_900156875.1_PRJEB18969_genomic.fna_11:364264-364471 Satlength=208 Nr
of Repeats=4 RepeatLength=52 seed=ATGAAGACCG Num.seqs=3
Similarity=0.863248
0 ATGAAGACCGTTAGTTTTGGTGAATGAGCAAGAACCGTTATCATAGTTGAG
GCF_900156875.1_PRJEB18969_genomic.fna_11:367968-368330 Satlength=363 Nr
of Repeats=7 RepeatLength=52 seed=AACCGTTAT Num.seqs=5
Similarity=0.858974
32 ATGAAGACCGTTAGTTTTGGTGAATGCNCAAGAACCGTTATCATAGTTGAG

Consensus:

ATGAAGACCGTTAGTTTTGGTGAATGagCAAGAACCGTTATCATAGTTGAG

>Bacillus_Fam_598_52_2 Nr. of seq. 2 Alignment length(with gaps) = 52
Alignment score = 1.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:1808457-1808873 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=GGCTTTCATT Num.seqs=8
Similarity=0.930403 0
GGCTTTCATTCTTCTCATGATGACCTTTTCTCTAGCTCTCTAGAATGATTTTC
GCF_900156875.1_PRJEB18969_genomic.fna_11:1817955-1818163 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=ATTTCCGGCTT Num.seqs=4
Similarity=0.948718 47
GGCTTTCATTCTTCTCATGATGACCTTTTCTCTAGCTCTCTAGAATGATTTTC

Consensus:

GGCTTTCATTCTTCTCATGATGACCTTTTCTCTAGCTCTCTAGAATGATTTTC

>Bacillus_Fam_599_51_2 Nr. of seq. 2 Alignment length(with gaps) = 51
Alignment score = 0.712418
GCF_000292245.2_ASM29224v2_genomic.fna_72:15429-15633 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=TTTCATTACC Num.seqs=4 Similarity=0.818910
82 TATTCGTACCCTAATTAAGGCAACCTCCATTTTCATTACCAATCCCCTGT

GCF_000292245.2_ASM29224v2_genomic.fna_80:13385-13741 Satlength=357 Nr of Repeats=7 RepeatLength=51 seed=TTTTTTCGTA Num.seqs=6 Similarity=0.836752
100 TTTTCGTACCCTAATTCAGCCAACACTCGAGTTTCATTACCTATTACCATT

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Consensus:

TTTCATTACCaATcaCCagTTaTTCGTACCCTAATTaAGcCAACaCTCcAg

>Bacillus_Fam_600_51_2 Nr. of seq. 2 Alignment length(with gaps) = 51
Alignment score = 0.895425
GCF_000292245.2_ASM29224v2_genomic.fna_92:17-274 Satlength=258 Nr of Repeats=5 RepeatLength=51 seed=TTCGGCTTAT Num.seqs=3 Similarity=0.895425
0 TTCGGCTTATAATTCTTACTCTCCATTCTTTTTACGCCGAACCTCTCTCTTA
Rev.of_GCF_000292245.2_ASM29224v2_genomic.fna_125:10-369 Satlength=360 Nr of Repeats=7 RepeatLength=51 seed=TCGGCGTAAA Num.seqs=5
Similarity=0.832680 40
TTCGGCTTATAATTCTTTTTCTCCATTCTTTTTACGCCGAACCTGGCTCTTA

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Consensus:

TTCGGCTTATAATTCTTAcTCTCCATTCTTTTTACGCCGAACtCgCTCTTA

>Bacillus_Fam_601_51_2 Nr. of seq. 2 Alignment length(with gaps) = 51
Alignment score = 1.000000
GCF_001420645.1_ASM142064v1_genomic.fna_44:115239-115443 Satlength=205 Nr of Repeats=5 RepeatLength=51 seed=TTCTTGCTCT Num.seqs=3
Similarity=0.912854 0
TTCTTGCTCTTCTCTAGCATCGTCCTCGCTGAGCTCTTCTGTACTGTCTTC
Rev.of_GCF_002019765.1_ASM201976v1_genomic.fna_1:514830-515034
Satlength=205 Nr of Repeats=5 RepeatLength=51 seed=GAGAAGAGCA Num.seqs=3
Similarity=0.912854 14
TTCTTGCTCTTCTCTAGCATCGTCCTCGCTGAGCTCTTCTGTACTGTCTTC

Consensus:

TTCTTGCTCTTCTCTAGCATCGTCCTCGCTGAGCTCTTCTGTACTGTCTTC

>Bacillus_Fam_602_51_2 Nr. of seq. 2 Alignment length(with gaps) = 51
Alignment score = 1.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:857991-858195 Satlength=205 Nr of Repeats=4 RepeatLength=51 seed=AAAAGGAAAAG Num.seqs=4
Similarity=0.908497
0 AAAAGGAAAGCGCCAAAAGCCCGTTTGTGAACACGAAAATCGAAAAACAGG
GCF_002019665.1_ASM201966v1_genomic.fna_1:859725-860133 Satlength=409 Nr of Repeats=8 RepeatLength=51 seed=CGTTTGTGAA Num.seqs=8
Similarity=0.884220
21 AAAAGGAAAGCGCCAAAAGCCCGTTTGTGAACACGAAAATCGAAAAACAGG

Consensus:

AAAAGGAAAGCGCCAAAAGCCCGTTTGTGAACACGAAAAATCGAAAAACAGG

>Bacillus_Fam_603_48_2 Nr. of seq. 2 Alignment length(with gaps) = 48
Alignment score = 1.000000
GCF_000153365.1_ASM15336v1_genomic.fna_17:211270-211939 Satlength=670 Nr
of Repeats=14 RepeatLength=48 seed=CAGATAGAGG Num.seqs=13
Similarity=0.835470 0
CAGATAGAGGAGGTTGAAGAACCGGAGCAAACCTGAGGAGTCAGAAGAG
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:4315874-4316543
Satlength=670 Nr of Repeats=14 RepeatLength=48 seed=CCTCTATCTG
Num.seqs=13 Similarity=0.839744
10 CAGATAGAGGAGGTTGAAGAACCGGAGCAAACCTGAGGAGTCAGAAGAG

Consensus:

CAGATAGAGGAGGTTGAAGAACCGGAGCAAACCTGAGGAGTCAGAAGAG

>Bacillus_Fam_604_48_2 Nr. of seq. 2 Alignment length(with gaps) = 48
Alignment score = 0.951389
GCF_000712615.1_ASM71261v1_genomic.fna_22:80497-81025 Satlength=529 Nr of
Repeats=11 RepeatLength=48 seed=TTGGATTATC Num.seqs=11
Similarity=0.853535
0 TTGGATTATCCACTGCATTACTTTCTTCTTGTGAAACAGCACTATTAC
GCF_000712615.1_ASM71261v1_genomic.fna_22:80497-81774 Satlength=1278 Nr
of Repeats=16 RepeatLength=48 seed=TTGGATTATC Num.seqs=15
Similarity=0.798942 0
TTGGATTATCCACTGCATTACTTCTTCTTGAGAAACAGCACTATTAC

Consensus:

TTGGATTATCCACTGCATTACTtTCTTCTTGaGAAACAGCACTATTAC

>Bacillus_Fam_605_48_2 Nr. of seq. 2 Alignment length(with gaps) = 48
Alignment score = 0.694444
GCF_000715205.1_SOAPdenovo_v1.05_genomic.fna_12:101104-101903
Satlength=800 Nr of Repeats=6 RepeatLength=48 seed=TCTTTTGGCT Num.seqs=5
Similarity=0.933333 0
TCTTTTGGCTCTTCCATTGACCCATCACCAGGCTTTGTTCCGTCCTGA
Rev.of_GCF_001578205.1_ASM157820v1_genomic.fna_1:1255656-1255848
Satlength=193 Nr of Repeats=4 RepeatLength=48 seed=GATCAGGATG Num.seqs=4
Similarity=0.907596 2
TCTTTCGGTTCTTCTGTTGTGCCATCGTCAGGTTTTGTCCCATCCTGA

Consensus:

TCTTTCGGcTCTTCcaTTGacCCATCacCAGGcTTTGTcCCaTCCTGA

>Bacillus_Fam_606_47_2 Nr. of seq. 2 Alignment length(with gaps) = 47
Alignment score = 1.000000

GCF_000153365.1_ASM15336v1_genomic.fna_34:533-722 Satlength=190 Nr of Repeats=4 RepeatLength=47 seed=TCCGTGGACA Num.seqs=3 Similarity=0.981087
0 TCCGTGGACAGATGGGGTGAAGTGTCTTTTGTGGTGCCAGGTACGC
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:4144621-4144810
Satlength=190 Nr of Repeats=4 RepeatLength=47 seed=AAAAGACACT Num.seqs=3
Similarity=0.943262 30
TCCGTGGACAGATGGGGTGAAGTGTCTTTTGTGGTGCCAGGTACGC

Consensus:

TCCGTGGACAGATGGGGTGAAGTGTCTTTTGTGGTGCCAGGTACGC

>Bacillus_Fam_607_46_2 Nr. of seq. 2 Alignment length(with gaps) = 46
Alignment score = 0.753623
GCF_001274915.1_ASM127491v1_genomic.fna_25:723071-723296 Satlength=226 Nr of Repeats=5 RepeatLength=45 seed=CCAGGTGAAG Num.seqs=5
Similarity=0.760000 0
CCAGGTGAAG-GAGAATCTGGCCAACCGGAAGAGGAAGTAACGGAG
Rev.of_GCF_000011145.1_ASM1114v1_genomic.fna_1:3424216-3424396
Satlength=181 Nr of Repeats=4 RepeatLength=45 seed=CTTCACCTGG Num.seqs=4
Similarity=0.737923 10
CCAGGTGAAGAGGGAATCTGGTCAGCCAGAGGAAGAAATAACGGAG

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Consensus:

CCAGGTGAAGaGaGAATCTGGcCAaCCaGAaGAaGAAaTAACGGAG

>Bacillus_Fam_608_45_2 Nr. of seq. 2 Alignment length(with gaps) = 45
Alignment score = 0.629630
GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_2:809286-809454
Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=AATCCAACGA Num.seqs=4
Similarity=0.962963 0
AATCCAACGACACCACCA--CAAGTGAAGGAAATAATGGAGAA
Rev.of_GCF_000712615.1_ASM71261v1_genomic.fna_1:387890-388565
Satlength=676 Nr of Repeats=15 RepeatLength=45 seed=CCACCTGTCTG
Num.seqs=15 Similarity=0.988713
29 AATCCAACAACACCACCAACGACAGGTGGAGACAACAACGGGGAT

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Consensus:

AATCCAACaACACCACCAAcgaCAaGTGaAGaaAAcAAcGGaGAa

>Bacillus_Fam_609_45_2 Nr. of seq. 2 Alignment length(with gaps) = 45
Alignment score = 0.614815
GCF_000612625.1_JCE_genomic.fna_6:32809-33331 Satlength=523 Nr of Repeats=6 RepeatLength=42 seed=GGCATTTGAC Num.seqs=4 Similarity=0.888889
0 GGCATTTGACCGTATCCGCTGGCA-TTTCT--CCAGCACCCATT
GCF_001591445.1_ASM159144v1_genomic.fna_9:113119-113479 Satlength=361 Nr of Repeats=7 RepeatLength=45 seed=GGCATTTGTC Num.seqs=6
Similarity=0.741844
0 GGCATTTGTCCATATCCTGCTGGTACTTGCTGACCATAACCCTGT

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Consensus:

GGCATTTGaCCaTATCCcGCTGGcAcTTgCTGaCCAgAACCcagT

>Bacillus_Fam_610_45_2 Nr. of seq. 2 Alignment length(with gaps) = 45

Alignment score = 0.874074

GCF_000161455.1_ASM16145v1_genomic.fna_1:4124623-4124845 Satlength=223 Nr of Repeats=5 RepeatLength=45 seed=GAAAAAAGAA Num.seqs=4

Similarity=0.851852

0

GAAAAAAGAAGCAGCAATGCAAGAACAACAAAAACAAGATAAAAT

GCF_000712615.1_ASM71261v1_genomic.fna_21:61395-61572 Satlength=178 Nr of Repeats=4 RepeatLength=45 seed=GAAAAAAGAA Num.seqs=3 Similarity=0.628118

0 GAAAAAAGAAGCAGCAATTCAGNNACAACAAAAACAAGATNAAAT

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Consensus:

GAAAAAAGAAGCAGCAATgCAagaACAACAAAAACAAGATaAAAT

>Bacillus_Fam_611_45_2 Nr. of seq. 2 Alignment length(with gaps) = 45

Alignment score = 0.822222

GCF_000724485.1_ASM72448v1_genomic.fna_1:628866-629091 Satlength=226 Nr of Repeats=5 RepeatLength=45 seed=GATTCCTCAT Num.seqs=5

Similarity=0.952593

0 GATTCCTCATCAGATTCATATTCATCGCTTGACTCGTTATCTTCA

GCF_000724485.1_ASM72448v1_genomic.fna_1:959830-960010 Satlength=181 Nr of Repeats=4 RepeatLength=45 seed=TCTTCAGATT Num.seqs=4

Similarity=0.925926

39 GATTCCTCGTCGGATTTCGTAACCATCGCTAGACTCGTTATCTTCA

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Consensus:

GATTCCTCaTCaGATTCaTAacCATCGCTaGACTCGTTATCTTCA

>Bacillus_Fam_612_43_2 Nr. of seq. 2 Alignment length(with gaps) = 43

Alignment score = 0.837209

GCF_000175075.1_ASM17507v1_genomic.fna_41:65761-65929 Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=GAAGCACCGG Num.seqs=4 Similarity=0.915344

0 GAAGC-ACCGGCTGAAGAACCTGTAAACAGAGGAACCAGCAGAG

GCF_001648575.1_ASM164857v1_genomic.fna_67:24594-24762 Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=GCTGAAGAGC Num.seqs=4

Similarity=0.906977

10 GAAGCTCCcNGCTGAAGAGCCTGTAAACAGAGGCACCAGCAGAG

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Consensus:

GAAGCtaCCgGCTGAAGaAcCTGTAAACAGAGGaACCAGCAGAG

>Bacillus_Fam_613_43_2 Nr. of seq. 2 Alignment length(with gaps) = 43

Alignment score = 0.689922

GCF_000430785.1_ASM43078v1_genomic.fna_16:70154-71534 Satlength=1381 Nr of Repeats=21 RepeatLength=42 seed=CATGCCGAAG Num.seqs=15
Similarity=0.532988 0
CATGCNGAAGGTNNNNNTACAACNGCAAGT-GGANATNCTTCN
GCF_000430785.1_ASM43078v1_genomic.fna_16:70112-70730 Satlength=619 Nr of Repeats=9 RepeatLength=42 seed=CATGCGGAAG Num.seqs=6 Similarity=0.576227
0 CATGCGGAAGGTNAAANCACAACAGCAAGTGGGANATGCTTCN

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Consensus:

CATGCgGAAGGTNaaaNcACAACaGCAAGTgGGANATgCTTCN

>Bacillus_Fam_614_43_2 Nr. of seq. 2 Alignment length(with gaps) = 43
Alignment score = 0.732558
GCF_000712615.1_ASM71261v1_genomic.fna_10:62613-63201 Satlength=589 Nr of Repeats=14 RepeatLength=42 seed=CCTTCCGCAT Num.seqs=14
Similarity=0.614123
0 CCTTCCGCATGCGAGNCAANTCCACTGGCTATTGTATTAANT-
GCF_000712615.1_ASM71261v1_genomic.fna_10:65183-65897 Satlength=715 Nr of Repeats=16 RepeatLength=42 seed=CCTTCCGCAT Num.seqs=15
Similarity=0.501622
0 CCTTCCGCATGCGANNANCTCCACTGGCTATTGTNTNCANNN

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Consensus:

CCTTCCGCATGCGAgNcAacTCCACTGGCTATTGTaTtaANtn

>Bacillus_Fam_615_43_2 Nr. of seq. 2 Alignment length(with gaps) = 43
Alignment score = 0.658915
GCF_000986785.1_ASM98678v1_genomic.fna_101:89286-89496 Satlength=211 Nr of Repeats=4 RepeatLength=42 seed=GGAGGAGCGA Num.seqs=3
Similarity=0.873016
0 GGAGGAGCGATGGACGCCAA-ATGCCGCACATGCCGAGGTG
Rev.of_GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_16:169506-169773
Satlength=268 Nr of Repeats=6 RepeatLength=42 seed=CTTGCGGCAT Num.seqs=5
Similarity=0.917460 40 GCAGGAGCAATGGATGCGCAATAT-
CCACATATGCCGCAAGTA

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Consensus:

GcAGGAGCaATGGAcGCCaCAAtATgCCaCAcATGCCGCAaGTa

>Bacillus_Fam_616_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.793651
GCF_000429725.1_ASM42972v1_genomic.fna_2:332298-332770 Satlength=473 Nr of Repeats=5 RepeatLength=41 seed=CGATTGTGAC Num.seqs=3
Similarity=0.913279
0 CGATTGTGACCAAGCGCGGCG-AAACTCCGGCCAATTGGCGA
Rev.of_GCF_000429725.1_ASM42972v1_genomic.fna_10:90786-91168
Satlength=383 Nr of Repeats=8 RepeatLength=41 seed=AATTGTCCGC Num.seqs=6

Similarity=0.785185
AGATTGTGACCAAGCGCGGCGNAAAGTGCGGACAATTGGCGG

37

Consensus:

aGATTGTGACCAAGCGCGGCGnAAAcTcCGGaCAATTGGCGa

>Bacillus_Fam_617_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.690476
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_1:1999822-2000150 Satlength=329 Nr of Repeats=8
RepeatLength=41 seed=ATTTTCGGATT Num.seqs=8 Similarity=0.809524 0
ATTTTCG-GATTTGCGGGCCGGAATCCATACTTTTCATGCCGG
Rev.of_GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_23:124770-125136 Satlength=367 Nr of Repeats=9
RepeatLength=41 seed=CGCAAATCAC Num.seqs=7 Similarity=0.14 A-
TTCGTGATTTGCGTGCCAGAACACACTCTTTTCNTGCCGG

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Consensus:

AtTTCGtGATTTGCGgGCCaGAaCaCacaCTTTTCaTGCCGG

>Bacillus_Fam_618_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.638889
GCF_002019665.1_ASM201966v1_genomic.fna_1:3639369-3639982 Satlength=614
Nr of Repeats=15 RepeatLength=41 seed=TTCGTCCCTA Num.seqs=13
Similarity=0.892850 0
TTCG-TCCCTATCCGTCGGTAAATCCCTTCATTCGTTGGTAG
Rev.of_GCF_002019665.1_ASM201966v1_genomic.fna_1:4598013-4598833
Satlength=821 Nr of Repeats=20 RepeatLength=41 seed=TTACCAACGA
Num.seqs=20 Similarity=0.827213
0 -CCGATCGCTATGCGTGGGTAAACTCGTTATTCGTTGGTAA

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Consensus:

tcCGaTcCCTATcCGTcGGTAAaCcCgTcATTTCGTTGGTAa

>Bacillus_Fam_619_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.809524
GCF_000007825.1_ASM782v1_genomic.fna_1:3435556-3435724 Satlength=169 Nr
of Repeats=4 RepeatLength=42 seed=GGAATAACTG Num.seqs=4
Similarity=0.968254
0 GGAATAACTGGTCCTACTGGGGTTACAGGTTCTACCGGAATC
GCF_000008505.1_ASM850v1_genomic.fna_1:3325303-3325513 Satlength=211 Nr
of Repeats=5 RepeatLength=42 seed=GGAATTGGCA Num.seqs=5
Similarity=0.923810
36 GGCATTACTGGTCCTACTGGAGTTACAGGACCTACCGGAATT

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Consensus:

GGaATaACTGGTCCTACTGGAATTACAGGacCTACCGGAATc

>Bacillus_Fam_620_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 1.000000
GCF_000009825.1_ASM982v1_genomic.fna_1:3313462-3313630 Satlength=169 Nr
of Repeats=4 RepeatLength=42 seed=CTTGCTTTCA Num.seqs=4
Similarity=0.899471
0 CTTGCTTTCAATGATGAAATGCGCCATTTCCAAAAGGAGCAG
GCF_900142675.1_IMG-
taxon_2654588196_annotated_assembly_genomic.fna_7:92101-92269
Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=CTTGCTTTCA Num.seqs=4
Similarity=0.920635 0
CTTGCTTTCAATGATGAAATGCGCCATTTCCAAAAGGAGCAG

Consensus:

CTTGCTTTCAATGATGAAATGCGCCATTTCCAAAAGGAGCAG

>Bacillus_Fam_621_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.809524
GCF_000169195.2_ASM16919v2_genomic.fna_1:2452745-2452955 Satlength=211 Nr
of Repeats=5 RepeatLength=42 seed=GGATCAGGTT Num.seqs=5
Similarity=0.841270 0
GGATCAGGTTCTGCATCCGGAACGACCGCAACGGGCAACACC
Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:1285270-1285522
Satlength=253 Nr of Repeats=6 RepeatLength=42 seed=GAACCCGATC Num.seqs=6
Similarity=0.832804 11
GGATCGGGTCCGCGTCCGGGACGACTGCAACGGGCAACACT

Consensus:

GGATCaGGTTcGCaTCCGGaACGACcGCAACGGGCAACACc

>Bacillus_Fam_622_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 1.000000
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_2:304102-304312
Satlength=211 Nr of Repeats=6 RepeatLength=42 seed=TTTGATTTCGG Num.seqs=4
Similarity=0.915344 0
TTTGATTTCGGTTGATCAGAAGTTTGATTCCATTGATCAGAGA
GCF_000294775.2_ASM29477v2_genomic.fna_1:4910289-4910520 Satlength=232 Nr
of Repeats=6 RepeatLength=42 seed=GATTCCATTG Num.seqs=5
Similarity=0.905426 24
TTTGATTTCGGTTGATCAGAAGTTTGATTCCATTGATCAGAGA

Consensus:

TTTGATTTCGGTTGATCAGAAGTTTGATTCCATTGATCAGAGA

>Bacillus_Fam_623_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.650794

GCF_000299035.1_ASM29903v1_genomic.fna_5:177403-178117 Satlength=715 Nr
of Repeats=17 RepeatLength=42 seed=AGTTGTAGTG Num.seqs=17
Similarity=0.981793 0
AGTTGTAGTGGAACTCGAGAAGAAGAGAGACCAGTAGAGCG
Rev.of_GCF_000712615.1_ASM71261v1_genomic.fna_6:43769-44105 Satlength=337
Nr of Repeats=8 RepeatLength=42 seed=ACTACTTCTT Num.seqs=8
Similarity=0.878685 9
AGAAGTAGTGGAGGCTCAAGCCGAAGAGAGACCGGTACATCA

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Consensus:

AGaaGTAGTGGAAaCTCaAGaaGAAGAGAGACCaGTAcAgCa

>Bacillus_Fam_624_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.690476
GCF_000307875.1_BABA1.0_genomic.fna_120:5376-5682 Satlength=307 Nr of
Repeats=7 RepeatLength=42 seed=GGAGAAATGC Num.seqs=5 Similarity=0.885714
0 GGAGAAATGCCACAAGGTTACGGCCAGATGCCGACAGGNTAC
GCF_000508325.1_BAVI_1_genomic.fna_148:13-268 Satlength=256 Nr of
Repeats=5 RepeatLength=42 seed=AATGCCGGGA Num.seqs=4 Similarity=0.814815
5 GGAGAAATGCCGGGAGCCTATGGCCAAATGCCAGCAGGATAC

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Consensus:

GGAGAAATGCCaCaAGccTAcGGCCaAATGCCaACAGGaTAC

>Bacillus_Fam_625_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.730159
GCF_000331575.1_ASM33157v1_genomic.fna_2:519806-520142 Satlength=337 Nr
of Repeats=8 RepeatLength=42 seed=AGATTCGTGG Num.seqs=8
Similarity=0.833333
0 AGATTCGTGGGTAAAGCACCGGGTTATGTGGGTATTCTACTA
GCF_000331575.1_ASM33157v1_genomic.fna_6:31803-31970 Satlength=168 Nr of
Repeats=4 RepeatLength=42 seed=GAGTTATATG Num.seqs=3 Similarity=0.839793
20 AAATCGTGGGTAAANCNCCGAGTTATATGGGTATTCCACCC

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Consensus:

AaAcTCGTGGGTAAAgCaCCGaGTTATaTGGGTATTCCaACca

>Bacillus_Fam_626_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42
Alignment score = 0.968254
GCF_000496285.1_ASM49628v1_genomic.fna_1:4580071-4580491 Satlength=421 Nr
of Repeats=10 RepeatLength=42 seed=CCAGGAGGCG Num.seqs=10
Similarity=0.899824 0
CCAGGAGGCGGAACGGGAACAGATAACGGAACCGGAGGAAAC
GCF_000831065.1_ASM83106v1_genomic.fna_1:1836001-1836505 Satlength=505 Nr
of Repeats=12 RepeatLength=42 seed=CCAGGAGGCG Num.seqs=12
Similarity=0.956229 0
CCAGGAGGCGGAACGGGAACAGACAACGGAACCGGAGGAAAC

Consensus:

CCAGGAGGCGGAACGGGAACAGAcAACGGAACCGGAGGAAAC

>Bacillus_Fam_627_42_2 Nr. of seq. 2 Alignment length(with gaps) = 42

Alignment score = 1.000000

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3545829-3546081

Satlength=253 Nr of Repeats=6 RepeatLength=42 seed=GAAGTCGCGA Num.seqs=6
Similarity=0.836176 0

GAAGTCGCGAAATTCCGGTGGGAAGTTGAAAGATTAACGGGA

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3549055-3549349

Satlength=295 Nr of Repeats=7 RepeatLength=42 seed=GAAGTCGCGA Num.seqs=7
Similarity=0.838686 0

GAAGTCGCGAAATTCCGGTGGGAAGTTGAAAGATTAACGGGA

Consensus:

GAAGTCGCGAAATTCCGGTGGGAAGTTGAAAGATTAACGGGA

>Bacillus_Fam_628_41_2 Nr. of seq. 2 Alignment length(with gaps) = 41

Alignment score = 0.617886

GCF_000321185.1_ASM32118v1_genomic.fna_73:13581-13737 Satlength=157 Nr of
Repeats=4 RepeatLength=39 seed=TTCTTTTACT Num.seqs=4 Similarity=0.794872
0 TTCTTTTACTGGAGCTGTTTTG--ACAATTGGCTTTGGCGC

Rev.of_GCF_000380245.2_ASM38024v2_genomic.fna_12:375741-376014

Satlength=274 Nr of Repeats=7 RepeatLength=39 seed=AAAGAAGCAC Num.seqs=7
Similarity=0.744404 6

TTCTTTTACT--ATTGGTTTTGTTACATTTGGCTGNGGTGC

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Consensus:

TTCTTTTACTggAgcgGTTTTGttACAaTTGGCTgtGGcGC

>Bacillus_Fam_629_41_2 Nr. of seq. 2 Alignment length(with gaps) = 41

Alignment score = 0.626016

GCF_001648575.1_ASM164857v1_genomic.fna_3:413-553 Satlength=141 Nr of

Repeats=4 RepeatLength=40 seed=GCGGATAAAA Num.seqs=3 Similarity=0.911111
0 GCGGATAAACGGA-AAAGTCGCGGATATATCGGAAAGTTA

Rev.of_GCF_000612805.1_FF3_genomic.fna_4:298364-298568 Satlength=205 Nr

of Repeats=5 RepeatLength=41 seed=AATATATCAG Num.seqs=4

Similarity=0.967480

32 GCTGATAAATCAAAGAAAGTCGCTGATATATTTTAAATTTC

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Consensus:

GCgGATAAAaCaaAgAAAGTCGcGATATATcggAAAgTTa

>Bacillus_Fam_630_40_2 Nr. of seq. 2 Alignment length(with gaps) = 40

Alignment score = 0.754167

GCF_001742425.1_ASM174242v1_genomic.fna_9:30829-31159 Satlength=331 Nr of Repeats=9 RepeatLength=39 seed=TGTTCTTCTG Num.seqs=7 Similarity=0.796500
0 TGTTCTTCTGTTGGCTCTGTAGCTTCTACTTCTTCAG-CT
GCF_001742425.1_ASM174242v1_genomic.fna_9:45797-45992 Satlength=196 Nr of Repeats=5 RepeatLength=39 seed=TTCTACTTCT Num.seqs=5 Similarity=0.816667
22 -G TTCATCTGTTGGCTCTGTTATTTCTACTTCTTCTGTCT

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Consensus:

tGTTCaTCTGTTGGCTCTGTaacTTCTACTTCTTCaGtCT

>Bacillus_Fam_631_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.897436

GCF_000007825.1_ASM782v1_genomic.fna_1:4838007-4838475 Satlength=469 Nr of Repeats=12 RepeatLength=39 seed=GGTTTCACTT Num.seqs=12
Similarity=0.948718 0

GGTTTCACTTCTGGCTCCTTCGGCTCTTTTCGGATCTTCC

GCF_000831065.1_ASM83106v1_genomic.fna_1:4592019-4592604 Satlength=586 Nr of Repeats=15 RepeatLength=39 seed=TTCACTTCTG Num.seqs=15
Similarity=0.890924 3

GGCTTCACTTCTGGTTTCCTTCGGTTCTTTTCGGATCTTCC

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Consensus:

GGcTTCACTTCTGGcTCCTTCGGcTCTTTTCGGATCTTCC

>Bacillus_Fam_632_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.897436

GCF_000008505.1_ASM850v1_genomic.fna_1:5094439-5094634 Satlength=196 Nr of Repeats=5 RepeatLength=39 seed=AATCCGGAAC Num.seqs=5
Similarity=0.972650

0 AATCCGGAACAAAATCCAGCAACTAAACCTGCTACTGAC

GCF_001645555.1_ASM164555v1_genomic.fna_13:56878-57034 Satlength=157 Nr of Repeats=4 RepeatLength=39 seed=CTAAACCTGT Num.seqs=4
Similarity=0.914530

22 AATCCGGAACAAAACCCAGCAACTAAACCTGTTACTGAT

Consensus:

AATCCGGAACAAAACCCAGCAACTAAACCTGcTACTGAc

>Bacillus_Fam_633_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.760684

GCF_000175075.1_ASM17507v1_genomic.fna_32:156308-156500 Satlength=193 Nr of Repeats=5 RepeatLength=39 seed=TGATCGTGCT Num.seqs=4
Similarity=0.886040

0 TGATCGTGCTCTTCCTCATGAGCTTCTTCTCATGCTCA

Rev.of_GCF_001648575.1_ASM164857v1_genomic.fna_58:140804-140999

Satlength=196 Nr of Repeats=5 RepeatLength=39 seed=CACGAGCATG Num.seqs=5
Similarity=0.835897 2

TGGTCATGGTCGTCGCCATGAGCTTCTTCTCATGCTCG

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Consensus:

TGaTCaTGcTCgTCccCATGAGCTTCTTCCTCATGCTCa

>Bacillus_Fam_634_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.641026
GCF_000331575.1_ASM33157v1_genomic.fna_6:36584-36779 Satlength=196 Nr of
Repeats=5 RepeatLength=39 seed=ATGACCATGA Num.seqs=5 Similarity=0.856410
0 ATGACCATGATGGAAGCCATAACCAGGGTAGTAACCGCC
Rev.of_GCF_001420715.1_ASM142071v1_genomic.fna_22:732730-732964
Satlength=235 Nr of Repeats=6 RepeatLength=39 seed=TACCATCATG Num.seqs=6
Similarity=0.783476 15
ATGTCCATGATGGTAGCCTTGACCTGGGTNATAGGTNCC

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Consensus:

ATGaCCATGATGGaAGCCaTaACCaGGGTaaTAaccgCC

>Bacillus_Fam_635_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.794872
GCF_000474275.1_Bmar1.0_genomic.fna_30:49658-49853 Satlength=196 Nr of
Repeats=6 RepeatLength=39 seed=CATGCTCGTG Num.seqs=4 Similarity=0.863248
0 CATGCTCGTGATCATGATCTTCCTCATGCCCCGTGCTCTT
GCF_002019665.1_ASM201966v1_genomic.fna_1:1072418-1072646 Satlength=229
Nr of Repeats=6 RepeatLength=39 seed=TGTGCGTCCT Num.seqs=5
Similarity=0.958974 26
CATGTTCTGATCATGATCTTCCTCATGTGCGTCCTCAC

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Consensus:

CATGcTCGTGATCATGATCTTCCTCATGccCGTcCTCac

>Bacillus_Fam_636_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.974359
GCF_000775975.1_ASM77597v1_genomic.fna_1:181115-181253 Satlength=139 Nr
of Repeats=4 RepeatLength=39 seed=AGAAGAAGTT Num.seqs=3
Similarity=0.836111
0 AGAAGAAGTTGTGGAATTAGAGAAATCTGAGGAAGCGAC
GCF_000832605.1_ASM83260v1_genomic.fna_1:1287745-1288135 Satlength=391 Nr
of Repeats=11 RepeatLength=39 seed=AGAAGAAGTT Num.seqs=9
Similarity=0.860185 0
AGAAGAAGTTGTGGAATTAGAGAAANCTGAGGAAGCGAC

Consensus:

AGAAGAAGTTGTGGAATTAGAGAAAtCTGAGGAAGCGAC

>Bacillus_Fam_637_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.666667

GCF_001654695.1_ASM165469v1_genomic.fna_23:241573-241729 Satlength=157 Nr
of Repeats=4 RepeatLength=39 seed=AAGAAGGAAG Num.seqs=4
Similarity=0.982906 0

AAGAAGGAAGAACAAGCACGTTTAGCTGAAGAACAGCGT

GCF_900156875.1_PRJEB18969_genomic.fna_11:570675-570870 Satlength=196 Nr
of Repeats=5 RepeatLength=39 seed=AAGCAAGAAG Num.seqs=5
Similarity=0.815385

0 AAGCAAGAAGAAGCAGATCGNTTAGCAGAGGAACAGCGA

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Consensus:

AAGaAaGAAGAAcaAGaaCGtTTAGCaGAaGAACAGCGa

>Bacillus_Fam_638_39_2 Nr. of seq. 2 Alignment length(with gaps) = 39
Alignment score = 0.940171

GCF_001877785.1_PlanoSAMM_genomic.fna_96:168466-169318 Satlength=853 Nr
of Repeats=16 RepeatLength=39 seed=GCTCCCATCA Num.seqs=14
Similarity=0.844839 0

GCTCCCATCANC CGGACGGCTGACCCATCGGGGATTGC

GCF_900094975.1_IMG-

taxon_2617270721_annotated_assembly_genomic.fna_4:1240438-1241134

Satlength=697 Nr of Repeats=13 RepeatLength=39 seed=GGCTGACCCA

Num.seqs=12 Similarity=0.864802 18

GCTCCCATCACTCCGACGGCTGACCCATCGGGGATTGT

Consensus:

GCTCCCATCACTCCGACGGCTGACCCATCGGGGATTGc

>Bacillus_Fam_639_37_2 Nr. of seq. 2 Alignment length(with gaps) = 37
Alignment score = 0.662162

GCF_000242895.2_ASM24289v3_genomic.fna_1:2712624-2712861 Satlength=238 Nr
of Repeats=5 RepeatLength=36 seed=TGTCTGGAT Num.seqs=3
Similarity=0.678063 0

TGTCTGGATAACCTCCCATGCCACCGTACCCGCCG-

GCF_001591665.1_ASM159166v1_genomic.fna_7:16103-16484 Satlength=382 Nr of
Repeats=8 RepeatLength=36 seed=ATCCTCCCAT Num.seqs=6 Similarity=0.823423

9 TG-CCTGGGTATCCTCCCATGCCTCCATAACCACCCA

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Consensus:

TGtCCTGGaTAaCCTCCCATGCCaCCaTAaCCaCCca

>Bacillus_Fam_640_37_2 Nr. of seq. 2 Alignment length(with gaps) = 37
Alignment score = 0.603604

GCF_000712615.1_ASM71261v1_genomic.fna_8:125406-125946 Satlength=541 Nr
of Repeats=15 RepeatLength=36 seed=TACGGGACCA Num.seqs=15
Similarity=0.931532 0

TACGGGACCAACGGGAG-AACCGGGATCTAGCGGAGT

Rev.of_GCF_000715205.1_SOAPdenovo_v1.05_genomic.fna_19:59022-60552

Satlength=1531 Nr of Repeats=42 RepeatLength=36 seed=GCTCCGGTTG

Num.seqs=34 Similarity=0.944808 0
CACGGGAGCCACGGGAGCAACC-GGTCCAACCGGAGC

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Consensus:

cACGGGACCaACGGGAGcAACCgGGacCaAcCGGAGc

>Bacillus_Fam_641_37_2 Nr. of seq. 2 Alignment length(with gaps) = 37
Alignment score = 0.747748
GCF_001578185.1_ASM157818v1_genomic.fna_1:1822790-1822970 Satlength=181
Nr of Repeats=5 RepeatLength=36 seed=TGCCACTGTT Num.seqs=5
Similarity=0.722522 0
TGCCACTGTTGCCAA-GTANCGTGAGGATGGTGCTGA
GCF_000025825.1_ASM2582v1_genomic.fna_1:3261851-3262067 Satlength=217 Nr
of Repeats=5 RepeatLength=36 seed=TGCCATTGAT Num.seqs=4
Similarity=0.594595
0 TGCCACTGATGCCAAGGTACNGTATGGATGCTGCTGA

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Consensus:

TGCCACTGaTGCCAAgGTAccGTaaGGATGcTGCTGA

>Bacillus_Fam_642_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.666667
GCF_000007825.1_ASM782v1_genomic.fna_1:2324878-2325328 Satlength=451 Nr
of Repeats=12 RepeatLength=36 seed=ACCGGAGCAA Num.seqs=9
Similarity=0.836420
0 ACCGGAGCAACAGGCCCGACTGGAATAACGGGCCCA
Rev.of_GCF_001038845.1_ASM103884v1_genomic.fna_46:6167-6671 Satlength=505
Nr of Repeats=11 RepeatLength=36 seed=CCCGTGGCTC Num.seqs=8
Similarity=0.851852 14
ACGGGAGCCACGGGTTCAACGGGAGTAACTGGCCCA

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Consensus:

ACcGGAGCaACaGGccCaACgGGAaTAACgGGCCCA

>Bacillus_Fam_643_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.898148
GCF_000008425.1_ASM842v1_genomic.fna_1:1177079-1177205 Satlength=127 Nr
of Repeats=4 RepeatLength=36 seed=AAAAGCAAGA Num.seqs=3
Similarity=0.777778
0 AAAAGCAAGAAACCCGATGACTGCAAAAAGCCTGAC
GCF_000408885.1_ASM40888v1_genomic.fna_1:1277423-1277564 Satlength=142 Nr
of Repeats=5 RepeatLength=36 seed=AAAAGCAAGA Num.seqs=3
Similarity=0.690058 0
AAAAGCAAGAAACCTGATGACTGCAAAAACNGAC

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Consensus:

AAAAGCAAGAAACCcGATGACTGCAAAAAaCctGAC

>Bacillus_Fam_644_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.925926
GCF_000025805.1_ASM2580v1_genomic.fna_1:706167-706311 Satlength=145 Nr of
Repeats=5 RepeatLength=36 seed=GAAATTAAGC Num.seqs=3 Similarity=0.861862
0 GAAATTAAGCAGGAAAAAGATATAGGAATTAaaaaG
GCF_000025825.1_ASM2582v1_genomic.fna_1:700384-700528 Satlength=145 Nr of
Repeats=4 RepeatLength=36 seed=CAGGAAAAAG Num.seqs=4 Similarity=0.938272
9 GAAATTAACAGGAAAAAGATATAGGAATTAAGAAG

Consensus:

GAAATTAaaCAGGAAAAAGATATAGGAATTAaaAAG

>Bacillus_Fam_645_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.925926
GCF_000025805.1_ASM2580v1_genomic.fna_1:2966155-2966335 Satlength=181 Nr
of Repeats=5 RepeatLength=36 seed=TCTTTTGTAG Num.seqs=5
Similarity=0.970370
0 TCTTTTGTAGCTTGTTGAGCTTGAGCCTGCTGCTGC
GCF_000025825.1_ASM2582v1_genomic.fna_1:2943369-2943663 Satlength=295 Nr
of Repeats=8 RepeatLength=36 seed=GCTTGAGCTT Num.seqs=7
Similarity=0.978836
18 TCTTTTGTAGCCTGTTGAGCTTGAGCTTGCTGCTGC

Consensus:

TCTTTTGTAGCcTGTTGAGCTTGAGCcTGCTGCTGC

>Bacillus_Fam_646_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 1.000000
GCF_000153365.1_ASM15336v1_genomic.fna_18:445614-445902 Satlength=289 Nr
of Repeats=7 RepeatLength=36 seed=GGTCCTTGAA Num.seqs=6
Similarity=0.790390
0 GGTCCTTGAACCCCTTGTTGTCCTTGATCTCCTTGC
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:507480-507768
Satlength=289 Nr of Repeats=7 RepeatLength=36 seed=TTCAAGGACC Num.seqs=6
Similarity=0.790390 10
GGTCCTTGAACCCCTTGTTGTCCTTGATCTCCTTGC

Consensus:

GGTCCTTGAACCCCTTGTTGTCCTTGATCTCCTTGC

>Bacillus_Fam_647_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.944444
GCF_000153365.1_ASM15336v1_genomic.fna_74:62534-62903 Satlength=370 Nr of
Repeats=10 RepeatLength=36 seed=CAAGGATCAA Num.seqs=9

Similarity=0.802469
0 CAAGGATCAACTGGNGCNCAGGGATCCCAAGGACCG
GCF_000473245.1_ASM47324v1_genomic.fna_1:2119185-2119554 Satlength=370 Nr
of Repeats=10 RepeatLength=36 seed=CAAGGATCAA Num.seqs=9
Similarity=0.802469 0
CAAGGATCAACTGGNGCNCAGGGATCCCAAGGACCG

Consensus:

CAAGGATCAACTGGNGCNCAGGGATCCCAAGGACCG

>Bacillus_Fam_648_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.666667
GCF_000161455.1_ASM16145v1_genomic.fna_1:2079145-2079325 Satlength=181 Nr
of Repeats=5 RepeatLength=36 seed=GGGAATACAA Num.seqs=5
Similarity=0.800000 0
GGGAATACAACTCCGCCAGGCAGTGGAATGGCCAA
Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:3388209-3388497
Satlength=289 Nr of Repeats=8 RepeatLength=36 seed=TGTATTTCCT Num.seqs=8
Similarity=0.866402 9
GGAAATACAACGCCCAAACAATGGTAGAGGCGAA

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Consensus:

GGaAATACAACgCCGCCAaaCAaTGGaAaaGGCcAA

>Bacillus_Fam_649_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.962963
GCF_000217835.1_ASM21783v1_genomic.fna_1:1229797-1230013 Satlength=217 Nr
of Repeats=5 RepeatLength=36 seed=GCAACAACCG Num.seqs=4
Similarity=0.919753 0
GCAACAACCGGAATAACGGGAACGGCCAGGCCGCAA
GCF_000832905.1_ASM83290v1_genomic.fna_1:203662-203842 Satlength=181 Nr
of Repeats=5 RepeatLength=36 seed=GCAACAACCG Num.seqs=5
Similarity=0.859259
0 GCAACAACCGGAATAACGGAAACGGCCAGGCCGCAA

Consensus:

GCAACAACCGGAATAACGGaAACGGCCAGGCCGCAA

>Bacillus_Fam_650_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36
Alignment score = 0.703704
GCF_000751775.1_A1A_genomic.fna_79:77245-77425 Satlength=181 Nr of
Repeats=5 RepeatLength=36 seed=CATTGATTGC Num.seqs=5 Similarity=0.855556
0 CATTGATTGCCGTGCCACCATTCGGGCCTTGACCTC
GCF_001420715.1_ASM142071v1_genomic.fna_23:27567-27783 Satlength=217 Nr
of Repeats=4 RepeatLength=36 seed=CCTCCTTGGG Num.seqs=3
Similarity=0.901235
32 CTTGGGCTGCAGTTCCACCATTCGGACCTTGGCCTC

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Consensus:

CaTgGacTGCaGTgCCACCATTCCGgACCTTGaCCTC

>Bacillus_Fam_651_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36

Alignment score = 0.629630

GCF_000769555.1_ASM76955v1_genomic.fna_1:1273558-1274494 Satlength=937 Nr
of Repeats=26 RepeatLength=36 seed=CGCCAGTAGC Num.seqs=26

Similarity=0.918405

0

CGCCAGTAGCGCCGGTAAATCCGGTCGGTCCGGTAA

Rev.of_GCF_001578205.1_ASM157820v1_genomic.fna_1:2833063-2833531

Satlength=469 Nr of Repeats=15 RepeatLength=36 seed=CTACTGGCGC

Num.seqs=11 Similarity=0.981145

9 CGCCAGTAGCCCCTGAAGGACCAGTAGGACCGGTAG

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Consensus:

CGCCAGTAGCcCCgGaAaaaCCaGTaGGaCCGGTAa

>Bacillus_Fam_652_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36

Alignment score = 0.666667

GCF_001590785.1_ASM159078v1_genomic.fna_10:48242-48455 Satlength=214 Nr
of Repeats=6 RepeatLength=36 seed=GGACCGACAG Num.seqs=4

Similarity=0.864198

0 GGACCGACAGGAGCAACAGGAATAGCAGGAATCACC

GCF_002019765.1_ASM201976v1_genomic.fna_1:2106260-2106764 Satlength=505

Nr of Repeats=10 RepeatLength=36 seed=TTAGACGGTG Num.seqs=6

Similarity=0.883951

21

GGTGCTACAGGAGCAACAGGATTAGACGGTGTCCT

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Consensus:

GGacCgACAGGAGCAACAGGAaTAGaaGGaaTCACc

>Bacillus_Fam_653_36_2 Nr. of seq. 2 Alignment length(with gaps) = 36

Alignment score = 0.824074

GCF_001887185.1_ASM188718v1_genomic.fna_215:57616-57874 Satlength=259 Nr
of Repeats=7 RepeatLength=36 seed=AGTACAGCAA Num.seqs=5

Similarity=0.718018

0 AGTACAGCAAACGGAAGAAATGCAGCCGAGAGTANC

Rev.of_GCF_002009555.1_ASM200955v1_genomic.fna_223:6085-6232

Satlength=148 Nr of Repeats=4 RepeatLength=36 seed=TTGCTGTACT Num.seqs=3

Similarity=0.728395

10

AGTACAGCAAGTGGAAGAAGAGCAGCCGAGAGTACC

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Consensus:

AGTACAGCAAacGGAAGAAaaGCAGCCGAGAGTAcC

>Bacillus_Fam_654_34_2 Nr. of seq. 2 Alignment length(with gaps) = 34
Alignment score = 1.000000
GCF_000153365.1_ASM15336v1_genomic.fna_18:81509-81679 Satlength=171 Nr of
Repeats=5 RepeatLength=34 seed=TCTGTCCCCT Num.seqs=5 Similarity=0.890196
0 TCTGTCCCCTTGGCCCAGTTTTTCGGGCCAGGGGG
Rev.of_GCF_000473245.1_ASM47324v1_genomic.fna_1:870777-870947
Satlength=171 Nr of Repeats=5 RepeatLength=34 seed=AAGGGGACAG Num.seqs=5
Similarity=0.890196 11
TCTGTCCCCTTGGCCCAGTTTTTCGGGCCAGGGGG

Consensus:

TCTGTCCCCTTGGCCCAGTTTTTCGGGCCAGGGGG

>Bacillus_Fam_655_33_2 Nr. of seq. 2 Alignment length(with gaps) = 33
Alignment score = 1.000000
GCF_001243895.1_Bacillus_testis_genomic.fna_9:552036-552300 Satlength=265
Nr of Repeats=8 RepeatLength=33 seed=CGGCGGGAAT Num.seqs=8
Similarity=0.874459 0
CGGCGGGAATGCCGGAATGCCAGGTCAAGGAAG
GCF_001243895.1_Bacillus_testis_genomic.fna_9:552088-552451 Satlength=364
Nr of Repeats=11 RepeatLength=33 seed=CCAGGCCAAG Num.seqs=11
Similarity=0.841322 19
CGGCGGGAATGCCGGAATGCCAGGTCAAGGAAG

Consensus:

CGGCGGGAATGCCGGAATGCCAGGTCAAGGAAG

>Bacillus_Fam_656_30_2 Nr. of seq. 2 Alignment length(with gaps) = 30
Alignment score = 1.000000
GCF_000759675.1_ASM75967v1_genomic.fna_60:16-166 Satlength=151 Nr of
Repeats=5 RepeatLength=30 seed=AAAATGAAAG Num.seqs=5 Similarity=0.902222
0 AAAATGAAAGAACTCCAAATGTAGTACCG
Rev.of_GCF_000759675.1_ASM75967v1_genomic.fna_80:1917-2127 Satlength=211
Nr of Repeats=7 RepeatLength=30 seed=TTCTTTCATT Num.seqs=7
Similarity=0.809524 12
AAAATGAAAGAACTCCAAATGTAGTACCG

Consensus:

AAAATGAAAGAACTCCAAATGTAGTACCG

>Bacillus_Fam_657_28_2 Nr. of seq. 2 Alignment length(with gaps) = 28
Alignment score = 0.601190
GCF_000712615.1_ASM71261v1_genomic.fna_14:9252-9900 Satlength=649 Nr of
Repeats=24 RepeatLength=27 seed=AGCGAAGCAA Num.seqs=24
Similarity=0.973341
0 AGCGAAGCAAAAGCAACAAGAAGAACA-
Rev.of_GCF_001243895.1_Bacillus_testis_genomic.fna_9:2243301-2243598
Satlength=298 Nr of Repeats=11 RepeatLength=27 seed=CGTTGTTGCT

Num.seqs=11 Similarity=0.910213
CGCCAAGCTCAAGC-ACAAGAGCAACAA

2

** **** * * * * *

Consensus:

aGCcAAGCaaAAGCaACAAGAcAACAA

>Bacillus_Fam_658_27_2 Nr. of seq. 2 Alignment length(with gaps) = 27
Alignment score = 0.697531
GCF_001877785.1_PlanoSAMM_genomic.fna_139:52829-52954 Satlength=126 Nr of
Repeats=5 RepeatLength=25 seed=TTGTACCTGG Num.seqs=5 Similarity=0.537179
0 TTGTACCTGGTACATNG-GNG-TNGAT
GCF_001877785.1_PlanoSAMM_genomic.fna_139:112839-112939 Satlength=101 Nr
of Repeats=4 RepeatLength=25 seed=TGTACCTGGT Num.seqs=4
Similarity=0.594246
0 -TGTACCTGGTACATGGAGCGTTTGAT

***** * * * * *

Consensus:

tTGTACCTGGTACATgGaGcGtTtGAT

>Bacillus_Fam_659_27_2 Nr. of seq. 2 Alignment length(with gaps) = 27
Alignment score = 0.654321
GCF_000831065.1_ASM83106v1_genomic.fna_1:4229089-4229503 Satlength=415 Nr
of Repeats=14 RepeatLength=27 seed=GCTCCCGTTG Num.seqs=9
Similarity=0.888889 12
GTTGAACCTGTCGCTCCCGTTGGACCT
GCF_001712755.1_ASM171275v1_genomic.fna_23:0-188 Satlength=189 Nr of
Repeats=7 RepeatLength=27 seed=GCTGTTCCAG Num.seqs=7 Similarity=0.971781
12 CCTGTCGCTCCAGCTGTTCCAGTTGCT

** *** * ** **

Consensus:

cCTccaGCTcccccaGgacCTccTGaa

>Bacillus_Fam_660_24_2 Nr. of seq. 2 Alignment length(with gaps) = 24
Alignment score = 0.631944
GCF_001591665.1_ASM159166v1_genomic.fna_19:22435-22519 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=GGACAGTAAA Num.seqs=4 Similarity=0.661376
0 GGACA-GTAAAA-CANAAAAAGT-
Rev.of_GCF_000496285.1_ASM49628v1_genomic.fna_1:1628788-1628908
Satlength=121 Nr of Repeats=4 RepeatLength=24 seed=ACTTCTTTTT Num.seqs=3
Similarity=0.814815 2
GTACAGGTAAAACCACAAAAAGAA

* *** * * * *

Consensus:

GgACAgGTAAAcCAcAAAAAGaa

>Bacillus_Fam_661_24_2 Nr. of seq. 2 Alignment length(with gaps) = 24
Alignment score = 0.833333
GCF_000005825.2_ASM582v2_genomic.fna_1:1602362-1602482 Satlength=121 Nr of Repeats=5 RepeatLength=24 seed=ATGGCCGGAG Num.seqs=5
Similarity=0.911111
0 ATGGCCGGAGCGAACATGGGGCCA
GCF_000474275.1_Bmar1.0_genomic.fna_8:180773-180917 Satlength=145 Nr of Repeats=6 RepeatLength=24 seed=ATGGCAGGAG Num.seqs=6 Similarity=0.907407
0 ATGGCAGGAGCGAACATGGCGCCG

Consensus:

ATGGCaGGAGCGAACATGGcGCCa

>Bacillus_Fam_662_24_2 Nr. of seq. 2 Alignment length(with gaps) = 24
Alignment score = 0.944444
GCF_000008505.1_ASM850v1_genomic.fna_1:1072242-1072386 Satlength=145 Nr of Repeats=6 RepeatLength=24 seed=CAGAAAAGAA Num.seqs=4
Similarity=0.632222
0 CAGAAAAGAATCAAAAACAGAGA
GCF_000831065.1_ASM83106v1_genomic.fna_1:895901-896096 Satlength=196 Nr of Repeats=5 RepeatLength=24 seed=AGAAAAAAT Num.seqs=3
Similarity=0.740741
1 CAGAAAAGAATCAAAAAGCAGAGA

Consensus:

CAGAAAAGAATCAAAAaCAGAGA

>Bacillus_Fam_663_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
Alignment score = 0.666667
GCF_001439915.1_ASM143991v1_genomic.fna_122:1-121 Satlength=121 Nr of Repeats=6 RepeatLength=20 seed=TATTTGCGTC Num.seqs=6 Similarity=0.590821
0 TATTTGCGTCGTCCTCCA--C-AT
Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_83:14858-15120
Satlength=263 Nr of Repeats=11 RepeatLength=20 seed=CGACGCAAAT
Num.seqs=8 Similarity=0.573499
11 TATTTGCGTCGNTTCANACNAT

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

Consensus:

TATTTGCGTCGgTcCCAnaCnAT

>Bacillus_Fam_664_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23
Alignment score = 0.717391
GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_4:1334318-1334418
Satlength=101 Nr of Repeats=5 RepeatLength=20 seed=ATTAGGATCG Num.seqs=5
Similarity=0.725397 0 ATTAGGATCGT--ATTCTG-GA
Rev.of_GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_4:483549-483629

Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=TACGATCCTA Num.seqs=4
Similarity=0.636364 11 -TTAGGATCGTAAATTTCTGAGA

***** **

Consensus:

aTTAGGATCGTaaATTTCTGaGA

>Bacillus_Fam_665_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23

Alignment score = 0.615942

GCF_001636315.1_ASM163631v1_genomic.fna_1:1446486-1446570 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=CCAACGGCG Num.seqs=4

Similarity=0.862434 0

CCAACGGCGGAT-A-CACGCTC

Rev.of_GCF_000612665.1_FF4_genomic.fna_75:18910-19034 Satlength=125 Nr of Repeats=5 RepeatLength=21 seed=ATCCGCTAGT Num.seqs=4 Similarity=0.576389

12 -CAACTAGCGGATAACCNCGATC

***** * * * *

Consensus:

cCAACTaGCGGATaAcCaCGaTC

>Bacillus_Fam_666_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23

Alignment score = 0.760870

GCF_001648575.1_ASM164857v1_genomic.fna_3:346105-346468 Satlength=364 Nr of Repeats=10 RepeatLength=21 seed=TTTATTTTCC Num.seqs=9

Similarity=0.555135 0

TTTATTTTCCATTNCAGCCG-A-

GCF_001648575.1_ASM164857v1_genomic.fna_3:354189-354315 Satlength=127 Nr of Repeats=6 RepeatLength=21 seed=TTTATTTTCC Num.seqs=6

Similarity=0.461111

0 TTTATTTTCCATTCAAGCCGNAT

***** *

Consensus:

TTTATTTTCCATTcaAGCCGnAt

>Bacillus_Fam_667_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23

Alignment score = 0.666667

GCF_000934845.1_ASM93484v1_genomic.fna_5:25497-25581 Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=ATTCCGCGAA Num.seqs=4 Similarity=0.468750

0 ATTCCGCGAAANAACC-AGAATA

GCF_001315165.1_ASM131516v1_genomic.fna_10:42593-42718 Satlength=126 Nr of Repeats=5 RepeatLength=21 seed=ATTCCGCGAA Num.seqs=4

Similarity=0.471014

0 ATTCCGCGAAA-AACNAACGATA

***** * * *

Consensus:

ATTCCGCGAAAnAACcaAcaATA

>Bacillus_Fam_668_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.772727
GCF_000007845.1_ASM784v1_genomic.fna_1:4827415-4827495 Satlength=81 Nr of
Repeats=4 RepeatLength=20 seed=TATATCAGCG Num.seqs=4 Similarity=0.593915
14 AGCGAAACTCCAAA--TATATC
GCF_000831065.1_ASM83106v1_genomic.fna_1:4391098-4391298 Satlength=201 Nr
of Repeats=9 RepeatLength=20 seed=TTATATCAGC Num.seqs=8
Similarity=0.688312 14
AGCGCAACTCCCAATTTATATC

***** **

Consensus:

tTATATCAGCGaAACTCCaAAt

>Bacillus_Fam_669_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.621212
GCF_000311725.1_ASM31172v1_genomic.fna_3:434751-434853 Satlength=103 Nr
of Repeats=5 RepeatLength=20 seed=ATTCCGGAAC Num.seqs=3
Similarity=0.814815
0 -ATTCCGGAACTTTT-GGATTA
GCF_000311725.1_ASM31172v1_genomic.fna_2:435289-435392 Satlength=104 Nr
of Repeats=5 RepeatLength=21 seed=AATTCCGGAA Num.seqs=3
Similarity=0.830688
0 AATTCCGTAACTTTTCGTGTT-

***** * **

Consensus:

aATTCCGgAACTTTTcGgaTTa

>Bacillus_Fam_670_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.643939
GCF_000331575.1_ASM33157v1_genomic.fna_3:82032-82150 Satlength=119 Nr of
Repeats=6 RepeatLength=20 seed=CTTACATATA Num.seqs=4 Similarity=1.000000
0 CTTAC-AT-ATATTTTGGGTC
Rev.of_GCF_900156875.1_PRJEB18969_genomic.fna_9:2524-2673 Satlength=150
Nr of Repeats=7 RepeatLength=21 seed=GTTATAGTTA Num.seqs=6
Similarity=0.932275 10
-TAACTATAACATTTTTGGGTC

* ** * *****

Consensus:

cTaActATaAcATTTTTGGGTC

>Bacillus_Fam_671_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.628788
GCF_000245315.1_ASM24531v1_genomic.fna_68:3612-3750 Satlength=139 Nr of
Repeats=7 RepeatLength=21 seed=AAAAAGTATT Num.seqs=6 Similarity=0.805291
0 -AAAAAGCATTATGATCATGAC
Rev.of_GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2731414-2731540
Satlength=127 Nr of Repeats=4 RepeatLength=21 seed=TTTTCTCTTC Num.seqs=3

Similarity=0.724868
GNTGAAGAG

4 AAAAAAGCATTA-

***** * * * **

Consensus:

aAAAAAGCATTTatGaTcAaGAc

>Bacillus_Fam_672_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.628788
GCF_000305495.1_BacPsy2.0_genomic.fna_37:40246-40493 Satlength=248 Nr of
Repeats=6 RepeatLength=21 seed=TATTCCCGTC Num.seqs=5 Similarity=0.513636
0 TATTCCCGTCTGCGNANGNTG-
Rev.of_GCF_000305495.1_BacPsy2.0_genomic.fna_243:5857-5941 Satlength=85
Nr of Repeats=4 RepeatLength=21 seed=AGACGGGAAT Num.seqs=4
Similarity=0.520202 11
TATTCCCGTCTGAGATGGAAGT

***** * * *

Consensus:

TATTCCCGTCTGaGaagGaaGt

>Bacillus_Fam_673_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.681818
GCF_000305495.1_BacPsy2.0_genomic.fna_66:16974-17058 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTATTCCCGT Num.seqs=4 Similarity=0.613636
0 TTATTCCCGTCTC-GAATAAGC
GCF_000305495.1_BacPsy2.0_genomic.fna_259:12228-12312 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TATTCCCGTC Num.seqs=4 Similarity=0.427083
1 TTATTCCCGTCTCATCATGNGC

***** ** **

Consensus:

TTATTCCCGTCTCagaATaaGC

>Bacillus_Fam_674_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.696970
GCF_000307875.1_BABA1.0_genomic.fna_7:26272-26417 Satlength=146 Nr of
Repeats=7 RepeatLength=21 seed=TGCGACAGTA Num.seqs=6 Similarity=0.658586
0 TGCGACAGTAAAGCGTGGC-TA
GCF_000307875.1_BABA1.0_genomic.fna_58:51271-51373 Satlength=103 Nr of
Repeats=5 RepeatLength=21 seed=TCCGACAGTA Num.seqs=4 Similarity=0.584541
0 TCCGACAGTAACG-GTGGCTTA

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Consensus:

TcCGACAGTAAaGcGTGGCtTA

>Bacillus_Fam_675_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.674242

GCF_000311725.1_ASM31172v1_genomic.fna_4:432525-432628 Satlength=104 Nr
of Repeats=5 RepeatLength=21 seed=TAATTCGGGA Num.seqs=3
Similarity=0.724868
0 TAATTCGGGAACCTTTNACCCA-
GCF_000311725.1_ASM31172v1_genomic.fna_1:120906-121010 Satlength=105 Nr
of Repeats=5 RepeatLength=21 seed=AATTCGGAA Num.seqs=4
Similarity=0.704545
1 NAATTCGGGAACCTTCGAGCAT

***** **
Consensus:

tAATTCGGGAACCTTTcaacCat

>Bacillus_Fam_676_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.643939
GCF_000331575.1_ASM33157v1_genomic.fna_1:755726-755838 Satlength=113 Nr
of Repeats=4 RepeatLength=21 seed=CTTTATTGTC Num.seqs=3
Similarity=0.601852
0 CTTTATTGTCCGGAATTGC-CN
Rev.of_GCF_000986785.1_ASM98678v1_genomic.fna_10:73543-73915
Satlength=373 Nr of Repeats=11 RepeatLength=21 seed=GACAATAGAA
Num.seqs=7 Similarity=0.621212
9 -TTTATTGTCCNGAAACGCTCT

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

cTTTATTGTCCgGAAacGcCt

>Bacillus_Fam_677_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.810606
GCF_000374345.1_ASM37434v1_genomic.fna_22:48552-48902 Satlength=351 Nr of
Repeats=13 RepeatLength=21 seed=TTCAATCCAA Num.seqs=9
Similarity=0.640572
0 TTCAATCCAAAA-TGGGNTTTT
GCF_000374345.1_ASM37434v1_genomic.fna_31:31-340 Satlength=310 Nr of
Repeats=11 RepeatLength=21 seed=TTCAATCCAA Num.seqs=7
Similarity=0.619048
0 TTCAATCCAAAAC-TGGGNTTT-

Consensus:

TTCAATCCAAAAC-TGGGNTTTt

>Bacillus_Fam_678_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.810606
GCF_000429705.1_ASM42970v1_genomic.fna_1:195033-195200 Satlength=168 Nr
of Repeats=7 RepeatLength=21 seed=CTAACTCGAC Num.seqs=5
Similarity=0.694444
0 CTAACTCGACTAAAGG-NGAGG
GCF_000429705.1_ASM42970v1_genomic.fna_1:361409-361556 Satlength=148 Nr
of Repeats=7 RepeatLength=21 seed=GCTAACTCGA Num.seqs=7

Similarity=0.863636
20 CTAAC TCGACTAAAGGCGGAG-

***** ***

Consensus:

CTAAC TCGACTAAAGGcgGAGg

>Bacillus_Fam_679_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.666667
GCF_000429705.1_ASM42970v1_genomic.fna_1:2283624-2283729 Satlength=106 Nr
of Repeats=4 RepeatLength=21 seed=TTTAAACAGG Num.seqs=3
Similarity=0.525253 0
TTTAAACAGGTTNGCACG-NCG
Rev.of_GCF_000429705.1_ASM42970v1_genomic.fna_6:55774-55879 Satlength=106
Nr of Repeats=4 RepeatLength=21 seed=AACCTGTTTA Num.seqs=3
Similarity=0.830688 12
TTTAAACAGGTTGG-AGGCGCG

***** * * * **

Consensus:

TTTAAACAGGTTgGcAcGcgCG

>Bacillus_Fam_680_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.674242
GCF_000430785.1_ASM43078v1_genomic.fna_6:52001-52085 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTTACTATCC Num.seqs=4 Similarity=0.664141
0 TTTACTATCCAAATTGAACCA-
GCF_001315085.1_ASM131508v1_genomic.fna_12:91450-91534 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTTATGATCC Num.seqs=4 Similarity=0.809524
0 TTTATGATCCAATT-AACCAA

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Consensus:

TTTAcgATCCAAaTTgAACCAa

>Bacillus_Fam_681_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.848485
GCF_000473245.1_ASM47324v1_genomic.fna_1:4442972-4443056 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=GGAATGATTA Num.seqs=4
Similarity=0.643939
0 GGAATGATTATT-GGCGAATCC
Rev.of_GCF_000153365.1_ASM15336v1_genomic.fna_17:84758-84842 Satlength=85
Nr of Repeats=4 RepeatLength=21 seed=ATAATCATTC Num.seqs=4
Similarity=0.644928 11
GGAATGATTATTCGCCGAATCC

***** * *****

Consensus:

GGAATGATTATTcGcCGAATCC

>Bacillus_Fam_682_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.628788
GCF_000496285.1_ASM49628v1_genomic.fna_1:367662-367830 Satlength=169 Nr
of Repeats=7 RepeatLength=21 seed=ACTTCTCCTT Num.seqs=6
Similarity=0.923810
0 ACTTCTCCTTTTGGATCTGTC-
Rev.of_GCF_000007845.1_ASM784v1_genomic.fna_1:554769-555177 Satlength=409
Nr of Repeats=15 RepeatLength=21 seed=AGAAGTTGAA Num.seqs=10
Similarity=0.668182 6
NCTTCTNTCTTTGGNTCTTTCA

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

Consensus:

aCTTCTcccTTTGGaTCTgTCa

>Bacillus_Fam_683_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.727273
GCF_000612625.1_JCE_genomic.fna_3:36022-36122 Satlength=101 Nr of
Repeats=5 RepeatLength=21 seed=ATTCTACAAA Num.seqs=3 Similarity=0.661376
0 ATTCTACAAAANT-AAAGANGA
Rev.of_GCF_000612625.1_JCE_genomic.fna_58:7998-8081 Satlength=84 Nr of
Repeats=4 RepeatLength=21 seed=TTTGTAAGAA Num.seqs=3 Similarity=0.525253
10 ATTCTACAAAAATCAAAG-GGA

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

Consensus:

ATTCTACAAAAaTcAAAGagGA

>Bacillus_Fam_684_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.613636
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:630800-630905
Satlength=106 Nr of Repeats=4 RepeatLength=21 seed=GTTACTCCCG Num.seqs=3
Similarity=0.767677 0
GTTACTCCCGCATAG-CTGCTC
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_15:11202-11572
Satlength=371 Nr of Repeats=16 RepeatLength=21 seed=TTACTCCCGT
Num.seqs=10 Similarity=0.802469
1 GTTACTCCCGTATCGACTCCA-

***** ** * ** *

Consensus:

GTTACTCCCGcATaGaCTcCac

>Bacillus_Fam_685_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.727273
GCF_000986785.1_ASM98678v1_genomic.fna_5:144649-145040 Satlength=392 Nr
of Repeats=15 RepeatLength=21 seed=GCAAATAGAA Num.seqs=11
Similarity=0.592496 12
ANTNGG-AAANCGGCAAATAGA
GCF_000986785.1_ASM98678v1_genomic.fna_4:84896-85225 Satlength=330 Nr of
Repeats=12 RepeatLength=21 seed=GCAAATAGAA Num.seqs=8

TCGCAAATAAACAgGaTAaGAT

>Bacillus_Fam_689_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.643939
GCF_001591805.1_ASM159180v1_genomic.fna_32:4437-4855 Satlength=419 Nr of
Repeats=4 RepeatLength=21 seed=TTTTGTCTAT Num.seqs=3 Similarity=0.606061
19 TTGTCTATTTTNNAGNTAG-TT
GCF_001591805.1_ASM159180v1_genomic.fna_34:3058-3142 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=GTTTTGTCTA Num.seqs=4 Similarity=0.683081
19 TTGTCTA-TTTTAATAGAGGTT

***** * * *

Consensus:

gTTTTGTCTAtTTTtaAgagAG

>Bacillus_Fam_690_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.659091
GCF_001648575.1_ASM164857v1_genomic.fna_62:153306-153390 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=AGTTCGTGCC Num.seqs=4
Similarity=0.544974
0 AGTTCGTGCCAAAATNAGACA-
Rev.of_GCF_001648575.1_ASM164857v1_genomic.fna_64:121834-121917
Satlength=84 Nr of Repeats=4 RepeatLength=21 seed=GGCACGAACT Num.seqs=3
Similarity=0.540404 10
AGTTCGTGCCAAAA-CNGNCCG

***** * *

Consensus:

AGTTCGTGCCAAAAtcaGaCag

>Bacillus_Fam_691_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.750000
GCF_002019665.1_ASM201966v1_genomic.fna_1:314590-315478 Satlength=889 Nr
of Repeats=19 RepeatLength=21 seed=AGGTTCCTCAC Num.seqs=14
Similarity=0.616883 0
AGGTTCCTCACGCTTCTC-GNAT
GCF_002019665.1_ASM201966v1_genomic.fna_1:3647860-3648050 Satlength=191
Nr of Repeats=9 RepeatLength=21 seed=CACGCTTCTC Num.seqs=8
Similarity=0.907029 6
-GGTTCCTCACGCTTCTCAGCAA

***** * *

Consensus:

aGGTTCCTCACGCTTCTCaGcAa

>Bacillus_Fam_692_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.621212
GCF_002019665.1_ASM201966v1_genomic.fna_1:3182387-3182471 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=AGGTTCCTCAC Num.seqs=4
Similarity=0.465278 0
AGGTTCCTCACGCTTCTC-CCTG

GCF_002019665.1_ASM201966v1_genomic.fna_1:4369800-4369884 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=AGGTTCTCAC Num.seqs=4
Similarity=0.646465 0
AGGTTCTCACATAACTCACNTG

***** *** * **

Consensus:

AGGTTCTCACagaaCTCaCtTG

>Bacillus_Fam_693_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.651515
GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_3:36555-36709
Satlength=155 Nr of Repeats=5 RepeatLength=21 seed=TTTGATAATA Num.seqs=3
Similarity=0.574879 0 TTCGATAATAAACTTNG-
ATT
GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_4:286502-286606
Satlength=105 Nr of Repeats=5 RepeatLength=21 seed=TTTTGATAAT Num.seqs=4
Similarity=0.629630 20 TTTGATAAT-AAATTTGGAATT

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

Consensus:

TTcGATAATaAAAcTTgGaATT

>Bacillus_Fam_694_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22
Alignment score = 0.795455
GCF_900103955.1_IMG-
taxon_2617270767_annotated_assembly_genomic.fna_6:34473-34708
Satlength=236 Nr of Repeats=5 RepeatLength=21 seed=TATACTTTAC Num.seqs=3
Similarity=0.830688 0 -
TATACTTTACTCCGATCTCTT
GCF_900103955.1_IMG-
taxon_2617270767_annotated_assembly_genomic.fna_7:19890-20391
Satlength=502 Nr of Repeats=6 RepeatLength=21 seed=CTATGCTTTA Num.seqs=4
Similarity=0.743687 0 CTATGCTTTACTCCGATC-
CTT

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Consensus:

cTATaCTTTACTCCGATCtCTT

>Bacillus_Fam_695_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.603175
GCF_001517135.1_ASM151713v1_genomic.fna_21:91763-91907 Satlength=145 Nr
of Repeats=8 RepeatLength=18 seed=AAGAACCTGA Num.seqs=8
Similarity=0.936508
0 AAGAACCTGATAACACA-G--
GCF_001645705.1_ASM164570v1_genomic.fna_60:514544-514944 Satlength=401 Nr
of Repeats=14 RepeatLength=20 seed=AAGAAGCCCA Num.seqs=10

Similarity=0.740388
AAGAACCCCATAACTCANGCT

0

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Consensus:

AAGAACCccATAACaCAnGct

>Bacillus_Fam_696_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.603175
GCF_001636325.1_ASM163632v1_genomic.fna_2:1329299-1329389 Satlength=91 Nr
of Repeats=5 RepeatLength=18 seed=CAAGCTCAAA Num.seqs=5
Similarity=0.970370 0
C-AAGCTCAAATGCCAATG--
Rev.of_GCF_000612665.1_FF4_genomic.fna_50:5-89 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=CCCATTTGGCA Num.seqs=4 Similarity=0.773990
0 CTACGGTCAGATGCCAATGGG

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Consensus:

CtAaGcTCaAATGCCAATGgg

>Bacillus_Fam_697_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.634921
GCF_001591465.1_ASM159146v1_genomic.fna_71:19109-19211 Satlength=103 Nr
of Repeats=5 RepeatLength=20 seed=TGCAAATAGA Num.seqs=3
Similarity=0.521739
0 TGCAAATAGAACGCTTTTT--
Rev.of_GCF_000986785.1_ASM98678v1_genomic.fna_10:28785-29115
Satlength=331 Nr of Repeats=10 RepeatLength=21 seed=TCTATTTGCC
Num.seqs=6 Similarity=0.663636
10 GGCAAATAGAACGAGGTTTCC

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Consensus:

gGCAAATAGAACGaggTTTcc

>Bacillus_Fam_698_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.658730
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_24:29769-29949
Satlength=181 Nr of Repeats=10 RepeatLength=18 seed=CTCCACCTTG
Num.seqs=10 Similarity=0.690643 0
CTCCACCTTGTGGATTG-GC-
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_59:13286-13410
Satlength=125 Nr of Repeats=6 RepeatLength=21 seed=CGCAAGTTGG Num.seqs=5
Similarity=0.707937 12
CTCCAACCTTGCGGATAGAGCN

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Consensus:

CTCCAACTTGcGGATaGaGCn

>Bacillus_Fam_699_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.785714
GCF_000175075.1_ASM17507v1_genomic.fna_5:45232-45332 Satlength=101 Nr of
Repeats=5 RepeatLength=20 seed=ATATATCAAG Num.seqs=5 Similarity=0.625758
0 ATATATCAAGAAATTTAG-GA
GCF_000175075.1_ASM17507v1_genomic.fna_32:297990-298092 Satlength=103 Nr
of Repeats=5 RepeatLength=20 seed=ATATCAAGAA Num.seqs=3
Similarity=0.777778
1 -TATATCAAGAAATTTGTGA

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Consensus:

aTATATCAAGAAATTTaGtGA

>Bacillus_Fam_700_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.626984
GCF_000175075.1_ASM17507v1_genomic.fna_41:62510-62591 Satlength=82 Nr of
Repeats=4 RepeatLength=20 seed=TCGCCCGTAA Num.seqs=3 Similarity=0.712121
0 TCGCCCGTAAATCTCAAAAN-
GCF_001877785.1_PlanoSAMM_genomic.fna_96:320102-320182 Satlength=81 Nr of
Repeats=4 RepeatLength=20 seed=TTTCGCCCTT Num.seqs=4 Similarity=0.648148
18 TCGCCCTTAAATC-CGANATT

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Consensus:

TCGCCCGTAAATCtCaAaAtt

>Bacillus_Fam_701_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.706349
GCF_000612805.1_FF3_genomic.fna_6:10-112 Satlength=103 Nr of Repeats=5
RepeatLength=20 seed=CGCAGATAAC Num.seqs=3 Similarity=0.911111
0 CGCAGATAACTCAAGAAATC-
GCF_000612805.1_FF3_genomic.fna_1:1030894-1030997 Satlength=104 Nr of
Repeats=5 RepeatLength=21 seed=CGCAGATAAC Num.seqs=3 Similarity=0.787879
0 CGCAGATAANTCATGAAAAAG

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Consensus:

CGCAGATAAcTCAaGAAAaag

>Bacillus_Fam_702_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.603175
GCF_000813125.1_ASM81312v1_genomic.fna_118:60365-60738 Satlength=374 Nr
of Repeats=7 RepeatLength=21 seed=TTTACGGTTG Num.seqs=5
Similarity=0.585507
0 TTTACGGTTGNACAACTTT-A
Rev.of_GCF_001591425.1_ASM159142v1_genomic.fna_85:16-117 Satlength=102 Nr
of Repeats=5 RepeatLength=20 seed=CGCAAATAAA Num.seqs=4

Similarity=0.656085
TTTGCGGTAGCACGATTTTNA

6

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Consensus:

TTTaCGGTaGcACaAcTTTnA

>Bacillus_Fam_703_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.682540
GCF_000986785.1_ASM98678v1_genomic.fna_6:41878-42012 Satlength=135 Nr of
Repeats=5 RepeatLength=21 seed=TTTGTCGTAA Num.seqs=3 Similarity=0.448718
0 TTTGTCGTAAAG-GCAGCNAGT
GCF_000986785.1_ASM98678v1_genomic.fna_11:136737-137027 Satlength=291 Nr
of Repeats=9 RepeatLength=21 seed=TTTGTCGTAA Num.seqs=7
Similarity=0.665224
0 TTTGTCGTAAAGTGCTGTTANT

Consensus:

TTTGTCGTAAAGtGCaGctAgT

>Bacillus_Fam_704_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.650794
GCF_001591445.1_ASM159144v1_genomic.fna_32:26340-26445 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=TTGGCGGAAT Num.seqs=5
Similarity=0.429333
0 TTGGCGGAATNACA-TCAAGN
Rev.of_GCF_000508325.1_BAVI_1_genomic.fna_81:19982-20417 Satlength=436 Nr
of Repeats=17 RepeatLength=21 seed=ATTCGCCAA Num.seqs=12
Similarity=0.524772 10
TTGGCGANATTACNGTCAAGN

Consensus:

TTGGCGaAATtACagTCAAGN

>Bacillus_Fam_705_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.666667
GCF_001636345.1_ASM163634v1_genomic.fna_1:492235-492415 Satlength=181 Nr
of Repeats=9 RepeatLength=20 seed=ACGGCGAAAA Num.seqs=9
Similarity=0.713404
0 AC-GGCGAAAAAACNTAATA
GCF_000508325.1_BAVI_1_genomic.fna_89:32-156 Satlength=125 Nr of
Repeats=5 RepeatLength=21 seed=ACTGGCGAGA Num.seqs=4 Similarity=0.538889
0 ACTGGCGAGAAAAAGCTAATT

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Consensus:

ACtGGCGAaAAAAAccTAATa

>Bacillus_Fam_706_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.706349
GCF_001712755.1_ASM171275v1_genomic.fna_37:245546-245745 Satlength=200 Nr
of Repeats=10 RepeatLength=20 seed=GCAAATAAAA Num.seqs=9
Similarity=0.735185 0
GCAAATAAAAACTGGNAATA-
Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_33:175176-175416
Satlength=241 Nr of Repeats=12 RepeatLength=20 seed=TTTTTATTTG
Num.seqs=12 Similarity=0.736412
11 GCAAATAAAAAATGTGTATAC

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Consensus:

GCAAATAAAAAaTGggaATAc

>Bacillus_Fam_707_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.666667
GCF_001877785.1_PlanoSAMM_genomic.fna_106:238188-238447 Satlength=260 Nr
of Repeats=5 RepeatLength=20 seed=TTATCAACAA Num.seqs=3
Similarity=0.733333
0 TTATCAACA-ATTTTTAGGAT
GCF_000759675.1_ASM75967v1_genomic.fna_13:38889-38973 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TATCTACACA Num.seqs=4 Similarity=0.498843
1 TTATCTACACACTTTTAGANT

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Consensus:

TTATCaACAcAcTTTTAGaaT

>Bacillus_Fam_708_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.666667
GCF_002019645.1_ASM201964v1_genomic.fna_1:280014-280475 Satlength=462 Nr
of Repeats=18 RepeatLength=21 seed=AAAATACGGC Num.seqs=12
Similarity=0.580369 0
AAAATACGGCGGNTTTGA-CA
GCF_002019645.1_ASM201964v1_genomic.fna_1:5314586-5314815 Satlength=230
Nr of Repeats=5 RepeatLength=21 seed=AATACGGCGG Num.seqs=3
Similarity=0.873016 2
CGAATACGGCGGGTTTGAGCC

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Consensus:

aaAATACGGCGGgTTTGAgCa

>Bacillus_Fam_709_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.619048
GCF_900111815.1_PRJEB17078_genomic.fna_1:2579479-2579833 Satlength=355 Nr
of Repeats=10 RepeatLength=21 seed=TTGGTTGATT Num.seqs=8
Similarity=0.642081 0
TTGGTTGATT-CTAGAGAAG

GCF_900111815.1_PRJEB17078_genomic.fna_1:2923151-2924173 Satlength=1023
Nr of Repeats=29 RepeatLength=21 seed=TTGGTTGATTT Num.seqs=19
Similarity=0.555217 1
TTGGTTGATTTCTGCTGNAN

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Consensus:

TTGGTTGATTTcCTacaGaAg

>Bacillus_Fam_710_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.690476
GCF_900156865.1_PRJEB18960_genomic.fna_3:4206861-4206941 Satlength=81 Nr
of Repeats=4 RepeatLength=20 seed=GACAGTATTT Num.seqs=4
Similarity=0.666667
0 GACAGTATTTCCAAAATAGC-
Rev.of_GCF_000712595.1_ASM71259v1_genomic.fna_14:34518-34623
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TCGGCTATTT Num.seqs=5
Similarity=0.665152 2
GAAAGTGTATCGAAAATAGCC

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Consensus:

GAaAGTaTaTcC AAAATAGCc

>Bacillus_Fam_711_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.809524
GCF_000169195.2_ASM16919v2_genomic.fna_1:1723063-1723231 Satlength=169 Nr
of Repeats=6 RepeatLength=21 seed=GCAACATCCT Num.seqs=4
Similarity=0.714286 0
GCAACATCCTGTTTCAGCACT
Rev.of_GCF_000832905.1_ASM83290v1_genomic.fna_1:1842445-1842529
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=GATGTTGCAG Num.seqs=4
Similarity=0.873016 8
GCAACATCTTGTTTTAGCCCT

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Consensus:

GCAACATCcTGTTTcAGCaT

>Bacillus_Fam_712_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.873016
GCF_000175075.1_ASM17507v1_genomic.fna_34:92519-92645 Satlength=127 Nr of
Repeats=4 RepeatLength=21 seed=TGTTAGTACA Num.seqs=3 Similarity=0.830688
0 TGTTAGTACATTAAAGAGTGA
Rev.of_GCF_001648575.1_ASM164857v1_genomic.fna_48:38804-38909
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=ACTAACATCA Num.seqs=5
Similarity=0.826087 7
TGTTAGTGTATTAAAGAGTGA

***** *****

Consensus:

TGTTAGTAcATTAAAGAGTGA

>Bacillus_Fam_713_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.746032
GCF_000175075.1_ASM17507v1_genomic.fna_36:48707-48854 Satlength=148 Nr of
Repeats=7 RepeatLength=21 seed=GGAGGCTCTT Num.seqs=7 Similarity=0.830688
0 GGAGGCTCTTCGCCATCACCC
Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:146949-147096
Satlength=148 Nr of Repeats=7 RepeatLength=21 seed=GGAGAAGAAA Num.seqs=7
Similarity=0.927438 14
GGTGTTTCTTCTCCATCACCC

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Consensus:

GGaGgcTCTTCgCCATCACCC

>Bacillus_Fam_714_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.746032
GCF_000307875.1_BABA1.0_genomic.fna_138:19368-19452 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=ATCCGACAGT Num.seqs=4 Similarity=0.723485
20 TCCGACAGTTAGCTGCGGTTA
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_22:13463-13608
Satlength=146 Nr of Repeats=7 RepeatLength=21 seed=ACTGTCGGAT Num.seqs=5
Similarity=0.675758 30
TCCGACAGTAAGCCGCTGCTA

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Consensus:

ATCCGACAGTaAGCcGCgGcT

>Bacillus_Fam_715_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.809524
GCF_000508325.1_BAVI_1_genomic.fna_59:240543-240669 Satlength=127 Nr of
Repeats=5 RepeatLength=21 seed=TTCAAAATTT Num.seqs=4 Similarity=0.820106
0 TTCAAAATTTCACTGTGATCG
Rev.of_GCF_000724485.1_ASM72448v1_genomic.fna_1:3059785-3059911
Satlength=127 Nr of Repeats=5 RepeatLength=21 seed=TTTGAAAGAA Num.seqs=4
Similarity=0.693122 6
TTCAAAAGTTTCACTGTGTTCT

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Consensus:

TTCAAAaTTTCACTGTGaTCg

>Bacillus_Fam_716_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.650794
GCF_000612625.1_JCE_genomic.fna_78:17147-17414 Satlength=268 Nr of
Repeats=5 RepeatLength=21 seed=TTTATCAACC Num.seqs=3 Similarity=0.666667
0 TTTATCAACCACTTTTCCTCN

GCF_002019635.1_ASM201963v1_genomic.fna_1:406736-407553 Satlength=818 Nr
of Repeats=28 RepeatLength=21 seed=TTCAACCACT Num.seqs=21
Similarity=0.616011 3
TNTTCAACCACTTCTCTGCT

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Consensus:

TtTaTCAACCACTTcTCcgCt

>Bacillus_Fam_717_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.873016

GCF_000708755.2_ASM70875v2_genomic.fna_7:112578-112785 Satlength=208 Nr
of Repeats=7 RepeatLength=21 seed=TTACTACCAA Num.seqs=5
Similarity=0.714286

0 TTACTACCAACTACCGCAGAT

GCF_000709935.2_ASM70993v2_genomic.fna_19:119838-120024 Satlength=187 Nr
of Repeats=6 RepeatLength=21 seed=TTACTACCAA Num.seqs=4
Similarity=0.671958

0 TTACTACCAACAACCACAGAT

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

Consensus:

TTACTACCAACaACCaCAGAT

>Bacillus_Fam_718_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.682540

GCF_000712595.1_ASM71259v1_genomic.fna_21:13433-13580 Satlength=148 Nr of
Repeats=7 RepeatLength=21 seed=ATAGCCGATA Num.seqs=7 Similarity=0.860922

0 ATAGCCGATACACCCGTGAAA

Rev.of_GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_12:4665-5905
Satlength=1241 Nr of Repeats=58 RepeatLength=21 seed=TTACGGGAGT

Num.seqs=45 Similarity=0.766697 19

AGCGCGGATACTCCCGTAAAA

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Consensus:

AgaGCcGATACaCCCGTaAAA

>Bacillus_Fam_719_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.698413

GCF_000813125.1_ASM81312v1_genomic.fna_142:26887-26971 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=AATCACTACG Num.seqs=4 Similarity=0.556713

0 AATCACTACGGAATTCAAANT

Rev.of_GCF_000813125.1_ASM81312v1_genomic.fna_142:36627-36711

Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TCGTAGTGAT Num.seqs=4
Similarity=0.612374 11

AATCACTACGAAAATTAGAAT

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Consensus:

AATCACTACGaAAATcAaAaT

>Bacillus_Fam_720_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.746032
GCF_000948175.1_BFA_2_A_genomic.fna_157:32173-32278 Satlength=106 Nr of
Repeats=5 RepeatLength=21 seed=GTATTCGACA Num.seqs=5 Similarity=0.974603
0 GTATTCGACACACTTTGGATT
GCF_000948175.1_BFA_2_A_genomic.fna_161:7622-7844 Satlength=223 Nr of
Repeats=4 RepeatLength=21 seed=GGATCGTATT Num.seqs=3 Similarity=1.000000
16 GTATTCGACAGAAGTTGGATC

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Consensus:

GTATTCGACAcAagTTGGATc

>Bacillus_Fam_721_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.888889
GCF_001273755.1_ASM127375v1_genomic.fna_17:235079-235207 Satlength=129 Nr
of Repeats=6 RepeatLength=21 seed=TTACGAGTA Num.seqs=5
Similarity=0.710145 30
TCNTGAAAATTCACGAGTAAA
Rev.of_GCF_001273755.1_ASM127375v1_genomic.fna_17:3961735-3962511
Satlength=777 Nr of Repeats=38 RepeatLength=21 seed=TTACTCGTGA
Num.seqs=27 Similarity=0.823814
41 TCGTGAAAACCTCACGAGTAAA

***** *****

Consensus:

cTCACGAGTAAATCgTGAAAA

>Bacillus_Fam_722_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.682540
GCF_001315065.1_ASM131506v1_genomic.fna_30:7615-7720 Satlength=106 Nr of
Repeats=5 RepeatLength=21 seed=GCCTTCATCT Num.seqs=5 Similarity=1.000000
0 GCCTTCATCTCCGTCCTCCAGG
GCF_002019635.1_ASM201963v1_genomic.fna_1:1180363-1180615 Satlength=253
Nr of Repeats=11 RepeatLength=21 seed=CTGGATCTTG Num.seqs=10
Similarity=0.880071 17
ATCTTGATCTCCGTCACCTGG

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Consensus:

acCTTcATCTCCGTCaCCaGG

>Bacillus_Fam_723_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.698413
GCF_001315165.1_ASM131516v1_genomic.fna_27:15017-15121 Satlength=105 Nr
of Repeats=4 RepeatLength=21 seed=GTGGTCGATA Num.seqs=3
Similarity=0.767196
0 GTGGTCGATATAATCANAAAA

GCF_002019645.1_ASM201964v1_genomic.fna_1:659769-659933 Satlength=165 Nr
of Repeats=8 RepeatLength=21 seed=CAATAAAACC Num.seqs=6
Similarity=0.817989
5 TTGGTCAATAAAACCAGAAAA

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Consensus:

gTGGTCaATAaAAcCAgAAAA

>Bacillus_Fam_724_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.619048

GCF_001591425.1_ASM159142v1_genomic.fna_40:10164-10290 Satlength=127 Nr
of Repeats=6 RepeatLength=21 seed=TGTTAAATAA Num.seqs=6
Similarity=0.654589

0 TGTTAAATAAAATCTCAAAGT

GCF_001591425.1_ASM159142v1_genomic.fna_132:2162-2350 Satlength=189 Nr of
Repeats=8 RepeatLength=21 seed=CTGTAAAGTA Num.seqs=6 Similarity=0.712169
20 TGTTAAGAAAAACCACAAACC

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Consensus:

TGTTAAaaAAAAcCaCAAacc

>Bacillus_Fam_725_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.825397

GCF_001591445.1_ASM159144v1_genomic.fna_9:109889-109973 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=CGCCAATAGA Num.seqs=4
Similarity=0.815657

0 CGCCAATAGAACCTCTGAATC

GCF_001591445.1_ASM159144v1_genomic.fna_9:169675-169822 Satlength=148 Nr
of Repeats=7 RepeatLength=21 seed=CGCCAATAGA Num.seqs=7
Similarity=0.779289

0 CGCCAATAGAACCTGNAAATC

***** *****

Consensus:

CGCCAATAGAACCTctaATC

>Bacillus_Fam_726_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.619048

GCF_001591665.1_ASM159166v1_genomic.fna_82:10-115 Satlength=106 Nr of
Repeats=5 RepeatLength=21 seed=ATCCGACAGT Num.seqs=5 Similarity=0.898413
0 ATCCGACAGTTGGAACACGCT

Rev.of_GCF_001591805.1_ASM159180v1_genomic.fna_15:119662-119746

Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=GCCAACTGTC Num.seqs=4
Similarity=0.904762

TTGCGACAGTTGGCTCTTGCT

14

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Consensus:

aTcCGACAGTTGGaaCacGCT

>Bacillus_Fam_727_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21
Alignment score = 0.682540
GCF_001591805.1_ASM159180v1_genomic.fna_15:30953-31058 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=TTGGCGAAAT Num.seqs=5
Similarity=0.587879

0 TTGGCGAAATNCNNNCACAGT

GCF_001591805.1_ASM159180v1_genomic.fna_15:39100-39247 Satlength=148 Nr
of Repeats=7 RepeatLength=21 seed=AGTTTGGCGA Num.seqs=7
Similarity=0.818594

18 TTGGCGAAATCCNGCGTAGT

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Consensus:

TTGGCGAAATcCcNgCacAGT

>Bacillus_Fam_728_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.800000
GCF_000175075.1_ASM17507v1_genomic.fna_29:50387-50489 Satlength=103 Nr of
Repeats=5 RepeatLength=20 seed=TATCCATTGT Num.seqs=3 Similarity=0.777778

0 TATCCATTGTAAATTTGATA

GCF_001648575.1_ASM164857v1_genomic.fna_66:142753-142855 Satlength=103 Nr
of Repeats=5 RepeatLength=20 seed=TATCCATTGT Num.seqs=3
Similarity=0.777778

0

TATCCATTGTTAATTGAATA

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

Consensus:

TATCCATTGTaAATTgaATA

>Bacillus_Fam_729_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.616667
GCF_000181495.1_ASM18149v1_genomic.fna_133:12224-12305 Satlength=82 Nr of
Repeats=4 RepeatLength=20 seed=GACGCAATTA Num.seqs=3 Similarity=0.544974

0 GACGCAATTATTTTCATATTA

Rev.of_GCF_000181495.1_ASM18149v1_genomic.fna_147:20393-20494
Satlength=102 Nr of Repeats=5 RepeatLength=20 seed=TAATTGCGTC Num.seqs=4
Similarity=0.498843

10

GACGCAATTAAACTGNATTA

***** ****

Consensus:

GACGCAATTAAaccatATTA

>Bacillus_Fam_730_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.700000
GCF_000285535.1_ASM28553v1_genomic.fna_2:785830-786454 Satlength=625 Nr
of Repeats=30 RepeatLength=20 seed=TTTGGCTCTC Num.seqs=25

```

Similarity=0.766222
TTTGCGTCTCCTCCNGATA
GCF_000285535.1_ASM28553v1_genomic.fna_62:31-473 Satlength=443 Nr of
Repeats=22 RepeatLength=20 seed=ATTTGCGTCT Num.seqs=21
Similarity=0.616594
19      TTTGCGTCTCCAGNTGATA

*****      ****
Consensus:

TTTGCGTCTCCcacctGATA

>Bacillus_Fam_731_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.750000
GCF_000311725.1_ASM31172v1_genomic.fna_2:224797-224897 Satlength=101 Nr
of Repeats=5 RepeatLength=20 seed=TATATCGGCG Num.seqs=5
Similarity=0.593651
14      GGCGNTTTTAGCAATATATC
GCF_000311725.1_ASM31172v1_genomic.fna_4:95730-95830 Satlength=101 Nr of
Repeats=5 RepeatLength=20 seed=TATATCGGCG Num.seqs=3 Similarity=0.671958
14      GGCGTTTTTTGAGATATATC

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

TATATCGGCGtTTTTaGaaA

>Bacillus_Fam_732_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.883333
GCF_000380245.2_ASM38024v2_genomic.fna_9:119172-119272 Satlength=101 Nr
of Repeats=5 RepeatLength=20 seed=CTCATATATT Num.seqs=5
Similarity=0.893333
0      CTCATATATTTGTTCTCNG
GCF_000380245.2_ASM38024v2_genomic.fna_9:119172-119412 Satlength=241 Nr
of Repeats=12 RepeatLength=20 seed=CTCATATATT Num.seqs=12
Similarity=0.859596
CTCATATATTTCGTTCTCCG

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

CTCATATATTTcGTTCTCcG

>Bacillus_Fam_733_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20
Alignment score = 0.750000
GCF_001591585.1_ASM159158v1_genomic.fna_8:146075-146177 Satlength=103 Nr
of Repeats=5 RepeatLength=20 seed=TTTGGCTGAT Num.seqs=3
Similarity=0.575758
0      TTTGGCTGATATTTTCTNC
Rev.of_GCF_001591585.1_ASM159158v1_genomic.fna_18:3-309 Satlength=307 Nr
of Repeats=15 RepeatLength=20 seed=ATCAGCCAAA Num.seqs=9
Similarity=0.798942
TTTGGCTGATATTTTCCCAG

```

0

0

10

***** *

Consensus:

TTTGGCTGATATTTTcCcac

>Bacillus_Fam_734_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19
Alignment score = 0.649123
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_3:387353-387569 Satlength=217 Nr of
Repeats=10 RepeatLength=18 seed=CCCGGATGAG Num.seqs=9
Similarity=0.872428 0
CCCGGATG-AGGTCCTGGT
Rev.of_GCF_001636325.1_ASM163632v1_genomic.fna_2:690747-691053
Satlength=307 Nr of Repeats=17 RepeatLength=18 seed=CCAGCACCAG
Num.seqs=17 Similarity=0.827887
5 GCTGG-TGAAGGTCCTGGT

* ** * *****

Consensus:

cCcGGaTGaAGGTCCTGGT

>Bacillus_Fam_735_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19
Alignment score = 0.622807
GCF_000008505.1_ASM850v1_genomic.fna_1:4938976-4939084 Satlength=109 Nr
of Repeats=6 RepeatLength=18 seed=CTGGACAAGC Num.seqs=6
Similarity=0.911111
0 CTGGACAAGCAAG-ACAAT
GCF_000430785.1_ASM43078v1_genomic.fna_13:56722-56902 Satlength=181 Nr of
Repeats=8 RepeatLength=18 seed=TTAGAGAAAGT Num.seqs=6 Similarity=0.782716
17 -TAGAGAAGCAAGAACACT

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

Consensus:

cTaGAcAAGCAAGaACAaT

>Bacillus_Fam_736_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19
Alignment score = 0.649123
GCF_000177235.2_ASM17723v2_genomic.fna_1:380562-380634 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=AAGCCAATGC Num.seqs=4 Similarity=0.962963
0 AAGCCAATGCTGCC-CACA
Rev.of_GCF_000242895.2_ASM24289v3_genomic.fna_1:1111116-1111242
Satlength=127 Nr of Repeats=7 RepeatLength=18 seed=GCGGCTTTGG Num.seqs=7
Similarity=0.978836 12 AA-
CCAAAGCCGCCACACA

** **** * ** *

Consensus:

AAgCCAAaGCcGCCaCACA

>Bacillus_Fam_737_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.666667

GCF_000007825.1_ASM782v1_genomic.fna_1:4701846-4702305 Satlength=460 Nr
of Repeats=12 RepeatLength=18 seed=ACGGGGAACA Num.seqs=10
Similarity=0.925926

0

ACGGGGAACACCGGACCC

GCF_000769555.1_ASM76955v1_genomic.fna_1:742609-742825 Satlength=217 Nr
of Repeats=8 RepeatLength=18 seed=ACCGGAGCAA Num.seqs=5
Similarity=0.770370

9 ACGGGGNTNACCGGAGCA

***** * * *

Consensus:

ACGGGGaacACCGGAcCa

>Bacillus_Fam_738_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630

GCF_000008505.1_ASM850v1_genomic.fna_1:1992091-1992343 Satlength=253 Nr
of Repeats=14 RepeatLength=18 seed=CCTGATACAG Num.seqs=14
Similarity=0.888482

0

CCTGATACAGGAGAAAAA

Rev.of_GCF_000161455.1_ASM16145v1_genomic.fna_1:1437244-1437370
Satlength=127 Nr of Repeats=7 RepeatLength=18 seed=TATCTGGTTT Num.seqs=5
Similarity=0.955556

7

CCAGATACACCAAATAAA

** * * * *

Consensus:

CCaGATACAccAaAaAAA

>Bacillus_Fam_739_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630

GCF_000161455.1_ASM16145v1_genomic.fna_1:4033827-4033917 Satlength=91 Nr
of Repeats=5 RepeatLength=18 seed=TGTTGATGCT Num.seqs=5
Similarity=0.970370

0 TGTTGATGCTGACCATGG

Rev.of_GCF_000832605.1_ASM83260v1_genomic.fna_1:1245276-1245432
Satlength=157 Nr of Repeats=6 RepeatLength=18 seed=CATCACCAAG Num.seqs=5
Similarity=0.874074

5

TGATGGTGTTGGCCTTGG

** * * * *

Consensus:

TGaTGaTGcTGaCCaTGG

>Bacillus_Fam_740_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.648148

GCF_000175075.1_ASM17507v1_genomic.fna_32:87599-88088 Satlength=490 Nr of
Repeats=18 RepeatLength=18 seed=AACAACAGCA Num.seqs=17
Similarity=0.869281

0 AACAACAGCAACAGCGGN

GCF_900104555.1_IMG-

taxon_2651870172_annotated_assembly_genomic.fna_17:3091-3181 Satlength=91

Nr of Repeats=5 RepeatLength=18 seed=ACAACAACAC Num.seqs=5
Similarity=0.940741 1 CACAACAACACCAGCAGT

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

Consensus:

aACAACAaCAaCAGCaGt

>Bacillus_Fam_741_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.925926
GCF_000177235.2_ASM17723v2_genomic.fna_1:532212-532500 Satlength=289 Nr
of Repeats=16 RepeatLength=18 seed=CCAGGCGAAG Num.seqs=16
Similarity=0.934568 0
CCAGGCGAAGGTGAAGGC
GCF_001315065.1_ASM131506v1_genomic.fna_40:23388-23478 Satlength=91 Nr of
Repeats=5 RepeatLength=18 seed=AGAAGGTGAA Num.seqs=5 Similarity=0.970370
5 CCAGGAGAAGGTGAAGGC

***** *****

Consensus:

CCAGGaGAAGGTGAAGGC

>Bacillus_Fam_742_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
GCF_000299035.1_ASM29903v1_genomic.fna_3:476185-476329 Satlength=145 Nr
of Repeats=8 RepeatLength=18 seed=ATCTTGGTCT Num.seqs=8
Similarity=0.960317
0 ATCTTGGTCTTTTCCTGG
Rev.of_GCF_001315065.1_ASM131506v1_genomic.fna_13:100988-101102
Satlength=115 Nr of Repeats=4 RepeatLength=18 seed=AGATGAAGAG Num.seqs=3
Similarity=1.000000 10
CTCTTCATCTAGTCCTGG

**** ** *****

Consensus:

aTCTTcaTCTagTCCTGG

>Bacillus_Fam_743_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
GCF_000299035.1_ASM29903v1_genomic.fna_4:44054-44162 Satlength=109 Nr of
Repeats=4 RepeatLength=18 seed=CACCTAATCC Num.seqs=3 Similarity=1.000000
0 CACCTAATCCAACCTCCGC
Rev.of_GCF_001439915.1_ASM143991v1_genomic.fna_85:15375-16048
Satlength=674 Nr of Repeats=4 RepeatLength=18 seed=GTGGATTTGG Num.seqs=3
Similarity=0.802469 12
CACCCAATCCACCTAATC

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

Consensus:

CACCCaATCCaACTaagC

>Bacillus_Fam_744_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.703704
GCF_000305495.1_BacPsy2.0_genomic.fna_210:5429-5585 Satlength=157 Nr of
Repeats=8 RepeatLength=18 seed=GCTTCTTGTT Num.seqs=6 Similarity=0.866667
0 GCCTCTTGTTTCAGCTTCT
GCF_000972245.2_ASM97224v2_genomic.fna_1:252282-252630 Satlength=349 Nr
of Repeats=18 RepeatLength=18 seed=TGAGCTTGAG Num.seqs=17
Similarity=0.881264
GCCTCTTGCTGAGCTTGA

9

***** * *****

Consensus:

GCCTCTTGcTcAGCTTca

>Bacillus_Fam_745_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.777778
GCF_000430785.1_ASM43078v1_genomic.fna_5:20934-21024 Satlength=91 Nr of
Repeats=5 RepeatLength=18 seed=ATTAGTACCA Num.seqs=5 Similarity=0.881481
0 ATTAGTACCAGTGCCTGG
GCF_000934845.1_ASM93484v1_genomic.fna_135:23551-23617 Satlength=67 Nr of
Repeats=4 RepeatLength=18 seed=GGATCAGTAC Num.seqs=3 Similarity=0.901235
16 ATCAGTACCAGTACCAGG

** ***** ** **

Consensus:

ATcAGTACCAGTaCCaGG

>Bacillus_Fam_746_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
GCF_000430785.1_ASM43078v1_genomic.fna_24:4949-5111 Satlength=163 Nr of
Repeats=8 RepeatLength=18 seed=AGAACTTTTA Num.seqs=7 Similarity=0.957672
0 AGAACTTTTAGAAGCCGT
Rev.of_GCF_001591445.1_ASM159144v1_genomic.fna_30:53287-53467
Satlength=181 Nr of Repeats=10 RepeatLength=18 seed=TTCTAGAAGT
Num.seqs=10 Similarity=0.917695
13 AATACTTCTAGAAACCGG

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

Consensus:

AaaACTTcTAGAAaCCGg

>Bacillus_Fam_747_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.777778
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_25:69856-70072 Satlength=217 Nr of Repeats=12
RepeatLength=18 seed=GGCCCGAATC Num.seqs=12 Similarity=0.987654 0
GGCCCGAATCCCATGCCG
Rev.of_GCF_001273755.1_ASM127375v1_genomic.fna_17:794926-795034
Satlength=109 Nr of Repeats=6 RepeatLength=18 seed=GGAATGGGAT Num.seqs=6
Similarity=0.891358
GGGCCGAATCCCATTTCCA

17

** ***** **

Consensus:

GGcCCGAATCCCATgCCa

>Bacillus_Fam_748_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18

Alignment score = 0.851852

GCF_000708755.2_ASM70875v2_genomic.fna_2:520937-521289 Satlength=353 Nr of Repeats=17 RepeatLength=18 seed=GGAGCACCTG Num.seqs=14

Similarity=0.822548

0

GGAGCACCTGTTACGCC

GCF_000709935.2_ASM70993v2_genomic.fna_1:1110697-1110931 Satlength=235 Nr of Repeats=13 RepeatLength=18 seed=GGAGCACCTG Num.seqs=13

Similarity=0.851852

0

GGAGCACCTGTTGCGCCT

***** ****

Consensus:

GGAGCACCTGTTaCGCCc

>Bacillus_Fam_749_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18

Alignment score = 0.629630

GCF_000709935.2_ASM70993v2_genomic.fna_6:62-278 Satlength=217 Nr of Repeats=10 RepeatLength=18 seed=CCGGCAGGTC Num.seqs=8

Similarity=0.777778

0 CCGGCAGGTCCAGTAACT

Rev.of_GCF_000712615.1_ASM71261v1_genomic.fna_82:4158-4356 Satlength=199

Nr of Repeats=8 RepeatLength=18 seed=CTCAAGGAAT Num.seqs=5

Similarity=0.911111

7

CCTTGAGATCCAGTAATT

** ** ***** *

Consensus:

CCggcAGaTCCAGTAaCT

>Bacillus_Fam_750_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18

Alignment score = 0.703704

GCF_000759675.1_ASM75967v1_genomic.fna_158:37496-37595 Satlength=100 Nr of Repeats=6 RepeatLength=18 seed=GGTGGTATTG Num.seqs=4

Similarity=0.802469

0 GGTGGTATTGGCGGTCCT

GCF_001591445.1_ASM159144v1_genomic.fna_87:10237-10345 Satlength=109 Nr of Repeats=6 RepeatLength=18 seed=GGACATGGTG Num.seqs=6

Similarity=0.925926

12 GGTGGAATGGGCGGACAT

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

Consensus:

GGTGGaATgGGCGGaCaT

>Bacillus_Fam_751_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.777778
GCF_000813125.1_ASM81312v1_genomic.fna_74:2375-2537 Satlength=163 Nr of
Repeats=9 RepeatLength=18 seed=ATACCGGAGG Num.seqs=9 Similarity=0.962963
0 ATACCGGAGGCGAAGGAG
GCF_001315165.1_ASM131516v1_genomic.fna_159:2411-2519 Satlength=109 Nr of
Repeats=6 RepeatLength=18 seed=GGTGGTGAAG Num.seqs=6 Similarity=0.841975
5 ATACCGGTGGTGAAGAAG

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

Consensus:

ATACCGGaGGcGAAGaAG

>Bacillus_Fam_752_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
GCF_001274935.1_ASM127493v1_genomic.fna_36:82635-84309 Satlength=1675 Nr
of Repeats=91 RepeatLength=18 seed=CCTACTGGTG Num.seqs=88
Similarity=0.883761 0
CCTACTGGTGCTGCTGGT
GCF_001636425.1_ASM163642v1_genomic.fna_1:2005510-2005852 Satlength=343
Nr of Repeats=19 RepeatLength=18 seed=GTGCTTGTGG Num.seqs=16
Similarity=0.973457 1
CGTGCTTGTGGTGCTCGT

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

Consensus:

CcTaCTgGTGcTGCTcGT

>Bacillus_Fam_753_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.666667
GCF_001420715.1_ASM142071v1_genomic.fna_22:3447196-3448294 Satlength=1099
Nr of Repeats=61 RepeatLength=18 seed=CCAGCAGGTG Num.seqs=61
Similarity=0.861486 0
CCAGCAGGTGCTACCGGA
Rev.of_GCF_001712755.1_ASM171275v1_genomic.fna_33:51006-51924
Satlength=919 Nr of Repeats=48 RepeatLength=18 seed=CCTGTTGCTC
Num.seqs=45 Similarity=0.793042
17 CCAGCNGGAGCAACAGGN

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

Consensus:

CCAGCaGGaGCaACaGGa

>Bacillus_Fam_754_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.703704
GCF_001578185.1_ASM157818v1_genomic.fna_1:2941947-2942073 Satlength=127
Nr of Repeats=7 RepeatLength=18 seed=CTGGCTTTGA Num.seqs=7
Similarity=0.887125 0
CTGGCTTTGATTGTTCTG
Rev.of_GCF_001591445.1_ASM159144v1_genomic.fna_68:19027-19129
Satlength=103 Nr of Repeats=5 RepeatLength=18 seed=CCACAACGAC Num.seqs=4

Similarity=0.913580
GTGGCTTTGGTCGTTGTG

1

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

cTGGCTTTGaTcGTTcTG

>Bacillus_Fam_755_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.648148
GCF_001654695.1_ASM165469v1_genomic.fna_9:27-117 Satlength=91 Nr of
Repeats=5 RepeatLength=18 seed=CTTGCTGTTT Num.seqs=5 Similarity=0.822222
0 CTTGCTGTTTTTGTGTT
Rev.of_GCF_001889165.1_ASM188916v1_genomic.fna_1:1564134-1564404
Satlength=271 Nr of Repeats=15 RepeatLength=18 seed=AGCAAGCAAA
Num.seqs=15 Similarity=0.886420
0 CCTGCTGNTTTGCTTGCT

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

CcTGCTGtTTTgCtTGcT

>Bacillus_Fam_756_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18
Alignment score = 0.629630
GCF_002019645.1_ASM201964v1_genomic.fna_1:3879414-3879792 Satlength=379
Nr of Repeats=16 RepeatLength=18 seed=GGAAGTGGAT Num.seqs=13
Similarity=0.867047 0
GGAAGTGGATTTGCTCCT
Rev.of_GCF_900111815.1_PRJEB17078_genomic.fna_1:557922-558030
Satlength=109 Nr of Repeats=6 RepeatLength=18 seed=CAAATCCGGA Num.seqs=6
Similarity=0.911111 13
GGATCCGATTTGGTGTT

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

GGAaCcGGATTTGcTccT

>Bacillus_Fam_757_16_2 Nr. of seq. 2 Alignment length(with gaps) = 16
Alignment score = 0.625000
GCF_000331575.1_ASM33157v1_genomic.fna_3:88190-88246 Satlength=57 Nr of
Repeats=4 RepeatLength=14 seed=CTAATCAACC Num.seqs=4 Similarity=0.952381
0 CT-AA-TCAACCAACA
GCF_900111815.1_PRJEB17078_genomic.fna_1:149733-149838 Satlength=106 Nr
of Repeats=7 RepeatLength=15 seed=GAAGTCAACC Num.seqs=7
Similarity=0.923810
2 CTGAAGTCAACCAA-A

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

CTgAAcTCAACCAAcA

>Bacillus_Fam_758_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
Alignment score = 0.688889
GCF_001591545.1_ASM159154v1_genomic.fna_1:1876062-1876140 Satlength=79 Nr
of Repeats=6 RepeatLength=13 seed=TTATTGTTTT Num.seqs=6
Similarity=1.000000 0
TTATT--GTTTTTCC
Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_25:2727-2817 Satlength=91
Nr of Repeats=6 RepeatLength=15 seed=AAAACATAAT Num.seqs=6
Similarity=0.917037 12
TTATTATGTTTTTCG

Consensus:

TTATTatGTTTTTCc

>Bacillus_Fam_759_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
Alignment score = 0.733333
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:254208-254418 Satlength=211 Nr of
Repeats=14 RepeatLength=15 seed=GGTGAACCCG Num.seqs=14
Similarity=0.940415 0
GGTGAACCCGGTGAT
GCF_000177235.2_ASM17723v2_genomic.fna_1:793103-793946 Satlength=844 Nr
of Repeats=20 RepeatLength=15 seed=GAACCAGGAG Num.seqs=19
Similarity=0.916829 3
GGCGAACCAGGAGAT

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

Consensus:

GGcGAACCaGGaGAT

>Bacillus_Fam_760_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
Alignment score = 0.666667
GCF_000299035.1_ASM29903v1_genomic.fna_1:1198325-1198505 Satlength=181 Nr
of Repeats=9 RepeatLength=15 seed=CAAAAACCAG Num.seqs=7
Similarity=0.751984 0
CAAAAACCAGAGGAN
GCF_001591445.1_ASM159144v1_genomic.fna_34:41259-41319 Satlength=61 Nr of
Repeats=4 RepeatLength=15 seed=GCTCCAAAAC Num.seqs=4 Similarity=0.851852
12 CCAAAAACCAGGGGCT

* ***** **

Consensus:

CaAAAACCAGaGGat

>Bacillus_Fam_761_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15
Alignment score = 0.733333
GCF_000474275.1_Bmar1.0_genomic.fna_33:30569-30884 Satlength=316 Nr of
Repeats=5 RepeatLength=15 seed=TTCTTGTTCT Num.seqs=3 Similarity=0.940741
1 ATTCTTGTTCTTTGT
GCF_001636325.1_ASM163632v1_genomic.fna_1:2526805-2527021 Satlength=217
Nr of Repeats=7 RepeatLength=15 seed=CTTTTCTTT Num.seqs=5

Similarity=0.822222

3

GTTCTTTTCTTTTT

***** * *

Consensus:

TTCTTgTTCTTTgTa

>Bacillus_Fam_762_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15

Alignment score = 1.000000

GCF_000508325.1_BAVI_1_genomic.fna_72:39782-39857 Satlength=76 Nr of Repeats=5 RepeatLength=15 seed=GGCATGATGT Num.seqs=5 Similarity=0.911111

0 GGCATGATGTGCGGC

GCF_001636315.1_ASM163631v1_genomic.fna_1:5617727-5617892 Satlength=166

Nr of Repeats=8 RepeatLength=15 seed=GGCATGATGT Num.seqs=5

Similarity=0.946667

0

GGCATGATGTGCGGC

Consensus:

GGCATGATGTGCGGC

>Bacillus_Fam_763_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15

Alignment score = 0.644444

GCF_001590785.1_ASM159078v1_genomic.fna_1:386490-386730 Satlength=241 Nr of Repeats=16 RepeatLength=15 seed=CCAGGCAATG Num.seqs=16

Similarity=0.902963

0

CCAGGCAATGGCGAT

Rev.of_GCF_001591665.1_ASM159166v1_genomic.fna_3:104200-104350

Satlength=151 Nr of Repeats=9 RepeatLength=15 seed=CCGCCACCGC Num.seqs=8

Similarity=0.866667

14

CCTGGCGGTGGCGGT

** *** * *

Consensus:

CCaGGCaaTGGCGaT

>Bacillus_Fam_764_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15

Alignment score = 0.844444

GCF_001591445.1_ASM159144v1_genomic.fna_9:114139-114289 Satlength=151 Nr of Repeats=10 RepeatLength=15 seed=GGCATTTCTT Num.seqs=10

Similarity=0.915062

0

GGCATTTCTTTGATC

Rev.of_GCF_001591485.1_ASM159148v1_genomic.fna_3:51079-51340

Satlength=262 Nr of Repeats=5 RepeatLength=15 seed=AAAGAAATAC Num.seqs=3

Similarity=0.733333

11

GGTATTTCTTTNATC

** * * * *

Consensus:

GGcATTTCTTTgATC

>Bacillus_Fam_765_14_2 Nr. of seq. 2 Alignment length(with gaps) = 14
Alignment score = 0.738095
GCF_000948175.1_BFA_2_A_genomic.fna_151:142349-142433 Satlength=85 Nr of
Repeats=7 RepeatLength=12 seed=TTCTCTTTT Num.seqs=5 Similarity=0.844444
9 TCTTTTTTC--TTC
GCF_001645555.1_ASM164555v1_genomic.fna_6:7244-7314 Satlength=71 Nr of
Repeats=5 RepeatLength=14 seed=TTCTTTTTTC Num.seqs=5 Similarity=1.000000
11 TCTTTTTTCTTTTT

** *****

Consensus:

TTcTCTTTTTTcTt

>Bacillus_Fam_766_14_2 Nr. of seq. 2 Alignment length(with gaps) = 14
Alignment score = 0.714286
GCF_000948175.1_BFA_2_A_genomic.fna_56:4896-4966 Satlength=71 Nr of
Repeats=5 RepeatLength=14 seed=TCATTACATA Num.seqs=5 Similarity=1.000000
0 TCATTACATATCCC
Rev.of_GCF_001578185.1_ASM157818v1_genomic.fna_1:2027719-2027775
Satlength=57 Nr of Repeats=4 RepeatLength=14 seed=TAAGTGATAA Num.seqs=4
Similarity=0.888889 3
TTATTACTTATCAC

* ***** *

Consensus:

TcATTACaTATCaC

>Bacillus_Fam_767_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
Alignment score = 0.666667
GCF_000008505.1_ASM850v1_genomic.fna_1:985966-986182 Satlength=217 Nr of
Repeats=17 RepeatLength=12 seed=GGAGGAGTAG Num.seqs=16
Similarity=0.905556
0 GGAGGAGTAGTT
GCF_000331575.1_ASM33157v1_genomic.fna_1:1528380-1528428 Satlength=49 Nr
of Repeats=4 RepeatLength=12 seed=GGATGAGTTA Num.seqs=4
Similarity=0.944444
0 GGATGAGTTATT

*** ***** **

Consensus:

GGAgGAGTaaTT

>Bacillus_Fam_768_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
Alignment score = 0.694444
GCF_000153365.1_ASM15336v1_genomic.fna_8:85710-85779 Satlength=70 Nr of
Repeats=5 RepeatLength=12 seed=CCTGAGCCTG Num.seqs=4 Similarity=0.759259
0 CCTGAACCTGAG
GCF_000294775.2_ASM29477v2_genomic.fna_2:295544-295664 Satlength=121 Nr
of Repeats=5 RepeatLength=12 seed=AGCCTAAGCC Num.seqs=3

Similarity=0.666667

4 CCTNAGCCTAAG

*** * *** **

Consensus:

CCTgAaCCTaAG

>Bacillus_Fam_769_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12

Alignment score = 0.666667

GCF_000161455.1_ASM16145v1_genomic.fna_1:5124264-5124372 Satlength=109 Nr of Repeats=4 RepeatLength=12 seed=TGGTTTTTCT Num.seqs=3

Similarity=1.000000

0

TGGTTTTTCTGT

Rev.of_GCF_000474275.1_Bmar1.0_genomic.fna_3:52284-52332 Satlength=49 Nr of Repeats=4 RepeatLength=12 seed=AAAGAAATGC Num.seqs=4

Similarity=0.925926

0 TGGCATTCTTT

*** ***** *

Consensus:

TGGCaTTCTgT

>Bacillus_Fam_770_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12

Alignment score = 0.805556

GCF_000334155.1_L1_genomic.fna_72:536-620 Satlength=85 Nr of Repeats=7 RepeatLength=12 seed=GATGCTGATG Num.seqs=7 Similarity=0.851852

0 GATGCTGATGCN

Rev.of_GCF_002019765.1_ASM201976v1_genomic.fna_1:3481582-3481660

Satlength=79 Nr of Repeats=5 RepeatLength=12 seed=GCATCCGCAT Num.seqs=3

Similarity=0.925926

5

GATGCCGATGCG

***** *****

Consensus:

GATGCcGATGCg

>Bacillus_Fam_771_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12

Alignment score = 0.666667

GCF_000430785.1_ASM43078v1_genomic.fna_20:47240-47348 Satlength=109 Nr of Repeats=9 RepeatLength=12 seed=CCTGGAGGAA Num.seqs=9 Similarity=0.913580

0 CCTGGAGGAACA

Rev.of_GCF_900093775.1_EVONIK_BGLY_genomic.fna_1:4560190-4560334

Satlength=145 Nr of Repeats=12 RepeatLength=12 seed=GTTGTTCCAC

Num.seqs=12 Similarity=0.922559

2 ACAGGTGGAACA

* ** *****

Consensus:

aCaGGaGGAACA

>Bacillus_Fam_772_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
Alignment score = 0.777778
GCF_000986785.1_ASM98678v1_genomic.fna_40:25576-25696 Satlength=121 Nr of
Repeats=8 RepeatLength=12 seed=TCATGGCTGT Num.seqs=6 Similarity=0.933333
0 TCATGGCTGTGA
GCF_002009555.1_ASM200955v1_genomic.fna_559:81-135 Satlength=55 Nr of
Repeats=4 RepeatLength=12 seed=TGATCATGGT Num.seqs=3 Similarity=0.925926
9 TCATGGTCGTGA

***** ****

Consensus:

TCATGGccGTGA

>Bacillus_Fam_773_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
Alignment score = 0.777778
GCF_001273755.1_ASM127375v1_genomic.fna_17:3004884-3004968 Satlength=85
Nr of Repeats=6 RepeatLength=12 seed=TTGAACTGGT Num.seqs=5
Similarity=0.866667 0
TTGAACTGGTTG
Rev.of_GCF_001315045.1_ASM131504v1_genomic.fna_15:59765-60074
Satlength=310 Nr of Repeats=6 RepeatLength=12 seed=ATGCAACAAC Num.seqs=4
Similarity=0.925926 6
TTGCATTGGTTG

*** * *****

Consensus:

TTGaAcTGGTTG

>Bacillus_Fam_774_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12
Alignment score = 0.777778
GCF_002019645.1_ASM201964v1_genomic.fna_1:1577470-1577590 Satlength=121
Nr of Repeats=10 RepeatLength=12 seed=CTGGAACAGA Num.seqs=10
Similarity=0.916049 0
CTGGAACAGACC
Rev.of_GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_22:386175-386367
Satlength=193 Nr of Repeats=15 RepeatLength=12 seed=TCTGTTCCTG
Num.seqs=14 Similarity=0.925519 10 CAGGAACAGATC

* ***** *

Consensus:

CaGGAACAGAcC

>Bacillus_Fam_775_11_2 Nr. of seq. 2 Alignment length(with gaps) = 11
Alignment score = 0.636364
GCF_000238675.1_Baci_smit_7_3_47FAA_V1_genomic.fna_4:38733-38800
Satlength=68 Nr of Repeats=4 RepeatLength=11 seed=GTTTCTATAT Num.seqs=3
Similarity=0.919192 0
GTTTCTATATG

Rev.of_GCF_000751775.1_A1A_genomic.fna_2:555-599 Satlength=45 Nr of
Repeats=4 RepeatLength=11 seed=GAAACAATAC Num.seqs=4 Similarity=0.939394
5 GTTTCGGTATT

***** ***

Consensus:

GTTTCgaTATg

>Bacillus_Fam_776_321_1 Nr. of seq. 1 Alignment length(with gaps) = 321
Alignment score = 0.000000
GCF_000242895.2_ASM24289v3_genomic.fna_1:4312051-4313392 Satlength=1342
Nr of Repeats=5 RepeatLength=321 seed=TGAACGTTAC Num.seqs=4
Similarity=0.939772 0
TGAACGTTACGGTATGTCTTCCATCTCTAAATTTGGTTGTGTCGAGAGTATAATGAAAGCCACCATTCCCATT
GTGGTACTCTGGAAAGACTTTCTGGACATCTGGTCTCGCATCTCCATAGATCGCCTGACCTGCCACTACACCG
TCTACCAGTACTTCAATTTTCGACACTCCGCTTTCATCTAAAAACCAGCCCCGTACGTTTTGGGACCCGATAA
GTGTTTTGCCAGAAACCGGATCATCGATATACCCGAGGACATTTGCAATCGTTATAGTCTTTTCAGGCAATGT
TGTGACATAGCCGTTTCCTGTTTCTC

Consensus:

TGAACGTTACGGTATGTCTTCCATCTCTAAATTTGGTTGTGTCGAGAGTATAATGAAAGCCACCATTCCCATT
GTGGTACTCTGGAAAGACTTTCTGGACATCTGGTCTCGCATCTCCATAGATCGCCTGACCTGCCACTACACCG
TCTACCAGTACTTCAATTTTCGACACTCCGCTTTCATCTAAAAACCAGCCCCGTACGTTTTGGGACCCGATAA
GTGTTTTGCCAGAAACCGGATCATCGATATACCCGAGGACATTTGCAATCGTTATAGTCTTTTCAGGCAATGT
TGTGACATAGCCGTTTCCTGTTTCTC

>Bacillus_Fam_777_255_1 Nr. of seq. 1 Alignment length(with gaps) = 255
Alignment score = 0.000000
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_16:50-1069 Satlength=1020 Nr of
Repeats=4 RepeatLength=255 seed=AGTAGGACGT Num.seqs=3
Similarity=0.920573
0

AGTAGGACGTTGCCAGGCAGATTAAACACANTCCTTTAGGGATGTGTTTTTTAATATGCATAAAGAGTATACT
CGGCGCAAAAAGAGCGCTGGTTCTGAAGAAGCAGCCCCCTACGAAGCGAAGCCCCGGAAGCGATCGAAGGAAGAA
AACCAAGTACGTTTCGCGAGACGAATCGGTTCTCTTCGTGCGACCTCGTGAGAGGCATCGGGGAAATCGCTACA
TGCCATACTTCCCCGAAGAAGAGAATCCGAAGAGAC

Consensus:

AGTAGGACGTTGCCAGGCAGATTAAACACANTCCTTTAGGGATGTGTTTTTTAATATGCATAAAGAGTATACT
CGGCGCAAAAAGAGCGCTGGTTCTGAAGAAGCAGCCCCCTACGAAGCGAAGCCCCGGAAGCGATCGAAGGAAGAA
AACCAAGTACGTTTCGCGAGACGAATCGGTTCTCTTCGTGCGACCTCGTGAGAGGCATCGGGGAAATCGCTACA
TGCCATACTTCCCCGAAGAAGAGAATCCGAAGAGAC

>Bacillus_Fam_778_252_1 Nr. of seq. 1 Alignment length(with gaps) = 252
Alignment score = 0.000000
GCF_000169195.2_ASM16919v2_genomic.fna_1:915504-916512 Satlength=1009 Nr
of Repeats=4 RepeatLength=252 seed=TTTGTCTCG Num.seqs=4
Similarity=0.906526 0
TTTTGCTTCGATTTAATCCTGACTGAGAAGCTACCTTTACTACTTGCTGTCCCTGTCCCCAGCACCGTTTTAC
CACGTTTAATCGTCACCTTTGGCGCCGGCTTCTGCTTTACCTGTAATCGTTGTTTGATTATCGCCAAACCGATT
GACGGACGGGGCTGATGGTGCTGTTTTGTCTTCCACTTTGAACGATTTGCCTGCACCCGTATTTCCAGCTTTA
TCTGTGCGCATAGGCTGTCAGAACCGTTCCTGCC

Consensus:

TTTTGCTTCGATTTAATCCTGACTGAGAAGCTACCTTTACTACTTGCTGTCCCTGTCCCCAGCACCGTTTTAC
CACGTTTAATCGTCACCTTTGGCGCCGGCTTCTGCTTTACCTGTAATCGTTGTTTGATTATCGCCAAACCGATT
GACGGACGGGGCTGATGGTGCTGTTTTGTCTTCCACTTTGAACGATTTGCCTGCACCCGTATTTCCAGCTTTA
TCTGTGCGCATAGGCTGTCAGAACCGTTCCTGCC

>Bacillus_Fam_779_249_1 Nr. of seq. 1 Alignment length(with gaps) = 249
Alignment score = 0.000000
GCF_000832905.1_ASM83290v1_genomic.fna_1:2746746-2747991 Satlength=1246
Nr of Repeats=5 RepeatLength=249 seed=AAACAAAAAG Num.seqs=5
Similarity=0.824409 0
AAACAAAAAGCAGGAACGAAGCTTGTCGTTTATGCGGAAGATGCGGCAGGGAACAAGAGCGNTGAAACNGTNG
TAACGGTTATTGATAAAACGGCTCCGGCAGCGCCGAAAGTCGGAGAAAGTAAGCGATACAAGTACTGTGGTTAC
AGGAACCACAGAAGCGGGCGCGAAAGTAACAGTAAATCCGGCTCGAACATTTTAGGNACGGCAACGGCTGAT
CATACCGGTGCATTTAAGGTAACCATTGCA

Consensus:

AAACAAAAAGCAGGAACGAAGCTTGTCGTTTATGCGGAAGATGCGGCAGGGAACAAGAGCGNTGAAACNGTNG
TAACGGTTATTGATAAAACGGCTCCGGCAGCGCCGAAAGTCGGAGAAAGTAAGCGATACAAGTACTGTGGTTAC
AGGAACCACAGAAGCGGGCGCGAAAGTAACAGTAAATCCGGCTCGAACATTTTAGGNACGGCAACGGCTGAT
CATACCGGTGCATTTAAGGTAACCATTGCA

>Bacillus_Fam_780_246_1 Nr. of seq. 1 Alignment length(with gaps) = 246
Alignment score = 0.000000
GCF_001591445.1_ASM159144v1_genomic.fna_67:6172-7645 Satlength=1474 Nr of
Repeats=5 RepeatLength=246 seed=GTTTTATCTA Num.seqs=3
Similarity=0.792231
0

GTTTTATCTACTTTTACTTCTACTGTGTTTTTATTTTCNGTATTACCNGCATTATCTACACTGTAGTAAGTTA
GAGTGTGGATGCCTTCTTTTTCTANGGTNAAGCTTGTGCCTTCGCTGAATTCAGCNCCATCGATAGAATAGTA
GGTTGCTTTCACACCGCTTAGGTCATCAGTTGCTGTCAGCTCAACATTCAGTCTTCTGTGTACCATTTGATCC
TCGACATTACTTACAGTAGTAGGAGCA

Consensus :

GTTTTATCTACTTTTACTTCTACTGTGTTTTTATTTTCNGTATTACCNGCATTATCTACACTGTAGTAAGTTA
GAGTGTGGATGCCTTCTTTTTCTANGGTNAAGCTTGTGCCTTCGCTGAATTCAGCNCCATCGATAGAATAGTA
GGTTGCTTTCACACCGCTTAGGTCATCAGTTGCTGTCAGCTCAACATTCACTGCTTCTGTGTACCATTGATCC
TCGACATTACTTACAGTAGTAGGAGCA

>Bacillus_Fam_781_237_1 Nr. of seq. 1 Alignment length(with gaps) = 237
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_37:21075-21996 Satlength=922 Nr of
Repeats=4 RepeatLength=237 seed=CCATTGGCTT Num.seqs=3
Similarity=0.889358

0
CCATTGGCTTTCACCCTTGCCAGCCGTTTCGATTTCGGATATCACTGATACTGCCGTTCCGCTGGACAGCTTGC
TTATCACTTTTCCTTGTGTAGACGCCTTGTCTCGGACATTTCAGCGAGGATCCAGAGTCGACTTTACATATTT
GGTAACCGGNTTGGCCGACGGTTTTGGTGTACCTGTGCTGGCTGACGGCTTGCTTGATGACAAATATTGTGAA
CTTACGTAGCCTGTTTTG

Consensus :

CCATTGGCTTTCACCCTTGCCAGCCGTTTCGATTTCGGATATCACTGATACTGCCGTTCCGCTGGACAGCTTGC
TTATCACTTTTCCTTGTGTAGACGCCTTGTCTCGGACATTTCAGCGAGGATCCAGAGTCGACTTTACATATTT
GGTAACCGGNTTGGCCGACGGTTTTGGTGTACCTGTGCTGGCTGACGGCTTGCTTGATGACAAATATTGTGAA
CTTACGTAGCCTGTTTTG

>Bacillus_Fam_782_237_1 Nr. of seq. 1 Alignment length(with gaps) = 237
Alignment score = 0.000000
GCF_001315065.1_ASM131506v1_genomic.fna_1:413-1597 Satlength=1185 Nr of
Repeats=5 RepeatLength=237 seed=TATACGTTTG Num.seqs=4
Similarity=0.781528

0
TATACGTTTGTTGGCTGGAACACCGAAGCGGATGGAAGTGGTGAAACCTATAAAGAGGGTGACACGTTTACCC
AAGGAATAGGAAATGTGACGTTCTATGCGCAGTGGTCTGTAAATCACTACGAGCTGCGATATGACGGGAACGG
GCAAGATGGAGGAAGTGCGCCAGAAGCGGAATCTGTTGCGTATGGAAGTGAAGTGGAGGTATCGGATTCTCAA
ACGTTAAGCCGAACCGGT

Consensus :

TATACGTTTGTTGGCTGGAACACCGAAGCGGATGGAAGTGGTGAAACCTATAAAGAGGGTGACACGTTTACCC
AAGGAATAGGAAATGTGACGTTCTATGCGCAGTGGTCTGTAAATCACTACGAGCTGCGATATGACGGGAACGG

GCAAGATGGAGGAAGTGCGCCAGAAGCGGAATCTGTTGCGTATGGAAGTGAAGTGGAGGTATCGGATTCTCAA
ACGTTAAGCCGAACCGGT

>Bacillus_Fam_783_234_1 Nr. of seq. 1 Alignment length(with gaps) = 234
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_7:32135-33194 Satlength=1060 Nr of
Repeats=5 RepeatLength=234 seed=TTACTTTTTC Num.seqs=4
Similarity=0.888889
0

TTACTTTTCTCCGTTTTTTTAAATTTCCGAGAATTGCACTATTTGTATTTGCTTGACTTCTTACTCGCAGGCT
CGTTGCGTTGATTGTTCCGCTTTCTTGTAATCCATTTGTGATGTCTTCAACTGGCTTTTCTTCTGTTTCCCA
GCTTCTAGCTTCACAACTCTAACGATACGTAACCTTCTTTTCTTTATAATTGATCTTCGCCCAGCCGTTTG
CTTTTCCTAAGATTG

Consensus:

TTACTTTTCTCCGTTTTTTTAAATTTCCGAGAATTGCACTATTTGTATTTGCTTGACTTCTTACTCGCAGGCT
CGTTGCGTTGATTGTTCCGCTTTCTTGTAATCCATTTGTGATGTCTTCAACTGGCTTTTCTTCTGTTTCCCA
GCTTCTAGCTTCACAACTCTAACGATACGTAACCTTCTTTTCTTTATAATTGATCTTCGCCCAGCCGTTTG
CTTTTCCTAAGATTG

>Bacillus_Fam_784_232_1 Nr. of seq. 1 Alignment length(with gaps) = 232
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:577590-580142
Satlength=2553 Nr of Repeats=11 RepeatLength=232 seed=TTCCATTTGA
Num.seqs=11 Similarity=0.994984 0

TTCCATTTGACTCCTCTGTGTTAGACGGAGAAATTCCGTTTATCTCGGGAAATACTACTATTTCCCTTGAATT
AAGGGAAGCTTTTCCGCTTATATGATCCAAATCCTTGGATTTTGCCTTTTTTGAAGGTAGTAAGCGGAATTC
TACCCTTATATCTCCCCTTTAAGCCGCAAAATTTTCATTAGACGGAAATTCCTCGCTTATGCTTCTCCACCTT
ATCCTTTGGCAAC

Consensus:

TTCCATTTGACTCCTCTGTGTTAGACGGAGAAATTCCGTTTATCTCGGGAAATACTACTATTTCCCTTGAATT
AAGGGAAGCTTTTCCGCTTATATGATCCAAATCCTTGGATTTTGCCTTTTTTGAAGGTAGTAAGCGGAATTC
TACCCTTATATCTCCCCTTTAAGCCGCAAAATTTTCATTAGACGGAAATTCCTCGCTTATGCTTCTCCACCTT
ATCCTTTGGCAAC

>Bacillus_Fam_785_231_1 Nr. of seq. 1 Alignment length(with gaps) = 231
Alignment score = 0.000000
GCF_000334155.1_L1_genomic.fna_143:18667-20053 Satlength=1387 Nr of
Repeats=6 RepeatLength=231 seed=GAAAAACTTG Num.seqs=6
Similarity=0.992304
0

GAAAAACTTGTTGCCGCTAGATTTTCTGTAAATTGCCCTCTTTACTTGTCATTTGCTGTCTTTCCATTCGAA
GATAGCAGTTCAGCGGCAGCCTTAGCTTTTTCTTACCTCCCTTCAGCCACGCTCTTTACCCCTTAATAATGG

TTGTTCAAGAAAAACAAGCCTGTTTTTCCACCTCTCTTTATGACAGGGAGGAATCACTTCTCTTTTTGCCTTC
AACCTTTATTTTC

Consensus:

GAAAAACTTGGTTGCCGCTAGATTTTCTGTAAATTGCCCTCTTTACTTGTTCATTTGCTGTCTTTCCATTTCGAA
GATAGCAGTTTCAGCGGCAGCCTTAGCTTTTTCTTACCTCCCTTCAGCCACGCTCTTTCACCCTTAATAATGG
TTGTTCAAGAAAAACAAGCCTGTTTTTCCACCTCTCTTTATGACAGGGAGGAATCACTTCTCTTTTTGCCTTC
AACCTTTATTTTC

>Bacillus_Fam_786_231_1 Nr. of seq. 1 Alignment length(with gaps) = 231
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:4450455-4451425 Satlength=971
Nr of Repeats=5 RepeatLength=231 seed=GTTGTCGATA Num.seqs=4
Similarity=0.870130 0
GTTGTCGATAAATATTTAGTACTGACATATCCTTCTTTTCCATTAGCTTTGATCTTCGCCCAACCTTTAGATT
CCGAATACACCGTTACCTGCATGCCTTTTCGAAAGCTTCGCAACTATGCTGGCAGTTTCCGTCCCACCTTTTTCG
CATATTGAGCGTCCCAGAACTTACATTTACATATTTTCGTTCGTTCGTTTAAACAGGGGTGGATGGTGTGGAACCC
GTTACAGGCTTC

Consensus:

GTTGTCGATAAATATTTAGTACTGACATATCCTTCTTTTCCATTAGCTTTGATCTTCGCCCAACCTTTAGATT
CCGAATACACCGTTACCTGCATGCCTTTTCGAAAGCTTCGCAACTATGCTGGCAGTTTCCGTCCCACCTTTTTCG
CATATTGAGCGTCCCAGAACTTACATTTACATATTTTCGTTCGTTCGTTTAAACAGGGGTGGATGGTGTGGAACCC
GTTACAGGCTTC

>Bacillus_Fam_787_230_1 Nr. of seq. 1 Alignment length(with gaps) = 230
Alignment score = 0.000000
GCF_000334155.1_L1_genomic.fna_48:14925-15845 Satlength=921 Nr of
Repeats=4 RepeatLength=230 seed=GAACAACCAT Num.seqs=4
Similarity=0.993237
0
GAACAACCATTTATGAAGGGTGAGAGAGGGGAAAAGTTTGGGAAGTAAGAAAAGCTAAGGGCTCTGCCGAACTTC
CGTCTTTGAAGGGAGGAAAGAGGACTTCGAAAAGAATGCACTCTTTAAAAAGAATCTGGCAGAGCCCAAGCTT
TGAAACAGAGGTTTATAAGGTCTGAAAAAGAGCGCCCTCCCTATCATAAAGAGGGGAGGAAAAACAGCGGT
CTGTTTTTCTC

Consensus:

GAACAACCATTTATGAAGGGTGAGAGAGGGGAAAAGTTTGGGAAGTAAGAAAAGCTAAGGGCTCTGCCGAACTTC
CGTCTTTGAAGGGAGGAAAGAGGACTTCGAAAAGAATGCACTCTTTAAAAAGAATCTGGCAGAGCCCAAGCTT

TGAAACAGAGGTTTATAAGGTCTGAAAAAGAGCGCCCCTCCCCTATCATAAAGAGGGGAGGAAAAACAGCGGT
CTGTTTTTCTC

>Bacillus_Fam_788_226_1 Nr. of seq. 1 Alignment length(with gaps) = 226
Alignment score = 0.000000
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_1:1737292-1738401 Satlength=1110 Nr of Repeats=5
RepeatLength=226 seed=ATTTACGTGC Num.seqs=3 Similarity=0.9724 0
ATTTACGTGCCGATTTGGCTTCTTTTCGGTCCGGAACGGAGCTCTTTCGTGCCGAAATCATCACTTTTCGAGC
GAGATTGGCGATTTTCGCGCCGGAGCTTAAATCTCTACGGTTCAACCACTTAATTACTATTTTTTTATGAACC
CCGTTGCTGTCCAGTTATGTTAGCTATGGCACATCAGCTAATGCACATGCACAAACCATCATTACGGGCCCG
ATTTCAA

Consensus:

ATTTACGTGCCGATTTGGCTTCTTTTCGGTCCGGAACGGAGCTCTTTCGTGCCGAAATCATCACTTTTCGAGC
GAGATTGGCGATTTTCGCGCCGGAGCTTAAATCTCTACGGTTCAACCACTTAATTACTATTTTTTTATGAACC
CCGTTGCTGTCCAGTTATGTTAGCTATGGCACATCAGCTAATGCACATGCACAAACCATCATTACGGGCCCG
ATTTCAA

>Bacillus_Fam_789_226_1 Nr. of seq. 1 Alignment length(with gaps) = 226
Alignment score = 0.000000
GCF_001274935.1_ASM127493v1_genomic.fna_27:538477-539381 Satlength=905 Nr
of Repeats=4 RepeatLength=226 seed=GCTTCGCTTT Num.seqs=4
Similarity=0.853314 0
GCTTCGCTTTCCTCGGGCGAGCGCTGAGCTTCCTCGTCGTTTCTCTCCTGCGGGATCTCACCTGTCTCGCTC
ATCCCGTAGGAGTCTTCTCATCTTTCACTGCCTTCCTTTGGTCTTTTCGACTAGGAAGTATTTAGTAGCCTGCT
TTTTGGAATGTGTATTTAGATAAGCTATGTTTATTCCACATGAAACACCCTTTACTTAGTCGGATTCCAGCT
CCAGATT

Consensus:

GCTTCGCTTTCCTCGGGCGAGCGCTGAGCTTCCTCGTCGTTTCTCTCCTGCGGGATCTCACCTGTCTCGCTC
ATCCCGTAGGAGTCTTCTCATCTTTCACTGCCTTCCTTTGGTCTTTTCGACTAGGAAGTATTTAGTAGCCTGCT
TTTTGGAATGTGTATTTAGATAAGCTATGTTTATTCCACATGAAACACCCTTTACTTAGTCGGATTCCAGCT
CCAGATT

>Bacillus_Fam_790_225_1 Nr. of seq. 1 Alignment length(with gaps) = 225
Alignment score = 0.000000
GCF_000011145.1_ASM1114v1_genomic.fna_1:3777785-3778688 Satlength=904 Nr
of Repeats=4 RepeatLength=225 seed=AAGCTTGATG Num.seqs=3
Similarity=0.854136 0
AAGCTTGATGAGGTTTTAAACGGGAAGTCTAGACCTGCCACTCTTCGCTTTGGTGACCGTCATCCGTACGTCA
TTCAGCTTAAAAAGATTTAGCTGAAGCAGGATTCCCGGTCTCCGGTAGCCCGACGGAGTATTTTGATCAGT
CACCGAATCCCAAGTCAAGGCTTTCCAACGAGCTCACGGACTTACTGCTAATGGCGTTGTCGGATCTGCTACT
TACGCA

Consensus:

AAGCTTGATGAGGTTTTAAACGGGAACCTCTAGACCTGCCACTCTTCGCTTTGGTGACCGTCATCCGTACGTCA
TTCAGCTTAAAAAAGATTTAGCTGAAGCAGGATTCCTCGGTCTCCGGTAGCCCCGACGGAGTATTTTGGATCAGT
CACCGAATCCCAAGTCAAGGCTTTCCAACGAGCTCACGGACTTACTGCTAATGGCGTTGTCGGATCTGCTACT
TACGCA

>Bacillus_Fam_791_222_1 Nr. of seq. 1 Alignment length(with gaps) = 222
Alignment score = 0.000000
GCF_001645705.1_ASM164570v1_genomic.fna_11:129111-130005 Satlength=895 Nr
of Repeats=4 RepeatLength=222 seed=TTATCCAAAC Num.seqs=3
Similarity=0.657698 0
TTATCCAAACTGATTAACCACGCAAAAACATATGAAAAGGATAAATATACCGAACTTCATACGGNGCNCTGC
AACAAGCAATTAGCCATGCNGAAGCAGTGGTACAAAATGCGAANACACAAGATGAAGTAACGGAAGCNATTAG
TCNTCTCCAAAAGCGATTAATGGATTAGAAAAAATAGCAGAACCAGAACCAGAANCTGAAGTAGATACGGGC
GAG

Consensus:

TTATCCAAACTGATTAACCACGCAAAAACATATGAAAAGGATAAATATACCGAACTTCATACGGNGCNCTGC
AACAAGCAATTAGCCATGCNGAAGCAGTGGTACAAAATGCGAANACACAAGATGAAGTAACGGAAGCNATTAG
TCNTCTCCAAAAGCGATTAATGGATTAGAAAAAATAGCAGAACCAGAACCAGAANCTGAAGTAGATACGGGC
GAG

>Bacillus_Fam_792_219_1 Nr. of seq. 1 Alignment length(with gaps) = 219
Alignment score = 0.000000
GCF_001484965.1_ASM148496v1_genomic.fna_12:79253-81209 Satlength=1957 Nr
of Repeats=8 RepeatLength=219 seed=GATGGGTTC Num.seqs=5
Similarity=0.860578 0
GATGGGTTCCTGCGGAGTACTTAAATGTCAGTGGGTCTGGGCAGCGATGCGAGTGAAGGGTCTTCCTCCATTGG
ATCGGCTACCACNACCGCAAGGCTTAACCTTCGCTCCGGTGCAGGGACTTCGAATCGTATTTTAACGACATTG
AACAACGGGCAGAACGTNGCCTTGCTTCAGAAACAAGGCAACTGGTATCAGGTAAAGCCGGTTCTCAGACGG

Consensus:

GATGGGTTCCTGCGGAGTACTTAAATGTCAGTGGGTCTGGGCAGCGATGCGAGTGAAGGGTCTTCCTCCATTGG
ATCGGCTACCACNACCGCAAGGCTTAACCTTCGCTCCGGTGCAGGGACTTCGAATCGTATTTTAACGACATTG
AACAACGGGCAGAACGTNGCCTTGCTTCAGAAACAAGGCAACTGGTATCAGGTAAAGCCGGTTCTCAGACGG

>Bacillus_Fam_793_214_1 Nr. of seq. 1 Alignment length(with gaps) = 214
Alignment score = 0.000000

GCF_002019645.1_ASM201964v1_genomic.fna_1:4390066-4391018 Satlength=953
Nr of Repeats=5 RepeatLength=214 seed=TCAGGGTAGA Num.seqs=3
Similarity=1.000000 0
TCAGGGTAGACCTTTATGCGAATAAGTATTGGCACCATGGAAGATGAAAAAGTTTTATACTCAGTGTGGAATG
AGCAGAGAGTCACCTGACTCCTGCGGGATCTAGCGGTCTCGTGAGACCCCGCAGGAGCCAAAAGCGACGAGGA
GGCTCACGGGGCGCCCCGCGGAAAGCAGGTGGATCGCAGCGAATGGAATCCACTATCTAAGTTATTT

Consensus:

TCAGGGTAGACCTTTATGCGAATAAGTATTGGCACCATGGAAGATGAAAAAGTTTTATACTCAGTGTGGAATG
AGCAGAGAGTCACCTGACTCCTGCGGGATCTAGCGGTCTCGTGAGACCCCGCAGGAGCCAAAAGCGACGAGGA
GGCTCACGGGGCGCCCCGCGGAAAGCAGGTGGATCGCAGCGAATGGAATCCACTATCTAAGTTATTT

>Bacillus_Fam_794_213_1 Nr. of seq. 1 Alignment length(with gaps) = 213
Alignment score = 0.000000
GCF_000009825.1_ASM982v1_genomic.fna_1:3219845-3221123 Satlength=1279 Nr
of Repeats=6 RepeatLength=213 seed=CGCCTTAACT Num.seqs=6
Similarity=0.931142 0
CGCCTTAACTTGCGTTCTGGAGCAGGCACTAACCATAGCATTATCACTACCCTTGCTAAAGGACAAAAAGTCG
AGTTGCTTAAAAAGCAAGGTGGCTGGTACCAAGTTAAAGCGGGCAACCGTACTGGATGGGTTTCTGTTGACTA
CTTAAATGTCAGCGGCTCTGGCAATGTGGACAACGCTCCTTCTAACGGCTCTGCCACAACCACTGCA

Consensus:

CGCCTTAACTTGCGTTCTGGAGCAGGCACTAACCATAGCATTATCACTACCCTTGCTAAAGGACAAAAAGTCG
AGTTGCTTAAAAAGCAAGGTGGCTGGTACCAAGTTAAAGCGGGCAACCGTACTGGATGGGTTTCTGTTGACTA
CTTAAATGTCAGCGGCTCTGGCAATGTGGACAACGCTCCTTCTAACGGCTCTGCCACAACCACTGCA

>Bacillus_Fam_795_213_1 Nr. of seq. 1 Alignment length(with gaps) = 213
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:414216-415493 Satlength=1278 Nr
of Repeats=6 RepeatLength=213 seed=CCACCAGAAA Num.seqs=5
Similarity=0.785426 0
CCACCAGAAAAAGAAGGCCATTCAATTCAAAGGATGGTATCAAGATGAGTTGCTCACAGAAGCGTGGGATTTTCG
AAACGAACACGGTTAGCGAAGATATGACCCTGTATGCAAAGTGGGAAATCAACGTTTATACTGTTAGTTTTGA
ATCGAATGGNGGCAGCCAAGTATCGGAAGTAGAAGCCGAGTATGGTTCGTCNATCACAGAGCCAGCT

Consensus:

CCACCAGAAAAAGAAGGCCATTCAATTCAAAGGATGGTATCAAGATGAGTTGCTCACAGAAGCGTGGGATTTTCG
AAACGAACACGGTTAGCGAAGATATGACCCTGTATGCAAAGTGGGAAATCAACGTTTATACTGTTAGTTTTGA
ATCGAATGGNGGCAGCCAAGTATCGGAAGTAGAAGCCGAGTATGGTTCGTCNATCACAGAGCCAGCT

>Bacillus_Fam_796_210_1 Nr. of seq. 1 Alignment length(with gaps) = 210
Alignment score = 0.000000

GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_41:390-1233 Satlength=844
Nr of Repeats=4 RepeatLength=210 seed=GACAAATCCGA Num.seqs=3
Similarity=0.763693 0
GACAATCCGAATGCTGNTTACGGTCCAACGACGACAACCTCGGGTGAAGGAATTCAGAAATATTATGGATTAG
TGGTCAACGGCATTGGTGATGAAGTAACACTTGCTAAAATTGAAGAGATTTTAGCATCNCCGCTCCAAAACGG
AGGCAGGCATGAAGACGTGATAGCGTTAAAGGAAAACCTTNTCTCGCCTCGGTTTCCATGTATCG

Consensus:

GACAATCCGAATGCTGNTTACGGTCCAACGACGACAACCTCGGGTGAAGGAATTCAGAAATATTATGGATTAG
TGGTCAACGGCATTGGTGATGAAGTAACACTTGCTAAAATTGAAGAGATTTTAGCATCNCCGCTCCAAAACGG
AGGCAGGCATGAAGACGTGATAGCGTTAAAGGAAAACCTTNTCTCGCCTCGGTTTCCATGTATCG

>Bacillus_Fam_797_208_1 Nr. of seq. 1 Alignment length(with gaps) = 208
Alignment score = 0.000000
GCF_000334155.1_L1_genomic.fna_10:13608-14440 Satlength=833 Nr of
Repeats=4 RepeatLength=208 seed=AGGGTGAGAG Num.seqs=4
Similarity=0.983974
0

AGGGTGAGAGAGGGAGGAGTTTGGGAGGTAAGAAAACTAAGGCCTCCGCCGATCTGCCGTCTTTGGTAAAGG
GAATCGGACAGTTTTTTAGGAGTGCTCTTCTTAACGGGATACAGGCAAGGTAGTGACGCTGAAAAACATCCCGA
TCCGCCCTGTCATAAAGAGCGGTGGAAGCAAGCTTGCTTTTCATGATTAACTTTATGAC

Consensus:

AGGGTGAGAGAGGGAGGAGTTTGGGAGGTAAGAAAACTAAGGCCTCCGCCGATCTGCCGTCTTTGGTAAAGG
GAATCGGACAGTTTTTTAGGAGTGCTCTTCTTAACGGGATACAGGCAAGGTAGTGACGCTGAAAAACATCCCGA
TCCGCCCTGTCATAAAGAGCGGTGGAAGCAAGCTTGCTTTTCATGATTAACTTTATGAC

>Bacillus_Fam_798_206_1 Nr. of seq. 1 Alignment length(with gaps) = 206
Alignment score = 0.000000
GCF_001274775.1_ASM127477v1_genomic.fna_6:313004-313829 Satlength=826 Nr
of Repeats=4 RepeatLength=206 seed=TCGTGCCTGC Num.seqs=3
Similarity=0.961165 0

TCGTGCCTGCGGGTCTCGGTCATCCCTCTTTTCCGAAGGAGTCCGGGCCCCCTTCGCTTCTTTTCACTCTTGG
TGATACTTTGATTCCCTTTTTTTCATTATTGTTTCCGCCTAGTTCGTTTTTGGTTCTGCTTCATTGGTGTGAT
GGATTGGGCGTTCCATCCCGCTGTGGGACCGCTTTTCTTGGGAGGGCGCCCGAGCCTCT

Consensus:

TCGTGCCTGCGGGTCTCGGTCATCCCTCTTTTCCGAAGGAGTCCGGGCCCCCTTCGCTTCTTTTCACTCTTGG
TGATACTTTGATTCCCTTTTTTTCATTATTGTTTCCGCCTAGTTCGTTTTTGGTTCTGCTTCATTGGTGTGAT
GGATTGGGCGTTCCATCCCGCTGTGGGACCGCTTTTCTTGGGAGGGCGCCCGAGCCTCT

>Bacillus_Fam_799_206_1 Nr. of seq. 1 Alignment length(with gaps) = 206
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:523574-525781
Satlength=2208 Nr of Repeats=11 RepeatLength=206 seed=AAAGAAAAGC
Num.seqs=10 Similarity=0.998706 0
AAAGAAAAGCGTAAACGCCCCGTTTAGCGACGTACAACTTTAATAATAAGGATGAACGGCTAAAGTCGCGCCG
TCCTGGCGCAACGCGGTTCTGACCAACGTCGTGTTGGCCCGAGATAAAGGAAACACAGCGAGGGACGAGCTGA
TGTTGACTTATCGTAGGAAGAAGCTGAAAGTTTGCTAGTCGTGGGCGTTGAAGCTGGAC

Consensus:

AAAGAAAAGCGTAAACGCCCCGTTTAGCGACGTACAACTTTAATAATAAGGATGAACGGCTAAAGTCGCGCCG
TCCTGGCGCAACGCGGTTCTGACCAACGTCGTGTTGGCCCGAGATAAAGGAAACACAGCGAGGGACGAGCTGA
TGTTGACTTATCGTAGGAAGAAGCTGAAAGTTTGCTAGTCGTGGGCGTTGAAGCTGGAC

>Bacillus_Fam_800_205_1 Nr. of seq. 1 Alignment length(with gaps) = 205
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:959082-960714 Satlength=1633 Nr
of Repeats=8 RepeatLength=204 seed=AAAGTGGAAG Num.seqs=8
Similarity=0.770301 0
AAAGTGGAAGATCTGTTACGAATGATAAGTTTCGACACATTGAAAGGAAGTACCGATCAAAGNGCGATTGATG
AAGCTCAAAAAGCNGTCAATAAACTTCCGGAAGGTCCAGAAAAAATCGNCTTGAANGATTTAGTGAACAAAG
CACAAGATCTATTAAATAAAAAAAAAACAAGCCGAAAAAGACTTGAACGATGCAAAGAAC

Consensus:

AAAGTGGAAGATCTGTTACGAATGATAAGTTTCGACACATTGAAAGGAAGTACCGATCAAAGNGCGATTGATG
AAGCTCAAAAAGCNGTCAATAAACTTCCGGAAGGTCCAGAAAAAATCGNCTTGAANGATTTAGTGAACAAAG
CACAAGATCTATTAAATAAAAAAAAAACAAGCCGAAAAAGACTTGAACGATGCAAAGAAC

>Bacillus_Fam_801_196_1 Nr. of seq. 1 Alignment length(with gaps) = 196
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:4043384-4044164 Satlength=781
Nr of Repeats=4 RepeatLength=195 seed=CGAATTAATA Num.seqs=4
Similarity=0.670875 0
CGAATTAATACGTGGATTGGACCGAAGTGGATCAAACCAAACAATCCACTAATAGGGGAACCAACTCCGATCT
CAACGAGGATNCACGATAACAGAAAATACCTATTTGCATAATCAACCGTGGAATAGTGCTAGAGAAGAAATGAAT
TTTTACGTCCGCAAACAGTGACAGCATTTGAAGAATGGAATGGATGGTAC

Consensus:

CGAATTAATACGTGGATTGGACCGAAGTGGATCAAACCAAACAATCCACTAATAGGGGAACCAACTCCGATCT
CAACGAGGATNCACGATAACAGAAAATACCTATTTGCATAATCAACCGTGGAATAGTGCTAGAGAAGAAATGAAT
TTTTACGTCCGCAAACAGTGACAGCATTTGAAGAATGGAATGGATGGTAC

>Bacillus_Fam_802_195_1 Nr. of seq. 1 Alignment length(with gaps) = 195
Alignment score = 0.000000
GCF_001274775.1_ASM127477v1_genomic.fna_6:301298-302231 Satlength=934 Nr
of Repeats=5 RepeatLength=195 seed=TCCATCACCA Num.seqs=3
Similarity=0.945299 0
TCCATCACCAAAAGTGCAATGCAGCGGAGACCGGCCGACTCCTTCGGAATAGAGTGAAGTTCGATACCCCG
GACGCGCAGCTGAGGAGGCTCGACTCACTCCCCGAGGAAAGCGGACGGCCGACGCGAAATGGAACGGACCTTG
ACTCCACCAAGATCCTCATCTAAAGCAGAAAGACATCATGCCTACCTCC

Consensus:

TCCATCACCAAAAGTGCAATGCAGCGGAGACCGGCCGACTCCTTCGGAATAGAGTGAAGTTCGATACCCCG
GACGCGCAGCTGAGGAGGCTCGACTCACTCCCCGAGGAAAGCGGACGGCCGACGCGAAATGGAACGGACCTTG
ACTCCACCAAGATCCTCATCTAAAGCAGAAAGACATCATGCCTACCTCC

>Bacillus_Fam_803_195_1 Nr. of seq. 1 Alignment length(with gaps) = 195
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:4034033-4035008 Satlength=976
Nr of Repeats=5 RepeatLength=195 seed=ATAATCAACC Num.seqs=5
Similarity=0.628407 0
ATAATCAACCATTTGCNAATACAAGAAGATCAGAAGTNTTACGTCCNCAAACGGTACAGGCAACAGGAGAATG
GAATGGCTGGTACCGAATTAATACATGGGTAGGACCAAAGTGGATTAAACCGTCGAATGCGATTGTAGGAGAA
ATTAAANAAATCTCGCAAANTATAACATTAACGCAAAATACGCATTTGC

Consensus:

ATAATCAACCATTTGCNAATACAAGAAGATCAGAAGTNTTACGTCCNCAAACGGTACAGGCAACAGGAGAATG
GAATGGCTGGTACCGAATTAATACATGGGTAGGACCAAAGTGGATTAAACCGTCGAATGCGATTGTAGGAGAA
ATTAAANAAATCTCGCAAANTATAACATTAACGCAAAATACGCATTTGC

>Bacillus_Fam_804_194_1 Nr. of seq. 1 Alignment length(with gaps) = 194
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_61:22691-23863 Satlength=1173 Nr
of Repeats=6 RepeatLength=195 seed=ACGTCGAATA Num.seqs=5
Similarity=0.575845 0
ACGTCGAATACACTAAGNCCGTTCCACTCGGATTGAGTTTGCTTATAAACACATCAAANTTCCGTTANAACCTT
TGATCATATGCTCCNGCGGTCGTTGGGAAATTGNTGATGTTGTATANCCNGTCACATACGCATTTCCATCCT
CATCGANNGCAATTCCATNTCCTNNATCANNATCACTTCNCCTAAAT

Consensus:

ACGTCGAATACACTAAGNCCGTTCCACTCGGATTGAGTTTGCTTATAAACACATCAAANTTCCGTTANAACCTT
TGATCATATGCTCCNGCGGTCGTTGGGAAATTGNTGATGTTGTATANCCNGTCACATACGCATTTCCATCCT
CATCGANNGCAATTCCATNTCCTNNATCANNATCACTTCNCCTAAAT

>Bacillus_Fam_805_190_1 Nr. of seq. 1 Alignment length(with gaps) = 190
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:2048397-2049156 Satlength=760
Nr of Repeats=4 RepeatLength=190 seed=TTAAATCAAA Num.seqs=3
Similarity=0.840023 0
TTAAATCAAAATTGGGATTGTACATAGANATANGCAGTGTCTAATCATCCTGCTGGGTTGATTTCGGTTGCA
GGCGCTCGCTTTCCGAGGCCTGCCGGGAGTCTCATCATAGTAAGCTCCTTCGGGGTTTCCATAAAGCCAGCTG
ATCCCGCAGGAGTCTCGCACCTTCCGCTCCAATCAACCTTTGAA

Consensus:

TTAAATCAAAATTGGGATTGTACATAGANATANGCAGTGTCTAATCATCCTGCTGGGTTGATTTCGGTTGCA
GGCGCTCGCTTTCCGAGGCCTGCCGGGAGTCTCATCATAGTAAGCTCCTTCGGGGTTTCCATAAAGCCAGCTG
ATCCCGCAGGAGTCTCGCACCTTCCGCTCCAATCAACCTTTGAA

>Bacillus_Fam_806_177_1 Nr. of seq. 1 Alignment length(with gaps) = 177
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:572602-573664 Satlength=1063 Nr
of Repeats=6 RepeatLength=177 seed=CAGAAACAAC Num.seqs=6
Similarity=0.773007 0
CAGAAACAACAAATGCTGAAGTAGTAGCAAAAACAGAAGCCATCCAAAAGCACTAGCAGGCTTAGAATTTGC
AGGCCAAAACAGCCTTAAATGCAGCAAAAGCAAAAGCTGAGGAAAAGCAAGAAGCCGACTACACATCTGAAAGC
TATAGCCCATTTAAAGCAGCATTAGAACTGC

Consensus:

CAGAAACAACAAATGCTGAAGTAGTAGCAAAAACAGAAGCCATCCAAAAGCACTAGCAGGCTTAGAATTTGC
AGGCCAAAACAGCCTTAAATGCAGCAAAAGCAAAAGCTGAGGAAAAGCAAGAAGCCGACTACACATCTGAAAGC
TATAGCCCATTTAAAGCAGCATTAGAACTGC

>Bacillus_Fam_807_172_1 Nr. of seq. 1 Alignment length(with gaps) = 172
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_6:82276-83300 Satlength=1025 Nr of
Repeats=6 RepeatLength=172 seed=TTACATATGG Num.seqs=5
Similarity=0.886364 0
TTACATATGGCTAGAGTAAAGCTTTGTGCGCTCTTTTACTTCGTCCATCATCGTTTGAATTTTTTGATCGTGT
AAAGCTTCGTTTTCAGAAAGCTTATCTTTTGAATCGTAATTTTAAAGAAAAAATTTGAAATATCATAATGT
AATCGCTCCTTTAGGTTGTTTTCGTA

Consensus:

TTACATATGGCTAGAGTAAAGCTTTGTGCGCTCTTTTACTTCGTCCATCATCGTTTGAATTTTTTGATCGTGT

AAAGCTTCGGTTTCAGAAAGCTTATCTTTTTGAATCGTAATTTTAAAAGAAAAAATTTGAAATATCATAATGT
AATCGCTCCTTTAGGTTGTTTTCGTA

>Bacillus_Fam_808_171_1 Nr. of seq. 1 Alignment length(with gaps) = 171
Alignment score = 0.000000

GCF_001274935.1_ASM127493v1_genomic.fna_19:74009-74687 Satlength=679 Nr
of Repeats=4 RepeatLength=171 seed=ATGTTGTTCC Num.seqs=3
Similarity=0.849253

0

ATGTTGTTCCACGATTGAAGTTGCGCTACGGTTACGCCGAATTTCACTGCAATTCCACTAAGTGTATCACCTG
ATTTAACGGTGTACGTGGATACGGTTGAATCGCCACCACCACTCGTAGGAGCTTTAACTTTCAAAACTTGTCC
AATCTTAATCACATCAGCGTTTGAG

Consensus:

ATGTTGTTCCACGATTGAAGTTGCGCTACGGTTACGCCGAATTTCACTGCAATTCCACTAAGTGTATCACCTG
ATTTAACGGTGTACGTGGATACGGTTGAATCGCCACCACCACTCGTAGGAGCTTTAACTTTCAAAACTTGTCC
AATCTTAATCACATCAGCGTTTGAG

>Bacillus_Fam_809_168_1 Nr. of seq. 1 Alignment length(with gaps) = 168
Alignment score = 0.000000

GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_1:2021519-2027779 Satlength=6261 Nr of
Repeats=38 RepeatLength=168 seed=TCTACCAATT Num.seqs=36 Similarity=0.77

0

TCTACCAATTTTAATNCCGAAAGTTCTTCCATCANTTCTTGATGTGTTTGTTTTAATTGTTCAAGTTCTTGGT
ACTGACTTTGTTCTTTCAANGTAGCINNCCGATAACTGTTGAGTACTTCTTCATATGATTGNTTTAATTTTTC
TAGTTCTTCGCTTTGGACTTGT

Consensus:

TCTACCAATTTTAATNCCGAAAGTTCTTCCATCANTTCTTGATGTGTTTGTTTTAATTGTTCAAGTTCTTGGT
ACTGACTTTGTTCTTTCAANGTAGCINNCCGATAACTGTTGAGTACTTCTTCATATGATTGNTTTAATTTTTC
TAGTTCTTCGCTTTGGACTTGT

>Bacillus_Fam_810_164_1 Nr. of seq. 1 Alignment length(with gaps) = 164
Alignment score = 0.000000

GCF_000177235.2_ASM17723v2_genomic.fna_1:4304399-4305217 Satlength=819 Nr
of Repeats=5 RepeatLength=164 seed=AACAGGGACG Num.seqs=3
Similarity=0.917172

0

AACAGGGACGGTTCTCACTTGCCAGTTTGATAGTTTTTTTATGATTTGGTCATAGTTATGTGCGATTTCTTTC
AAGTTACACGCGATTTTGATCGAGTTACGCGCGATTTACACGAGTTTGAAGCGATTTGGAAACCAACTGGAA
AAACACTTCAATTAGGCT

Consensus:

AACAGGGACGGTTCCTCACTTGCCAGTTTGATAGTTTTTTTTATGATTTGGTCATAGTTATGTGCGATTTCTTTC
AAGTTACACGCGATTTTGATCGAGTTACGCGCGATTTACACGAGTTTGAAGCGATTTGGAAACCAACTGGAA
AAACACTTCAATTAGGCT

>Bacillus_Fam_811_164_1 Nr. of seq. 1 Alignment length(with gaps) = 164
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_16:30431-31253 Satlength=823 Nr
of Repeats=5 RepeatLength=164 seed=GGTCACATTC Num.seqs=4
Similarity=0.967480

0
GGTCACATTCATGAGGTAAGATTTCAGCTTGTTTCAGTGATTTGATCACCGCACTCGGGACATTGTTTAGGTGG
TAGGGTTCTAAAGAACTCCAACGGATTTTTAGTTTGCATGATGGTTTCCTCCTTTAAATGGTTTAGTAGTCTT
CGCGTTTAGAAAGGCAGT

Consensus:

GGTCACATTCATGAGGTAAGATTTCAGCTTGTTTCAGTGATTTGATCACCGCACTCGGGACATTGTTTAGGTGG
TAGGGTTCTAAAGAACTCCAACGGATTTTTAGTTTGCATGATGGTTTCCTCCTTTAAATGGTTTAGTAGTCTT
CGCGTTTAGAAAGGCAGT

>Bacillus_Fam_812_156_1 Nr. of seq. 1 Alignment length(with gaps) = 156
Alignment score = 0.000000
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_4:22903-23527 Satlength=625 Nr of Repeats=4
RepeatLength=156 seed=ATAAAGTGAA Num.seqs=4 Similarity=0.968661 0
ATAAAGTGAATCTTCCATCAGTGAGGGTTTGCTTCATCCTCCACTGATGGTTAGTTGAACCAATCGGGGTTT
TACAGGCTGTTTTATCACTACACACTTCTCTCTATTTCTCCAACGAAAATGAAAGAGGGATTATTACAGCCTG
TTAAACCGGG

Consensus:

ATAAAGTGAATCTTCCATCAGTGAGGGTTTGCTTCATCCTCCACTGATGGTTAGTTGAACCAATCGGGGTTT
TACAGGCTGTTTTATCACTACACACTTCTCTCTATTTCTCCAACGAAAATGAAAGAGGGATTATTACAGCCTG
TTAAACCGGG

>Bacillus_Fam_813_156_1 Nr. of seq. 1 Alignment length(with gaps) = 156
Alignment score = 0.000000
GCF_001591585.1_ASM159158v1_genomic.fna_12:122004-122892 Satlength=889 Nr
of Repeats=6 RepeatLength=156 seed=TTCTTTCTTA Num.seqs=5
Similarity=0.862420 0

TTCTTTCTTAATAGTATTTTAAAGAATTAACAGAAGAACCAGCTTGCGTGACTACTTCCTTTACATTGAATGC
TTTTAGAGGATTTTGCTTTTAGTTGTACATCTTTTGATACAGCTTCTTTTTGTAAAGATAATACTTTGTTTCAT
TTCTCATTC

Consensus:

TTCTTTCTTAATAGTATTTTAAAGAATTAACAGAAGAACCAGCTTGCGTGACTACTTCCTTTACATTGAATGC
TTTGTAGAGGATTTTGCTTTTAGTTGTACATCTTTTGATACAGCTTCTTTTGTAAAGATAATACTTTGTTTCAT
TTCTCATTC

>Bacillus_Fam_814_156_1 Nr. of seq. 1 Alignment length(with gaps) = 156
Alignment score = 0.000000
GCF_001887185.1_ASM188718v1_genomic.fna_192:71627-72199 Satlength=573 Nr
of Repeats=5 RepeatLength=156 seed=ATTTGACTG Num.seqs=3
Similarity=0.723270 0
ATTTTGACTGGGGCGGGAACCTAAGGGTGCGGTTGATTACCGAGAAGGAAGAAATTCGGGGGTTTCGGGAAC
CTAAGGGAGGGTTTGGTTACCGGGATGGAGAAAAATGNCTGTGNTCGGTAACCTAAAGAGTGTGGTTGGTTACC
CTGGTGGGGA

Consensus:

ATTTTGACTGGGGCGGGAACCTAAGGGTGCGGTTGATTACCGAGAAGGAAGAAATTCGGGGGTTTCGGGAAC
CTAAGGGAGGGTTTGGTTACCGGGATGGAGAAAAATGNCTGTGNTCGGTAACCTAAAGAGTGTGGTTGGTTACC
CTGGTGGGGA

>Bacillus_Fam_815_156_1 Nr. of seq. 1 Alignment length(with gaps) = 156
Alignment score = 0.000000
GCF_002019595.1_ASM201959v1_genomic.fna_1:3715909-3716689 Satlength=781
Nr of Repeats=6 RepeatLength=156 seed=AAAAAGGACT Num.seqs=4
Similarity=0.764241 0
AAAAAGGACTGCCTGGCACTGGAGCAAACCCGCCTGAACCATTACCTAAAAAACCGAGACATCATCGGAACC
AAAGTTCACGACCGCAAGATCCATAATCCCGTCTCCATTAAAAATCTGCAGACGTGATGGAANTTGGACCCAAA
CCTCCACTAG

Consensus:

AAAAAGGACTGCCTGGCACTGGAGCAAACCCGCCTGAACCATTACCTAAAAAACCGAGACATCATCGGAACC
AAAGTTCACGACCGCAAGATCCATAATCCCGTCTCCATTAAAAATCTGCAGACGTGATGGAANTTGGACCCAAA
CCTCCACTAG

>Bacillus_Fam_816_155_1 Nr. of seq. 1 Alignment length(with gaps) = 155
Alignment score = 0.000000
GCF_000299035.1_ASM29903v1_genomic.fna_2:237491-238103 Satlength=613 Nr
of Repeats=4 RepeatLength=153 seed=CGCTTGCCAT Num.seqs=4
Similarity=0.618896 0
CGCTTGCCATTCGGACCACCACGTTTCTCCCAAATAGCAGCATAACGATCCTGACCATTACTACCGTAACCA
CTTACNTGCATATCAACCGATAGCCTTGCGCAACCAGTTCATTGAACGTCCGCTGATATTGCTCTGCTGTCAA
ACCATGTCG

Consensus:

CGCTTGCCATTCCGGACCACCACGTTTCTCCCAAATAGCAGCATAACGATCCTGACCATTACTACCGTAACCA
CTTACNTGCATATCAACCGATAGCCTTGCGCAACCAGTTCATTGAACGTCGCTGATATTGCTCTGCTGTCAA
ACCATGTCTG

>Bacillus_Fam_817_155_1 Nr. of seq. 1 Alignment length(with gaps) = 155
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:755995-757235 Satlength=1241 Nr
of Repeats=8 RepeatLength=155 seed=TGCTCTACCG Num.seqs=8
Similarity=0.986645 0
TGCTCTACCGACTGAGCTATCGAGCCATAATAATATTTAACTTACAACCTTTATACTCCACTTGCAAAACGTCC
TCTGTCCCTTCCTCTTCTAGCTTATTCTTTGATGCTTATGCGTCGGGACAACCTCGCAGCTGATTCGCTGATGT
GGTGCTCGT

Consensus:

TGCTCTACCGACTGAGCTATCGAGCCATAATAATATTTAACTTACAACCTTTATACTCCACTTGCAAAACGTCC
TCTGTCCCTTCCTCTTCTAGCTTATTCTTTGATGCTTATGCGTCGGGACAACCTCGCAGCTGATTCGCTGATGT
GGTGCTCGT

>Bacillus_Fam_818_155_1 Nr. of seq. 1 Alignment length(with gaps) = 155
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:4026577-4027197 Satlength=621 Nr
of Repeats=4 RepeatLength=155 seed=TTTGTGTAA Num.seqs=4
Similarity=0.853763 0
TTTGTGTAAACAAAAGCAGAAAAAACCATGCACAAATCCAGAATGCGCATGCATTTCAATTAATAGCTGAAGC
AAAGCCATGTGTAATATCCAGGACATGGAAGAAAAACCCATAAAGTCAGTTATAACAGTAAAAAAGTTCCACA
CCCGCATGA

Consensus:

TTTGTGTAAACAAAAGCAGAAAAAACCATGCACAAATCCAGAATGCGCATGCATTTCAATTAATAGCTGAAGC
AAAGCCATGTGTAATATCCAGGACATGGAAGAAAAACCCATAAAGTCAGTTATAACAGTAAAAAAGTTCCACA
CCCGCATGA

>Bacillus_Fam_819_154_1 Nr. of seq. 1 Alignment length(with gaps) = 154
Alignment score = 0.000000
GCF_900098925.1_PRJEB15625_genomic.fna_18:275436-276206 Satlength=771 Nr
of Repeats=5 RepeatLength=154 seed=GGTTCTCCTA Num.seqs=5
Similarity=0.977489 0
GGTTCTCTATATCTCGCTCGGCATCAGTCCAGGTCATACGGCGATGAACAGGACCCTTTTCGCTTTTTCGTTTT
TGTCCAGCAGCAGGGCCCTATCGCCTAGTGTCCTTCCCTTACCTCGGGTCGATAAGTCGAAAACGAAAGGAGA
GCCCTTTC

Consensus:

GGTTCCTCTATATCTCGCTCGGCATCAGTCCAGGTCATACGGCGATGAACAGGACCCTTTCGCTTTTCGTTTT
TGTCCAGCAGCAGGGCCCTATCGCCTAGTGTCTTCCCTTACCTCGGGTCGATAAGTCGAAAACGAAAGGAGA
GCCCTTTC

>Bacillus_Fam_820_153_1 Nr. of seq. 1 Alignment length(with gaps) = 153
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:4446177-4446943 Satlength=767 Nr
of Repeats=5 RepeatLength=153 seed=CTAGAAACT Num.seqs=4
Similarity=0.816198 0
CTAGAAACTCGTAAAACCCATGCGAATCTCACGGTTTCACATGGTTTTATCAAAAGATCTCAAGAAAAGCAT
GTGGAAGTGGAAAAGTTCTCAAATATTGACCGTTTTAGAGCTAGAATTTCAAACATATGGATGTTGCGCATG
CCATTTTC

Consensus:

CTAGAAACTCGTAAAACCCATGCGAATCTCACGGTTTCACATGGTTTTATCAAAAGATCTCAAGAAAAGCAT
GTGGAAGTGGAAAAGTTCTCAAATATTGACCGTTTTAGAGCTAGAATTTCAAACATATGGATGTTGCGCATG
CCATTTTC

>Bacillus_Fam_821_150_1 Nr. of seq. 1 Alignment length(with gaps) = 150
Alignment score = 0.000000
GCF_000238675.1_Baci_smit_7_3_47FAA_V1_genomic.fna_8:63370-64378
Satlength=1009 Nr of Repeats=5 RepeatLength=150 seed=TTCCGGCAAT
Num.seqs=3 Similarity=0.845926
0
TTCCGGCAATGAATTTTTAATGTGCTTCAAACCTCGATCGTCCACAAACACATCCGGAGTGGACAACGAAGTC
GAAAACAATGAGTTATAAGAATCTCCTCTCATCGGTTCAAAAATTTCTTTTGTACCGGGTTAGGAAGCACAT
AGTT

Consensus:

TTCCGGCAATGAATTTTTAATGTGCTTCAAACCTCGATCGTCCACAAACACATCCGGAGTGGACAACGAAGTC
GAAAACAATGAGTTATAAGAATCTCCTCTCATCGGTTCAAAAATTTCTTTTGTACCGGGTTAGGAAGCACAT
AGTT

>Bacillus_Fam_822_150_1 Nr. of seq. 1 Alignment length(with gaps) = 150
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_42:22825-23572 Satlength=748 Nr of
Repeats=5 RepeatLength=150 seed=TATGGTGGAT Num.seqs=4
Similarity=0.920000
0
TATGGTGGATTGGAGCAAACGGCTCAGTGCAAGGGGCTTATTGGTATGAAGGAATGGCACGACGAGAGAGTTA
TGAATTAGCACCAGCGGGAAGCGCTTCTACCAATGGAGGTATTGCAGCGGTGTCGAGAAGGCCAAACACTTTC
GAAC

Consensus:

TATGGTGGATTGGAGCAAACGGCTCAGTGCAAGGGGCTTATTGGTATGAAGGAATGGCAGCAGAGAGAGTTA
TGAATTAGCACCAGCGGGAAGCGCTTCTACCAATGGAGGTATTGCAGCGGTGTCGAGAAGGCCAAACACTTTC
GAAC

>Bacillus_Fam_823_150_1 Nr. of seq. 1 Alignment length(with gaps) = 150
Alignment score = 0.000000

GCF_000712615.1_ASM71261v1_genomic.fna_110:463-1366 Satlength=904 Nr of
Repeats=6 RepeatLength=150 seed=ACTACCCACA Num.seqs=5
Similarity=0.584458

0

ACTACCCACATAACGTTTACACGTCCNTGNTTATCTACGAAAAACAAATCAAGTTGCTCATCGGTTTGACGTG
CAGTTGCTNNNACCGNATCCAATGGAACGTAGTTNGGTGCAGTNAGAGGAATTGGTCCTTGCCAATTTCCGGT
TCCG

Consensus:

ACTACCCACATAACGTTTACACGTCCNTGNTTATCTACGAAAAACAAATCAAGTTGCTCATCGGTTTGACGTG
CAGTTGCTNNNACCGNATCCAATGGAACGTAGTTNGGTGCAGTNAGAGGAATTGGTCCTTGCCAATTTCCGGT
TCCG

>Bacillus_Fam_824_148_1 Nr. of seq. 1 Alignment length(with gaps) = 148
Alignment score = 0.000000

GCF_000161455.1_ASM16145v1_genomic.fna_1:395331-396141 Satlength=811 Nr
of Repeats=4 RepeatLength=148 seed=GAACTTTAA Num.seqs=3
Similarity=0.892593

0

GAACTTTAAAGCAGTAATGTAAGTTCATTATTCCGCAATTATTTATAAAAATTATCATACTTAATACGAA
AAAAGAGGAGGAAATCATATGGCAATCGCAATGGCAGTTTAAAAATTTGTAGGTGGAGCACTTCCATTAGTAC
AA

**

Consensus:

GAACTTTAAAGCAGTAATGTAAGTTCATTATTCCGCAATTATTTATAAAAATTATCATACTTAATACGAA
AAAAGAGGAGGAAATCATATGGCAATCGCAATGGCAGTTTAAAAATTTGTAGGTGGAGCACTTCCATTAGTAC
AA

>Bacillus_Fam_825_147_1 Nr. of seq. 1 Alignment length(with gaps) = 147
Alignment score = 0.000000

GCF_000430765.1_ASM43076v1_genomic.fna_6:140808-141395 Satlength=588 Nr
of Repeats=4 RepeatLength=147 seed=TTTTCTTTG Num.seqs=3
Similarity=0.877628

0

TTTTTCTTTGGTGGCTGCATCAAGATTTGCGAACATGCCGTGGCGTTCACCCTTTTCCGGAAGTGTTACACCA
AGCTTTTTCAGCTGGTCCTGTGCCTGGGTCTGTGTCTAGGGTGCCGGCCTTCAGCTTTTCCATAATCGCCCCGCG
C

*

Consensus:

TTTTTCTTTGGTGGCTGCATCAAGATTTGCGAACATGCCGTGGCGTTCACCCTTTTCCGGAAGTGTTACACCA
AGCTTTTTCAGCTGGTCCTGTGCCTGGGTCTGTGTCTAGGGTGCCGGCCTTCAGCTTTTCCATAATCGCCCCGCG
C

>Bacillus_Fam_826_144_1 Nr. of seq. 1 Alignment length(with gaps) = 144
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_14:117958-118822 Satlength=865 Nr
of Repeats=6 RepeatLength=144 seed=ATGAAATTAC Num.seqs=6
Similarity=0.946296 0
ATGAAATTACCGAGCTGACTAATCTCGATCCCTCAATGGAAGATACCAATTTGGATGAAGTGGCGTCTGTAAA
GGAAATCACTAATTCCATCGAGATTATTTCTACAAATGAAGATATCGAGACGATCGAAGGTGTCACTTCAC

Consensus:

ATGAAATTACCGAGCTGACTAATCTCGATCCCTCAATGGAAGATACCAATTTGGATGAAGTGGCGTCTGTAAA
GGAAATCACTAATTCCATCGAGATTATTTCTACAAATGAAGATATCGAGACGATCGAAGGTGTCACTTCAC

>Bacillus_Fam_827_143_1 Nr. of seq. 1 Alignment length(with gaps) = 143
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:919080-919888 Satlength=809 Nr
of Repeats=4 RepeatLength=143 seed=ACTTTTTCAG Num.seqs=3
Similarity=0.962704 0
ACTTTTTCAGTGCCCTTTTATTTGTATTGCAATGGCTACGTTTCGTTGCGCGCCTGATAGGATAAACCCACTCC
TATCAGGCTTTTAAACGATTGCAACGACTACGCACATTGCTTAGGGGCACTTCAAAAGTGAAAGAACACC

Consensus:

ACTTTTTCAGTGCCCTTTTATTTGTATTGCAATGGCTACGTTTCGTTGCGCGCCTGATAGGATAAACCCACTCC
TATCAGGCTTTTAAACGATTGCAACGACTACGCACATTGCTTAGGGGCACTTCAAAAGTGAAAGAACACC

>Bacillus_Fam_828_139_1 Nr. of seq. 1 Alignment length(with gaps) = 139
Alignment score = 0.000000
GCF_000334155.1_L1_genomic.fna_81:1145-1840 Satlength=696 Nr of Repeats=5
RepeatLength=139 seed=TTTTGTGGAA Num.seqs=5 Similarity=0.984652 0
TTTTGTGGAAAAGGGGACGGAGCTTACAGGATGATAAAGCAGGAAGCCTATCGCTCACACCCCTTCATTGAAA
GGTTACTCAGCGTTACTGGACGTACTCATTTTCATCCAGTGGAAGAGCGAGCCACTTATGCTAA

Consensus :

TTTTGTGGAAAAGGGGACGGAGCTTACAGGATGATAAAGCAGGAAGCCTATCGCTCACACCCCTTCATTGAAA
GGTTACTCAGCGTTACTGGACGTACTCATTTTCATCCAGTGGAAGAGCGAGCCACTTATGCTAA

>Bacillus_Fam_829_135_1 Nr. of seq. 1 Alignment length(with gaps) = 135
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_82:4706-5375 Satlength=670 Nr of
Repeats=5 RepeatLength=135 seed=GACGGTTCCC Num.seqs=3
Similarity=0.802469

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GACGGTTCCCGTGCCCTACACAGCAAATGTTAACAATGACACGGTTTCCGTGATCGGCACGGCCACGAATACTG
TCTTGACCACCATTTCGCTCGCTCCCGCAGGAAACGGTCCTNNTGCTATTGCCATCACGCCG

Consensus :

GACGGTTCCCGTGCCCTACACAGCAAATGTTAACAATGACACGGTTTCCGTGATCGGCACGGCCACGAATACTG
TCTTGACCACCATTTCGCTCGCTCCCGCAGGAAACGGTCCTNNTGCTATTGCCATCACGCCG

>Bacillus_Fam_830_132_1 Nr. of seq. 1 Alignment length(with gaps) = 132
Alignment score = 0.000000
GCF_000225265.1_ASM22526v1_genomic.fna_2:43307-43811 Satlength=505 Nr of
Repeats=4 RepeatLength=126 seed=CATCAATGAC Num.seqs=4
Similarity=0.431287

0
CATCAATGACAGAAACNGTATCACTATTTTCNTCATTAGCTACATAAATACGATTATTAGAGGGATTAACACC
TACATCAGAAGGCTGANTCTCCGACAGGTACTATTCCAATAACAGCATTTGTNNACCTG

Consensus :

CATCAATGACAGAAACNGTATCACTATTTTCNTCATTAGCTACATAAATACGATTATTAGAGGGATTAACACC
TACATCAGAAGGCTGANTCTCCGACAGGTACTATTCCAATAACAGCATTTGTNNACCTG

>Bacillus_Fam_831_132_1 Nr. of seq. 1 Alignment length(with gaps) = 132
Alignment score = 0.000000
GCF_001590785.1_ASM159078v1_genomic.fna_20:27981-28774 Satlength=794 Nr
of Repeats=5 RepeatLength=132 seed=TTTTCTTCCC Num.seqs=3
Similarity=0.673300

0
TTTTCTTCCCAGAACAATTGAATTTGCTCCAATGCTCCAGAAATAATCTCACTTATAAATGCCATTGCCTCTG
AAATAATGGTCCCTACAACCTCCATCGTACTAGTCAATATTTCCATTATCCATGTGCCG

Consensus :

TTTTCTTCCCAGAACAATTGAATTTGCTCCAATGCTCCAGAAATAATCTCACTTATAAATGCCATTGCCTCTG
AAATAATGGTCCCTACAACCTCCATCGTACTAGTCAATATTTCCATTATCCATGTGCCG

>Bacillus_Fam_832_132_1 Nr. of seq. 1 Alignment length(with gaps) = 132
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:1113610-1114144 Satlength=535
Nr of Repeats=4 RepeatLength=132 seed=TCGCGGGGTG Num.seqs=3
Similarity=0.993266 0
TCGCGGGGTGGAGCATGGAGCAAAGCTTCTTGATTTTACATCGACATGTCGTGACGCATCAAGCTACAAAGCG
TTACGAGAAGAGGAAACGATGACCTCTTAGAAAAAACATCATCTGTAAGCTATATAACG

Consensus:

TCGCGGGGTGGAGCATGGAGCAAAGCTTCTTGATTTTACATCGACATGTCGTGACGCATCAAGCTACAAAGCG
TTACGAGAAGAGGAAACGATGACCTCTTAGAAAAAACATCATCTGTAAGCTATATAACG

>Bacillus_Fam_833_131_1 Nr. of seq. 1 Alignment length(with gaps) = 131
Alignment score = 0.000000
GCF_001590785.1_ASM159078v1_genomic.fna_4:31738-32230 Satlength=493 Nr of
Repeats=4 RepeatLength=123 seed=CATTAAACCA Num.seqs=4
Similarity=0.312261
0

CATTAAACCATNNACTTAAGANTAGCCCATTTGTTCCATNACCTAATCCTTTACAGCATCCACCCATCTGAAA
GCCAGTCCNANNGTTGTCAAATNTCAACATCTTCCTATAATGGCTCCCATACAGTTT

Consensus:

CATTAAACCATNNACTTAAGANTAGCCCATTTGTTCCATNACCTAATCCTTTACAGCATCCACCCATCTGAAA
GCCAGTCCNANNGTTGTCAAATNTCAACATCTTCCTATAATGGCTCCCATACAGTTT

>Bacillus_Fam_834_129_1 Nr. of seq. 1 Alignment length(with gaps) = 129
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_35:27208-27724
Satlength=517 Nr of Repeats=4 RepeatLength=129 seed=TTTTGAACA
Num.seqs=4 Similarity=0.613946 0
TTTTTGAACAATCACGAAACGATGAGCGAACAGCCGCAACGCTTTTAAGCCAGTCATGAACGCATTTGTCATG
ATTGGCGAGCGGGGAGGAAGCCATCGTCCTACAAATAAAAAAGGGCGCTTTTCCC

Consensus:

TTTTTGAACAATCACGAAACGATGAGCGAACAGCCGCAACGCTTTTAAGCCAGTCATGAACGCATTTGTCATG
ATTGGCGAGCGGGGAGGAAGCCATCGTCCTACAAATAAAAAAGGGCGCTTTTCCC

>Bacillus_Fam_835_128_1 Nr. of seq. 1 Alignment length(with gaps) = 128
Alignment score = 0.000000
GCF_000615945.1_ASM61594v1_genomic.fna_82:23663-24293 Satlength=631 Nr of
Repeats=4 RepeatLength=126 seed=TGGTTTACAG Num.seqs=3
Similarity=0.464869
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TGGTTTACAGAAATACAGGTAACAAAATAGGAAGAATNNCAACGGANGGTGAAATTACAGAATATNATATNC
CTACNNCAGATGCAGGTGCNTATNGATTATAGCNNNAGGTNCTGATGGTGCAC TN

Consensus :

TGGTTTACAGAAATACAGGTAACAAAATAGGAAGAATNNCAACGGANGGTGAAATTACAGAATATNATATNC
CTACNNCAGATGCAGGTGCNTATNGATTATAGCNNNAGGTNCTGATGGTGCAC TN

>Bacillus_Fam_836_127_1 Nr. of seq. 1 Alignment length(with gaps) = 127
Alignment score = 0.000000

GCF_000025825.1_ASM2582v1_genomic.fna_7:28124-28628 Satlength=505 Nr of
Repeats=4 RepeatLength=126 seed=TTTCTGTAA T Num.seqs=4
Similarity=0.602865

0

TTTCTGTAA TTGATGGGTTAACAAATACTGTAATTGCCACGATTCCAGTAGGAACTCAACCGACCGGTATAG
AGATCAATCCATACATCAATCGAATTTATATAACAAATAGAGGTAGTAATACAG

Consensus :

TTTCTGTAA TTGATGGGTTAACAAATACTGTAATTGCCACGATTCCAGTAGGAACTCAACCGACCGGTATAG
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>Bacillus_Fam_837_127_1 Nr. of seq. 1 Alignment length(with gaps) = 127
Alignment score = 0.000000

GCF_900107275.1_IMG-

taxon_2675903024_annotated_assembly_genomic.fna_38:105111-105565

Satlength=455 Nr of Repeats=4 RepeatLength=127 seed=CGTCGTTTTT

Num.seqs=3 Similarity=0.979003 0

CGTCGTTTTTCCAAAAGGGAAATGCGCCCTTTTATTTTAGTTTACGATGGCTCGCTTTTGTGCGACGTCGGTT
ATGACAAATGCGCTCATAACCTACTTAAAAAACGCGACAGCTCCCTCATCGTAC

Consensus :

CGTCGTTTTTCCAAAAGGGAAATGCGCCCTTTTATTTTAGTTTACGATGGCTCGCTTTTGTGCGACGTCGGTT
ATGACAAATGCGCTCATAACCTACTTAAAAAACGCGACAGCTCCCTCATCGTAC

>Bacillus_Fam_838_126_1 Nr. of seq. 1 Alignment length(with gaps) = 126
Alignment score = 0.000000

GCF_001636345.1_ASM163634v1_genomic.fna_1:2067064-2067694 Satlength=631

Nr of Repeats=5 RepeatLength=126 seed=GATGTTGAAG Num.seqs=5

Similarity=0.789418 0

GATGTTGAAGCATTAACAACAGAAAAAGAAGCTGTATCTTCTTCATNCTGAAGGAAAAGAAACACACGATT
CAGTAAGCAAGGAAGAGAAAGCATCATCTCTAGTTGATGTAAGCGGACTTA

Consensus :

GATGTTGAAGCATTAACAACAGAAAAAGAAGCTGTATCTTCTTCATNCTGAAGGAAAAGAAACACACGATT
CAGTAAGCAAGGAAGAGAAAGCATCATCTCTAGTTGATGTAAAAGCGGACTTA

>Bacillus_Fam_839_125_1 Nr. of seq. 1 Alignment length(with gaps) = 125
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:4638716-4643591 Satlength=4876
Nr of Repeats=39 RepeatLength=125 seed=AGCGCCCTCC Num.seqs=39
Similarity=0.991795 0
AGCGCCCTCCGCATTTTCCTTGTCCAGCTTCGGGCGCTATCGGCTCGAGGGCAAATGCCCAGATGCCCCAAGAGG
TGGAAGAGCGATCTTCCGTGTCATCTGGGCTTTGGCTGGTCGCCGATGGGCC

Consensus:

AGCGCCCTCCGCATTTTCCTTGTCCAGCTTCGGGCGCTATCGGCTCGAGGGCAAATGCCCAGATGCCCCAAGAGG
TGGAAGAGCGATCTTCCGTGTCATCTGGGCTTTGGCTGGTCGCCGATGGGCC

>Bacillus_Fam_840_124_1 Nr. of seq. 1 Alignment length(with gaps) = 124
Alignment score = 0.000000
GCF_000429725.1_ASM42972v1_genomic.fna_10:14934-15732 Satlength=799 Nr of
Repeats=5 RepeatLength=124 seed=GAACGTCCGA Num.seqs=3
Similarity=0.956989
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GAACGTCCGAGCCGGCCGGCGGAGTGTCCGCCCAGCGCCGGAGTGACCGCTTTGCTCTTCGATGTGACCGCTC
ACCTCCTCCGAAGCGCCGTCCGCGGCCGCCTTCCGACCGCTTTTCCCGGCC

Consensus:

GAACGTCCGAGCCGGCCGGCGGAGTGTCCGCCCAGCGCCGGAGTGACCGCTTTGCTCTTCGATGTGACCGCTC
ACCTCCTCCGAAGCGCCGTCCGCGGCCGCCTTCCGACCGCTTTTCCCGGCC

>Bacillus_Fam_841_124_1 Nr. of seq. 1 Alignment length(with gaps) = 124
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_48:14425-15293 Satlength=869 Nr of
Repeats=7 RepeatLength=124 seed=GGAAGCGCCT Num.seqs=7
Similarity=0.996928
0
GGAAGCGCCTTGGTCAGACCCGACCAGCATAAGTCGCTCCAGGATAGAAGGCGTCCTTTGCCTTCAATCCTGG
AGTGGCTTATGACTCGAGGGTCTAGGCGCTGGAGCTGGACAATCGAAAAGC

Consensus:

GGAAGCGCCTTGGTCAGACCCGACCAGCATAAGTCGCTCCAGGATAGAAGGCGTCCTTTGCCTTCAATCCTGG
AGTGGCTTATGACTCGAGGGTCTAGGCGCTGGAGCTGGACAATCGAAAAGC

>Bacillus_Fam_842_123_1 Nr. of seq. 1 Alignment length(with gaps) = 123
Alignment score = 0.000000

GCF_000986785.1_ASM98678v1_genomic.fna_50:5702-6836 Satlength=1135 Nr of Repeats=9 RepeatLength=123 seed=GCTTCCGCTT Num.seqs=8
Similarity=0.997290
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GCTTCCGCTTTTCTTATTGTCCAGCTGCAGCGGCTAGCCCCCTCGAGACACTTCGGTCCATCACCTGAAGGCAA
AGAACGCCTTCAACTGCTGGCCCTCCAGTGCTTTTCGGGGCTGGACAGCC

Consensus:

GCTTCCGCTTTTCTTATTGTCCAGCTGCAGCGGCTAGCCCCCTCGAGACACTTCGGTCCATCACCTGAAGGCAA
AGAACGCCTTCAACTGCTGGCCCTCCAGTGCTTTTCGGGGCTGGACAGCC

>Bacillus_Fam_843_122_1 Nr. of seq. 1 Alignment length(with gaps) = 122
Alignment score = 0.000000

GCF_000708755.2_ASM70875v2_genomic.fna_2:743902-744385 Satlength=484 Nr of Repeats=4 RepeatLength=122 seed=CGAAAAGCGG Num.seqs=3
Similarity=0.729391
0

CGAAAAGCGGAAGCGCTCGTTTAGCTCCGGGAGTCAGATAAGGAAGTGGCGGAAAAGGCGCTTTTTGCCTTTN
CNGACAATTCGGTTCTGACAGAGGAGCTGAGCGCTGGAGCTAGACAATG

Consensus:

CGAAAAGCGGAAGCGCTCGTTTAGCTCCGGGAGTCAGATAAGGAAGTGGCGGAAAAGGCGCTTTTTGCCTTTN
CNGACAATTCGGTTCTGACAGAGGAGCTGAGCGCTGGAGCTAGACAATG

>Bacillus_Fam_844_122_1 Nr. of seq. 1 Alignment length(with gaps) = 122
Alignment score = 0.000000

GCF_000709935.2_ASM70993v2_genomic.fna_5:41241-41730 Satlength=490 Nr of Repeats=4 RepeatLength=122 seed=CGAAAAGCGG Num.seqs=3
Similarity=0.704000
0

CGAAAAGCGGAGCCGACTGTTCAGTCCTNTCAGTCAGATAAGAAATCACCGGAAAAGTCCGGTTTTGACTTTT
TCGGGGATTTTGTTCAGACAAGGACTAGGAGGCGGAGCTGGACAATG

Consensus:

CGAAAAGCGGAGCCGACTGTTCAGTCCTNTCAGTCAGATAAGAAATCACCGGAAAAGTCCGGTTTTGACTTTT
TCGGGGATTTTGTTCAGACAAGGACTAGGAGGCGGAGCTGGACAATG

>Bacillus_Fam_845_122_1 Nr. of seq. 1 Alignment length(with gaps) = 122
Alignment score = 0.000000

GCF_001636425.1_ASM163642v1_genomic.fna_1:3988479-3988970 Satlength=492
Nr of Repeats=4 RepeatLength=122 seed=GCATCATTTCT Num.seqs=3
Similarity=0.775986
0

GCATCATTTCTTTGTTTCCATTGGTTGTTGTTTCATAAAAGCAACATCTCCTTTGGGTCATGAGAATGGTTTAT
ACTTATTAGNTTACAGGTATTCATNTTTAGTCGCCGGGACTAAAAACN

Consensus:

GCATCATCTCTTGTTCATTGGTTGTTGTTTCATAAAAGCAACATCTCCTTTGGGTCATGAGAATGGTTTAT
ACTTATTAGNTTACAGGTATTCCATNTTTAGTCGCCGGGACTAAAAACN

>Bacillus_Fam_846_121_1 Nr. of seq. 1 Alignment length(with gaps) = 121
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_142:19481-19965 Satlength=485 Nr
of Repeats=4 RepeatLength=121 seed=GAAATTCGCC Num.seqs=4
Similarity=0.970615

0

GAAATTCGCCGCAATCTCTCCTCCCCTGACGAACGAGAAGCAAGAAGTTCAAGGAGATGAGAGAGAGAGGACC
GGAGCGTATCTATAATACGTGAGGATCCGAGCGAGCGAAATCGACGCA

Consensus:

GAAATTCGCCGCAATCTCTCCTCCCCTGACGAACGAGAAGCAAGAAGTTCAAGGAGATGAGAGAGAGAGGACC
GGAGCGTATCTATAATACGTGAGGATCCGAGCGAGCGAAATCGACGCA

>Bacillus_Fam_847_120_1 Nr. of seq. 1 Alignment length(with gaps) = 120
Alignment score = 0.000000

GCF_000161455.1_ASM16145v1_genomic.fna_1:886062-886479 Satlength=418 Nr
of Repeats=4 RepeatLength=120 seed=TGGTATTACT Num.seqs=3
Similarity=0.861566

0

TGGTATTACTTTGAGAGTAATGGCGTAATGAAAACAGATTGGTATTTTGATGGAACGAATTGGTTTTATATGA
ATAGCAATGGTGGAATGGAGACAGGATGGAAAAAGATTCAAGGAACG

Consensus:

TGGTATTACTTTGAGAGTAATGGCGTAATGAAAACAGATTGGTATTTTGATGGAACGAATTGGTTTTATATGA
ATAGCAATGGTGGAATGGAGACAGGATGGAAAAAGATTCAAGGAACG

>Bacillus_Fam_848_120_1 Nr. of seq. 1 Alignment length(with gaps) = 120
Alignment score = 0.000000

GCF_000169195.2_ASM16919v2_genomic.fna_1:2868366-2869215 Satlength=850 Nr
of Repeats=4 RepeatLength=120 seed=GAAGAAATCG Num.seqs=3
Similarity=0.595556

0

GAAGAAATCGATGTGATTCTTTCCANGAAACCGACAATGCCGGGCAACGCGAAAAGCTGCCATCAGATGCGG
AAAATGAAACAGTTGGCGGTGCGANAGGTGAAGACACAGACGAACCG

Consensus:

GAAGAAATCGATGTGATTCTTTCCANGAAACCGACAATGCCGGGCAACGCGAAAAGCTGCCATCAGATGCGG
AAAATGAAACAGTTGGCGGTGCGANAGGTGAAGACACAGACGAACCG

>Bacillus_Fam_849_118_1 Nr. of seq. 1 Alignment length(with gaps) = 118
Alignment score = 0.000000
Bacillus_murimartini_genomic.fna_9:918630-919220 Satlength=591 Nr of
Repeats=5 RepeatLength=118 seed=GCTTATAAGA Num.seqs=5
Similarity=0.995480 0
GCTTATAAGAAACCTCGCCTTTTTGAACTGCGCCGTGCTGTAGCAGCTGGCGGCCATTAATCTCATATAGCAT
TTGACATCTAGTACTCTATTTTAGGAGGGATGCTCAATGAAAAAA

Consensus:

GCTTATAAGAAACCTCGCCTTTTTGAACTGCGCCGTGCTGTAGCAGCTGGCGGCCATTAATCTCATATAGCAT
TTGACATCTAGTACTCTATTTTAGGAGGGATGCTCAATGAAAAAA

>Bacillus_Fam_850_116_1 Nr. of seq. 1 Alignment length(with gaps) = 116
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:1679718-1680414 Satlength=697 Nr
of Repeats=6 RepeatLength=116 seed=CAAAAGGTCG Num.seqs=6
Similarity=0.989272 0
CAAAAGGTCGAACCTTTACCTTTTGGGGATTTTACGTAACGAGAGCGAAGTCGTCACAAAGAAGAGCACAAATG
GAGTGAACCTCTCCATTAGTGCGAGTGACGAACGGAGCCTCGC

Consensus:

CAAAAGGTCGAACCTTTACCTTTTGGGGATTTTACGTAACGAGAGCGAAGTCGTCACAAAGAAGAGCACAAATG
GAGTGAACCTCTCCATTAGTGCGAGTGACGAACGGAGCCTCGC

>Bacillus_Fam_851_115_1 Nr. of seq. 1 Alignment length(with gaps) = 115
Alignment score = 0.000000
GCF_000751775.1_A1A_genomic.fna_102:38116-38692 Satlength=577 Nr of
Repeats=5 RepeatLength=115 seed=CTCATAGAAC Num.seqs=4
Similarity=0.868599 0
CTCATAGAACGGCTATATGAGACAAAATTAGTTGAAAATCAAGCCAAAATGTCCCATAGAATTGCCCGGATCC
CCTGCTATGGGACAAAACCAGCGGAAGCCGAAGCAAAAATGG

Consensus:

CTCATAGAACGGCTATATGAGACAAAATTAGTTGAAAATCAAGCCAAAATGTCCCATAGAATTGCCCGGATCC
CCTGCTATGGGACAAAACCAGCGGAAGCCGAAGCAAAAATGG

>Bacillus_Fam_852_114_1 Nr. of seq. 1 Alignment length(with gaps) = 114
Alignment score = 0.000000
GCF_000621445.1_ASM62144v1_genomic.fna_8:58648-59360 Satlength=713 Nr of
Repeats=4 RepeatLength=114 seed=AAAAGGTATA Num.seqs=3
Similarity=0.992203 0

AAAAGGTATAGGGCGACATTTTGGGTCGGGAGACGCTCGTTGCTCGCCATTTCAGAAGTACACTGAATGGCTTT
AAGAGCGGGCAACGGCTTTCCCCCTCTTACGAGAAAGAACC

Consensus:

AAAAGGTATAGGGCGACATTTTGGGTCGGGAGACGCTCGTTGCTCGCCATTTCAGAAGTACACTGAATGGCTTT
AAGAGCGGGCAACGGCTTTCCCCCTCTTACGAGAAAGAACC

>Bacillus_Fam_853_114_1 Nr. of seq. 1 Alignment length(with gaps) = 114
Alignment score = 0.000000
GCF_001274935.1_ASM127493v1_genomic.fna_37:230037-231096 Satlength=1060
Nr of Repeats=5 RepeatLength=114 seed=TTCTCTGTT Num.seqs=3
Similarity=0.937622 0
TTCTCTGTTCCTTCACTTTCCGACTCCGCTGTTTTTTCTCTTCTGCTTCGCGAGAGCCTGTGCTTTTGCCTTT
GCGGCTGCTGCGGCCTTTTTCTTCGCCAGGGCTAGTGCGTC

Consensus:

TTCTCTGTTCCTTCACTTTCCGACTCCGCTGTTTTTTCTCTTCTGCTTCGCGAGAGCCTGTGCTTTTGCCTTT
GCGGCTGCTGCGGCCTTTTTCTTCGCCAGGGCTAGTGCGTC

>Bacillus_Fam_854_114_1 Nr. of seq. 1 Alignment length(with gaps) = 114
Alignment score = 0.000000
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_28:73806-74259
Satlength=454 Nr of Repeats=4 RepeatLength=114 seed=CACTTGATTC
Num.seqs=3 Similarity=0.924638 0
CACTTGATTCATGGAAGAAGATGACTCCTCGTCTGAGACCTCCGAATCAATGCTACTGGATTCATCCGGTGA
GGGGGCAGAGTCATCGCAACAGGTAACCGTTTCATCCTCCA

Consensus:

CACTTGATTCATGGAAGAAGATGACTCCTCGTCTGAGACCTCCGAATCAATGCTACTGGATTCATCCGGTGA
GGGGGCAGAGTCATCGCAACAGGTAACCGTTTCATCCTCCA

>Bacillus_Fam_855_111_1 Nr. of seq. 1 Alignment length(with gaps) = 111
Alignment score = 0.000000
GCF_000334155.1_L1_genomic.fna_160:15-793 Satlength=779 Nr of Repeats=7
RepeatLength=111 seed=TGTGGCGGAA Num.seqs=6 Similarity=1.000000
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TGTGGCGGAATGGCAGACGCGCTAGACTTAGGATCTAGTGTCTTATGACGTGGGGGTTCAAGTCCCTTCACCC
GCACTTTGAATTTTATAGAGTGATGAAACTGAAGCGGT

Consensus:

TGTGGCGGAATGGCAGACGCGCTAGACTTAGGATCTAGTGTCTTATGACGTGGGGGTTCAAGTCCCTTCACCC
GCACTTTGAATTTTTAGAGTGATGAAAAGTGAAGCGGT

>Bacillus_Fam_856_111_1 Nr. of seq. 1 Alignment length(with gaps) = 111
Alignment score = 0.000000

GCF_001648575.1_ASM164857v1_genomic.fna_66:59259-59688 Satlength=430 Nr
of Repeats=4 RepeatLength=111 seed=TTGCTGCTG Num.seqs=3
Similarity=0.927928

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TTGCTGCTGCGGCGGCTTTCTTTTTGGCTAGCTCCTTGGCGTCATCTGTTTCGGTTGCTGGAGCTTCGCCTG
CTTCACTCTTTTGTTTTGCCAGTGCGGCAGCCTTTGCT

Consensus:

TTGCTGCTGCGGCGGCTTTCTTTTTGGCTAGCTCCTTGGCGTCATCTGTTTCGGTTGCTGGAGCTTCGCCTG
CTTCACTCTTTTGTTTTGCCAGTGCGGCAGCCTTTGCT

>Bacillus_Fam_857_111_1 Nr. of seq. 1 Alignment length(with gaps) = 111
Alignment score = 0.000000

GCF_900111815.1_PRJEB17078_genomic.fna_1:2921195-2921687 Satlength=493 Nr
of Repeats=5 RepeatLength=111 seed=CAGCGGCTTT Num.seqs=4
Similarity=0.949950

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CAGCGGCTTTTTCTTCGCTAAGTCGTCTGCTTCCCCAGCTGGCGGCGTTTCTGAGTCTGACTCTTTCGCTTT
CATTTTCGCGAGTGCGGCAGCCTTTGCTTTTCGCTGCTG

Consensus:

CAGCGGCTTTTTCTTCGCTAAGTCGTCTGCTTCCCCAGCTGGCGGCGTTTCTGAGTCTGACTCTTTCGCTTT
CATTTTCGCGAGTGCGGCAGCCTTTGCTTTTCGCTGCTG

>Bacillus_Fam_858_110_1 Nr. of seq. 1 Alignment length(with gaps) = 110
Alignment score = 0.000000

GCF_000161455.1_ASM16145v1_genomic.fna_1:5374739-5375117 Satlength=379 Nr
of Repeats=4 RepeatLength=111 seed=GATATGGCAA Num.seqs=3
Similarity=0.448118

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GATATGGCAAAAGTGTTCATGTTTTATATGTGTCAAATATTANNGAAACANCTATAAAACGTTGATATATAA
GGGNTATAAGATGTTTCNNATATTTATTAGGTCAAG

Consensus:

GATATGGCAAAAGTGTTCATGTTTTATATGTGTCAAATATTANNGAAACANCTATAAAACGTTGATATATAA
GGGNTATAAGATGTTTCNNATATTTATTAGGTCAAG

>Bacillus_Fam_859_110_1 Nr. of seq. 1 Alignment length(with gaps) = 110
Alignment score = 0.000000

GCF_000712615.1_ASM71261v1_genomic.fna_61:8384-8914 Satlength=531 Nr of
Repeats=5 RepeatLength=112 seed=AGGATACCGC Num.seqs=3

Similarity=0.546448

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AGGATACCGCAAACGTGTTGCAAGTTAAGTTATANGTATATGAATAAGAAAAAACGNCTATCCTTTGATATA
TAAGGNATTCGAGTNAAATGACAAAAAAGTTAGGGTA

Consensus:

AGGATACCGCAAACGTGTTGCAAGTTAAGTTATANGTATATGAATAAGAAAAAACGNCTATCCTTTGATATA
TAAGGNATTCGAGTNAAATGACAAAAAAGTTAGGGTA

>Bacillus_Fam_860_108_1 Nr. of seq. 1 Alignment length(with gaps) = 108

Alignment score = 0.000000

GCF_000374565.1_ASM37456v1_genomic.fna_3:32442-32847 Satlength=406 Nr of
Repeats=4 RepeatLength=108 seed=ACAGGTCCAG Num.seqs=3

Similarity=0.732510

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ACAGGTCCAGTTGGTCCNCNAGGAGCGACGGGCCCCCGGNCCTACAGGAGCAGTAGGCCAGCAGGGCCAA
CAGGAGCCCCAGGCCCGATCGGCCCAATGGGAGCG

Consensus:

ACAGGTCCAGTTGGTCCNCNAGGAGCGACGGGCCCCCGGNCCTACAGGAGCAGTAGGCCAGCAGGGCCAA
CAGGAGCCCCAGGCCCGATCGGCCCAATGGGAGCG

>Bacillus_Fam_861_106_1 Nr. of seq. 1 Alignment length(with gaps) = 106

Alignment score = 0.000000

GCF_900156865.1_PRJEB18960_genomic.fna_3:3352570-3353080 Satlength=511 Nr
of Repeats=5 RepeatLength=106 seed=TTTTTAGGAG Num.seqs=4

Similarity=0.830189

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TTTTTAGGAGATAGCGAACCTGCAACATGCCTTTGCGGGTTCGCAATTGGATAATATTAGGAAACACCATTCC
TGTATAACTCATTTGCATCCTCGCACTTGGATA

Consensus:

TTTTTAGGAGATAGCGAACCTGCAACATGCCTTTGCGGGTTCGCAATTGGATAATATTAGGAAACACCATTCC
TGTATAACTCATTTGCATCCTCGCACTTGGATA

>Bacillus_Fam_862_105_1 Nr. of seq. 1 Alignment length(with gaps) = 105

Alignment score = 0.000000

GCF_000017425.1_ASM1742v1_genomic.fna_1:3693939-3694896 Satlength=958 Nr
of Repeats=4 RepeatLength=105 seed=CTGAAACAGC Num.seqs=3

Similarity=0.932275

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CTGAAACAGCAACTGGAAACGAAAGACGAGCAGATTGAGAAGCTAGAACAAGAAAAGCAAAAGTTAGAAACCC
AAATGAATCAGTTGCAAGGAGGGCCAGAAAAT

Consensus:

CTGAAACAGCAACTGGAAACGAAAGACGAGCAGATTGAGAAGCTAGAACAAGAAAAGCAAAAGTTAGAAACCC
AAATGAATCAGTTGCAAGGAGGGCCAGAAAAT

>Bacillus_Fam_863_105_1 Nr. of seq. 1 Alignment length(with gaps) = 105
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:913685-914101 Satlength=417 Nr
of Repeats=4 RepeatLength=104 seed=AGCGCCCAT Num.seqs=4
Similarity=0.926455

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AGCGCCCCATTCTAAAGGGAAAAATATATGTAGAAAGGCGCACAAATCGAAATAGCGGGCCATTGAGAGAAAG
AAAAAGCAATAGAAATGGCCAGCAAAATAAAAT

Consensus:

AGCGCCCCATTCTAAAGGGAAAAATATATGTAGAAAGGCGCACAAATCGAAATAGCGGGCCATTGAGAGAAAG
AAAAAGCAATAGAAATGGCCAGCAAAATAAAAT

>Bacillus_Fam_864_105_1 Nr. of seq. 1 Alignment length(with gaps) = 105
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_80:7351-7877 Satlength=527 Nr of
Repeats=5 RepeatLength=105 seed=TATCTATGTC Num.seqs=4
Similarity=0.879365

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TATCTATGTCAACTGGTATAGCAATGAAGCAATTCGATCAAAGCTTAAAAAACTAACGGCTCTTCCAACTGA
GAATCTAAACAGTGTAAATAAATTCCTCATTGC

Consensus:

TATCTATGTCAACTGGTATAGCAATGAAGCAATTCGATCAAAGCTTAAAAAACTAACGGCTCTTCCAACTGA
GAATCTAAACAGTGTAAATAAATTCCTCATTGC

>Bacillus_Fam_865_105_1 Nr. of seq. 1 Alignment length(with gaps) = 105
Alignment score = 0.000000
GCF_001591485.1_ASM159148v1_genomic.fna_104:1301-1875 Satlength=575 Nr of
Repeats=5 RepeatLength=105 seed=CTTCAGACAG Num.seqs=3
Similarity=0.690112

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CTTCAGACAGAGGCNGGCATGCCTTTCTCTTTGTTGTCCGAACCTACGGTAACTTCGGACTGTACTCGAGTTT
TTCTTGAGGTTAAGTGTCCAAACCTTCTNCGA

Consensus:

CTTCAGACAGAGGCNGGCATGCCTTTCTCTTTGTTGTCCGAACCTACGGTAACTTCGGACTGTACTCGAGTTT
TTCTTGAGGTTAAGTGTCCAAACCTTCTNCGA

>Bacillus_Fam_866_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000

GCF_000294775.2_ASM29477v2_genomic.fna_1:3556334-3556750 Satlength=417 Nr
of Repeats=4 RepeatLength=104 seed=GGACTCTGGT Num.seqs=4
Similarity=0.833074 0
GGACTCTGGTTGAGGATATCACGTATTTTGGGTCCAAACCTGAGCCTACTTCAGACTCTGGTTGAGCTCATCC
TGAAATGTGAGTCCGAACCTAGTACAACCTC

Consensus:

GGACTCTGGTTGAGGATATCACGTATTTTGGGTCCAAACCTGAGCCTACTTCAGACTCTGGTTGAGCTCATCC
TGAAATGTGAGTCCGAACCTAGTACAACCTC

>Bacillus_Fam_867_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:159625-160145
Satlength=521 Nr of Repeats=5 RepeatLength=104 seed=TGGTTTCTTA
Num.seqs=5 Similarity=0.882243 0
TGGTTTCTTACCGTACCAATGATTTCCCTCTTTCTAGGGCAAATCAACGCTTGATTTTTACCGCCTGAACC
GTTTTTCTCTTCCTTGGGAAAATTCATTAA

Consensus:

TGGTTTCTTACCGTACCAATGATTTCCCTCTTTCTAGGGCAAATCAACGCTTGATTTTTACCGCCTGAACC
GTTTTTCTCTTCCTTGGGAAAATTCATTAA

>Bacillus_Fam_868_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:1851553-1851970 Satlength=418
Nr of Repeats=4 RepeatLength=104 seed=GAGGTGTGTT Num.seqs=3
Similarity=0.923077 0
GAGGTGTGTTTCGGAGCTAAACGCGACTATGAAATCCTATATATGGAAAATAGTGTCGTGGAAATGCTCTAAT
CACGACAGAATAATCCAATAAATGGATAACA

Consensus:

GAGGTGTGTTTCGGAGCTAAACGCGACTATGAAATCCTATATATGGAAAATAGTGTCGTGGAAATGCTCTAAT
CACGACAGAATAATCCAATAAATGGATAACA

>Bacillus_Fam_869_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000
GCF_001645705.1_ASM164570v1_genomic.fna_56:37601-38537 Satlength=937 Nr
of Repeats=9 RepeatLength=104 seed=TTTCTGAAT Num.seqs=9
Similarity=0.892450
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TTTTCTGAATTGCAACGCTTTATGGGTTCTATGAAACCTGCTATATTACCACTTTTGAAGATTACAACCCATT
ACGGGAACCTATGAACCGCACTATGCGACCGC

Consensus:

TTTTCTGAATTGCAACGCTTTATGGGTTCATGAAACCTGCTATATTACCACTTTTGAAGATTACAACCCATT
ACGGGAACCTATGAACCGCACTATGCGACCGC

>Bacillus_Fam_870_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:591573-591926 Satlength=354 Nr
of Repeats=4 RepeatLength=104 seed=CGTCAAGTCC Num.seqs=3
Similarity=0.891005 0
CGTCAAGTCCCGGTGTANGATTAAAAATCCGGCGGGTTCCGAATGAAATCGGGCCAGATGGAAGACAAATCGG
GCGGGAATCAAGGTAAATCCGGCAAGCCGGG

Consensus:

CGTCAAGTCCCGGTGTANGATTAAAAATCCGGCGGGTTCCGAATGAAATCGGGCCAGATGGAAGACAAATCGG
GCGGGAATCAAGGTAAATCCGGCAAGCCGGG

>Bacillus_Fam_871_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:2399755-2400142 Satlength=388
Nr of Repeats=4 RepeatLength=104 seed=GAAAGCGGCG Num.seqs=3
Similarity=0.910256 0
GAAAGCGGCGACTTTTCAGAAAGAATCCGGCGGGAAAGCGAGGAAATCCGGCGAGANACATTTCGAGTGACTGGT
TCGGGTGAAAAAACGGGCGGGATTTAGAAG

Consensus:

GAAAGCGGCGACTTTTCAGAAAGAATCCGGCGGGAAAGCGAGGAAATCCGGCGAGANACATTTCGAGTGACTGGT
TCGGGTGAAAAAACGGGCGGGATTTAGAAG

>Bacillus_Fam_872_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:4123904-4124424 Satlength=521
Nr of Repeats=5 RepeatLength=104 seed=ACCCGCCCGA Num.seqs=3
Similarity=0.940171 0
ACCCGCCCGATTATTCACTTTTCTCGCCGGATAATTGACCCGGATTTGACCCAGATTCCAGAACTGGCCCCGAT
TTTCTTTGGATCCCGCCGCATTTCGAGCTCAC

Consensus:

ACCCGCCCGATTATTCACTTTTCTCGCCGGATAATTGACCCGGATTTGACCCAGATTCCAGAACTGGCCCCGAT
TTTCTTTGGATCCCGCCGCATTTCGAGCTCAC

>Bacillus_Fam_873_104_1 Nr. of seq. 1 Alignment length(with gaps) = 104
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:1022316-1022802 Satlength=487
Nr of Repeats=5 RepeatLength=104 seed=ACAAGAAATT Num.seqs=3

Similarity=0.931624 0
ACAAGAAATTGGGTCTGAATAAAATCGTAATTCAGACAAGAGATCTGCTAAGGTGAGAAATCAAGTCCGAATG
GGCGGGGGATTTCAGACAGAAAAGAGACTTCA

Consensus:

ACAAGAAATTGGGTCTGAATAAAATCGTAATTCAGACAAGAGATCTGCTAAGGTGAGAAATCAAGTCCGAATG
GGCGGGGGATTTCAGACAGAAAAGAGACTTCA

>Bacillus_Fam_874_103_1 Nr. of seq. 1 Alignment length(with gaps) = 103
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:3310743-3311151 Satlength=409 Nr
of Repeats=4 RepeatLength=103 seed=TTTATTCTAC Num.seqs=3
Similarity=0.892125 0
TTTATTCTACCTTCACACGATTCTCCNCGTCATGACGGGACTTTAAAACATGGTTCTTACCCCTTCAGACCGG
GGCGTTCACTCTAAAAGGATATTAAATCGT

Consensus:

TTTATTCTACCTTCACACGATTCTCCNCGTCATGACGGGACTTTAAAACATGGTTCTTACCCCTTCAGACCGG
GGCGTTCACTCTAAAAGGATATTAAATCGT

>Bacillus_Fam_875_103_1 Nr. of seq. 1 Alignment length(with gaps) = 103
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:278070-278585 Satlength=516 Nr
of Repeats=5 RepeatLength=103 seed=AACTTTTGG Num.seqs=5
Similarity=0.919741 0
AACTTTTGGAAAAAGTGCTGAACTAAAGAGTGGAACGCGGAACCGCCAGAGGAATGCTGAAAAAATGGAGA
TTAACGCTGAAATAGGGGAGGAAAACGCTG

Consensus:

AACTTTTGGAAAAAGTGCTGAACTAAAGAGTGGAACGCGGAACCGCCAGAGGAATGCTGAAAAAATGGAGA
TTAACGCTGAAATAGGGGAGGAAAACGCTG

>Bacillus_Fam_876_102_1 Nr. of seq. 1 Alignment length(with gaps) = 102
Alignment score = 0.000000
GCF_000217835.1_ASM21783v1_genomic.fna_1:395335-395743 Satlength=409 Nr
of Repeats=4 RepeatLength=102 seed=GGTTGGAAGC Num.seqs=4
Similarity=0.906419
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GGTTGGAAGCACATGGAACCTCTGCAATCAAAAATATAGATACACTAAAATCATTCTCTGACCCTTTGAAAGAT
ACACGAAAAGCCCTTGCTTCAATTGCAGA

Consensus:

GGTTGGAAGCACATGGAACCTCTGCAATCAAAAATATAGATACACTAAAATCATTCTCTGACCCTTTGAAAGAT
ACACGAAAAGCCCTTGCTTCAATTGCAGA

>Bacillus_Fam_877_99_1 Nr. of seq. 1 Alignment length(with gaps) = 99
Alignment score = 0.000000
GCF_000299035.1_ASM29903v1_genomic.fna_2:1202161-1203221 Satlength=1061
Nr of Repeats=7 RepeatLength=99 seed=AACAAAAATA Num.seqs=6
Similarity=1.000000 0
AACAAAAATAACAGTAACGATGAAGATACAGAAACAACATCGAATGAAAAATAAACAATACAAAACAAGATA
ACGATAATCAACAAAATTCTAACAAC

Consensus:

AACAAAAATAACAGTAACGATGAAGATACAGAAACAACATCGAATGAAAAATAAACAATACAAAACAAGATA
ACGATAATCAACAAAATTCTAACAAC

>Bacillus_Fam_878_99_1 Nr. of seq. 1 Alignment length(with gaps) = 99
Alignment score = 0.000000
GCF_000831065.1_ASM83106v1_genomic.fna_1:1522811-1523306 Satlength=496 Nr
of Repeats=5 RepeatLength=99 seed=CGAAGAAGAA Num.seqs=3
Similarity=0.637540 0
CGAAGAAGAACTACATGTAGANAACTACTAAGCATNAATTTGGAAAAACGCTAGAAACGTATGCGCAAAGT
GGTGAGATAGCAGAACAAATNGAACG

Consensus:

CGAAGAAGAACTACATGTAGANAACTACTAAGCATNAATTTGGAAAAACGCTAGAAACGTATGCGCAAAGT
GGTGAGATAGCAGAACAAATNGAACG

>Bacillus_Fam_879_93_1 Nr. of seq. 1 Alignment length(with gaps) = 93
Alignment score = 0.000000
GCF_000430785.1_ASM43078v1_genomic.fna_27:11652-12024 Satlength=373 Nr of
Repeats=4 RepeatLength=93 seed=ATTACCCAAC Num.seqs=4 Similarity=0.947431
0
ATTACCCAAC TAGAAATGAACCTGCACCTCCAGATACACAACACATAATGCAAATGATGACAAGTCTCGAGGA
TCGATTAAATAAACTCACTA

Consensus:

ATTACCCAAC TAGAAATGAACCTGCACCTCCAGATACACAACACATAATGCAAATGATGACAAGTCTCGAGGA
TCGATTAAATAAACTCACTA

>Bacillus_Fam_880_90_1 Nr. of seq. 1 Alignment length(with gaps) = 90
Alignment score = 0.000000
GCF_000008505.1_ASM850v1_genomic.fna_2:8851-9571 Satlength=721 Nr of
Repeats=7 RepeatLength=90 seed=CGTTCTACTT Num.seqs=6 Similarity=0.952593
0

CGTTCTACTTGCTGACGATCACCTTTTGCCTGATCGTTTGGCACTTCATTTCTTCCTGGGTTATTTATTTCGAT
TAGCTACTTCCAATTCT

Consensus:

CGTTCTACTTGCTGACGATCACCTTTTGCCTGATCGTTTGGCACTTCATTTCTTCCTGGGTTATTTATTTCGAT
TAGCTACTTCCAATTCT

>Bacillus_Fam_881_84_1 Nr. of seq. 1 Alignment length(with gaps) = 84
Alignment score = 0.000000
GCF_000008505.1_ASM850v1_genomic.fna_2:8167-8587 Satlength=421 Nr of
Repeats=5 RepeatLength=84 seed=ACTTCTCGTT Num.seqs=5 Similarity=0.876863
0
ACTTCTCGTTGAACTGTCGTTCCATTTACGCTCACGTTTCCGCTATTTACTGATCCTTGATTCTTCACATTAT
CCTGTACGTTT

Consensus:

ACTTCTCGTTGAACTGTCGTTCCATTTACGCTCACGTTTCCGCTATTTACTGATCCTTGATTCTTCACATTAT
CCTGTACGTTT

>Bacillus_Fam_882_84_1 Nr. of seq. 1 Alignment length(with gaps) = 84
Alignment score = 0.000000
GCF_000831065.1_ASM83106v1_genomic.fna_1:918773-919151 Satlength=379 Nr
of Repeats=5 RepeatLength=84 seed=AATTAGCAGA Num.seqs=3
Similarity=0.862434
0
AATTAGCAGATGGCTCAAGTCAAGTAACAGGCGGTTTAGGAACATTATCTGTAGGAGCAAATCAAATGGCAGG
TGGAGTAAATC

Consensus:

AATTAGCAGATGGCTCAAGTCAAGTAACAGGCGGTTTAGGAACATTATCTGTAGGAGCAAATCAAATGGCAGG
TGGAGTAAATC

>Bacillus_Fam_883_84_1 Nr. of seq. 1 Alignment length(with gaps) = 84
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_23:202276-202863 Satlength=588 Nr
of Repeats=7 RepeatLength=84 seed=AACTCTTCT Num.seqs=6
Similarity=0.671318 0
AACTCTTCTTTGCGCATTCAATTACTTCTTCGCTAATAAATGGTGCCACNCNTGTTAATCCTTTAATAC
CATTCGTTTCA

Consensus:

AACTCTTTCTTTGCGCATTCATCAATTACTTCTTCGCTAATAAATGGTGCCACNCNTGTTAATCCTTTAATAC
CATTCGTTTCA

>Bacillus_Fam_884_84_1 Nr. of seq. 1 Alignment length(with gaps) = 84
Alignment score = 0.000000
GCF_002019765.1_ASM201976v1_genomic.fna_1:1293407-1293689 Satlength=283
Nr of Repeats=4 RepeatLength=84 seed=AAGCTGTGGA Num.seqs=3
Similarity=0.947090 0
AAGCTGTGGAACAAGAAGACACAGAATCGAAACAAGCTGATGCAGAAATCGCTGTTCAAGAAAAGGAAGAGCT
AAAACAAGTTG

Consensus:

AAGCTGTGGAACAAGAAGACACAGAATCGAAACAAGCTGATGCAGAAATCGCTGTTCAAGAAAAGGAAGAGCT
AAAACAAGTTG

>Bacillus_Fam_885_81_1 Nr. of seq. 1 Alignment length(with gaps) = 81
Alignment score = 0.000000
GCF_001315085.1_ASM131508v1_genomic.fna_36:14169-14493 Satlength=325 Nr
of Repeats=4 RepeatLength=81 seed=ACTCAGGTTG Num.seqs=4
Similarity=0.895748
0
ACTCAGGTTGGTTGACTTGGTCATTAAGATCTTCAATAACTTCTGTGATTGGAGCAGAGTCAATAGGTATTTCT
TGAACCTG

Consensus:

ACTCAGGTTGGTTGACTTGGTCATTAAGATCTTCAATAACTTCTGTGATTGGAGCAGAGTCAATAGGTATTTCT
TGAACCTG

>Bacillus_Fam_886_78_1 Nr. of seq. 1 Alignment length(with gaps) = 78
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:1482589-1482958 Satlength=370
Nr of Repeats=5 RepeatLength=78 seed=AGGAGCAAGA Num.seqs=3
Similarity=0.886040 0
AGGAGCAAGAATCGGAAGAAGAAGTAGCATTAAATTCTGATGCAAATCAACCAGAAGTAGAAGAACAATCACT
GCAAG

Consensus:

AGGAGCAAGAATCGGAAGAAGAAGTAGCATTAAATTCTGATGCAAATCAACCAGAAGTAGAAGAACAATCACT
GCAAG

>Bacillus_Fam_887_78_1 Nr. of seq. 1 Alignment length(with gaps) = 78
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_42:634601-635147

Satlength=547 Nr of Repeats=7 RepeatLength=78 seed=CAGAGAACAA Num.seqs=7
Similarity=0.931624 0
CAGAGAACAATCAGGAAGGAACAGCGAAAACAGTGTTGGCAGAAAGTAATCAGGCAGGAGCATCAGAACCAGC
GTCGT

Consensus:

CAGAGAACAATCAGGAAGGAACAGCGAAAACAGTGTTGGCAGAAAGTAATCAGGCAGGAGCATCAGAACCAGC
GTCGT

>Bacillus_Fam_888_76_1 Nr. of seq. 1 Alignment length(with gaps) = 76
Alignment score = 0.000000
GCF_001700275.1_ASM170027v1_genomic.fna_23:136895-137354 Satlength=460 Nr
of Repeats=6 RepeatLength=76 seed=TGAAGCTTGA Num.seqs=5
Similarity=0.957895 0
TGAAGCTTGACGCGAAAAGATGAAGTAAAACGTTGATATAAGGGATAGAACTGCGCATAGCTTGACGTAAGCA
ACG

Consensus:

TGAAGCTTGACGCGAAAAGATGAAGTAAAACGTTGATATAAGGGATAGAACTGCGCATAGCTTGACGTAAGCA
ACG

>Bacillus_Fam_889_75_1 Nr. of seq. 1 Alignment length(with gaps) = 75
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:1713467-1714367 Satlength=901
Nr of Repeats=12 RepeatLength=75 seed=TATTATCTGG Num.seqs=12
Similarity=0.997037 0
TATTATCTGGGTCAGTTGCATCTTTAGGGTCTTCAATCGGATCTTCTTTATTAGTGCCCCCATCATTTTCATC
GA

**
Consensus:

TATTATCTGGGTCAGTTGCATCTTTAGGGTCTTCAATCGGATCTTCTTTATTAGTGCCCCCATCATTTTCATC
GA

>Bacillus_Fam_890_75_1 Nr. of seq. 1 Alignment length(with gaps) = 75
Alignment score = 0.000000
GCF_002019705.1_ASM201970v1_genomic.fna_1:1610549-1611374 Satlength=826
Nr of Repeats=11 RepeatLength=75 seed=GAGCAAGATT Num.seqs=11
Similarity=0.929535 0
GAGCAAGATTCTGATTCCTCTCTAGATGAAGATGTTTCTCTTGATAACGACGCTTCTGAAGACCAGGATGCAG
AT

**
Consensus:

GAGCAAGATTCTGATTCTCTCTAGATGAAGATGTTTCTCTTGATAACGACGCTTCTGAAGACCAGGATGCAG
AT

>Bacillus_Fam_891_74_1 Nr. of seq. 1 Alignment length(with gaps) = 74
Alignment score = 0.000000
GCF_001591485.1_ASM159148v1_genomic.fna_259:34-767 Satlength=734 Nr of
Repeats=10 RepeatLength=73 seed=CTTTC AATCC Num.seqs=6
Similarity=0.458642
0
CTTTC AATCCCCTAAATCGGGTCACATCTTTTGCTACGANNTATGAAGATTCGTTAANAATCTAACAGTTATT
N

*
Consensus:

CTTTC AATCCCCTAAATCGGGTCACATCTTTTGCTACGANNTATGAAGATTCGTTAANAATCTAACAGTTATT
N

>Bacillus_Fam_892_73_1 Nr. of seq. 1 Alignment length(with gaps) = 73
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:228971-229263 Satlength=293 Nr
of Repeats=4 RepeatLength=73 seed=CACGCAAGTA Num.seqs=4
Similarity=0.978691
0
CACGCAAGTATCACTATGGTAATTTGACGGACATAACTCCACAACGAGATCCCAGAAAGAATCTCTAAAATGA

Consensus:

CACGCAAGTATCACTATGGTAATTTGACGGACATAACTCCACAACGAGATCCCAGAAAGAATCTCTAAAATGA

>Bacillus_Fam_893_72_1 Nr. of seq. 1 Alignment length(with gaps) = 72
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_39:34707-34986 Satlength=280 Nr of
Repeats=4 RepeatLength=72 seed=CAGTAACACC Num.seqs=3 Similarity=0.618656
0
CAGTAACACCAGTTGCGCCAATCGAAAATGAAGTACCAAATTCAGAAGTGGCCGCTGGGCCAATGTCAACAC

Consensus:

CAGTAACACCAGTTGCGCCAATCGAAAATGAAGTACCAAATTCAGAAGTGGCCGCTGGGCCAATGTCAACAC

>Bacillus_Fam_894_70_1 Nr. of seq. 1 Alignment length(with gaps) = 70
Alignment score = 0.000000
GCF_900142675.1_IMG-
taxon_2654588196_annotated_assembly_genomic.fna_5:575590-575991
Satlength=402 Nr of Repeats=6 RepeatLength=66 seed=TGAGTGC GTG Num.seqs=4
Similarity=0.434942 0
TGAGTGC GTGGATTGAAATAACTACGNCNTTGANCAATGCAATATCNCAATTAGCTAGTCGCACTTTTTG

Consensus:

TGAGTGC GTGGATTGAAATAACTACGNCNTTGANCAATGCAATATCNCAATTAGCTAGTCGCACTTTTGTG

>Bacillus_Fam_895_69_1 Nr. of seq. 1 Alignment length(with gaps) = 69
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_3:79046-79529 Satlength=484 Nr of
Repeats=7 RepeatLength=69 seed=TAATTTCTGA Num.seqs=7 Similarity=0.994479
0

TAATTTCTGACTTTGTACCTTCAATAGATGTTCCGTTTGTTAATGTTTCAGGTAAAGAGAATTATATGGT

Consensus:

TAATTTCTGACTTTGTACCTTCAATAGATGTTCCGTTTGTTAATGTTTCAGGTAAAGAGAATTATATGGT

>Bacillus_Fam_896_69_1 Nr. of seq. 1 Alignment length(with gaps) = 69
Alignment score = 0.000000
GCF_000508325.1_BAVI_1_genomic.fna_9:15902-17486 Satlength=1585 Nr of
Repeats=24 RepeatLength=66 seed=GTCGCACCT Num.seqs=16
Similarity=0.306590
0

GTCGCACCTTACATGGGTGCGTGGATTGAAATNAANGNGNCAATNAANNCGNATNNTTNATNAGNNNCN

Consensus:

GTCGCACCTTACATGGGTGCGTGGATTGAAATNAANGNGNCAATNAANNCGNATNNTTNATNAGNNNCN

>Bacillus_Fam_897_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
GCF_000948175.1_BFA_2_A_genomic.fna_164:33120-33442 Satlength=323 Nr of
Repeats=5 RepeatLength=64 seed=GTTTTATCTG Num.seqs=4 Similarity=0.452635
0 GTTTTATCTGAACGTAGTGGGATATAAAGTTTAANTTCGCATAANAANCTNTNACCTTAGCCGANNNT

Consensus:

GTTTTATCTGAACGTAGTGGGATATAAAGTTTAANTTCGCATAANAANCTNTNACCTTAGCCGANNNT

>Bacillus_Fam_898_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_13:136989-137520
Satlength=532 Nr of Repeats=8 RepeatLength=66 seed=GTCGCACTCT Num.seqs=5
Similarity=0.485897
0

GTCGCACTCTATGTGAGTGCGTGGATTGAAATANCTNTTTGNNCCNGNTCAGCNTANNTTNCAGTACN

Consensus:

GTCGCACTCTATGTGAGTGCGTGGATTGAAATANCTNTTTGNNCCNGNTCAGCNTANNTTNCAGTACN

>Bacillus_Fam_899_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_13:161926-162191
Satlength=266 Nr of Repeats=4 RepeatLength=66 seed=TCGCACTCTA Num.seqs=3
Similarity=0.526190 0
TCGCACTCTATATGAGTGCGTGGATTGAAATTCCTTCTNCTNTTCTTTAGCCGTTCCNNCGNTTGCAG

Consensus:

TCGCACTCTATATGAGTGCGTGGATTGAAATTCCTTCTNCTNTTCTTTAGCCGTTCCNNCGNTTGCAG

>Bacillus_Fam_900_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
GCF_900142675.1_IMG-
taxon_2654588196_annotated_assembly_genomic.fna_5:556930-557330
Satlength=401 Nr of Repeats=6 RepeatLength=67 seed=GTCGCACTCT Num.seqs=4
Similarity=0.700980 0
GTCGCACTCTTAGTGAGTGCGTGGATTGAAATNTAATGGCAACTACACCCAAAAGAAAAGGCAAATC

Consensus:

GTCGCACTCTTAGTGAGTGCGTGGATTGAAATNTAATGGCAACTACACCCAAAAGAAAAGGCAAATC

>Bacillus_Fam_901_68_1 Nr. of seq. 1 Alignment length(with gaps) = 68
Alignment score = 0.000000
GCF_900142675.1_IMG-
taxon_2654588196_annotated_assembly_genomic.fna_5:580013-580479
Satlength=467 Nr of Repeats=7 RepeatLength=66 seed=TGGATTGAAA Num.seqs=5
Similarity=0.446053 0
TGGATTGAAATNNGATTANNCAGNNTTNAATGATTNNAATAATCNNTGTGCACTCCTTGTGAGTGCG

Consensus:

TGGATTGAAATNNGATTANNCAGNNTTNAATGATTNNAATAATCNNTGTGCACTCCTTGTGAGTGCG

>Bacillus_Fam_902_67_1 Nr. of seq. 1 Alignment length(with gaps) = 67
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_72:8860-10166 Satlength=1307 Nr of
Repeats=20 RepeatLength=66 seed=GTCATATCTC Num.seqs=13
Similarity=0.412873
0 GTCATATCTCCATCTAATCCGTTGCTGTGATATGATANNNGCNNTCANCANNTNGATGNTGNNAANN

Consensus:

GTCATATCTCCATCTAATCCGTTGCTGTGATATGATANNNGCNNTCANCANNTNGATGNTGNNAANN

>Bacillus_Fam_903_67_1 Nr. of seq. 1 Alignment length(with gaps) = 67
Alignment score = 0.000000

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2530174-2531360
Satlength=1187 Nr of Repeats=18 RepeatLength=66 seed=AAAACTGAA
Num.seqs=16 Similarity=0.346635
AAAAACTGAAAGAGTGCCAAACTANGTTNANATNGTNCATNTTNTCNANANNGTTTTCTATACC

0

Consensus:

AAAAACTGAAAGAGTGCCAAACTANGTTNANATNGTNCATNTTNTCNANANNGTTTTCTATACC

>Bacillus_Fam_904_67_1 Nr. of seq. 1 Alignment length(with gaps) = 67
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_53:71-465 Satlength=395 Nr of
Repeats=6 RepeatLength=66 seed=GGTACTCTCT Num.seqs=4 Similarity=0.532724
0 GGTACTCTCTCAGTTTTCGGTATAGAGAAACAAGTCCACGANTGTGNAAGANTACGATTNNGTTTT

Consensus:

GGTACTCTCTCAGTTTTCGGTATAGAGAAACAAGTCCACGANTGTGNAAGANTACGATTNNGTTTT

>Bacillus_Fam_905_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GCF_000017425.1_ASM1742v1_genomic.fna_1:3154400-3155030 Satlength=631 Nr
of Repeats=5 RepeatLength=66 seed=ATCTTTTGAT Num.seqs=3
Similarity=0.905724
0 ATCTTTTGATAATTCGTAGCCCGCTGGTGCTTCTATTTCAACGATTTTGTATTACCTATCGGTAA

Consensus:

ATCTTTTGATAATTCGTAGCCCGCTGGTGCTTCTATTTCAACGATTTTGTATTACCTATCGGTAA

>Bacillus_Fam_906_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GCF_000238675.1_Baci_smit_7_3_47FAA_V1_genomic.fna_17:14392-16174
Satlength=1783 Nr of Repeats=27 RepeatLength=66 seed=ATCATATCAC
Num.seqs=25 Similarity=0.325146
ATCATATCACAGCAATAATCTTAGGGGAAGTATGACNGNTNNTNNGANNATNTNNGNTNNNNN

0

Consensus:

ATCATATCACAGCAATAATCTTAGGGGAAGTATGACNGNTNNTNNGANNATNTNNGNTNNNNN

>Bacillus_Fam_907_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GCF_000307855.1_BAZO1.0_genomic.fna_92:44514-45037 Satlength=524 Nr of
Repeats=8 RepeatLength=65 seed=GTCGCATCCC Num.seqs=5 Similarity=0.490909
0 GTCGCATCCCACGCGGATGCGTGGATTGAAATGNCNANCATGNCGAGATANANCCGNANTCTNGN

Consensus:

GTCGCATCCCACGCGGATGCGTGGATTGAAATGNCNANCATGNCGAGATANANCCGNNANTCTNGN

>Bacillus_Fam_908_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GCF_000429705.1_ASM42970v1_genomic.fna_2:243049-243709 Satlength=661 Nr
of Repeats=10 RepeatLength=66 seed=GACAGCACCA Num.seqs=10
Similarity=0.846016
GACAGCACCAACGCTACTGATACTTCCACCGCTACAAGCGGCTCCACCAGCGAGTCCGACACG

0

Consensus:

GACAGCACCAACGCTACTGATACTTCCACCGCTACAAGCGGCTCCACCAGCGAGTCCGACACG

>Bacillus_Fam_909_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GCF_001274935.1_ASM127493v1_genomic.fna_31:6009-6274 Satlength=266 Nr of
Repeats=4 RepeatLength=66 seed=ATCATAATAC Num.seqs=3 Similarity=0.558559
0 ATCATAATACAGCAATGGCTTTAATGGAAGTATGACNTACAAATGTANGANAAATATTNGATTNA

Consensus:

ATCATAATACAGCAATGGCTTTAATGGAAGTATGACNTACAAATGTANGANAAATATTNGATTNA

>Bacillus_Fam_910_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GCF_900096965.1_IMG-
taxon_2671180223_annotated_assembly_genomic.fna_7:104929-105260
Satlength=332 Nr of Repeats=5 RepeatLength=66 seed=GGATTGAAAT Num.seqs=3
Similarity=0.470209 0
GGATTGAAATNCGNTNGTATGCTNANNAGGTTGTTGGCNGNCGTCGCATCCCATGTGGGTGCGC

Consensus:

GGATTGAAATNCGNTNGTATGCTNANNAGGTTGTTGGCNGNCGTCGCATCCCATGTGGGTGCGC

>Bacillus_Fam_911_66_1 Nr. of seq. 1 Alignment length(with gaps) = 66
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_49:6168-6961
Satlength=794 Nr of Repeats=12 RepeatLength=66 seed=GTCGCACTCT
Num.seqs=8 Similarity=0.424771 0
GTCGCACTCTTCATGAGTGCGTGGATTGAAATNTTATANTCNTGATGGTCGAGNGCATNNGATCGN

Consensus:

GTCGCACTCTTCATGAGTGCGTGGATTGAAATNTTATANTCNTGATGGTCGAGNGCATNNGATCGN

>Bacillus_Fam_912_65_1 Nr. of seq. 1 Alignment length(with gaps) = 65
Alignment score = 0.000000

GCF_000374345.1_ASM37434v1_genomic.fna_66:11358-11621 Satlength=264 Nr of Repeats=4 RepeatLength=66 seed=ATTTCAATCC Num.seqs=3 Similarity=0.460526
0 ATTTCAATCCTCGCACTCACATGGAGTGC GACCANTAAGTCTATTNCTGTTATGCAAGANNGNCT

Consensus:

ATTTCAATCCTCGCACTCACATGGAGTGC GACCANTAAGTCTATTNCTGTTATGCAAGANNGNCT

>Bacillus_Fam_913_65_1 Nr. of seq. 1 Alignment length(with gaps) = 65
Alignment score = 0.000000

GCF_001484965.1_ASM148496v1_genomic.fna_8:75646-77564 Satlength=1919 Nr of Repeats=29 RepeatLength=66 seed=TCCACGCACT Num.seqs=19
Similarity=0.282332

TCCACGCACTCACATGGAGTGC GATTACGNCNNANNNATNNCGNNGANAACGTCNGANATTTCAA

Consensus:

TCCACGCACTCACATGGAGTGC GATTACGNCNNANNNATNNCGNNGANAACGTCNGANATTTCAA

>Bacillus_Fam_914_65_1 Nr. of seq. 1 Alignment length(with gaps) = 65
Alignment score = 0.000000

GCF_900142675.1_IMG-
taxon_2654588196_annotated_assembly_genomic.fna_5:564317-564649
Satlength=333 Nr of Repeats=5 RepeatLength=66 seed=GTCGCACTCT Num.seqs=3
Similarity=0.526636

GTCGCACTCTTTGTGAGTGC GTGATTGAAATAANCATNTTTCTGTAANCGGCAAAATAATNCNG

Consensus:

GTCGCACTCTTTGTGAGTGC GTGATTGAAATAANCATNTTTCTGTAANCGGCAAAATAATNCNG

>Bacillus_Fam_915_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000

GCF_000429705.1_ASM42970v1_genomic.fna_3:200483-201166 Satlength=684 Nr of Repeats=8 RepeatLength=63 seed=TTTTTTCTAC Num.seqs=5
Similarity=0.664646

0 TTTTTTCTACCGCAAAGAGAGATATTCCTACCACAAANAGCAATAATCCTACCGAAAATCCGA

Consensus:

TTTTTTCTACCGCAAAGAGAGATATTCCTACCACAAANAGCAATAATCCTACCGAAAATCCGA

>Bacillus_Fam_916_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000

GCF_000430785.1_ASM43078v1_genomic.fna_32:20641-20977 Satlength=337 Nr of Repeats=5 RepeatLength=63 seed=CAAGAAATAG Num.seqs=4 Similarity=0.915344
0 CAAGAAATAGAAAATTTAAATGAAACAATCATCAGTTACAAAACAAAAGAACTGAACATAAA

Consensus:

CAAGAAATAGAAAATTTAAATGAAACAATCATCAGTTACAAAACAAAAGAACTGAACATAAA

>Bacillus_Fam_917_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
GCF_000508325.1_BAVI_1_genomic.fna_19:13794-14166 Satlength=373 Nr of
Repeats=4 RepeatLength=63 seed=AATACCATTT Num.seqs=3 Similarity=0.823633
0 AATACCATTTTNCNCCNGATTGAACCCATGCTTTTGTACCATAGCTCCATCAGCACCTAAGT

Consensus:

AATACCATTTTNCNCCNGATTGAACCCATGCTTTTGTACCATAGCTCCATCAGCACCTAAGT

>Bacillus_Fam_918_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
GCF_000751775.1_A1A_genomic.fna_22:47265-47558 Satlength=294 Nr of
Repeats=5 RepeatLength=63 seed=TTTGTCCCAT Num.seqs=3 Similarity=0.887125
0 TTTGTCCCATAGACCGTGAATCCGGAATTCTATGGGACATTTTATTTTACTTTTCAACTAAA

Consensus:

TTTGTCCCATAGACCGTGAATCCGGAATTCTATGGGACATTTTATTTTACTTTTCAACTAAA

>Bacillus_Fam_919_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
GCF_001274935.1_ASM127493v1_genomic.fna_16:22732-23194 Satlength=463 Nr of
Repeats=5 RepeatLength=63 seed=TAGGAAAACCT Num.seqs=4
Similarity=0.841270
0 TAGGAAAACCTATCTGACGGATCTACTCAGCTAGCAACAGGAAAAGGCGATTTATCAAATGGTT

Consensus:

TAGGAAAACCTATCTGACGGATCTACTCAGCTAGCAACAGGAAAAGGCGATTTATCAAATGGTT

>Bacillus_Fam_920_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_12:70-2906 Satlength=2837 Nr of
Repeats=44 RepeatLength=66 seed=AGAGTACCAA Num.seqs=38
Similarity=0.266813
0 AGAGTACCAAAACNTNNNNANANNNNTNNGNTANTANGTNGTTTCTCTATACCGAAAACCTGAG

Consensus:

AGAGTACCAAAACNTNNNNANANNNNTNNGNTANTANGTNGTTTCTCTATACCGAAAACCTGAG

>Bacillus_Fam_921_63_1 Nr. of seq. 1 Alignment length(with gaps) = 63
Alignment score = 0.000000
GCF_002019595.1_ASM201959v1_genomic.fna_1:3679532-3679910 Satlength=379
Nr of Repeats=6 RepeatLength=63 seed=GAAAAAGAGC Num.seqs=6

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Similarity=0.646875
GAAAAAGAGCAGCAAGCCAGNCTTACCATCCAAGAGCTGGAGAACAAAATCCAACACTCTTTG

*****
Consensus:

GAAAAAGAGCAGCAAGCCAGNCTTACCATCCAAGAGCTGGAGAACAAAATCCAACACTCTTTG

>Bacillus_Fam_922_62_1 Nr. of seq. 1 Alignment length(with gaps) = 62
Alignment score = 0.000000
GCF_000374345.1_ASM37434v1_genomic.fna_18:23841-24079 Satlength=239 Nr of
Repeats=4 RepeatLength=62 seed=ATGAAAGCCA Num.seqs=3 Similarity=0.600694
0 ATGAAAGCCATNATGAAGGAAAAACGCGGGTNAANTNGCTTTCATCTGTAAAAAAGATCCAA

*****
Consensus:

ATGAAAGCCATNATGAAGGAAAAACGCGGGTNAANTNGCTTTCATCTGTAAAAAAGATCCAA

>Bacillus_Fam_923_61_1 Nr. of seq. 1 Alignment length(with gaps) = 61
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:1321762-1322553 Satlength=792
Nr of Repeats=13 RepeatLength=61 seed=AATCGAAACA Num.seqs=11
Similarity=0.861302
0 AATCGAAACAAGGACGAAATACTCCAATGTAGGCCGAATTAATAGCAGTCAAGGCCGGATT

*****
Consensus:

AATCGAAACAAGGACGAAATACTCCAATGTAGGCCGAATTAATAGCAGTCAAGGCCGGATT

>Bacillus_Fam_924_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:1619478-1620237 Satlength=760 Nr
of Repeats=7 RepeatLength=60 seed=AATACCAAGT Num.seqs=5
Similarity=0.661376
0 AATACCAAGTAGATCCTTCTTTTAACCAGCCAGTAGCCATAGAACCATTTGCATTTAGAT

*****
Consensus:

AATACCAAGTAGATCCTTCTTTTAACCAGCCAGTAGCCATAGAACCATTTGCATTTAGAT

>Bacillus_Fam_925_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
GCF_000496285.1_ASM49628v1_genomic.fna_1:3811091-3811391 Satlength=301 Nr
of Repeats=4 RepeatLength=60 seed=TGGTATTACT Num.seqs=3
Similarity=0.644444
0 TGGTATTACTTGAAAGAAAATGGATCNATGATGACAGGTTGGACGTTAGTAAATGGTNAG

*****
Consensus:

TGGTATTACTTGAAAGAAAATGGATCNATGATGACAGGTTGGACGTTAGTAAATGGTNAG

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>Bacillus_Fam_926_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
GCF_000496285.1_ASM49628v1_genomic.fna_1:3813346-3813826 Satlength=481 Nr of Repeats=7 RepeatLength=60 seed=TGGTATTATT Num.seqs=6
Similarity=0.575788 0
TGGTATTATTTTAAACGCTAATGGAGCAATGAAAACGGGCTGGCTATTANATCAAGGAGTT

Consensus:

TGGTATTATTTTAAACGCTAATGGAGCAATGAAAACGGGCTGGCTATTANATCAAGGAGTT

>Bacillus_Fam_927_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_18:41788-42208 Satlength=421 Nr of Repeats=7 RepeatLength=60 seed=TAGTACCAAG Num.seqs=7 Similarity=0.572161
0 TAGTACCAAGTATTANCAAGNTGAAGCCATCCNGTATGCATNNCACCGTTATTNTTTAAN

Consensus:

TAGTACCAAGTATTANCAAGNTGAAGCCATCCNGTATGCATNNCACCGTTATTNTTTAAN

>Bacillus_Fam_928_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_59:11461-11761 Satlength=301 Nr of Repeats=5 RepeatLength=60 seed=ATTTACATTT Num.seqs=5 Similarity=0.769312
0 ATTTACATTTTTCTTACATTCACTCTCTTGATACCCCTTGCTTTTACCTCATCCTTTGA

Consensus:

ATTTACATTTTTCTTACATTCACTCTCTTGATACCCCTTGCTTTTACCTCATCCTTTGA

>Bacillus_Fam_929_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
GCF_000832605.1_ASM83260v1_genomic.fna_2:284188-284428 Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=ATCACAACAC Num.seqs=4
Similarity=0.933333
0 ATCACAACACCACAGTCAGGAACAACACCATCACCAGCGAATCCGATGGAAAGTAAGCCA

Consensus:

ATCACAACACCACAGTCAGGAACAACACCATCACCAGCGAATCCGATGGAAAGTAAGCCA

>Bacillus_Fam_930_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_105:204636-204873 Satlength=238
Nr of Repeats=4 RepeatLength=60 seed=CCCAACCACT Num.seqs=3
Similarity=0.664903 0
CCCAACCACTAGCCATCGCACCCTAGGATGCATGAAGTACCAGGTGCTCCCATCNNNTA

Consensus:

CCCAACCAGTAGCCATCGCACCCTAGGATGCATGAAGTACCAGGTGCTCCCATCENNNTA

>Bacillus_Fam_931_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60

Alignment score = 0.000000

GCF_001591485.1_ASM159148v1_genomic.fna_100:1375-1615 Satlength=241 Nr of
Repeats=4 RepeatLength=60 seed=AGGTAGTACC Num.seqs=4 Similarity=0.685792
0 AGGTAGTACCCTTCCCACCTGTATAAAGCCAACCGGTCTTCATCGAGCCATTACTAGTC

Consensus:

AGGTAGTACCCTTCCCACCTGTATAAAGCCAACCGGTCTTCATCGAGCCATTACTAGTC

>Bacillus_Fam_932_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60

Alignment score = 0.000000

GCF_001591485.1_ASM159148v1_genomic.fna_130:5865-6531 Satlength=667 Nr of
Repeats=5 RepeatLength=60 seed=TCAGCCAGCC Num.seqs=3 Similarity=0.336650
0 TCAGCCAGCCNTTNTGAATNAGACCGTTTGATNCAAAGTAATANTGCTNNNATCCCTNGG

Consensus:

TCAGCCAGCCNTTNTGAATNAGACCGTTTGATNCAAAGTAATANTGCTNNNATCCCTNGG

>Bacillus_Fam_933_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60

Alignment score = 0.000000

GCF_001591805.1_ASM159180v1_genomic.fna_49:31667-31967 Satlength=301 Nr
of Repeats=5 RepeatLength=60 seed=AAGAGCGGAG Num.seqs=3
Similarity=0.911111
0 AAGAGCGGAGCCATGCAAACGGGCTGGCTGAAAGACGGATCGAAATGGTACTACCTCGGT

Consensus:

AAGAGCGGAGCCATGCAAACGGGCTGGCTGAAAGACGGATCGAAATGGTACTACCTCGGT

>Bacillus_Fam_934_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60

Alignment score = 0.000000

GCF_001712755.1_ASM171275v1_genomic.fna_3:55980-56220 Satlength=241 Nr of
Repeats=4 RepeatLength=60 seed=GGAGTAATGA Num.seqs=4 Similarity=0.769841
0 GGAGTAATGAAACTAGTTGGTTAGTATTAGGTAATAAACATTATTACTTTGATAAATAT

Consensus:

GGAGTAATGAAACTAGTTGGTTAGTATTAGGTAATAAACATTATTACTTTGATAAATAT

>Bacillus_Fam_935_60_1 Nr. of seq. 1 Alignment length(with gaps) = 60

Alignment score = 0.000000

GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_16:475148-475388
Satlength=241 Nr of Repeats=4 RepeatLength=60 seed=TGACGGTAGC Num.seqs=4
Similarity=0.933333 0
TGACGGTAGCCATGAGGAGGCAGGACATGAAGACGAAAATCATGAAGCTGACGCTCATGG

Consensus:

TGACGGTAGCCATGAGGAGGCAGGACATGAAGACGAAAATCATGAAGCTGACGCTCATGG

>Bacillus_Fam_936_58_1 Nr. of seq. 1 Alignment length(with gaps) = 58
Alignment score = 0.000000
GCF_001591485.1_ASM159148v1_genomic.fna_14:19820-20120 Satlength=301 Nr
of Repeats=5 RepeatLength=60 seed=TGGTATTATT Num.seqs=5
Similarity=0.504040
0 TGGTATTATTTTGATNNNACCGGTGCAATGAAAACAGGNTGGCTGCTATNGTGGCAAN

Consensus:

TGGTATTATTTTGATNNNACCGGTGCAATGAAAACAGGNTGGCTGCTATNGTGGCAAN

>Bacillus_Fam_937_58_1 Nr. of seq. 1 Alignment length(with gaps) = 58
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_42:885338-885570
Satlength=233 Nr of Repeats=4 RepeatLength=58 seed=AGGATGGCGA Num.seqs=4
Similarity=1.000000 0
AGGATGGCGACATTCCGCTGTTACTCACAGGACGTGAGTGGTACTTAAGCGGAATTGG

Consensus:

AGGATGGCGACATTCCGCTGTTACTCACAGGACGTGAGTGGTACTTAAGCGGAATTGG

>Bacillus_Fam_938_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_16:66119-66404 Satlength=286 Nr of
Repeats=5 RepeatLength=57 seed=TTTCCAATGC Num.seqs=5 Similarity=0.887719
0 TTTCCAATGCCAAGCCACCATGGAGGAATGATGCCAATGCCAGAGCAAAGTGGAGGA

Consensus:

TTTCCAATGCCAAGCCACCATGGAGGAATGATGCCAATGCCAGAGCAAAGTGGAGGA

>Bacillus_Fam_939_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
GCF_000321185.1_ASM32118v1_genomic.fna_73:59292-59609 Satlength=318 Nr of
Repeats=5 RepeatLength=57 seed=AATGACTCAT Num.seqs=3 Similarity=0.953216
0 AATGACTCATAAATACTCGATTCTTTTTTATCATGGATTCTTCAGCTGGTCTTATT

Consensus:

AATGACTCATAAATACTCGATTCTTTTTTATCATGGATTCTTCAGCTGGTCTTATT

>Bacillus_Fam_940_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_6:87271-88026 Satlength=756 Nr of
Repeats=7 RepeatLength=57 seed=CAAATGTTGG Num.seqs=5 Similarity=0.985965
0 CAAATGTTGGAAATGTAGTTGGTGCTCCTACTGGAACCTCCGCCTTGCGCCCCCTCCTA

Consensus:

CAAATGTTGGAAATGTAGTTGGTGCTCCTACTGGAACCTCCGCCTTGCGCCCCCTCCTA

>Bacillus_Fam_941_57_1 Nr. of seq. 1 Alignment length(with gaps) = 57
Alignment score = 0.000000
GCF_000775975.1_ASM77597v1_genomic.fna_1:2705156-2705429 Satlength=274 Nr
of Repeats=6 RepeatLength=57 seed=GGGCCTACTG Num.seqs=4
Similarity=0.910331 0
GGGCCTACTGGACCTACCGGAATAACTGGAGCAACTGGACCTTCTGGTGGACCTCCA

Consensus:

GGGCCTACTGGACCTACCGGAATAACTGGAGCAACTGGACCTTCTGGTGGACCTCCA

>Bacillus_Fam_942_56_1 Nr. of seq. 1 Alignment length(with gaps) = 56
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_120:58369-58681 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=TTTGGAGGTA Num.seqs=4
Similarity=0.625000
0 TTTGGAGGTACTTCCTTTTAGCTATTCGCTAGCATGATGTGACNTCATGACACTCT

Consensus:

TTTGGAGGTACTTCCTTTTAGCTATTCGCTAGCATGATGTGACNTCATGACACTCT

>Bacillus_Fam_943_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
GCF_000217835.1_ASM21783v1_genomic.fna_1:697043-697355 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=GTCTTCCTTA Num.seqs=6
Similarity=0.674206
0 GTCTTCCTTAACNTAGANGCGNTTCTACGTTAAGATACCCGAAAAATTCCGANG

Consensus:

GTCTTCCTTAACNTAGANGCGNTTCTACGTTAAGATACCCGAAAAATTCCGANG

>Bacillus_Fam_944_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000

GCF_000331575.1_ASM33157v1_genomic.fna_1:1650370-1650647 Satlength=278 Nr
of Repeats=5 RepeatLength=55 seed=GGACCATGAT Num.seqs=3
Similarity=0.903030 0
GGACCATGATTAAGCTGCTATTTGTTGGTAGTTTTATACATAGCACTTGATTTCGC

Consensus:

GGACCATGATTAAGCTGCTATTTGTTGGTAGTTTTATACATAGCACTTGATTTCGC

>Bacillus_Fam_945_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:511669-512190 Satlength=522 Nr
of Repeats=11 RepeatLength=52 seed=ATGAAGGACA Num.seqs=8
Similarity=0.624362 0
ATGAAGGACAANTTGAAGGAAAGAATCGAAGGAAAATCAGTCCTTCATCGGAAGT

Consensus:

ATGAAGGACAANTTGAAGGAAAGAATCGAAGGAAAATCAGTCCTTCATCGGAAGT

>Bacillus_Fam_946_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:1907579-1907897 Satlength=319
Nr of Repeats=6 RepeatLength=53 seed=CTTTATTTTG Num.seqs=6
Similarity=0.823434 0
CTTTATTTTGACCGGTGACCTCCTTCTTGGTACCTTTGCGGGAAGAATCNGACGN

Consensus:

CTTTATTTTGACCGGTGACCTCCTTCTTGGTACCTTTGCGGGAAGAATCNGACGN

>Bacillus_Fam_947_55_1 Nr. of seq. 1 Alignment length(with gaps) = 55
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:2333462-2333670 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=CTCATGAACC Num.seqs=4
Similarity=0.606061 0
CTCATGAACCCTCTATGAGAACAATTGCNAGCACCTCCTTCANCCAGTCTGTC

Consensus:

CTCATGAACCCTCTATGAGAACAATTGCNAGCACCTCCTTCANCCAGTCTGTC

>Bacillus_Fam_948_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_000169195.2_ASM16919v2_genomic.fna_1:140555-140771 Satlength=217 Nr
of Repeats=4 RepeatLength=54 seed=CCCGTCTTTC Num.seqs=4
Similarity=0.786008
0 CCCGTCTTTCAGCATGATGTTTCAGGCAAATCCGGGGGAACACGGCGCTCTATTT

Consensus:

CCCGTCTTTCAGCATGATGTTTCAGGCAAATCCGGGGGAACACGGCGCTCTATTT

>Bacillus_Fam_949_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_000169195.2_ASM16919v2_genomic.fna_1:451571-451779 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TGTCCTTTCAT Num.seqs=4
Similarity=0.507937
0 TGTCTTTCATCANACCGATGAAGGACAAATAGCTACCAGCCACNCCTTGTA AAA

Consensus:

TGTCTTTCATCANACCGATGAAGGACAAATAGCTACCAGCCACNCCTTGTA AAA

>Bacillus_Fam_950_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_000708755.2_ASM70875v2_genomic.fna_2:1546077-1546501 Satlength=425 Nr
of Repeats=8 RepeatLength=53 seed=TTTCAGTGCCA Num.seqs=8
Similarity=0.784832
0
TTTCAGTGCCATCAAAACCGATTCCGGACGCTTCTTGAGGGTTCTTATCCTGNTG

Consensus:

TTTCAGTGCCATCAAAACCGATTCCGGACGCTTCTTGAGGGTTCTTATCCTGNTG

>Bacillus_Fam_951_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_14:27849-28929 Satlength=1081 Nr
of Repeats=20 RepeatLength=54 seed=ACAAAGACTT Num.seqs=20
Similarity=0.765132
0
ACAAAGACTTCCGGCTCTTCTTGGNTTTCCTCTACAACCTTCTGCTTCAGGTTCC

Consensus:

ACAAAGACTTCCGGCTCTTCTTGGNTTTCCTCTACAACCTTCTGCTTCAGGTTCC

>Bacillus_Fam_952_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_77:5423-5639 Satlength=217 Nr of
Repeats=4 RepeatLength=54 seed=ATTGTTGGAA Num.seqs=4 Similarity=0.897119
0 ATTGTTGGAAACACAAACATCACGATGATTGTTCAAAACATAAACATCATTGTG

Consensus:

ATTGTTGGAAACACAAACATCACGATGATTGTTCAAAACATAAACATCATTGTG

>Bacillus_Fam_953_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000

GCF_000775975.1_ASM77597v1_genomic.fna_1:2007949-2008246 Satlength=298 Nr
of Repeats=6 RepeatLength=54 seed=AGAGAAAAGAA Num.seqs=5
Similarity=0.690476 0
AGAGAAAAGAAAGTGAAGAACTGAATCAAAAAAGAAGATAAAGCAATTGAATT

Consensus:

AGAGAAAAGAAAGTGAAGAACTGAATCAAAAAAGAAGATAAAGCAATTGAATT

>Bacillus_Fam_954_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_101:238687-238999 Satlength=313 Nr
of Repeats=5 RepeatLength=52 seed=CTGACAGCCC Num.seqs=4
Similarity=0.763375 0
CTGACAGCCCTCCTCAGTGCCCGTTTCTTGGAATAGGAAACCATTTTAGGGCT

Consensus:

CTGACAGCCCTCCTCAGTGCCCGTTTCTTGGAATAGGAAACCATTTTAGGGCT

>Bacillus_Fam_955_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_001243895.1_Bacillus_testis_genomic.fna_9:434776-435244 Satlength=469
Nr of Repeats=5 RepeatLength=54 seed=ATGGGGCCAA Num.seqs=4
Similarity=0.864198 0
ATGGGGCCAAACAGGAGCCACCGATTAGCAGGAGCAACCGGGCCAGCAGGAGTA

Consensus:

ATGGGGCCAAACAGGAGCCACCGATTAGCAGGAGCAACCGGGCCAGCAGGAGTA

>Bacillus_Fam_956_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:201591-201847
Satlength=257 Nr of Repeats=5 RepeatLength=51 seed=TTTGTCTCTG Num.seqs=4
Similarity=0.598765 0
TTTGTCTCTGAGCACGTCTATCAGAGACATTAATTATCCAATTAAAAGCGAAGA

Consensus:

TTTGTCTCTGAGCACGTCTATCAGAGACATTAATTATCCAATTAAAAGCGAAGA

>Bacillus_Fam_957_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_002019705.1_ASM201970v1_genomic.fna_1:3847198-3848008 Satlength=811
Nr of Repeats=14 RepeatLength=54 seed=TAAGCCAGTA Num.seqs=9
Similarity=1.000000 0
TAAGCCAGTAGCGCCAGTAGGCCAGGATCGCCGGTGGCCCCAGTAGCCCCAGC

Consensus:

TAAGCCAGTAGCGCCAGTAGGCCAGGATCGCCGGTGGCCCCAGTAGCCCCAGC

>Bacillus_Fam_958_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_32:122431-122863
Satlength=433 Nr of Repeats=8 RepeatLength=54 seed=CTCAGCCAGC Num.seqs=8
Similarity=0.973545 0
CTCAGCCAGCAGCTCGGTTTCTTCTGCAGCCTCTTCGAGTAATTCTGTCTCATT

Consensus:

CTCAGCCAGCAGCTCGGTTTCTTCTGCAGCCTCTTCGAGTAATTCTGTCTCATT

>Bacillus_Fam_959_54_1 Nr. of seq. 1 Alignment length(with gaps) = 54
Alignment score = 0.000000
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_26:45696-46032
Satlength=337 Nr of Repeats=4 RepeatLength=54 seed=AAAGCAGAAG Num.seqs=3
Similarity=0.983539 0
AAAGCAGAAGAGCAACAGCGTGAAGCATTGAAGAAACAAGAAGAGGCCCGTAAA

Consensus:

AAAGCAGAAGAGCAACAGCGTGAAGCATTGAAGAAACAAGAAGAGGCCCGTAAA

>Bacillus_Fam_960_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_3:207312-207737 Satlength=426 Nr of
Repeats=8 RepeatLength=53 seed=GGTCGACATG Num.seqs=7 Similarity=0.892183
0 GGTTCGACATGATCGAGGAGAAAATAGAGAAAGAACAGGTCGATGAGTAGCCGA

Consensus:

GGTCGACATGATCGAGGAGAAAATAGAGAAAGAACAGGTCGATGAGTAGCCGA

>Bacillus_Fam_961_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000153365.1_ASM15336v1_genomic.fna_16:88973-89184 Satlength=212 Nr of
Repeats=4 RepeatLength=53 seed=ATATGAGTCA Num.seqs=3 Similarity=0.740042
0 ATATGAGTCACTNTGGTGGTGGNGAAAGCCGNACAGAGTGACTCAAGAGGAAG

Consensus:

ATATGAGTCACTNTGGTGGTGGNGAAAGCCGNACAGAGTGACTCAAGAGGAAG

>Bacillus_Fam_962_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000169195.2_ASM16919v2_genomic.fna_1:2227978-2228290 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GCTTCCTTAA Num.seqs=6 Similarity=0.792243 0
GCTTCCTTAACATAGAAGCGCTCTACATTAAGGAAAGGCGAAAATTCGTGACN

Consensus:

GCTTCCTTAACATAGAAGCGCTCTACATTAAGGAAAGGCGAAAATTCGTGACN

>Bacillus_Fam_963_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_71:4024-4448 Satlength=425 Nr of Repeats=8 RepeatLength=53 seed=GAATCGGTAG Num.seqs=8 Similarity=0.919137
0 GAATCGGTAGGGTCAAAAGAGCACTTAGACATGGTCTGAATCCAGGTAAGAGAA

Consensus:

GAATCGGTAGGGTCAAAAGAGCACTTAGACATGGTCTGAATCCAGGTAAGAGAA

>Bacillus_Fam_964_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_89:2084-2402 Satlength=319 Nr of Repeats=6 RepeatLength=53 seed=GTAGGTCATA Num.seqs=6 Similarity=0.932914
0 GTAGGTCATAAGGGTCTCAACATGAAAATGAAGCCATGCGCTCGTCCCGCGCG

Consensus:

GTAGGTCATAAGGGTCTCAACATGAAAATGAAGCCATGCGCTCGTCCCGCGCG

>Bacillus_Fam_965_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_99:4910-5176 Satlength=267 Nr of Repeats=4 RepeatLength=53 seed=TCTCAATGGG Num.seqs=3 Similarity=0.829218
0 TCTCAATGGGCTAATTACGTCGTTTACGGGCCAACACCTCATCAAAAAGTCAA

Consensus:

TCTCAATGGGCTAATTACGTCGTTTACGGGCCAACACCTCATCAAAAAGTCAA

>Bacillus_Fam_966_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_130:505-717 Satlength=213 Nr of Repeats=4 RepeatLength=53 seed=TACATGAGTT Num.seqs=4 Similarity=0.689727
0 TACATGAGTTACTTCAGATGGTCCGACTCATGTATGAAAACTNGATCNTTGA

Consensus:

TACATGAGTTACTTCAGATGGTCCGACTCATGTATGAAAACTNGATCNTTGA

>Bacillus_Fam_967_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_138:4971-5501 Satlength=531 Nr of
Repeats=10 RepeatLength=53 seed=GTCCCTTTGA Num.seqs=10
Similarity=0.877009
0 GTCCCTTTGACGACTCCGATTCTCCCTGACTTCCGATTCCACACCCTCATTGA

Consensus:

GTCCCTTTGACGACTCCGATTCTCCCTGACTTCCGATTCCACACCCTCATTGA

>Bacillus_Fam_968_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_140:18323-18531 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CTAAAGACCA Num.seqs=4
Similarity=0.901468
0 CTAAAGACCAAAACGAATGAAATTCCAGGTGTAAAAGTGTCTTTAGAGACGTT

Consensus:

CTAAAGACCAAAACGAATGAAATTCCAGGTGTAAAAGTGTCTTTAGAGACGTT

>Bacillus_Fam_969_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_141:950-1213 Satlength=264 Nr of
Repeats=5 RepeatLength=53 seed=AAAGGGTGTA Num.seqs=4 Similarity=0.916143
0 AAAGGGTGTAACGGGCCAACGAGAAAGCAGAACCAGAAGGATGCTGGCCCCG

Consensus:

AAAGGGTGTAACGGGCCAACGAGAAAGCAGAACCAGAAGGATGCTGGCCCCG

>Bacillus_Fam_970_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_150:24659-25400 Satlength=742 Nr
of Repeats=14 RepeatLength=53 seed=CATCAAAAGG Num.seqs=13
Similarity=0.894856
CATCAAAAGGTGTGGACGGTGAAAATGATGTATGAAAAGAGGGATGATTCCAG

0

Consensus:

CATCAAAAGGTGTGGACGGTGAAAATGATGTATGAAAAGAGGGATGATTCCAG

>Bacillus_Fam_971_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_157:28244-28774 Satlength=531 Nr
of Repeats=10 RepeatLength=53 seed=ACGTTTCTTC Num.seqs=10
Similarity=0.838435
ACGTTTCTTCTCTAATCGTGCACCTTCACNTCAGATTCCCGCCTTCTAGGGGC

0

Consensus:

ACGTTTCTTCTCTAATCGTGCACCTTCACNTCAGATTCCCGCCTTCTAGGGGC

>Bacillus_Fam_972_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_166:38412-38623 Satlength=212 Nr
of Repeats=4 RepeatLength=53 seed=GTTGTTGAAG Num.seqs=3
Similarity=0.932914

0 GTTGTTGAAGGGTAAAGTTTAAGAGCTAAACGTACCCCTTGAGTGCAGATTGA

Consensus:

GTTGTTGAAGGGTAAAGTTTAAGAGCTAAACGTACCCCTTGAGTGCAGATTGA

>Bacillus_Fam_973_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_173:33950-34639 Satlength=690 Nr
of Repeats=13 RepeatLength=53 seed=GTACATCATT Num.seqs=13
Similarity=0.832608

GTACATCATTCGAGAGTCAACCAGGAAATGACACCCCGCGCGGGAGGAGCGCG

0

Consensus:

GTACATCATTCGAGAGTCAACCAGGAAATGACACCCCGCGCGGGAGGAGCGCG

>Bacillus_Fam_974_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_173:43930-44406 Satlength=477 Nr
of Repeats=8 RepeatLength=53 seed=CCAACATCTC Num.seqs=6
Similarity=0.823251

0 CCAACATCTCGAGGAATTCTGAATCACAATGGTCCGATAACCCTCTAAACGGA

Consensus:

CCAACATCTCGAGGAATTCTGAATCACAATGGTCCGATAACCCTCTAAACGGA

>Bacillus_Fam_975_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_174:16203-16625 Satlength=423 Nr
of Repeats=8 RepeatLength=53 seed=GTAAACGTAC Num.seqs=7
Similarity=0.832285

47 GTACCACTACAGAAGGNGAATCGGGCTTCTAATGGTACGATTAGCTTGTAAC

Consensus:

GTAAACGTACCACTACAGAAGGNGAATCGGGCTTCTAATGGTACGATTAGCTT

>Bacillus_Fam_976_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_175:7654-7968 Satlength=315 Nr of
Repeats=6 RepeatLength=52 seed=AAAAGAGAAT Num.seqs=4 Similarity=0.752058
0 AAAAGAGAATCGACCCTGTCTGAAGAGGCGTAAAGACCAGGTCGAATGGTTGCA

Consensus:

AAAAGAGAATCGACCCTGTCTGAAGAGGCGTAAAGACCAGGTCGAATGGTTGCA

>Bacillus_Fam_977_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_178:36078-36870 Satlength=793 Nr
of Repeats=13 RepeatLength=53 seed=GGCTTCATTT Num.seqs=11
Similarity=0.778072
GGCTTCATTTGTGGATTCAGGTGCTTATGACAACACGCGCTCGAGGTGCGCGG 0

Consensus:

GGCTTCATTTGTGGATTCAGGTGCTTATGACAACACGCGCTCGAGGTGCGCGG

>Bacillus_Fam_978_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_179:78015-78438 Satlength=424 Nr
of Repeats=7 RepeatLength=53 seed=CATCATTTCTG Num.seqs=5
Similarity=0.864151
0 CATCATTTCTGGGCCGCCGTGAAAAATGATGTAGGAAAAACAATCGGAATTAGGG

Consensus:

CATCATTTCTGGGCCGCCGTGAAAAATGATGTAGGAAAAACAATCGGAATTAGGG

>Bacillus_Fam_979_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_181:51513-52096 Satlength=584 Nr
of Repeats=11 RepeatLength=53 seed=TTGGTACATC Num.seqs=11
Similarity=0.914923
TTGGTACATCAAATCAAGGTGGTCCACGCAATGATGTCCTAATAAAGTCAGAA 0

Consensus:

TTGGTACATCAAATCAAGGTGGTCCACGCAATGATGTCCTAATAAAGTCAGAA

>Bacillus_Fam_980_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_183:56196-56408 Satlength=213 Nr
of Repeats=4 RepeatLength=53 seed=TGGCCCATTT Num.seqs=4
Similarity=0.767677
0 TGGCCCATTTAACCATTTAATGGACCAACACCCTTTAGAGTCGCAACTCTCAT

Consensus:

TGGCCCATTTAACCATTTAATGGACCAACACCCTTTAGAGTCGCAACTCTCAT

>Bacillus_Fam_981_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_184:47614-48038 Satlength=425 Nr
of Repeats=8 RepeatLength=53 seed=GTCATTTTGT Num.seqs=8
Similarity=0.828593

0 GTCATTTTGTGAGAATTGGTCGAATGACACCCNGCGCCCCGTCCGCGCGGTAG

Consensus:

GTCATTTTGTGAGAATTGGTCGAATGACACCCNGCGCCCCGTCCGCGCGGTAG

>Bacillus_Fam_982_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_186:247447-247818 Satlength=372 Nr
of Repeats=7 RepeatLength=53 seed=CACTGGCCCA Num.seqs=7
Similarity=0.744834

CACTGGCCCAATAATCCAATAAATGGGCCAACATGATCTGGTTTGTAGCAATCT

0

Consensus:

CACTGGCCCAATAATCCAATAAATGGGCCAACATGATCTGGTTTGTAGCAATCT

>Bacillus_Fam_983_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_186:666606-666977 Satlength=372 Nr
of Repeats=7 RepeatLength=53 seed=AAATGATGAC Num.seqs=7
Similarity=0.856244

AAATGATGACATGCGCGCGNGNGCGCGGGGTGTCATTGTGTTGGATTTGCGG

0

Consensus:

AAATGATGACATGCGCGCGNGNGCGCGGGGTGTCATTGTGTTGGATTTGCGG

>Bacillus_Fam_984_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_186:674905-675223 Satlength=319 Nr
of Repeats=6 RepeatLength=53 seed=GTAATCGACC Num.seqs=6
Similarity=0.839506

CGACCCAACATCTTCTCCAAAACCCAATCTCCTTGGGCTGTTTACCTCGTAAT

48

Consensus:

GTAATCGACCCAACATCTTCTCCAAAACCCAATCTCCTTGGGCTGTTTACCTC

>Bacillus_Fam_985_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000285535.1_ASM28553v1_genomic.fna_3:225928-226269 Satlength=342 Nr
of Repeats=8 RepeatLength=53 seed=ATACCATTTA Num.seqs=5
Similarity=0.793711
0 ATACCATTTATCGTTGCTCGGCTTCGTGATATTCCGTTTACGCCGTTTGCGGT

Consensus:

ATACCATTTATCGTTGCTCGGCTTCGTGATATTCCGTTTACGCCGTTTGCGGT

>Bacillus_Fam_986_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000285535.1_ASM28553v1_genomic.fna_61:20-436 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=ATGAAGAGGA Num.seqs=8 Similarity=0.769180
0 ATGAAGAGGATACACCACGAATGAAAGCTACGAAATCCCCTTCATGAGAGCTA

Consensus:

ATGAAGAGGATACACCACGAATGAAAGCTACGAAATCCCCTTCATGAGAGCTA

>Bacillus_Fam_987_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_27:54281-54494 Satlength=214 Nr of
Repeats=4 RepeatLength=53 seed=GAGGAAAGTC Num.seqs=3 Similarity=0.823899
0 GAGGAAAGTCAGAAGGAGAAGCTNNGNACGCGTCGGCAGGTTTCAGACTTTAGG

Consensus:

GAGGAAAGTCAGAAGGAGAAGCTNNGNACGCGTCGGCAGGTTTCAGACTTTAGG

>Bacillus_Fam_988_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000311725.1_ASM31172v1_genomic.fna_2:378341-378913 Satlength=573 Nr
of Repeats=11 RepeatLength=52 seed=TTGTCCGAAT Num.seqs=11
Similarity=0.674931
TTGTCCGAATAANCCTTCTATTTCGGACTIONAACCCTTGGTGCTTCNNTCNTC 0

Consensus:

TTGTCCGAATAANCCTTCTATTTCGGACTIONAACCCTTGGTGCTTCNNTCNTC

>Bacillus_Fam_989_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000311725.1_ASM31172v1_genomic.fna_3:509966-510547 Satlength=582 Nr
of Repeats=11 RepeatLength=53 seed=TTTGTCTCAT Num.seqs=9
Similarity=0.858840
0 TTTGTCTCATGGAGCNTTCATGTTACATGAGTTACTCCCTTTCTTGAGGAAAG

Consensus:

TTTGTCTCATGGAGCNTTCATGTTACATGAGTTACTCCCTTTCTTGAGGAAAG

>Bacillus_Fam_990_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_4:225418-226666 Satlength=1249 Nr
of Repeats=24 RepeatLength=52 seed=ATTAGTGACC Num.seqs=24
Similarity=0.592525 0
ATTAGTGACCGTTTTCTNTTGCAACTACAAAAACGGGCATCTANTACACTCG

Consensus:

ATTAGTGACCGTTTTCTNTTGCAACTACAAAAACGGGCATCTANTACACTCG

>Bacillus_Fam_991_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000708755.2_ASM70875v2_genomic.fna_6:240161-240426 Satlength=266 Nr
of Repeats=5 RepeatLength=53 seed=ATTATAACGT Num.seqs=5
Similarity=0.854088
0 ATTATAACGTAAGGAAACACTCGAATCGTACGCTATACGTACACCGGATGAAA

Consensus:

ATTATAACGTAAGGAAACACTCGAATCGTACGCTATACGTACACCGGATGAAA

>Bacillus_Fam_992_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_1:146658-146976 Satlength=319 Nr
of Repeats=6 RepeatLength=53 seed=CCAGAAATGG Num.seqs=6
Similarity=0.773585
0 CCAGAAATGGTGACCGGAAACAGAGAAAAGTGGCGTCACTAAGGCGAGTGGCG

Consensus:

CCAGAAATGGTGACCGGAAACAGAGAAAAGTGGCGTCACTAAGGCGAGTGGCG

>Bacillus_Fam_993_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_1:748009-748380 Satlength=372 Nr
of Repeats=7 RepeatLength=53 seed=AGAGTGCTGC Num.seqs=7
Similarity=0.783169
0 AGAGTGCTGCCACTTTTGCCGTTGAGGGATCATCGGAAGTGGCGTCAATCCAC

Consensus:

AGAGTGCTGCCACTTTTGCCGTTGAGGGATCATCGGAAGTGGCGTCAATCCAC

>Bacillus_Fam_994_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000709935.2_ASM70993v2_genomic.fna_17:22189-22454 Satlength=266 Nr of Repeats=5 RepeatLength=53 seed=TGACGCCACA Num.seqs=5 Similarity=0.778616
0 TGACGCCACAAAGCTGTTTGCAATATAAGTGAAAGTGGCGCAACTCNCCGGAG

Consensus:

TGACGCCACAAAGCTGTTTGCAATATAAGTGAAAGTGGCGCAACTCNCCGGAG

>Bacillus_Fam_995_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000709935.2_ASM70993v2_genomic.fna_24:63175-63438 Satlength=264 Nr of Repeats=5 RepeatLength=53 seed=TGCCACTTTT Num.seqs=3 Similarity=0.882600
0 TGCCACTTTTTGCGTGATGGGTTTGCCAATTGTGGTGTTCATTGGCCGTAGTGG

Consensus:

TGCCACTTTTTGCGTGATGGGTTTGCCAATTGTGGTGTTCATTGGCCGTAGTGG

>Bacillus_Fam_996_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:288723-288988 Satlength=266 Nr of Repeats=5 RepeatLength=53 seed=CGGGCTCCTA Num.seqs=5 Similarity=0.909434
0 CGGGCTCCTATTTCAACGATTGGCTACCGTTTCCACTCCTTGAGAGCTACGCT

Consensus:

CGGGCTCCTATTTCAACGATTGGCTACCGTTTCCACTCCTTGAGAGCTACGCT

>Bacillus_Fam_997_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000759675.1_ASM75967v1_genomic.fna_151:483245-483566 Satlength=322 Nr of Repeats=5 RepeatLength=53 seed=GTTTTGTCCT Num.seqs=3 Similarity=0.740042
0 GTTTTGTCCTCAAGACCCCCGATTGAGGACGAATCCTCTGGGGACTCTTGNTA

Consensus:

GTTTTGTCCTCAAGACCCCCGATTGAGGACGAATCCTCTGGGGACTCTTGNTA

>Bacillus_Fam_998_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_000813125.1_ASM81312v1_genomic.fna_10:31192-31510 Satlength=319 Nr of Repeats=6 RepeatLength=53 seed=AAGAAAGATA Num.seqs=6 Similarity=0.788683
0 AAGAAAGATACCCTTATGCAGCCGTTTGTTCATCACATAAGGGTACGAAAACCG

Consensus:

AAGAAAGATACCCTTATGCAGCCGTTTGTTCATCACATAAGGGTACGAAAACCG

>Bacillus_Fam_999_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_118:4594-4855 Satlength=262 Nr of
Repeats=5 RepeatLength=52 seed=TATTGGTTAC Num.seqs=4 Similarity=0.660377
0 TATTGGTTACCTATAATTCTAGTTTCAGCCCTTTTATAGGGCACCAATAACGCC

Consensus:

TATTGGTTACCTATAATTCTAGTTTCAGCCCTTTTATAGGGCACCAATAACGCC

>Bacillus_Fam_1000_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_001315165.1_ASM131516v1_genomic.fna_1:59355-59632 Satlength=278 Nr of
Repeats=5 RepeatLength=53 seed=GTACCCTTAT Num.seqs=4 Similarity=0.878407
0 GTACCCTTATGGAGAGCTTTCGCTTGGTATAAGGATACGATTAGGAGAAAATC

Consensus:

GTACCCTTATGGAGAGCTTTCGCTTGGTATAAGGATACGATTAGGAGAAAATC

>Bacillus_Fam_1001_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_001315165.1_ASM131516v1_genomic.fna_18:0-258 Satlength=259 Nr of
Repeats=5 RepeatLength=52 seed=CTTCAGACAA Num.seqs=4 Similarity=0.834382
0 CTTCAGACAAAATCTGCACGCCTAAGACGTGGTTTTGGCCGAACATGGCATCA

Consensus:

CTTCAGACAAAATCTGCACGCCTAAGACGTGGTTTTGGCCGAACATGGCATCA

>Bacillus_Fam_1002_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_001315165.1_ASM131516v1_genomic.fna_110:6-377 Satlength=372 Nr of
Repeats=7 RepeatLength=53 seed=TATCCTTATG Num.seqs=7 Similarity=0.834681
0 TATCCTTATGAGGTAAAATCCAGCAACATAAGGGTACCGTTCAAGCCNAATCG

Consensus:

TATCCTTATGAGGTAAAATCCAGCAACATAAGGGTACCGTTCAAGCCNAATCG

>Bacillus_Fam_1003_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_83:366387-367075 Satlength=689 Nr of
Repeats=13 RepeatLength=53 seed=CCTAAAAAGA Num.seqs=12
Similarity=0.861254
0 CCTAAAAAGAGGAAAATGGTGACCGTCAAAACGAAAGCAATGGTCACCAATCT

Consensus:

CCTAAAAAGAGGAAAATGGTGACCGTCAAAACGAAAGCAATGGTCACCAATCT

>Bacillus_Fam_1004_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_116:264620-264828 Satlength=209

Nr of Repeats=4 RepeatLength=52 seed=GTATTGCGAC Num.seqs=4

Similarity=0.578704

0

GTATTGCGACACAAAGCAAGAATTTTCAGCAAGCCGAGTCCGAATANAGCNTC

Consensus:

GTATTGCGACACAAAGCAAGAATTTTCAGCAAGCCGAGTCCGAATANAGCNTC

>Bacillus_Fam_1005_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_125:212481-212689 Satlength=209

Nr of Repeats=4 RepeatLength=52 seed=CTTATGAAGA Num.seqs=4

Similarity=0.859539

0

CTTATGAAGACCTTTTCGACGAGCCACGAGTTCTGATTGAGTCTTCATCACG

Consensus:

CTTATGAAGACCTTTTCGACGAGCCACGAGTTCTGATTGAGTCTTCATCACG

>Bacillus_Fam_1006_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001591485.1_ASM159148v1_genomic.fna_83:11410-11726 Satlength=317 Nr

of Repeats=6 RepeatLength=53 seed=ATGAAAGACA Num.seqs=5

Similarity=0.849057

0 ATGAAAGACAAAACTCAGGAGAATGGGTGAGGGAATTGTCCTTCATCCGGTGT

Consensus:

ATGAAAGACAAAACTCAGGAGAATGGGTGAGGGAATTGTCCTTCATCCGGTGT

>Bacillus_Fam_1007_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001591485.1_ASM159148v1_genomic.fna_133:5376-5693 Satlength=318 Nr of

Repeats=5 RepeatLength=53 seed=GATGAAGCCC Num.seqs=3 Similarity=0.614256

0 GATGAAGCCCCAAANCCCACTAAGCCACNCAAGGATATGTNCTTCATAGGCNC

Consensus:

GATGAAGCCCCAAANCCCACTAAGCCACNCAAGGATATGTNCTTCATAGGCNC

>Bacillus_Fam_1008_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001591665.1_ASM159166v1_genomic.fna_7:59019-59227 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GTCAATGAAA Num.seqs=4 Similarity=0.701010
0 GTCAATGAAAGCCTCTTCCATTTACCATGGAGGCCCNATTATTTCTCTTTTCG

Consensus:

GTCAATGAAAGCCTCTTCCATTTACCATGGAGGCCCNATTATTTCTCTTTTCG

>Bacillus_Fam_1009_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001591665.1_ASM159166v1_genomic.fna_89:10754-11013 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=TATTGGAGCC Num.seqs=4
Similarity=0.840671

0 TATTGGAGCCCATCTCTGTTTGAAAACCTGGGCAAAAGGTATCCAATCGATCCG

Consensus:

TATTGGAGCCCATCTCTGTTTGAAAACCTGGGCAAAAGGTATCCAATCGATCCG

>Bacillus_Fam_1010_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:69909-70760 Satlength=852 Nr of Repeats=9 RepeatLength=53 seed=TTTTTACCGC Num.seqs=6 Similarity=0.647879
0 TTTTTACCGCCTGACCCCTTCTCAGCACTCCGCGGGCAATAGAACCATCTTC

Consensus:

TTTTTACCGCCTGACCCCTTCTCAGCACTCCGCGGGCAATAGAACCATCTTC

>Bacillus_Fam_1011_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:3822748-3823380 Satlength=633
Nr of Repeats=12 RepeatLength=53 seed=TATTGCCCGA Num.seqs=8
Similarity=0.682760 0

TATTGCCCGATTGNGGTGTCCAAGGGGTGCAAACGGTAAAAAGAACAGGCTTC

Consensus:

TATTGCCCGATTGNGGTGTCCAAGGGGTGCAAACGGTAAAAAGAACAGGCTTC

>Bacillus_Fam_1012_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000

GCF_001636335.1_ASM163633v1_genomic.fna_1:112399-112815 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=TGTCCATCAT Num.seqs=8
Similarity=0.780423

0 TGTCCATCATCCGTTAGATGAAGGCCATTTTATGAGGCAAATCATGGAGTAA

Consensus:

TGTCCATCATCCGTTAGATGAAGGCCATTTTTCAGGCAAATCATGGAGTAA

>Bacillus_Fam_1013_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_42:309000-309527
Satlength=528 Nr of Repeats=10 RepeatLength=53 seed=TTCTGTCCCG
Num.seqs=7 Similarity=0.952081 0
TTCTGTCCCGAATCCGTTTCATACGGGACACTAGGGCATAAAAAGTGCAGACGC

Consensus:

TTCTGTCCCGAATCCGTTTCATACGGGACACTAGGGCATAAAAAGTGCAGACGC

>Bacillus_Fam_1014_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:2816531-2816795 Satlength=265 Nr
of Repeats=5 RepeatLength=53 seed=GTCTCATCC Num.seqs=4
Similarity=0.879115 0
GTCTCATCCCTACCATGATAACAATTCCGAACCCTACTTTCTCTCCAAACAT

Consensus:

GTCTCATCCCTACCATGATAACAATTCCGAACCCTACTTTCTCTCCAAACAT

>Bacillus_Fam_1015_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:2955854-2956755 Satlength=902 Nr
of Repeats=17 RepeatLength=53 seed=TTGCGGGTTC Num.seqs=17
Similarity=0.813356 0
TTGCGGGTTCGCACTTGGAACCTTTCTAGGAGATACCGAACCCGATTCCACCAC

Consensus:

TTGCGGGTTCGCACTTGGAACCTTTCTAGGAGATACCGAACCCGATTCCACCAC

>Bacillus_Fam_1016_53_1 Nr. of seq. 1 Alignment length(with gaps) = 53
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:3971592-3971910 Satlength=319 Nr
of Repeats=6 RepeatLength=53 seed=AGAAAATAGG Num.seqs=6
Similarity=0.914465 0
AGAAAATAGGTAACAGCGAACCGTAAACCATTATAGTGGTATGCAAATGGA

Consensus:

AGAAAATAGGTAACAGCGAACCGTAAACCATTATAGTGGTATGCAAATGGA

>Bacillus_Fam_1017_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:394969-395177 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TAATCGTGTA Num.seqs=4 Similarity=0.797694
0 TAATCGTGTAGATACTGTGACCATTGTGGGGAGTAACTGACATGAAAAGGGC

Consensus:

TAATCGTGTAGATACTGTGACCATTGTGGGGAGTAACTGACATGAAAAGGGC

>Bacillus_Fam_1018_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

BACILLUS_PSEUDALCALIPHILUS_genomic.fna_12:22087-22323 Satlength=237 Nr of Repeats=4 RepeatLength=52 seed=TAGCAACATA Num.seqs=3 Similarity=0.931624
0 TAGCAACATATCGAGTGAAAAGGGCAGAGTTGTTGTAGGAAAAGTCGGGAAG

Consensus:

TAGCAACATATCGAGTGAAAAGGGCAGAGTTGTTGTAGGAAAAGTCGGGAAG

>Bacillus_Fam_1019_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000169195.2_ASM16919v2_genomic.fna_1:619606-619865 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=GCTTTTGTCC Num.seqs=4
Similarity=0.811966

0 GCTTTTGTCCATTTAGAACAGCTAACGGGACAATTCCACCGGAGCTGCCAGC

Consensus:

GCTTTTGTCCATTTAGAACAGCTAACGGGACAATTCCACCGGAGCTGCCAGC

>Bacillus_Fam_1020_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000169195.2_ASM16919v2_genomic.fna_1:1522401-1523027 Satlength=627 Nr of Repeats=12 RepeatLength=52 seed=TGAAGGACAT Num.seqs=10
Similarity=0.525016 0

TGAAGGACATTTTAGGGTTGTGGCGNCTTTGTTTTGTCCTTCATNGGGCGGA

Consensus:

TGAAGGACATTTTAGGGTTGTGGCGNCTTTGTTTTGTCCTTCATNGGGCGGA

>Bacillus_Fam_1021_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000169195.2_ASM16919v2_genomic.fna_1:1523363-1523674 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=AAAAGCCAAA Num.seqs=5
Similarity=0.700000 0

AAAAGCCAAAAGGCACCTGGNNANCGTCCAAACTGTCCTTTAGAACGTCTCA

Consensus:

AAAAGCCAAAAGGCACCTGGNNANCGTCCAAACTGTCCTTTAGAACGTCTCA

>Bacillus_Fam_1022_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000171615.1_ASM17161v1_genomic.fna_81:65762-66019 Satlength=258 Nr of
Repeats=5 RepeatLength=52 seed=GCTCTTCTCT Num.seqs=4 Similarity=0.747379
0 GCTCTTCTCTTCTTCCTGCTGCCTTTGAGACACGCGCTACCCCTAGCGCGGC

Consensus:

GCTCTTCTCTTCTTCCTGCTGCCTTTGAGACACGCGCTACCCCTAGCGCGGC

>Bacillus_Fam_1023_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000171615.1_ASM17161v1_genomic.fna_88:78004-78212 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=GGCGCGGTGC Num.seqs=4 Similarity=0.854701
0 GGCGCGGTGCAGAAAGTAGGTTTGGGCAGGGGTGAGAGCACCGCGCGGGGGT

Consensus:

GGCGCGGTGCAGAAAGTAGGTTTGGGCAGGGGTGAGAGCACCGCGCGGGGGT

>Bacillus_Fam_1024_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000171615.1_ASM17161v1_genomic.fna_129:29159-29367 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TTTTGGGCAC Num.seqs=4
Similarity=0.813941
0 TTTTGGGCACCGCGCGGACGCGGCGGCGCTCTTCTCACGCTGCAACTCAC

Consensus:

TTTTGGGCACCGCGCGGACGCGGCGGCGCTCTTCTCACGCTGCAACTCAC

>Bacillus_Fam_1025_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000175075.1_ASM17507v1_genomic.fna_3:45105-45313 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=GAGATGTCTT Num.seqs=4 Similarity=0.897436
0 GAGATGTCTTCATCCATGCGATGAGGACCTGTCTACGCACAAATAGGAACGA

Consensus:

GAGATGTCTTCATCCATGCGATGAGGACCTGTCTACGCACAAATAGGAACGA

>Bacillus_Fam_1026_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000175075.1_ASM17507v1_genomic.fna_29:76482-76950 Satlength=469 Nr of
Repeats=9 RepeatLength=52 seed=AGGTCTTCAT Num.seqs=9 Similarity=0.832285
0 AGGTCTTCATACACCTTATGAAGACACTTCCAAGCCTGAAATCCTTCCACTA

Consensus:

AGGTCTTCATACACCTTATGAAGACACTTCCAAGCCTGAAATCCTTCCACTA

>Bacillus_Fam_1027_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_31:72973-73233 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GACATCTCTC Num.seqs=5 Similarity=0.851282

0 GACATCTCTCCACCGGAAATCTTCTCTCACATGTCTTCATTCCGCTTATGAG

Consensus:

GACATCTCTCCACCGGAAATCTTCTCTCACATGTCTTCATTCCGCTTATGAG

>Bacillus_Fam_1028_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_31:101319-101579 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GATGAAGACA Num.seqs=5

Similarity=0.907692

0 GATGAAGACATTCCTCATGATGATTTCTTTTCCAAAGTGTCTTCATCATGCG

Consensus:

GATGAAGACATTCCTCATGATGATTTCTTTTCCAAAGTGTCTTCATCATGCG

>Bacillus_Fam_1029_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_32:508521-508729 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CAACATTGTC Num.seqs=4

Similarity=0.747863

0 CAACATTGTCCTCGTAGGTAGCGTACGACTCCCTGAGAAGGTGAAAACCCGC

Consensus:

CAACATTGTCCTCGTAGGTAGCGTACGACTCCCTGAGAAGGTGAAAACCCGC

>Bacillus_Fam_1030_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_34:87713-88025 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=AACGAGGACA Num.seqs=6 Similarity=0.912821

0 AACGAGGACAATGTTGACGTGATTTCTGGGGTTACCGGGTTTCATAGGAGTTC

Consensus:

AACGAGGACAATGTTGACGTGATTTCTGGGGTTACCGGGTTTCATAGGAGTTC

>Bacillus_Fam_1031_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_36:83466-83673 Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=TGTTTGGTAA Num.seqs=3 Similarity=0.863248
0 TGTTTGGTAAGATAGAGGGGTTCTATACGCCCCGAAGCAGCATGGTAAAAGGC

Consensus:

TGTTTGGTAAGATAGAGGGGTTCTATACGCCCCGAAGCAGCATGGTAAAAGGC

>Bacillus_Fam_1032_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_38:28329-28537 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=GCTTCTATAC Num.seqs=4 Similarity=0.806080
0 GCTTCTATACTACCGAAGACCTCGGGATTCTTACCGTTCGGGCGTATAGAAC

Consensus:

GCTTCTATACTACCGAAGACCTCGGGATTCTTACCGTTCGGGCGTATAGAAC

>Bacillus_Fam_1033_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_39:50471-50679 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=AGGTAGTCAT Num.seqs=4 Similarity=0.710391
0 AGGTAGTCATACGCTTTGAACGAGGACAATGTTTTACACTTTTCAGTGGGGA

Consensus:

AGGTAGTCATACGCTTTGAACGAGGACAATGTTTTACACTTTTCAGTGGGGA

>Bacillus_Fam_1034_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_44:72380-72692 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=CTATACGACC Num.seqs=6 Similarity=0.864957
0 CTATACGACCGAAGCTACTTATCAAGCTCCCCTTCCGTCTTATAGAACCCCT

Consensus:

CTATACGACCGAAGCTACTTATCAAGCTCCCCTTCCGTCTTATAGAACCCCT

>Bacillus_Fam_1035_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_46:18322-18634 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GACCGAAGCA Num.seqs=6 Similarity=0.909402
0 GACCGAAGCAACCCCTATTACCTCGAAACGTCGTATAGAACGCTTCTATAC

Consensus:

GACCGAAGCAACCCCTATTACCTCGAAACGTCGTATAGAACGCTTCTATAC

>Bacillus_Fam_1036_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:339003-339210 Satlength=208 Nr
of Repeats=4 RepeatLength=52 seed=CCCGTTAGAG Num.seqs=3
Similarity=0.931624
0 CCCGTTAGAGCAGGATTCAATAACTAAGTGTGCGATTAAACAGGGTTTAAAT

Consensus:

CCCGTTAGAGCAGGATTCAATAACTAAGTGTGCGATTAAACAGGGTTTAAAT

>Bacillus_Fam_1037_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:650939-651407 Satlength=469 Nr
of Repeats=8 RepeatLength=52 seed=GTGTCATAGC Num.seqs=7
Similarity=0.668464
0 GTGTCATAGCACTCGTATGACGCATCTTATATTGAATCTCTAGCTATGTNGT

Consensus:

GTGTCATAGCACTCGTATGACGCATCTTATATTGAATCTCTAGCTATGTNGT

>Bacillus_Fam_1038_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:857866-858230 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=TAGTCTGAGT Num.seqs=7
Similarity=0.904163
0 TAGTCTGAGTGGATATAAAACACGAAATAAAATCTCGTTGTGATGGTGAGTC

Consensus:

TAGTCTGAGTGGATATAAAACACGAAATAAAATCTCGTTGTGATGGTGAGTC

>Bacillus_Fam_1039_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:1710465-1710724 Satlength=260 Nr
of Repeats=5 RepeatLength=52 seed=CCCGTTAGAA Num.seqs=4
Similarity=0.893162 0
CCCGTTAGAAATGATTATCCCGTGCTGAAGGTAGATAAAACAGCGTTTAAAG

Consensus:

CCCGTTAGAAATGATTATCCCGTGCTGAAGGTAGATAAAACAGCGTTTAAAG

>Bacillus_Fam_1040_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:3148329-3148588 Satlength=260 Nr
of Repeats=5 RepeatLength=52 seed=TGCGAGTGGA Num.seqs=4
Similarity=0.824786 0
TGCGAGTGGACTTTAAAGTGCCTATAAAATCCCATGAGGTAGAGGGAGCATG

Consensus:

TGCGAGTGGACTTTTAAAGTGCCTATAAAATCCCATGAGGTAGAGGGAGCATG

>Bacillus_Fam_1041_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:3704894-3705310 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=TTTTCCGTTC Num.seqs=8
Similarity=0.891941 0
TTTTCCGTTCAGTGGATCCTCTCTTCCTTGAACGGAATTCTTTGTCATTTTC

Consensus:

TTTTCCGTTCAGTGGATCCTCTCTTCCTTGAACGGAATTCTTTGTCATTTTC

>Bacillus_Fam_1042_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:3773627-3773939 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=TTGCTTTCCT Num.seqs=6
Similarity=0.904274 0
TTGCTTTCCTTTCTAAGGCACTCAGCTTCCTGGAAAGGAATACTAAGCCACT

Consensus:

TTGCTTTCCTTTCTAAGGCACTCAGCTTCCTGGAAAGGAATACTAAGCCACT

>Bacillus_Fam_1043_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:3821441-3821909 Satlength=469 Nr
of Repeats=9 RepeatLength=52 seed=AATGGGTTC Num.seqs=9
Similarity=0.868274 0
AATGGGTTCATTTTGTTCGCGTGCCTTTTGCGCGTTGTTTTCTGCTCG

Consensus:

AATGGGTTCATTTTGTTCGCGTGCCTTTTGCGCGTTGTTTTCTGCTCG

>Bacillus_Fam_1044_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:3996570-3997090 Satlength=521 Nr
of Repeats=10 RepeatLength=52 seed=AAGGAATGGG Num.seqs=10
Similarity=0.924217 0
AAGGAATGGGCGCTATTCTTATTGCTGGCCTTTACCTCTGATTTTGTGTA

Consensus:

AAGGAATGGGCGCTATTCTTATTGCTGGCCTTTACCTCTGATTTTGTGTA

>Bacillus_Fam_1045_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:4116764-4117128 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=CTTTCTCGGA Num.seqs=7
Similarity=0.888889 0
CTTTCTCGGATAGTTTTCTTTTCAGAGACTTTTTCTTCTTTGAACGGAACG

Consensus:

CTTTCTCGGATAGTTTTCTTTTCAGAGACTTTTTCTTCTTTGAACGGAACG

>Bacillus_Fam_1046_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:4188801-4189419 Satlength=619 Nr
of Repeats=11 RepeatLength=52 seed=TTCTTTCTTA Num.seqs=9
Similarity=0.856125 0
TTCTTTCTACTAGTAAAATCAGCCATGAAAGGAATACTAAACGCCTTCACT

Consensus:

TTCTTTCTACTAGTAAAATCAGCCATGAAAGGAATACTAAACGCCTTCACT

>Bacillus_Fam_1047_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:4365838-4366774 Satlength=937 Nr
of Repeats=18 RepeatLength=52 seed=TAAAGGAATA Num.seqs=18
Similarity=0.863415 59
CTCGTCCTAAAGGAATACTAAGCACTCTGGCTTTCCTTTCTACGTCGATTCC

Consensus:

TAAAGGAATACTAAGCACTCTGGCTTTCCTTTCTACGTCGATTCCCTCGTCC

>Bacillus_Fam_1048_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_145:9012-9583 Satlength=572 Nr of
Repeats=11 RepeatLength=52 seed=GTTGTCGATT Num.seqs=10
Similarity=0.876353
0 GTTGTCGATTAGGATTATGAAAAAATCGATGGTGCCAAAAGGTGCGAATGGG

Consensus:

GTTGTCGATTAGGATTATGAAAAAATCGATGGTGCCAAAAGGTGCGAATGGG

>Bacillus_Fam_1049_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_158:13126-13858 Satlength=733 Nr
of Repeats=14 RepeatLength=52 seed=CCCCGTCAAA Num.seqs=10
Similarity=0.862678 0
CCCCGTCAAAAGAGAGGGTATGAGGGTGTGCAATTGAATTTTGGTTGAATCGG

Consensus:

CCCCGTCAAAGAGAGGGTATGAGGGTGTCTGAATTGAATTTGGTTGAATCGG

>Bacillus_Fam_1050_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_163:107-991 Satlength=885 Nr of
Repeats=17 RepeatLength=52 seed=GAAACGTACC Num.seqs=15
Similarity=0.871795

0 GAAACGTACCAATATAGAGTCAGAATCCTGCTGTAGTGGTAAGATTCGAGAA

Consensus:

GAAACGTACCAATATAGAGTCAGAATCCTGCTGTAGTGGTAAGATTCGAGAA

>Bacillus_Fam_1051_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_174:41004-41469 Satlength=466 Nr
of Repeats=9 RepeatLength=52 seed=AGGAATGATG Num.seqs=6
Similarity=0.909402

0 AGGAATGATGTAGGAATGCAGGGGTAATTAGAGCATCAAATCGGAGAAGTGA

Consensus:

AGGAATGATGTAGGAATGCAGGGGTAATTAGAGCATCAAATCGGAGAAGTGA

>Bacillus_Fam_1052_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_175:27082-27342 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=GGGTGTCTCA Num.seqs=5
Similarity=0.830769

0 GGGTGTCTCATGAACGCTTCATGGGGCCATTTTGCCTGCATATTTGAAGTTA

Consensus:

GGGTGTCTCATGAACGCTTCATGGGGCCATTTTGCCTGCATATTTGAAGTTA

>Bacillus_Fam_1053_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000181495.1_ASM18149v1_genomic.fna_178:14811-15278 Satlength=468 Nr
of Repeats=9 RepeatLength=52 seed=GGTGGTCGAA Num.seqs=8
Similarity=0.883700

0 GGTGGTCGAATCCCAAAAAAGAGAATCGGCCCCGTCAAAGTGCTGCTTCGA

Consensus:

GGTGGTCGAATCCCAAAAAAGAGAATCGGCCCCGTCAAAGTGCTGCTTCGA

>Bacillus_Fam_1054_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_186:206325-206533 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GGTGGAATTT Num.seqs=4
Similarity=0.751048 0
GGTGGAATTTAGTTTTGGAGAAATCGGCATGGTCAAAGCGGGCGAAAGACAG

Consensus:

GGTGGAATTTAGTTTTGGAGAAATCGGCATGGTCAAAGCGGGCGAAAGACAG

>Bacillus_Fam_1055_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_4:74543-74803
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CTCAACCAGA Num.seqs=3
Similarity=0.676955 0
CTCAACCAGAGTCCGAAGTTGTACTAGGTTTCGGACTCAAATTNCAGGATGAG

Consensus:

CTCAACCAGAGTCCGAAGTTGTACTAGGTTTCGGACTCAAATTNCAGGATGAG

>Bacillus_Fam_1056_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_4:197835-198199
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=ATGAAGCCGA Num.seqs=7
Similarity=0.710758 0
ATGAAGCCGAAAAGTCGTGNAGCGATAAGAAAACGGTCGCCATGAGGCAGTC

Consensus:

ATGAAGCCGAAAAGTCGTGNAGCGATAAGAAAACGGTCGCCATGAGGCAGTC

>Bacillus_Fam_1057_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_5:287610-288102
Satlength=493 Nr of Repeats=9 RepeatLength=52 seed=GACGAAAATT Num.seqs=7
Similarity=0.750916 0
GACGAAAATTCAGTGGCTCACCAANAAATGGTCGACATAGAGCCTTCATGAA

Consensus:

GACGAAAATTCAGTGGCTCACCAANAAATGGTCGACATAGAGCCTTCATGAA

>Bacillus_Fam_1058_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000285535.1_ASM28553v1_genomic.fna_1:1333233-1333493 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TCACAGACAA Num.seqs=5
Similarity=0.776923 0
TCACAGACAATTCATTCAACTTTTTACTNCGNTTGTCTTCGAGACTGGCTA

Consensus:

TCACAGACAATTCACTCAACTTTTTACTNCGNTTTGTCTTCGAGACTGGCTA

>Bacillus_Fam_1059_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000285535.1_ASM28553v1_genomic.fna_2:421697-421905 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TATGAAGGAC Num.seqs=4
Similarity=0.738994

0 TATGAAGGACTTTCTACCGGCCAGGCTGCTCGTTTCGAGGCTTCATCGGCCT

Consensus:

TATGAAGGACTTTCTACCGGCCAGGCTGCTCGTTTCGAGGCTTCATCGGCCT

>Bacillus_Fam_1060_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000285535.1_ASM28553v1_genomic.fna_2:945617-946345 Satlength=729 Nr
of Repeats=14 RepeatLength=52 seed=TCAGTTTCTC Num.seqs=14
Similarity=0.766234

TCAGTTTCTCAGACCNAATCCCCTTCATAGACCACTTGAAGAGGATACACCT

0

Consensus:

TCAGTTTCTCAGACCNAATCCCCTTCATAGACCACTTGAAGAGGATACACCT

>Bacillus_Fam_1061_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000285535.1_ASM28553v1_genomic.fna_3:73213-73421 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=CCTCGGCATA Num.seqs=4 Similarity=0.901709

0 CCTCGGCATACTCCGGTTTGTCTTGTCTCCGAGAGCAGCTATCAAACACTTT

Consensus:

CCTCGGCATACTCCGGTTTGTCTTGTCTCCGAGAGCAGCTATCAAACACTTT

>Bacillus_Fam_1062_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000285535.1_ASM28553v1_genomic.fna_3:346534-347418 Satlength=885 Nr
of Repeats=17 RepeatLength=52 seed=TTCAATGCCT Num.seqs=17
Similarity=0.826934

TTCAATGCCTCGATGAAGAGCATAACGCAACAGAACTATGCTCGAATTCCTC

0

Consensus:

TTCAATGCCTCGATGAAGAGCATAACGCAACAGAACTATGCTCGAATTCCTC

>Bacillus_Fam_1063_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_3:32494-32754 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=TTGGACATTC Num.seqs=5 Similarity=0.833333
0 TTGGACATTCTGACTACCTCCACTTTCTCCTTTGTCCTTTAAACTTGGGATA

Consensus:

TTGGACATTCTGACTACCTCCACTTTCTCCTTTGTCCTTTAAACTTGGGATA

>Bacillus_Fam_1064_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_9:64736-64996 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=TACATGTTTT Num.seqs=5 Similarity=0.938462
0 TACATGTTTTGGCTGGTTGCTGACCATTATTTGGGTGCCATACTCATTGGG

Consensus:

TACATGTTTTGGCTGGTTGCTGACCATTATTTGGGTGCCATACTCATTGGG

>Bacillus_Fam_1065_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_29:13895-14099 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=TAATTCGTAA Num.seqs=4 Similarity=0.692387
0 TAATTCGTAATGTAATTTCCCACTATGNACTAATTACGGTGCGTATAACCCC

Consensus:

TAATTCGTAATGTAATTTCCCACTATGNACTAATTACGGTGCGTATAACCCC

>Bacillus_Fam_1066_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000294775.2_ASM29477v2_genomic.fna_1:1113586-1113995 Satlength=410 Nr
of Repeats=6 RepeatLength=52 seed=GTTCGACAG Num.seqs=4
Similarity=0.786325 0
GTTCGACAGGAGAAGAGGAAAAACCGTGGATTGAGTCCGAAGTCGCCCTAT

Consensus:

GTTCGACAGGAGAAGAGGAAAAACCGTGGATTGAGTCCGAAGTCGCCCTAT

>Bacillus_Fam_1067_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000294775.2_ASM29477v2_genomic.fna_1:4788379-4788640 Satlength=262 Nr
of Repeats=5 RepeatLength=52 seed=TTTCGACAGA Num.seqs=4
Similarity=0.863248 0
TTTCGACAGACTCTGGACTTTTTCTGCCTTGCTGTCCGAAGTGGCCAGG

Consensus:

TTCGGACAGACTCTGGACTTTTTCTGCCTTGCTGTCCGAACTTGCCCCAGG

>Bacillus_Fam_1068_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000307855.1_BAZO1.0_genomic.fna_40:158681-158889 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TTTATCCTCA Num.seqs=4 Similarity=0.923077
0 TTTATCCTCACCAAACCGAGCCTAGATGAGGTTTGATAGTAAATAACTCGTG

Consensus:

TTTATCCTCACCAAACCGAGCCTAGATGAGGTTTGATAGTAAATAACTCGTG

>Bacillus_Fam_1069_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000307855.1_BAZO1.0_genomic.fna_128:3586-3794 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TTTGGTGAGG Num.seqs=4 Similarity=0.829060
0 TTTGGTGAGGATAAAAGCAGGTTATCTACTACCAAAGTAAGTAGAGTGGA

Consensus:

TTTGGTGAGGATAAAAGCAGGTTATCTACTACCAAAGTAAGTAGAGTGGA

>Bacillus_Fam_1070_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000307875.1_BABA1.0_genomic.fna_114:10800-11164 Satlength=365 Nr of
Repeats=7 RepeatLength=52 seed=AAAATCTAGC Num.seqs=7 Similarity=0.875458
0 AAAATCTAGCGGACTGTCCTTAATAGGCGCTGTTGAGGACAAAACGGGGTTG

Consensus:

AAAATCTAGCGGACTGTCCTTAATAGGCGCTGTTGAGGACAAAACGGGGTTG

>Bacillus_Fam_1071_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000311725.1_ASM31172v1_genomic.fna_4:536064-536636 Satlength=573 Nr
of Repeats=11 RepeatLength=52 seed=TCTGTCCGAA Num.seqs=11
Similarity=0.756253
TCTGTCCGAATGCACCTCTTATTCGGAATCCTTCACCTCTCTACTACCTTT

Consensus:

TCTGTCCGAATGCACCTCTTATTCGGAATCCTTCACCTCTCTACTACCTTT

>Bacillus_Fam_1072_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000311725.1_ASM31172v1_genomic.fna_7:13528-13944 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=ATTCGGACAA Num.seqs=8 Similarity=0.889194
0 ATTCGGACAAGCCTATGGCTTCTTGCTTCCTACTTGTCCGAATATCCTTCG

Consensus:

ATTCGGACAAGCCTATGGCTTCTTGCTTCCTACTTGTCCGAATATCCTTCCG

>Bacillus_Fam_1073_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:30506-31078 Satlength=573 Nr of
Repeats=11 RepeatLength=52 seed=TGTCCGAAC T Num.seqs=11
Similarity=0.902098
0 TGTCCGAAC TAGGCTTAAGTTCGGACAGAAATGACCGCTTTTCTCAAATGG

Consensus:

TGTCCGAAC TAGGCTTAAGTTCGGACAGAAATGACCGCTTTTCTCAAATGG

>Bacillus_Fam_1074_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_3:87769-87977 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=ATTGCGTTGC Num.seqs=4 Similarity=0.871795
0 ATTGCGTTGCTCTCGATCAAGAAATGGACTTCATAGCCGAGGTAACGATCGT

Consensus:

ATTGCGTTGCTCTCGATCAAGAAATGGACTTCATAGCCGAGGTAACGATCGT

>Bacillus_Fam_1075_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000374345.1_ASM37434v1_genomic.fna_4:25818-26244 Satlength=427 Nr of
Repeats=6 RepeatLength=52 seed=CGTTCATAAG Num.seqs=5 Similarity=0.779487
0 CGTTCATAAGGCGGATGAAAGCCATTGTAAAGAGAAAAACAGGTGAGAAGG

Consensus:

CGTTCATAAGGCGGATGAAAGCCATTGTAAAGAGAAAAACAGGTGAGAAGG

>Bacillus_Fam_1076_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000374345.1_ASM37434v1_genomic.fna_7:32632-33048 Satlength=417 Nr of
Repeats=8 RepeatLength=52 seed=AATGGCGTTC Num.seqs=8 Similarity=0.884615
0 AATGGCGTTCATCAGCCGTATGAACGCTATCTCTACCGGGTTGATCCTTGA

Consensus:

AATGGCGTTCATCAGCCGTATGAACGCTATCTCTACCGGGTTGATCCTTGA

>Bacillus_Fam_1077_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374345.1_ASM37434v1_genomic.fna_7:56200-56512 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=CGGGCTTTCA Num.seqs=6 Similarity=0.731070
0 CGGGCTTTCATATCCCCAATGAACGACCGTTTCCCCGGGCACTTGCCTGATT

Consensus:

CGGGCTTTCATATCCCCAATGAACGACCGTTTCCCCGGGCACTTGCCTGATT

>Bacillus_Fam_1078_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374345.1_ASM37434v1_genomic.fna_9:65991-66356 Satlength=366 Nr of Repeats=7 RepeatLength=52 seed=GCGAAATGAA Num.seqs=6 Similarity=0.789727
0 GCGAAATGAAGTTCATCAGGCCTATGAAAGCAATCGCGGCCGAAATTTTAGA

Consensus:

GCGAAATGAAGTTCATCAGGCCTATGAAAGCAATCGCGGCCGAAATTTTAGA

>Bacillus_Fam_1079_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374345.1_ASM37434v1_genomic.fna_24:14134-14498 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GGGCTTTCAT Num.seqs=7 Similarity=0.714585
0 GGGCTTTCATTTCGACCGATGATCGACCGCGCGGATGGTTTTTCTCTCGCGT

Consensus:

GGGCTTTCATTTCGACCGATGATCGACCGCGCGGATGGTTTTTCTCTCGCGT

>Bacillus_Fam_1080_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374345.1_ASM37434v1_genomic.fna_26:26410-26774 Satlength=365 Nr of Repeats=6 RepeatLength=52 seed=ATGAACGCGA Num.seqs=5 Similarity=0.803086
0 ATGAACGCGATCACGAATGAAAAAGGGGGTTACGATGGTGTTCATAAGNCCG

Consensus:

ATGAACGCGATCACGAATGAAAAAGGGGGTTACGATGGTGTTCATAAGNCCG

>Bacillus_Fam_1081_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374345.1_ASM37434v1_genomic.fna_44:13486-13902 Satlength=417 Nr of Repeats=8 RepeatLength=52 seed=ATAGCGTTCA Num.seqs=8 Similarity=0.722527
0 ATAGCGTTCATCCCGGTATGAACTTCATCTTGANTATCTTTTTTACTTGNA

Consensus:

ATAGCGTTCATCCCGGTATGAACTTCATCTTGANTATCTTTTTTACTTGNA

>Bacillus_Fam_1082_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000374345.1_ASM37434v1_genomic.fna_80:5979-6392 Satlength=414 Nr of
Repeats=8 RepeatLength=52 seed=GCTTATGAAC Num.seqs=5 Similarity=0.861538
0 GCTTATGAACTGCATTTGGCATGGATTTTTTTACCGAGATAGCGTTCATTCC

Consensus:

GCTTATGAACTGCATTTGGCATGGATTTTTTTACCGAGATAGCGTTCATTCC

>Bacillus_Fam_1083_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_1:689690-690002 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=CGGGCACTTT Num.seqs=6
Similarity=0.786373
0 CGGGCACTTTTAGCCTCTATTAGTGACCGGTTCTCTCGACAAACTCTATTTG

Consensus:

CGGGCACTTTTAGCCTCTATTAGTGACCGGTTCTCTCGACAAACTCTATTTG

>Bacillus_Fam_1084_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_3:204349-204867 Satlength=519 Nr
of Repeats=10 RepeatLength=52 seed=AATCGGTAAC Num.seqs=8
Similarity=0.749084
0 AATCGGTAAC TAATAGGCAGGAAAGATGCCCGAATCCGNTGTGTCTCGTCCCGC

Consensus:

AATCGGTAAC TAATAGGCAGGAAAGATGCCCGAATCCGNTGTGTCTCGTCCCGC

>Bacillus_Fam_1085_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_5:148962-149638 Satlength=677 Nr
of Repeats=13 RepeatLength=52 seed=CGTATATCCC Num.seqs=13
Similarity=0.844541
CGTATATCCCAAAAAGCGGTCACCAATCGTATGGATTAGTGCCCGTTCTGAG

0

Consensus:

CGTATATCCCAAAAAGCGGTCACCAATCGTATGGATTAGTGCCCGTTCTGAG

>Bacillus_Fam_1086_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_6:158147-158511 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=AAAAGCGGTC Num.seqs=5
Similarity=0.769811
0 AAAAGCGGTCACGATTAGTGAGGAAAGATGCCCGTTT TAGTCGGTTTT CAGT

Consensus:

AAAAGCGGTCACGATTAGTGAGGAAAGATGCCCGTTTTAGTCGGTTTTTCAGT

>Bacillus_Fam_1087_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374565.1_ASM37456v1_genomic.fna_7:2370-2942 Satlength=573 Nr of
Repeats=11 RepeatLength=52 seed=TATTTGTGAC Num.seqs=11
Similarity=0.857343

0 TATTTGTGACCGGATTTCTGATTTCTCCCTTCAAACGGGCATCTTCCACTAC

Consensus:

TATTTGTGACCGGATTTCTGATTTCTCCCTTCAAACGGGCATCTTCCACTAC

>Bacillus_Fam_1088_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374565.1_ASM37456v1_genomic.fna_12:88054-88651 Satlength=598 Nr of
Repeats=8 RepeatLength=52 seed=TCCTAAAAA Num.seqs=7 Similarity=0.860806

0 TCCTAAAAAGTGCTAAAAAGTGCCCGTAATGTGGTGAATCACGAAAATCCGG

Consensus:

TCCTAAAAAGTGCTAAAAAGTGCCCGTAATGTGGTGAATCACGAAAATCCGG

>Bacillus_Fam_1089_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374565.1_ASM37456v1_genomic.fna_16:33589-34317 Satlength=729 Nr of
Repeats=12 RepeatLength=52 seed=ACCGCTTTTT Num.seqs=10
Similarity=0.750105

0 ACCGCTTTTTACCAAAATCTCTCGTAACGGGCACCTTTCTCCAACATTAGTG

Consensus:

ACCGCTTTTTACCAAAATCTCTCGTAACGGGCACCTTTCTCCAACATTAGTG

>Bacillus_Fam_1090_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374565.1_ASM37456v1_genomic.fna_22:20071-20488 Satlength=418 Nr of
Repeats=8 RepeatLength=52 seed=ACCAATAAAG Num.seqs=7 Similarity=0.912088

0 ACCAATAAAGGTTAATAGTGCCCGAAAAGGAGAAAAAAGTGCTCTAATGGTC

Consensus:

ACCAATAAAGGTTAATAGTGCCCGAAAAGGAGAAAAAAGTGCTCTAATGGTC

>Bacillus_Fam_1091_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000374565.1_ASM37456v1_genomic.fna_29:30054-30365 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=GATTAGTGAC Num.seqs=5 Similarity=0.826415
50 TTAGTGACCGNTTTTCGGATTAACGCAACTTTTCGGGCATCTTTTACTCCGA

Consensus:

GATTAGTGACCGNTTTTCGGATTAACGCAACTTTTCGGGCATCTTTTACTCC

>Bacillus_Fam_1092_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000401235.1_BacNeaAAU1_genomic.fna_144:20-332 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=GTTTCATCTTG Num.seqs=6 Similarity=0.859829
0 GTTCATCTTGTTTATGAACGATAGTTTTGCCCTCTTCTTTTGAAAAAGTGGC

Consensus:

GTTCATCTTGTTTATGAACGATAGTTTTGCCCTCTTCTTTTGAAAAAGTGGC

>Bacillus_Fam_1093_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000401235.1_BacNeaAAU1_genomic.fna_153:115-374 Satlength=260 Nr of Repeats=5 RepeatLength=52 seed=TGGCTTTCAT Num.seqs=4 Similarity=0.871795
0 TGGCTTTCATTCCCTTGATGAACGCCACTTTCCTCCAAGATTACCTTAAAC

Consensus:

TGGCTTTCATTCCCTTGATGAACGCCACTTTCCTCCAAGATTACCTTAAAC

>Bacillus_Fam_1094_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000430765.1_ASM43076v1_genomic.fna_3:286133-286444 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=TGTCCGAAGT Num.seqs=5 Similarity=0.861538
0 TGTCCGAAGTGGGTCTGTGTTTCGACAACCTCCGGATGAATCCAAGCCAAC

Consensus:

TGTCCGAAGTGGGTCTGTGTTTCGACAACCTCCGGATGAATCCAAGCCAAC

>Bacillus_Fam_1095_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000430765.1_ASM43076v1_genomic.fna_5:148049-148621 Satlength=573 Nr of Repeats=11 RepeatLength=52 seed=TCTCTGAACC Num.seqs=9 Similarity=0.735755
0 TCTCTGAACCATTTNCCAGCGGAGCAGCCTCNGTTTTGGTCTTGAGACGCCT

Consensus:

TCTCTGAACCATTTNCCAGCGGAGCAGCCTCNGTTTTGGTCTTGAGACGCCT

>Bacillus_Fam_1096_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_6:140008-140268 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TCTCATGACC Num.seqs=5
Similarity=0.979487
0 TCTCATGACCAAACTTCTGCCGCTTCCCCTCTTTATGGTTCTGAGACGCAC

Consensus:

TCTCATGACCAAACTTCTGCCGCTTCCCCTCTTTATGGTTCTGAGACGCAC

>Bacillus_Fam_1097_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_7:289548-290021 Satlength=474 Nr
of Repeats=9 RepeatLength=52 seed=CCTCTCAAGA Num.seqs=6
Similarity=0.858700
0 CCTCTCAAGACCAAAATTCCTTTAAGCAAGCGGAGAAGTGGTTCAGAGAGGG

Consensus:

CCTCTCAAGACCAAAATTCCTTTAAGCAAGCGGAGAAGTGGTTCAGAGAGGG

>Bacillus_Fam_1098_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_9:15-224 Satlength=210 Nr of
Repeats=4 RepeatLength=52 seed=GGATGACGAA Num.seqs=3 Similarity=0.811321
0 GGATGACGAAGATAGGTCAATGAGAAGGGTTCTAATGGACACTACGCTGAAN

Consensus:

GGATGACGAAGATAGGTCAATGAGAAGGGTTCTAATGGACACTACGCTGAAN

>Bacillus_Fam_1099_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_12:149140-149400 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TCAGGACCAA Num.seqs=5
Similarity=0.948718
7 GGGCGTCTCAGGACCAAAACAAAGACAGAGCTGGTGAAAGTGGTTCAGAGG

Consensus:

TCAGGACCAAAACAAAGACAGAGCTGGTGAAAGTGGTTCAGAGGGGCGTC

>Bacillus_Fam_1100_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000473245.1_ASM47324v1_genomic.fna_1:4633527-4633839 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=GGGTCTTAGT Num.seqs=6
Similarity=0.859829
GGGTCTTAGTTTCTCTGACTAGCACCTCTGGTTTGGTTTTTGTGATTCAGA

0

Consensus:

GGGTCTTAGTTTCTCTGACTAGCACCTCTGGTTTGGTTTTGTGATTCAGA

>Bacillus_Fam_1101_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000508325.1_BAVI_1_genomic.fna_69:22489-22749 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=CGATAAGCTA Num.seqs=5 Similarity=0.775472
0 CGATAAGCTACCCAACCTGGTTCTTTCTTGATGGATTCGGTCGCTTATAANCC

Consensus:

CGATAAGCTACCCAACCTGGTTCTTTCTTGATGGATTCGGTCGCTTATAANCC

>Bacillus_Fam_1102_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000508325.1_BAVI_1_genomic.fna_161:5891-6101 Satlength=211 Nr of
Repeats=4 RepeatLength=52 seed=GGGCACTCTG Num.seqs=3 Similarity=0.846154
0 GGGCACTCTGGCTACTCCACAGTGCCCGGTTGATGCTTTTTTCTCCTCACAT

Consensus:

GGGCACTCTGGCTACTCCACAGTGCCCGGTTGATGCTTTTTTCTCCTCACAT

>Bacillus_Fam_1103_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000612665.1_FF4_genomic.fna_19:82518-82985 Satlength=468 Nr of
Repeats=9 RepeatLength=52 seed=CGGTCATTAA Num.seqs=8 Similarity=0.904762
0 CGGTCATTAAAGCGGGGCTCTAAATGCCCCGCGGAGAGCGAAAAAGGAAGGGAG

Consensus:

CGGTCATTAAAGCGGGGCTCTAAATGCCCCGCGGAGAGCGAAAAAGGAAGGGAG

>Bacillus_Fam_1104_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000612665.1_FF4_genomic.fna_65:35468-35676 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TCTTAGTTAC Num.seqs=4 Similarity=0.850427
0 TCTTAGTTACCGCGAGACCCGCATTTTCTCCTTCGCGGGCATTTAGAGCCCT

Consensus:

TCTTAGTTACCGCGAGACCCGCATTTTCTCCTTCGCGGGCATTTAGAGCCCT

>Bacillus_Fam_1105_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000612665.1_FF4_genomic.fna_66:181657-182736 Satlength=1080 Nr of Repeats=9 RepeatLength=52 seed=TTATAGCCTT Num.seqs=8 Similarity=0.807692
0 TTATAGCCTTTATAAATGACCGACCGACCGGAAAAANCGCCAGCTCGGGCAT

Consensus:

TTATAGCCTTTATAAATGACCGACCGACCGGAAAAANCGCCAGCTCGGGCAT

>Bacillus_Fam_1106_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000708755.2_ASM70875v2_genomic.fna_1:477291-477603 Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=AACCAAGTAA Num.seqs=6
Similarity=0.882051

0 AACCAAGTAAGTGTTCTATACCGTCAATAGCAACACTTTCCTCATCAATTG

Consensus:

AACCAAGTAAGTGTTCTATACCGTCAATAGCAACACTTTCCTCATCAATTG

>Bacillus_Fam_1107_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000708755.2_ASM70875v2_genomic.fna_1:508584-508844 Satlength=261 Nr of Repeats=4 RepeatLength=52 seed=TCGTTTAAGA Num.seqs=3
Similarity=0.836478

0 TCGTTTAAGAGCACTTTGGTCTTGCTGTGAATCGGAGTTCTTGTTGCAAACA

Consensus:

TCGTTTAAGAGCACTTTGGTCTTGCTGTGAATCGGAGTTCTTGTTGCAAACA

>Bacillus_Fam_1108_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000708755.2_ASM70875v2_genomic.fna_2:662686-662998 Satlength=313 Nr of Repeats=5 RepeatLength=52 seed=TATTCAGCCG Num.seqs=4
Similarity=0.863248

0 TATTCAGCCGCAACCAATTTATAGGGTTGCATTTGCCAGTATGGTACCCTC

Consensus:

TATTCAGCCGCAACCAATTTATAGGGTTGCATTTGCCAGTATGGTACCCTC

>Bacillus_Fam_1109_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000708755.2_ASM70875v2_genomic.fna_2:713425-713736 Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=TAGAACACTT Num.seqs=5
Similarity=0.723077

0 TAGAACACTTTCTGCGGTCGGGATNCCNACTTAATGTTGCTTACTCCGGTT

Consensus:

TAGAACACTTTCTGCGGTCGGGATNCCNACTTAATGTTGCTTACTCCGGTT

>Bacillus_Fam_1110_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000708755.2_ASM70875v2_genomic.fna_2:1183664-1183924 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CAAAATGTTG Num.seqs=5
Similarity=0.784906 0
CAAAATGTTGCTAAAGCCAGGTTAGAACACTTTCNGGGCTTTCTGGCCTCTG

Consensus:

CAAAATGTTGCTAAAGCCAGGTTAGAACACTTTCNGGGCTTTCTGGCCTCTG

>Bacillus_Fam_1111_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000708755.2_ASM70875v2_genomic.fna_2:1324156-1324364 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CTGAAGGGCA Num.seqs=4
Similarity=0.854701 0
CTGAAGGGCACATTCCTGCCTGGTTTTTCGACCTTCAGCTTACTTCCTTTTCC

Consensus:

CTGAAGGGCACATTCCTGCCTGGTTTTTCGACCTTCAGCTTACTTCCTTTTCC

>Bacillus_Fam_1112_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000708755.2_ASM70875v2_genomic.fna_2:1620621-1620829 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=ACCCTTCACA Num.seqs=4
Similarity=0.735043 0
ACCCTTCACACAATCCCCTGATAAACGGTCATATCTTATCCACTTATA

Consensus:

ACCCTTCACACAATCCCCTGATAAACGGTCATATCTTATCCACTTATA

>Bacillus_Fam_1113_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000708755.2_ASM70875v2_genomic.fna_2:1684021-1684385 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=ACCTTCAGCT Num.seqs=5
Similarity=0.810256 0
ACCTTCAGCTTCTTCTCCACCAACTGAAGGGCACGATCCATCCGCTTTTGTG

Consensus:

ACCTTCAGCTTCTTCTCCACCAACTGAAGGGCACGATCCATCCGCTTTTGTG

>Bacillus_Fam_1114_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000708755.2_ASM70875v2_genomic.fna_6:178665-178925 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TAAGTGCCT Num.seqs=5
Similarity=0.789091
0 TAAGTGCCTTATCTCGGTTTTAGAACACTTTCACAGATANTGCNCTTTGGC

Consensus:

TAAGTGCCTTATCTCGGTTTTAGAACACTTTCACAGATANTGCNCTTTGGC

>Bacillus_Fam_1115_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000708755.2_ASM70875v2_genomic.fna_6:348631-348839 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GCTGCGGCGG Num.seqs=4
Similarity=0.841880
0 GCTGCGGCGGAAAGGCATGAAGGGTCATAAGAGGCTTGGATTGTTACCTTCA

Consensus:

GCTGCGGCGGAAAGGCATGAAGGGTCATAAGAGGCTTGGATTGTTACCTTCA

>Bacillus_Fam_1116_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000708755.2_ASM70875v2_genomic.fna_7:130520-130728 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TTTCTCCAG Num.seqs=4
Similarity=0.829060
0 TTTCTCCAGGCTCACGCTCCACTTTGTGCTCTTAACCCGCGGAAGCGCAC

Consensus:

TTTCTCCAGGCTCACGCTCCACTTTGTGCTCTTAACCCGCGGAAGCGCAC

>Bacillus_Fam_1117_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_1:71045-71305 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=GAAATATAGG Num.seqs=5 Similarity=0.762963
0 GAAATATAGGGCAGCAAAACATGAAAATGCAACCCTATAAAATGCGCCATCT

Consensus:

GAAATATAGGGCAGCAAAACATGAAAATGCAACCCTATAAAATGCGCCATCT

>Bacillus_Fam_1118_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_1:1027951-1028263 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=CTGTATTTTG Num.seqs=6
Similarity=0.776520
0 CTGTATTTTGGACAAGCNGATTTATAGGGCAGCATTTACCTTTTGGTGCC

Consensus:

CTGTATTTTGGACAAGCNGATTTATAGGGCAGCATTTACCTTTTTGGTGCC

>Bacillus_Fam_1119_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_1:1073715-1073923 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CATAAGTGCT Num.seqs=4
Similarity=0.688034 0
CATAAGTGCTGCAAAGCTGGTTTAACAACATAAACTCAGCTGCAGGAAGCCG

Consensus:

CATAAGTGCTGCAAAGCTGGTTTAACAACATAAACTCAGCTGCAGGAAGCCG

>Bacillus_Fam_1120_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_5:462972-463648 Satlength=677 Nr
of Repeats=13 RepeatLength=52 seed=TTCTTATCGG Num.seqs=13
Similarity=0.793904 0
TTCTTATCGGACGAATNGGTGCCATCAAANCTGATTCTTCTCTGCTTGAGGG

Consensus:

TTCTTATCGGACGAATNGGTGCCATCAAANCTGATTCTTCTCTGCTTGAGGG

>Bacillus_Fam_1121_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_19:19072-19436 Satlength=365 Nr of
Repeats=7 RepeatLength=52 seed=GAACCCCTCAA Num.seqs=7 Similarity=0.848596
0 GAACCCCTCAAGCTTTGGATTCTGTGGATTGATGGCACTTATAGCAGAGTTTA

Consensus:

GAACCCCTCAAGCTTTGGATTCTGTGGATTGATGGCACTTATAGCAGAGTTTA

>Bacillus_Fam_1122_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_19:109951-110159 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=AAGTGTCTT Num.seqs=4
Similarity=0.769231
0 AAGTGTCTTATCCTGCTTTTACAGCACTTATCTTCGCTCCGGAGTCACTCA

Consensus:

AAGTGTCTTATCCTGCTTTTACAGCACTTATCTTCGCTCCGGAGTCACTCA

>Bacillus_Fam_1123_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:243707-244693
Satlength=987 Nr of Repeats=19 RepeatLength=52 seed=AGCGGGTAAA

Num.seqs=17 Similarity=0.943439 0
AGCGGGTAAAATAAAGCGCCGTTTTTTACCGGTGATAGCCTTTTTTCGCTCC

Consensus:

AGCGGGTAAAATAAAGCGCCGTTTTTTACCGGTGATAGCCTTTTTTCGCTCC

>Bacillus_Fam_1124_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:495149-495669

Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=CGCTTATACC

Num.seqs=10 Similarity=0.908262 0

CGCTTATACCCTTTATTGGTGACCGAACCAAGTGTCAAACCCATGGTTCCGGG

Consensus:

CGCTTATACCCTTTATTGGTGACCGAACCAAGTGTCAAACCCATGGTTCCGGG

>Bacillus_Fam_1125_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_24:501342-502175

Satlength=834 Nr of Repeats=16 RepeatLength=52 seed=TTATTGGCGA

Num.seqs=15 Similarity=0.867155 0

TTATTGGCGACCGCTCACTACTGGAGNTCCTTCGCTCGGGCGCTTATCTCCC

Consensus:

TTATTGGCGACCGCTCACTACTGGAGNTCCTTCGCTCGGGCGCTTATCTCCC

>Bacillus_Fam_1126_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_24:95882-96453

Satlength=572 Nr of Repeats=11 RepeatLength=52 seed=GACCTTTTCA

Num.seqs=10 Similarity=0.829060

0 GACCTTTTCAACCTTTTTTACCACAATTCGGGCGTCTACAACCTTTCTAGAG

Consensus:

GACCTTTTCAACCTTTTTTACCACAATTCGGGCGTCTACAACCTTTCTAGAG

>Bacillus_Fam_1127_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_43:160186-160819

Satlength=634 Nr of Repeats=4 RepeatLength=52 seed=AGGGTTCTCA Num.seqs=3
Similarity=0.948718 0

AGGGTTCTCAAGACAAAGTGCACGCAAAACCGGTGAAACTGTCCTAGACA

Consensus:

AGGGTTCTCAAGGACAAAGTGCACGCAAAAACCGGTGAAACTGTCCTAGACA

>Bacillus_Fam_1128_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_19:237050-237362 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=TCTTAAGGAC Num.seqs=6
Similarity=0.936752
0 TCTTAAGGACAAATCTTCTAGTTCTCTTTAGAGATTTGTCCTTCATACCCCT

Consensus:

TCTTAAGGACAAATCTTCTAGTTCTCTTTAGAGATTTGTCCTTCATACCCCT

>Bacillus_Fam_1129_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_126:195884-196092 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GTAACGATTA Num.seqs=4
Similarity=0.850427 0
GTAACGATTAGTCGCTAATCGTGCCCTTCTCCTCGATTTTTTGGAGTTTGCG

Consensus:

GTAACGATTAGTCGCTAATCGTGCCCTTCTCCTCGATTTTTTGGAGTTTGCG

>Bacillus_Fam_1130_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_151:38292-38799 Satlength=508 Nr
of Repeats=8 RepeatLength=52 seed=TATGAGTGAC Num.seqs=6
Similarity=0.814675
0 TATGAGTGACCGCTTGTCTTTTTCCAGGAGGTTCTTGGGCTCTCATGAACCT

Consensus:

TATGAGTGACCGCTTGTCTTTTTCCAGGAGGTTCTTGGGCTCTCATGAACCT

>Bacillus_Fam_1131_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_158:33598-34014 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=TGTGACCAAA Num.seqs=8
Similarity=0.889194
0 TGTGACCAAAACTCATGGATGAAACTATCAAAATGGTCACAAGAAGGGTCGC

Consensus:

TGTGACCAAAACTCATGGATGAAACTATCAAAATGGTCACAAGAAGGGTCGC

>Bacillus_Fam_1132_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000787375.1_ASM78737v1_genomic.fna_1:349174-349686 Satlength=513 Nr
of Repeats=4 RepeatLength=52 seed=CTTGCTCTTT Num.seqs=3
Similarity=0.880342
0 CTTGCTCTTTTCGGTAGGCAATACATCTTGTTGTCTACTCTTATTGCGGCT

Consensus:

CTTGCTCTTTTCGGTAGGCAATACATCTTGTTGTCTACTCTTATTGCGGCT

>Bacillus_Fam_1133_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_2:125037-125349 Satlength=313 Nr
of Repeats=5 RepeatLength=52 seed=CTACCCAAAT Num.seqs=4
Similarity=0.790598
0 CTACCCAAATACGGGGGACCTCTCAAGTTCGGGCGCCATCACATCCCTTTGA

Consensus:

CTACCCAAATACGGGGGACCTCTCAAGTTCGGGCGCCATCACATCCCTTTGA

>Bacillus_Fam_1134_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_2:172325-172585 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CTCTTTTCGG Num.seqs=5
Similarity=0.853846
26 TTGACTCCCTTCCTCACNCCTCCTCACTCTTTTCGGTAGCCATTCCACCCCT

Consensus:

CTCTTTTCGGTAGCCATTCCACCCCTTTGACTCCCTTCCTCACNCCTCCTCA

>Bacillus_Fam_1135_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_3:17378-17794 Satlength=417 Nr of
Repeats=7 RepeatLength=52 seed=TTGCTTCTC Num.seqs=6 Similarity=0.875472
0 TTGCTTCTCTTCGGGAGTCAACACCCTCCTTTAGCTACCGTTCTCTTTGTC

Consensus:

TTGCTTCTCTTCGGGAGTCAACACCCTCCTTTAGCTACCGTTCTCTTTGTC

>Bacillus_Fam_1136_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_4:209708-209916 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=ACATTCGGGC Num.seqs=4
Similarity=0.846154
0 ACATTCGGGCTCCAGATCCCTCTTCTGCTTCCCTACTTTTCCCATTCCCACC

Consensus:

ACATTCGGGCTCCAGATCCCTCTTCTGCTTCCCTACTTTTCCCATTCCCACC

>Bacillus_Fam_1137_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_16:30256-30516 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=ACGGGAGCCA Num.seqs=5 Similarity=0.912821
0 ACGGGAGCCATTCCCTTCCTTTGACTACCCAAATCCNGTTCGGTCCTTCTGC

Consensus:

ACGGGAGCCATTCCCTTCCTTTGACTACCCAAATCCNGTTCGGTCCTTCTGC

>Bacillus_Fam_1138_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_22:64949-65313 Satlength=365 Nr of
Repeats=7 RepeatLength=52 seed=TCGTTGACTA Num.seqs=7 Similarity=0.693710
0 TCGTTGACTACCCAAATTTGTGATNGACTCAGAGTTCGAGTGCCANTGNGCT

Consensus:

TCGTTGACTACCCAAATTTGTGATNGACTCAGAGTTCGAGTGCCANTGNGCT

>Bacillus_Fam_1139_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_40:17325-17638 Satlength=314 Nr of
Repeats=6 RepeatLength=52 seed=AGTCAATACA Num.seqs=5 Similarity=0.841026
0 AGTCAATACACCTTATTGGCTACCGTCCACTCCTCCTCCCTCGCTTTTCGGG

Consensus:

AGTCAATACACCTTATTGGCTACCGTCCACTCCTCCTCCCTCGCTTTTCGGG

>Bacillus_Fam_1140_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_56:13660-13868 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TTTCGGTAGT Num.seqs=4 Similarity=0.839099
0 TTTCGGTAGTCAACCCTTCTCTTTGTCTACCAAAATCCTCGCCCTCTCCCTT

Consensus:

TTTCGGTAGTCAACCCTTCTCTTTGTCTACCAAAATCCTCGCCCTCTCCCTT

>Bacillus_Fam_1141_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_8:33426-33634 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TAGACATTTT Num.seqs=4 Similarity=0.880342
0 TAGACATTTTGTAGTCAATTGGCATTGAAATGTACATTAAACAAGGTTTTT

Consensus:

TAGACATTTTGTAGTCAATTGGCATTTCGAAATGTACATTAAACAAGGTTTTT

>Bacillus_Fam_1142_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_55:28017-28329 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=TCATTTGGGT Num.seqs=6 Similarity=0.830769
0 TCATTTGGGTAAGAGGAAAGCCCCTGCATTGCCCGAAAAAGCGCCAACTCCA

Consensus:

TCATTTGGGTAAGAGGAAAGCCCCTGCATTGCCCGAAAAAGCGCCAACTCCA

>Bacillus_Fam_1143_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_62:7988-8195 Satlength=208 Nr of
Repeats=4 RepeatLength=52 seed=GATGACGGAC Num.seqs=3 Similarity=0.758910
51 ATGACGGACACTTTCCCAGCGTTTTGGGCTATTTCTGTCCGTCATAGGCTGG

Consensus:

GATGACGGACACTTTCCCAGCGTTTTGGGCTATTTCTGTCCGTCATAGGCTG

>Bacillus_Fam_1144_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_65:29-237 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=AAAAAGGGTA Num.seqs=4 Similarity=0.905983
0 AAAAAGGGTAAAAGGAAAGGCTCTGCATTACCCGAAAATGCTGGAGAGAAGT

Consensus:

AAAAAGGGTAAAAGGAAAGGCTCTGCATTACCCGAAAATGCTGGAGAGAAGT

>Bacillus_Fam_1145_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_67:47637-47845 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TGTCCATTAA Num.seqs=4 Similarity=0.910256
0 TGTCCATTAAATGCACTTTCTTAGACATTTTCGGTTTGGAACATCATGCTGAAA

Consensus:

TGTCCATTAAATGCACTTTCTTAGACATTTTCGGTTTGGAACATCATGCTGAAA

>Bacillus_Fam_1146_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_88:82704-82913 Satlength=210 Nr of
Repeats=4 RepeatLength=52 seed=TTTTGTCCGA Num.seqs=3 Similarity=0.897436
0 TTTTGTCCGAACCTGCCCTACTTCAGACAATTTCCGCTTGTACGCCGAGA

Consensus:

TTTTGTCCGAACCTGCCCCTACTTCAGACAATTTCCGCTGTACGGCCGAGA

>Bacillus_Fam_1147_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000813125.1_ASM81312v1_genomic.fna_92:44793-45053 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=TTAATAGACA Num.seqs=5 Similarity=0.846541

0 TTAATAGACATTTTGACGTCCGTTACTCTTCGAAATGTCTAAGAAGTGCTGT

Consensus:

TTAATAGACATTTTGACGTCCGTTACTCTTCGAAATGTCTAAGAAGTGCTGT

>Bacillus_Fam_1148_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000813125.1_ASM81312v1_genomic.fna_102:37405-37665 Satlength=261 Nr of Repeats=4 RepeatLength=52 seed=AAACAGGTCA Num.seqs=3

Similarity=0.551440

0 AAACAGGTCACCAATACCCNTGATTGGTGACCTAAAAATCCATATTTCCGNA

Consensus:

AAACAGGTCACCAATACCCNTGATTGGTGACCTAAAAATCCATATTTCCGNA

>Bacillus_Fam_1149_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000813125.1_ASM81312v1_genomic.fna_103:5511-5928 Satlength=418 Nr of Repeats=7 RepeatLength=52 seed=GTTCGGACAT Num.seqs=6 Similarity=0.838155

0 GTTCGGACATTTCAACGGCCTCTTCATTGAGTTTTGTCCGAAGTAGGATCAA

Consensus:

GTTCGGACATTTCAACGGCCTCTTCATTGAGTTTTGTCCGAAGTAGGATCAA

>Bacillus_Fam_1150_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000813125.1_ASM81312v1_genomic.fna_105:68233-68494 Satlength=262 Nr of Repeats=5 RepeatLength=52 seed=GAAAAGCTGT Num.seqs=4

Similarity=0.580939

0 GAAAAGCTGTCAAGATTATCCCGGAATTATGACAGGCTCAAGCCCATAAAGC

Consensus:

GAAAAGCTGTCAAGATTATCCCGGAATTATGACAGGCTCAAGCCCATAAAGC

>Bacillus_Fam_1151_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_000813125.1_ASM81312v1_genomic.fna_121:45604-46123 Satlength=520 Nr
of Repeats=10 RepeatLength=52 seed=GTTCGGACAA Num.seqs=9
Similarity=0.829060
0 GTTCGGACAAATCATCGGGAGTGACGGTACTTTTTGTCCGAAGGTGACCCAT

Consensus:

GTTCGGACAAATCATCGGGAGTGACGGTACTTTTTGTCCGAAGGTGACCCAT

>Bacillus_Fam_1152_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_129:124410-124826 Satlength=417 Nr
of Repeats=9 RepeatLength=52 seed=TCCCTCATCC Num.seqs=7
Similarity=0.846154 0
TCCCTCATCCGGGCACATATTTTCCCTTTATGTGCCCCGTCTCCCTTCATCT

Consensus:

TCCCTCATCCGGGCACATATTTTCCCTTTATGTGCCCCGTCTCCCTTCATCT

>Bacillus_Fam_1153_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000832905.1_ASM83290v1_genomic.fna_1:2082727-2083091 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=TATGAAGGAC Num.seqs=7
Similarity=0.817011 0
TATGAAGGACATTTTGGGGGCGNGGGATTCTCCTTTTGTCTTTCATCCCTGT

Consensus:

TATGAAGGACATTTTGGGGGCGNGGGATTCTCCTTTTGTCTTTCATCCCTGT

>Bacillus_Fam_1154_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000934845.1_ASM93484v1_genomic.fna_1:28106-28314 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TTATTTTGAC Num.seqs=4 Similarity=0.881027
7 AGAGAGGTTATTTTGACAACTTTCAGGTGAAAAGGGCAAAGTTGTCAAGAA

Consensus:

TTATTTTGACAACTTTCAGGTGAAAAGGGCAAAGTTGTCAAGAAAGAGAGG

>Bacillus_Fam_1155_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_6:11778-12141 Satlength=364 Nr of
Repeats=7 RepeatLength=52 seed=TGATAGGCGC Num.seqs=6 Similarity=0.801467
0 TGATAGGCGCCCGTGGCGGTTGAAATAGGAGTTGGCGGTCGCCAATAGGGT

Consensus:

TGATAGGCGCCCGTGGCGGTTGAAAATAGGAGTTGGCGGTCGCCAATAGGGT

>Bacillus_Fam_1156_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_15:1-313 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=GGGCACTGAG Num.seqs=6 Similarity=0.801258
0 GGGCACTGAGAACACCTGTCAGCACCCAAAATCCCTGGCCCCCTCCTAAAAAT

Consensus:

GGGCACTGAGAACACCTGTCAGCACCCAAAATCCCTGGCCCCCTCCTAAAAAT

>Bacillus_Fam_1157_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_19:60234-60494 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=TGTCAGTGCC Num.seqs=5 Similarity=0.675472
0 TGTCAGTGCCCCAAAAGTGGAGCAGNTCGTNAAAAAGGTTACTGAGGGTCGN

Consensus:

TGTCAGTGCCCCAAAAGTGGAGCAGNTCGTNAAAAAGGTTACTGAGGGTCGN

>Bacillus_Fam_1158_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_31:25184-25444 Satlength=261 Nr of
Repeats=5 RepeatLength=52 seed=CCTCTTTTTC Num.seqs=5 Similarity=0.887179
0 CCTCTTTTTCGGTAAACTCTCGGAAAAAGGTACCTGACAGGCTGCCTCAGTA

Consensus:

CCTCTTTTTCGGTAAACTCTCGGAAAAAGGTACCTGACAGGCTGCCTCAGTA

>Bacillus_Fam_1159_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_38:27020-27332 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=TTGGTCGTCC Num.seqs=6 Similarity=0.841026
0 TTGGTCGTCCATACCCGATGGAGGCCCGTTTTTCAGAATCAGCTTCAGTA

Consensus:

TTGGTCGTCCATACCCGATGGAGGCCCGTTTTTCAGAATCAGCTTCAGTA

>Bacillus_Fam_1160_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_100:49503-49815 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=GGGCTTCCAT Num.seqs=6
Similarity=0.876923
0 GGGCTTCCATCCACTTGATGGAGACCTTTTTTGCGGCTTCCTGCGAAAAC

Consensus:

GGGCTTCCATCCACTTGATGGAGGACCTTTTTTGGCGCTTCCTGCGAAAAC

>Bacillus_Fam_1161_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_000986785.1_ASM98678v1_genomic.fna_101:18847-19056 Satlength=210 Nr
of Repeats=4 RepeatLength=52 seed=TTTTTTGGTG Num.seqs=3
Similarity=0.700855

10 NTCAGAGCCCTTTTTTGGTGGTTGCATGAATTTTGGTACTGAGGAGGAGT

Consensus:

TTTTTTGGTGGTTTGCATGAATTTTGGTACTGAGGAGGAGTNTCAGAGCCC

>Bacillus_Fam_1162_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001278705.1_ASM127870v1_genomic.fna_1:2331510-2331718 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=GTCCTTCATC Num.seqs=4
Similarity=0.854701

0

GTCCTTCATCCAGGGTCTGAAGGACATAACAACACTAGTGATCACGTGAATT

Consensus:

GTCCTTCATCCAGGGTCTGAAGGACATAACAACACTAGTGATCACGTGAATT

>Bacillus_Fam_1163_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001315045.1_ASM131504v1_genomic.fna_43:27341-27549 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TAGTCCGAAG Num.seqs=4
Similarity=0.846154

0 TAGTCCGAAGGCAGGTCAAGTTCGGACAGAAAGCAGACATCAAAGCGCAAAC

Consensus:

TAGTCCGAAGGCAGGTCAAGTTCGGACAGAAAGCAGACATCAAAGCGCAAAC

>Bacillus_Fam_1164_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001315165.1_ASM131516v1_genomic.fna_82:7303-7614 Satlength=312 Nr of
Repeats=6 RepeatLength=52 seed=TTCGGCCAAA Num.seqs=5 Similarity=0.787179

0 TTCGGCCAAATCAGGAGCGNCGAGCCGTTGAAATGTCCGAAGTTGGTGTAGG

Consensus:

TTCGGCCAAATCAGGAGCGNCGAGCCGTTGAAATGTCCGAAGTTGGTGTAGG

>Bacillus_Fam_1165_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2141488-2141852
Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=CATTTTCCA Num.seqs=7
Similarity=0.792430 0
CATTTTCCAGGGCTATGGTCTATGACAGACGTTATCATGACCCGTTGGCTG

Consensus:

CATTTTCCAGGGCTATGGTCTATGACAGACGTTATCATGACCCGTTGGCTG

>Bacillus_Fam_1166_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2366660-2366868
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CTCTCATGGA Num.seqs=4
Similarity=0.927350 0
CTCTCATGGACCTTTTCGCATGTAAAAGTCGCTGCAATGGGACACGACAACGA

Consensus:

CTCTCATGGACCTTTTCGCATGTAAAAGTCGCTGCAATGGGACACGACAACGA

>Bacillus_Fam_1167_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2468093-2468561
Satlength=469 Nr of Repeats=9 RepeatLength=52 seed=GAATCGTTAC Num.seqs=9
Similarity=0.769204 0
GAATCGTTACCGTCATGCGANGCTTTCAAGNCTAACGGGCACGATTCACTTC

Consensus:

GAATCGTTACCGTCATGCGANGCTTTCAAGNCTAACGGGCACGATTCACTTC

>Bacillus_Fam_1168_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:2662491-2662803
Satlength=313 Nr of Repeats=6 RepeatLength=52 seed=CCTCTCATGT Num.seqs=6
Similarity=0.854701 0
CCTCTCATGTCCCGTATCATTGAAAAAGGATGTGCTTGGGACATGAGACCA

Consensus:

CCTCTCATGTCCCGTATCATTGAAAAAGGATGTGCTTGGGACATGAGACCA

>Bacillus_Fam_1169_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3404396-3408244
Satlength=3849 Nr of Repeats=74 RepeatLength=52 seed=CTATTCGCCC
Num.seqs=74 Similarity=0.942760 0
CTATTCGCCCCGAGGAGGAAGAAAAGTGTATCTAGGGGTAGAATAGGACGTCT

Consensus:

CTATTCGCCCCGAGGAGGAAGAAAAGTGTATCTAGGGGTAGAATAGGACGTCT

>Bacillus_Fam_1170_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3437377-3438313

Satlength=937 Nr of Repeats=18 RepeatLength=52 seed=GGTCGAATAG

Num.seqs=16 Similarity=0.812631

0

GGTCGAATAGGGCGTCTCTATTCGCCCCGAAGCGCCAGGTCGAGTCGTTCAAA

Consensus:

GGTCGAATAGGGCGTCTCTATTCGCCCCGAAGCGCCAGGTCGAGTCGTTCAAA

>Bacillus_Fam_1171_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3623417-3629501

Satlength=6085 Nr of Repeats=99 RepeatLength=52 seed=CCTTGAATGG

Num.seqs=81 Similarity=0.818276

0

CCTTGAATGGGACGTGATGAGTGTTATCAAAGCCCGATCGCCANCTTTTTTN

Consensus:

CCTTGAATGGGACGTGATGAGTGTTATCAAAGCCCGATCGCCANCTTTTTTN

>Bacillus_Fam_1172_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4106934-4107141

Satlength=208 Nr of Repeats=4 RepeatLength=52 seed=ACGGTAACGA Num.seqs=3

Similarity=0.863248

0

ACGGTAACGATTGAGGCCGAATCGTTCCCGCACCGTGCTATTTTTGGGAGTT

Consensus:

ACGGTAACGATTGAGGCCGAATCGTTCCCGCACCGTGCTATTTTTGGGAGTT

>Bacillus_Fam_1173_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001420595.1_ASM142059v1_genomic.fna_11:959883-960403 Satlength=521 Nr

of Repeats=10 RepeatLength=52 seed=CGATTGAGTT Num.seqs=10

Similarity=0.834032

0

CGATTGAGTTCAGTTTATCCAAAATTACCCGCTAACGGGAACCAATGAGCT

Consensus:

CGATTGAGTTCAGTTTATCCAAAATTACCCGCTAACGGGAACCAATGAGCT

>Bacillus_Fam_1174_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:1190597-1190910 Satlength=314
Nr of Repeats=6 RepeatLength=52 seed=TTCGGACAAG Num.seqs=5
Similarity=0.779487 0
TTCGGACAAGCCCAGGTGATTTTGAGCAATCNTAGTCCGAATAGCCGTCGAG

Consensus:

TTCGGACAAGCCCAGGTGATTTTGAGCAATCNTAGTCCGAATAGCCGTCGAG

>Bacillus_Fam_1175_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:1214278-1214746 Satlength=469
Nr of Repeats=9 RepeatLength=52 seed=GTCGCCAATA Num.seqs=9
Similarity=0.757512 0
GTCGCCAATAAGGTGTATTGGTACCCGAAACTCTACTATATTTAATAAAACG

Consensus:

GTCGCCAATAAGGTGTATTGGTACCCGAAACTCTACTATATTTAATAAAACG

>Bacillus_Fam_1176_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:1222858-1223222 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=GACAACCACA Num.seqs=7
Similarity=0.880342 0
GACAACCACACTCAAAATTCGGCTGAAGAAGTCCGAAGTGGTAGTGGGTTC

Consensus:

GACAACCACACTCAAAATTCGGCTGAAGAAGTCCGAAGTGGTAGTGGGTTC

>Bacillus_Fam_1177_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:1804770-1804979 Satlength=210
Nr of Repeats=4 RepeatLength=52 seed=AGGGAACCAA Num.seqs=3
Similarity=0.842767 0
AGGGAACCAATGACTCCTATTGATACCTCAAACAACGCTAATTTGCCAAATA

Consensus:

AGGGAACCAATGACTCCTATTGATACCTCAAACAACGCTAATTTGCCAAATA

>Bacillus_Fam_1178_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:2856360-2856620 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=GGAAACAAGC Num.seqs=5
Similarity=0.835897 0
GGAAACAAGCAGCCCTATTGAGTACACTATTCACTCGAATTCTTTAAAAATG

Consensus:

GGAAACAAGCAGCCCTATTGAGTACACTATTCACTCGAATTCTTTAAAAATG

>Bacillus_Fam_1179_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:3118694-3118954 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=TGCTCTGAACT Num.seqs=5
Similarity=0.787179 0
TGCTCTGAACTTGACTGGTGTTCGGACTCGATTACCTTAAAAATCGCCATTGC

Consensus:

TGCTCTGAACTTGACTGGTGTTCGGACTCGATTACCTTAAAAATCGCCATTGC

>Bacillus_Fam_1180_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:3296695-3296903 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=CTTTTTTCTC Num.seqs=4
Similarity=0.816239 0
CTTTTTTCTCCAGTGTTCGGTCAACAATAACGGCGATTGGATACCCTTCTGT

Consensus:

CTTTTTTCTCCAGTGTTCGGTCAACAATAACGGCGATTGGATACCCTTCTGT

>Bacillus_Fam_1181_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:3743605-3744124 Satlength=520
Nr of Repeats=10 RepeatLength=52 seed=TACTTCAGAC Num.seqs=9
Similarity=0.759971 0
TACTTCAGACTTCTTTTNCGCAATCAAGGGCTAACCTGTCCGAACCTGAGGC

Consensus:

TACTTCAGACTTCTTTTNCGCAATCAAGGGCTAACCTGTCCGAACCTGAGGC

>Bacillus_Fam_1182_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:3931578-3931889 Satlength=312
Nr of Repeats=6 RepeatLength=52 seed=GGCTATTGAT Num.seqs=5
Similarity=0.892308 0
GGCTATTGATAACCTTTTTTGCTTTTTTTTACAGGAAAACTGAACTCAATAGA

Consensus:

GGCTATTGATAACCTTTTTTGCTTTTTTTTACAGGAAAACTGAACTCAATAGA

>Bacillus_Fam_1183_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:4472676-4473040 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=TCTTGTTTCAG Num.seqs=7
Similarity=0.801737 0
TCTTGTTTCAGACTCGATCTCTTATTTTCACCAAACCTGTCCGAACCTTGAC

Consensus:

TCTTGTTTCAGACTCGATCTCTTATTTTCACCAAACCTGTCCGAACCTTGAC

>Bacillus_Fam_1184_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:4647606-4648228 Satlength=623
Nr of Repeats=12 RepeatLength=52 seed=CCTAACCTGT Num.seqs=10
Similarity=0.855556 0
CCTAACCTGTCCGAACCTCATCCCAAGTTCGGACTTCTTTGCTCTTGAATCCT

Consensus:

CCTAACCTGTCCGAACCTCATCCCAAGTTCGGACTTCTTTGCTCTTGAATCCT

>Bacillus_Fam_1185_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_12:256320-256580 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=AGAAAAGCGA Num.seqs=5
Similarity=0.861538 0
AGAAAAGCGAACTCAACAAGCGTTATTGGTTCCCGAAAACCTAGCAGAAAGGC

Consensus:

AGAAAAGCGAACTCAACAAGCGTTATTGGTTCCCGAAAACCTAGCAGAAAGGC

>Bacillus_Fam_1186_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:194482-194899 Satlength=418 Nr
of Repeats=8 RepeatLength=52 seed=AGATGTCCTT Num.seqs=7
Similarity=0.699001 0
AGATGTCCTTCATCAATGAAATGAAGGCCAAGNTATAGGGTTTCTACTGTC

Consensus:

AGATGTCCTTCATCAATGAAATGAAGGCCAAGNTATAGGGTTTCTACTGTC

>Bacillus_Fam_1187_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:204926-205656 Satlength=731 Nr
of Repeats=14 RepeatLength=52 seed=TGAATTGTTC Num.seqs=13
Similarity=0.747702 0
TGAATTGTTCCTTCATCAACACCATCCACGATTGCGGTCACGATACNTCG

Consensus:

TGAATTGTTCCCGTTCATCAACACCATCCACGATTGCGGTCACGATACNTCG

>Bacillus_Fam_1188_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001420715.1_ASM142071v1_genomic.fna_22:348610-349234 Satlength=625 Nr

of Repeats=12 RepeatLength=52 seed=AGAGGAAGTA Num.seqs=12

Similarity=0.812655

0

AGAGGAAGTATTGTGCCCGAAAGGGAAAGCTCGAGAAGAAACGGGAACAAA

Consensus:

AGAGGAAGTATTGTGCCCGAAAGGGAAAGCTCGAGAAGAAACGGGAACAAA

>Bacillus_Fam_1189_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001420715.1_ASM142071v1_genomic.fna_22:408865-409073 Satlength=209 Nr

of Repeats=4 RepeatLength=52 seed=GTATTGTTCC Num.seqs=4

Similarity=0.734277

0

GTATTGTTCCCATATCCTCTGGGAAAGACAGAAACGGTAACGATTAGTTGA

Consensus:

GTATTGTTCCCATATCCTCTGGGAAAGACAGAAACGGTAACGATTAGTTGA

>Bacillus_Fam_1190_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001420715.1_ASM142071v1_genomic.fna_22:580070-580538 Satlength=469 Nr

of Repeats=9 RepeatLength=52 seed=GGGAACAATA Num.seqs=9

Similarity=0.837607

0

GGGAACAATAGAAAGTAGAATCGTGCCCGAAATCAGGAGAGAGCAGTGNCCCC

Consensus:

GGGAACAATAGAAAGTAGAATCGTGCCCGAAATCAGGAGAGAGCAGTGNCCCC

>Bacillus_Fam_1191_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001420715.1_ASM142071v1_genomic.fna_22:603974-604181 Satlength=208 Nr

of Repeats=4 RepeatLength=52 seed=ACAACGGTAA Num.seqs=3

Similarity=0.760684

0

ACAACGGTAACGATCAGAGGTGGAATGTGCCCGTAGCGGAGGAAATCTCGGG

Consensus:

ACAACGGTAACGATCAGAGGTGGAATGTGCCCGTAGCGGAGGAAATCTCGGG

>Bacillus_Fam_1192_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:614742-615418 Satlength=677 Nr
of Repeats=13 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=9
Similarity=0.781971 0
TGTCCTTCATGAAGGTAATGAAGTCCAACTAGGTGTACCAAAATCGAAAAG

Consensus:

TGTCCTTCATGAAGGTAATGAAGTCCAACTAGGTGTACCAAAATCGAAAAG

>Bacillus_Fam_1193_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:972888-973200 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=AGCGATGAAG Num.seqs=6
Similarity=0.835897 0
AGCGATGAAGGCCAAAATGTGCTCGGTAACAAGAGCAGATGACCTTCATAAA

Consensus:

AGCGATGAAGGCCAAAATGTGCTCGGTAACAAGAGCAGATGACCTTCATAAA

>Bacillus_Fam_1194_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:2501988-2502560 Satlength=573
Nr of Repeats=11 RepeatLength=52 seed=ATCGTGCCCA Num.seqs=11
Similarity=0.738721 0
ATCGTGCCCAATACCGAGGCNGACATGGAATAACGGGAACAATACCAGGAGA

Consensus:

ATCGTGCCCAATACCGAGGCNGACATGGAATAACGGGAACAATACCAGGAGA

>Bacillus_Fam_1195_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:3462522-3462781 Satlength=260
Nr of Repeats=5 RepeatLength=52 seed=TGAAGGACAC Num.seqs=4
Similarity=0.777778 23
TATCTTGTCCTCATAACCCCGATGAAGGACACTTCCCTTGTTTTCTATCAC

Consensus:

TGAAGGACACTTCCCTTGTTTTCTATCACTATCTTGTCCTCATAACCCCGA

>Bacillus_Fam_1196_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_24:148824-149188 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=CTTTGGTCTT Num.seqs=7
Similarity=0.863133 0
CTTTGGTCTTTATAACCCGCTTAAAGGACAATTCCTTTAAAATATTTGATTC

Consensus:

CTTTGGTCTTTATAACCCGCTTAAAGGACAATTCCTTTAAAATATTTGATTC

>Bacillus_Fam_1197_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_24:150600-151016 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=TGTCCTTCAT Num.seqs=8
Similarity=0.746855 0
TGTCCTTCATATGCTCCATGAAGGACATGTCCATGGGTATTTTCGGTTGTCT

Consensus:

TGTCCTTCATATGCTCCATGAAGGACATGTCCATGGGTATTTTCGGTTGTCT

>Bacillus_Fam_1198_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_83:3882-4089 Satlength=208 Nr of
Repeats=4 RepeatLength=52 seed=ATTAGAGTAA Num.seqs=3 Similarity=0.811966
0 ATTAGAGTAAAAGGTCTTCATCGATGTTATGAAGACCAAACCGGGTTCAGAG

Consensus:

ATTAGAGTAAAAGGTCTTCATCGATGTTATGAAGACCAAACCGGGTTCAGAG

>Bacillus_Fam_1199_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_83:129734-130312 Satlength=579 Nr
of Repeats=11 RepeatLength=52 seed=TGATTGCGAC Num.seqs=7
Similarity=0.740153 0
TGATTGCGACACGGATTTTCGGNAAAATTCAAAGATGAGTCCGAATAAGAGTG

Consensus:

TGATTGCGACACGGATTTTCGGNAAAATTCAAAGATGAGTCCGAATAAGAGTG

>Bacillus_Fam_1200_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_83:602105-602677 Satlength=573 Nr
of Repeats=11 RepeatLength=52 seed=CTTGTGTTGT Num.seqs=11
Similarity=0.875058 0
CTTGTGTTGTCCGAATCAAGGCGTCATTTCGGACAGCTACGCCAGATTTTCCTG

Consensus:

CTTGTGTTGTCCGAATCAAGGCGTCATTTCGGACAGCTACGCCAGATTTTCCTG

>Bacillus_Fam_1201_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_83:693863-694070 Satlength=208 Nr
of Repeats=4 RepeatLength=52 seed=ATGATTCGGA Num.seqs=3
Similarity=0.708595 0
ATGATTCGGACACAGATCAGGAAAAACCGCACCCCTCGAGTCCGAATGAAGCG

Consensus:

ATGATTCGGACACAGATCAGGAAAAACCGCACCCCTCGAGTCCGAATGAAGCG

>Bacillus_Fam_1202_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_84:126495-127119 Satlength=625 Nr
of Repeats=12 RepeatLength=52 seed=AGTCCGAATG Num.seqs=12
Similarity=0.750143 0
AGTCCGAATGCAAGGCTGATTCGGACAGTTGGGTCAGGGGAATNCAGAAGCG

Consensus:

AGTCCGAATGCAAGGCTGATTCGGACAGTTGGGTCAGGGGAATNCAGAAGCG

>Bacillus_Fam_1203_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_87:45812-46177 Satlength=366 Nr
of Repeats=7 RepeatLength=52 seed=CTGTCAGAAT Num.seqs=6
Similarity=0.776955
0 CTGTCAGAATCAACCCTTCATTCGGACTCAACTACTCGTATTCCTTACTTCT

Consensus:

CTGTCAGAATCAACCCTTCATTCGGACTCAACTACTCGTATTCCTTACTTCT

>Bacillus_Fam_1204_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_105:73746-74108 Satlength=363 Nr
of Repeats=7 RepeatLength=52 seed=AGGTCTTCAT Num.seqs=6
Similarity=0.714747
0 AGGTCTTCATGAGGTTGATGAAGACCTATTTGCAACTAGTATTCTCTCGGAA

Consensus:

AGGTCTTCATGAGGTTGATGAAGACCTATTTGCAACTAGTATTCTCTCGGAA

>Bacillus_Fam_1205_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_116:280129-280960 Satlength=832
Nr of Repeats=16 RepeatLength=52 seed=GAATCGTACC Num.seqs=15
Similarity=0.837118 0
GAATCGTACCCGATTCGGGGCAATTGCAAGGAAAAGGGTAACGCAAACGTGG

Consensus:

GAATCGTACCCGATTCGGGGCAATTGCAAGGAAAAGGGTAACGCAAACGTGG

>Bacillus_Fam_1206_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_122:196858-197329 Satlength=472

Nr of Repeats=9 RepeatLength=52 seed=CTGTCCGAAT Num.seqs=7

Similarity=0.686791

0

CTGTCCGAATGAGGCATGAATTCGGAATCATAAACGTTTTTTGGGACCTACA

Consensus:

CTGTCCGAATGAGGCATGAATTCGGAATCATAAACGTTTTTTGGGACCTACA

>Bacillus_Fam_1207_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_122:208982-209396 Satlength=415

Nr of Repeats=8 RepeatLength=52 seed=TGGTCTTCAT Num.seqs=6

Similarity=0.796581

0

TGGTCTTCATCACCTCAATGATAACCGTTTCCGCGATTCAGCGAACGAGTTT

Consensus:

TGGTCTTCATCACCTCAATGATAACCGTTTCCGCGATTCAGCGAACGAGTTT

>Bacillus_Fam_1208_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_122:222503-222814 Satlength=312

Nr of Repeats=6 RepeatLength=52 seed=TGTCCGAATC Num.seqs=5

Similarity=0.902564

0

TGTCCGAATCATAGGCTCATTCGGAATTAAGGCAACAGAATCCTTTGCGACG

Consensus:

TGTCCGAATCATAGGCTCATTCGGAATTAAGGCAACAGAATCCTTTGCGACG

>Bacillus_Fam_1209_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_123:110275-110849 Satlength=575

Nr of Repeats=11 RepeatLength=52 seed=GAATCGTTCC Num.seqs=9

Similarity=0.688823

0

GAATCGTTCCCGATTGCAAATAAAAATCATAAAAAGAGTAACGCAAGCCCTC

Consensus:

GAATCGTTCCCGATTGCAAATAAAAATCATAAAAAGAGTAACGCAAGCCCTC

>Bacillus_Fam_1210_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439965.1_ASM143996v1_genomic.fna_12:79325-79844 Satlength=520 Nr
of Repeats=10 RepeatLength=52 seed=TTACCGGGGA Num.seqs=9
Similarity=0.804131
0 TTACCGGGGACTCTTGATTTCTCCTTCACGGTAAGCATACTCCCTCTTTGN

Consensus:

TTACCGGGGACTCTTGATTTCTCCTTCACGGTAAGCATACTCCCTCTTTGN

>Bacillus_Fam_1211_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001439965.1_ASM143996v1_genomic.fna_121:100541-100822 Satlength=282
Nr of Repeats=5 RepeatLength=52 seed=ACCGAAAGAG Num.seqs=4
Similarity=0.805556
ACCGAAAGAGGCCCAAGTCCCGCTCCAGGTAACCAAAACCCAGTAAAGGTA 0

Consensus:

ACCGAAAGAGGCCCAAGTCCCGCTCCAGGTAACCAAAACCCAGTAAAGGTA

>Bacillus_Fam_1212_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_2:11105-11469 Satlength=365 Nr of
Repeats=7 RepeatLength=52 seed=ATGGTACCGG Num.seqs=7 Similarity=0.814408
0 ATGGTACCGGAAAAGAGAGAAGCTGTACGATGGCAACGCGAATCTCGTAGCC

Consensus:

ATGGTACCGGAAAAGAGAGAAGCTGTACGATGGCAACGCGAATCTCGTAGCC

>Bacillus_Fam_1213_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_20:46870-47181 Satlength=312 Nr
of Repeats=6 RepeatLength=52 seed=TGCTCTATCG Num.seqs=5
Similarity=0.766038
0 TGCTCTATCGGTTTCGCTTTTGNCTCTTGCAAGTACCATTGGCGTTNGTGCTCC

Consensus:

TGCTCTATCGGTTTCGCTTTTGNCTCTTGCAAGTACCATTGGCGTTNGTGCTCC

>Bacillus_Fam_1214_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_20:50326-50534 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GATCTTCCCG Num.seqs=4
Similarity=0.846154
0 GATCTTCCCGCATACCGGGATTCCGGTACTTCATGCAATGCTAGCTGCCGC

Consensus:

GATCTTCCCGCATCACCGGGATTCTGGGTACTTCATGCAATGCTAGCTGCCGC

>Bacillus_Fam_1215_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001587375.1_ASM158737v1_genomic.fna_52:33919-34179 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CAAAAATGTA Num.seqs=5
Similarity=0.782051

0 CAAAAATGTAAAAGGAANGCCGGCTTGTATATAGATTTTCGGTGTAGAAGGT

Consensus:

CAAAAATGTAAAAGGAANGCCGGCTTGTATATAGATTTTCGGTGTAGAAGGT

>Bacillus_Fam_1216_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001587375.1_ASM158737v1_genomic.fna_68:1509-1873 Satlength=365 Nr of Repeats=7 RepeatLength=52 seed=GCACAGCAAT Num.seqs=7 Similarity=0.821734

0 GCACAGCAATGGTACCGCTTCTCCTTTAACCGGTTCATAGCAGTACGCCCCG

Consensus:

GCACAGCAATGGTACCGCTTCTCCTTTAACCGGTTCATAGCAGTACGCCCCG

>Bacillus_Fam_1217_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001587375.1_ASM158737v1_genomic.fna_89:4001-4209 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CAAGTGGACG Num.seqs=4 Similarity=0.901709

0 CAAGTGGACGAATCCGCCGGATGCGGGAAGATAAGGATGGATGAACCCTGCT

Consensus:

CAAGTGGACGAATCCGCCGGATGCGGGAAGATAAGGATGGATGAACCCTGCT

>Bacillus_Fam_1218_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001587375.1_ASM158737v1_genomic.fna_89:39868-40128 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=CCAACTTGGT Num.seqs=3
Similarity=0.794872

0 CCAACTTGGTCGCCAAAGCCCCGGAATGAAGCCCAAGAACGAAGCAANNAGT

Consensus:

CCAACTTGGTCGCCAAAGCCCCGGAATGAAGCCCAAGAACGAAGCAANNAGT

>Bacillus_Fam_1219_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001587375.1_ASM158737v1_genomic.fna_98:17349-17608 Satlength=260 Nr
of Repeats=4 RepeatLength=52 seed=TGCCCGAAAAG Num.seqs=3
Similarity=0.948718
0 TGCCCGAAAAGAGCCGTATGCGGGAATTTGAACAAGACCCATCAATCCCGAAG

Consensus:

TGCCCGAAAAGAGCCGTATGCGGGAATTTGAACAAGACCCATCAATCCCGAAG

>Bacillus_Fam_1220_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_154:82039-82563 Satlength=525 Nr
of Repeats=10 RepeatLength=52 seed=CAAAATTAAA Num.seqs=9
Similarity=0.890313 0
CAAAATTAAAACAAGAAGTGCTTCATACAGCGTTTATGAGGTACATGGTTTT

Consensus:

CAAAATTAAAACAAGAAGTGCTTCATACAGCGTTTATGAGGTACATGGTTTT

>Bacillus_Fam_1221_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_167:65422-65630 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TACATTTTAC Num.seqs=4
Similarity=0.803419
0 TACATTTTACAAGCATCTATTCAAAAATGTAAAAGCAAAGCAAGGATACCTA

Consensus:

TACATTTTACAAGCATCTATTCAAAAATGTAAAAGCAAAGCAAGGATACCTA

>Bacillus_Fam_1222_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_171:145480-145896 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=GTCCGATGGA Num.seqs=8
Similarity=0.862637 0
GTCCGATGGAGAAGGAAAGCGTGAGGCTATGAGGCTGGAAAGAAGAGAAGCG

Consensus:

GTCCGATGGAGAAGGAAAGCGTGAGGCTATGAGGCTGGAAAGAAGAGAAGCG

>Bacillus_Fam_1223_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001590785.1_ASM159078v1_genomic.fna_17:35789-35997 Satlength=209 Nr
of Repeats=5 RepeatLength=52 seed=GCTCCCTTTT Num.seqs=3
Similarity=0.693416
0 GCTCCCTTTTGACCNCTTTTCGAGTTCAGCGCTNTTTTCNGGTGAATAGGTG

Consensus:

GCTCCCTTTTGACCNCTTTTCGAGTTCAGCGCTNTTTTCNGGTGAATAGGTG

>Bacillus_Fam_1224_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591445.1_ASM159144v1_genomic.fna_10:32260-32468 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=TCTTTCTTAC Num.seqs=4
Similarity=0.914530
0 TCTTTCTTACCGTAACCACCTCTCAAACCTAGTCTTCGGTCGTTTAAGAGCCC

Consensus:

TCTTTCTTACCGTAACCACCTCTCAAACCTAGTCTTCGGTCGTTTAAGAGCCC

>Bacillus_Fam_1225_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591485.1_ASM159148v1_genomic.fna_48:825-1138 Satlength=314 Nr of
Repeats=6 RepeatLength=52 seed=TTCCAATCAA Num.seqs=5 Similarity=0.812820
0 TTCCAATCAAGGGNATTGGTGCATGAACCCGAAAAAAACCGNGTAGTTCAAG

Consensus:

TTCCAATCAAGGGNATTGGTGCATGAACCCGAAAAAAACCGNGTAGTTCAAG

>Bacillus_Fam_1226_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591585.1_ASM159158v1_genomic.fna_5:97301-97510 Satlength=210 Nr of
Repeats=4 RepeatLength=52 seed=GCCACTTTTT Num.seqs=3 Similarity=0.982906
0 GCCACTTTTTTCGCTTCTCCCTTCCATTTTGGCTTTCATCTTGGTAATGAAC

Consensus:

GCCACTTTTTTCGCTTCTCCCTTCCATTTTGGCTTTCATCTTGGTAATGAAC

>Bacillus_Fam_1227_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591585.1_ASM159158v1_genomic.fna_8:46370-46578 Satlength=209 Nr of
Repeats=4 RepeatLength=52 seed=ATAAGTGGTT Num.seqs=4 Similarity=0.893162
0 ATAAGTGGTTTTTCATTCAACAAATGAACGCCACTTTTTATGGAAAAGATGGC

Consensus:

ATAAGTGGTTTTTCATTCAACAAATGAACGCCACTTTTTATGGAAAAGATGGC

>Bacillus_Fam_1228_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591585.1_ASM159158v1_genomic.fna_13:90669-90981 Satlength=313 Nr of
Repeats=6 RepeatLength=52 seed=GTTCATCAGT Num.seqs=6

Similarity=0.924786

0 GTTCATCAGTTGGATGAAAGCCGAAATCCCGTGGAGCAAGAGGAAAAGAGGC

Consensus:

GTTCATCAGTTGGATGAAAGCCGAAATCCCGTGGAGCAAGAGGAAAAGAGGC

>Bacillus_Fam_1229_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591645.1_ASM159164v1_genomic.fna_1:671330-671590 Satlength=261 Nr

of Repeats=5 RepeatLength=52 seed=TTTAGTGCCC Num.seqs=5

Similarity=0.866667

0 TTTAGTGCCCGCGTATACCAGAAATTAGTAGAATGAGGTCACTAAAAGTTAA

Consensus:

TTTAGTGCCCGCGTATACCAGAAATTAGTAGAATGAGGTCACTAAAAGTTAA

>Bacillus_Fam_1230_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591645.1_ASM159164v1_genomic.fna_1:803082-803290 Satlength=209 Nr

of Repeats=4 RepeatLength=52 seed=TCCAGATATT Num.seqs=4

Similarity=0.743590

0 TCCAGATATTAGGAAAACCAGGGCACTATATTCAGATTTAACACCCTTAAAA

Consensus:

TCCAGATATTAGGAAAACCAGGGCACTATATTCAGATTTAACACCCTTAAAA

>Bacillus_Fam_1231_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591645.1_ASM159164v1_genomic.fna_1:810484-810796 Satlength=313 Nr

of Repeats=6 RepeatLength=52 seed=AGTCCGAATG Num.seqs=6

Similarity=0.801709

0 AGTCCGAATGACGGTCTGATTAGGACAGCAACAGCAGCTCAAACCTAATTCAC

Consensus:

AGTCCGAATGACGGTCTGATTAGGACAGCAACAGCAGCTCAAACCTAATTCAC

>Bacillus_Fam_1232_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591645.1_ASM159164v1_genomic.fna_5:34073-34385 Satlength=313 Nr of

Repeats=6 RepeatLength=52 seed=GAAGTTCATC Num.seqs=6 Similarity=0.806838

0 GAAGTTCATCTGGCTCATGAACGTCATTACAAAGAGAAAAGACTGAGCAAAT

Consensus:

GAAGTTCATCTGGCTCATGAACGTCATTACAAAGAGAAAAGACTGAGCAAAT

>Bacillus_Fam_1233_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591645.1_ASM159164v1_genomic.fna_18:93814-94126 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=TCTCTTACCA Num.seqs=6
Similarity=0.747009
0 TCTCTTACCATCCATCATGATTTTCCGCCCCGTTTGGGCACTGAGACGCCTTC

Consensus:

TCTCTTACCATCCATCATGATTTTCCGCCCCGTTTGGGCACTGAGACGCCTTC

>Bacillus_Fam_1234_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591665.1_ASM159166v1_genomic.fna_28:471-678 Satlength=208 Nr of
Repeats=4 RepeatLength=52 seed=ATCTTTCCCT Num.seqs=3 Similarity=0.897436
0 ATCTTTCCCTTCCTTTTTTCAGCCAAACGTCGAAGTAGAACCACCTCTACTTCA

Consensus:

ATCTTTCCCTTCCTTTTTTCAGCCAAACGTCGAAGTAGAACCACCTCTACTTCA

>Bacillus_Fam_1235_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591665.1_ASM159166v1_genomic.fna_41:6030-6288 Satlength=259 Nr of
Repeats=5 RepeatLength=52 seed=GAAAGGGAGA Num.seqs=4 Similarity=0.893162
0 GAAAGGGAGAAACGGTCGATAAGAGCGGTTTCATAACGACCATTGTTGGTTGAG

Consensus:

GAAAGGGAGAAACGGTCGATAAGAGCGGTTTCATAACGACCATTGTTGGTTGAG

>Bacillus_Fam_1236_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591665.1_ASM159166v1_genomic.fna_57:81030-81238 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CTCATGAGGA Num.seqs=4
Similarity=0.820513
0 CTCATGAGGACAGGAATCATGTTTAATTCACATTTTTTGTCTCATGAAAGG

Consensus:

CTCATGAGGACAGGAATCATGTTTAATTCACATTTTTTGTCTCATGAAAGG

>Bacillus_Fam_1237_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591665.1_ASM159166v1_genomic.fna_60:22815-23075 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=ATCGACCGTA Num.seqs=5
Similarity=0.912821
0 ATCGACCGTAATTGACTTTCAGCTTGGCTATCGGGCTTTATAAACCTTTCTT

Consensus:

ATCGACCGTAATTGACTTTCAGCTTGGCTATCGGGCTTTATAAACCTTTCTT

>Bacillus_Fam_1238_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591665.1_ASM159166v1_genomic.fna_94:124-764 Satlength=641 Nr of
Repeats=7 RepeatLength=52 seed=ATGAAGGACT Num.seqs=5 Similarity=0.808805
0 ATGAAGGACTAATCCCTATTAGAAAGACAGCGTTTTGTCCTTCATCAAGCAT

Consensus:

ATGAAGGACTAATCCCTATTAGAAAGACAGCGTTTTGTCCTTCATCAAGCAT

>Bacillus_Fam_1239_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591665.1_ASM159166v1_genomic.fna_102:8439-8701 Satlength=263 Nr of
Repeats=5 RepeatLength=52 seed=GGTTTCCAAT Num.seqs=3 Similarity=0.769231
0 GGTTTCCAATCAGCCCTATTGGAACAAGTTAAGGCNAAAAAGTCGGTCAAAA

Consensus:

GGTTTCCAATCAGCCCTATTGGAACAAGTTAAGGCNAAAAAGTCGGTCAAAA

>Bacillus_Fam_1240_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591665.1_ASM159166v1_genomic.fna_108:0-209 Satlength=210 Nr of
Repeats=4 RepeatLength=52 seed=TTTTGTCCTC Num.seqs=3 Similarity=0.846154
0 TTTTGTCTCATGAAGCACTCATGCGGACAGTTTCGCCTTGGGAACCCCGGG

Consensus:

TTTTGTCTCATGAAGCACTCATGCGGACAGTTTCGCCTTGGGAACCCCGGG

>Bacillus_Fam_1241_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591805.1_ASM159180v1_genomic.fna_10:197189-197658 Satlength=470 Nr of
Repeats=9 RepeatLength=52 seed=TCATAGTGCC Num.seqs=8
Similarity=0.825092 0

TCATAGTGCCCGAAACCTGAAAAAACCAGCCACTCGGGCACTGAGAGCAGT

Consensus:

TCATAGTGCCCGAAACCTGAAAAAACCAGCCACTCGGGCACTGAGAGCAGT

>Bacillus_Fam_1242_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_001591805.1_ASM159180v1_genomic.fna_28:10204-10514 Satlength=311 Nr of Repeats=6 RepeatLength=52 seed=CTATTGGACA Num.seqs=4 Similarity=0.858974
0 CTATTGGACAGTTGGGGTTGTATCTTCGTCGATATTGTCCTATAGACCGCTT

Consensus:

CTATTGGACAGTTGGGGTTGTATCTTCGTCGATATTGTCCTATAGACCGCTT

>Bacillus_Fam_1243_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52 Alignment score = 0.000000
GCF_001591805.1_ASM159180v1_genomic.fna_38:47701-47961 Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=GGATAACGGG Num.seqs=5 Similarity=0.861538
0 GGATAACGGGCTCCAATGAGGGTTATTGGCGACCGAAACGCTCTCGAATTCC

Consensus:

GGATAACGGGCTCCAATGAGGGTTATTGGCGACCGAAACGCTCTCGAATTCC

>Bacillus_Fam_1244_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52 Alignment score = 0.000000
GCF_001591805.1_ASM159180v1_genomic.fna_49:18770-18980 Satlength=211 Nr of Repeats=4 RepeatLength=52 seed=GGTCACAGAG Num.seqs=3 Similarity=0.811966
0 GGTCACAGAGAGCGATCCTCAGTGCCCGAAGAGAGGCAAAAAGCTGTCTAGC

Consensus:

GGTCACAGAGAGCGATCCTCAGTGCCCGAAGAGAGGCAAAAAGCTGTCTAGC

>Bacillus_Fam_1245_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52 Alignment score = 0.000000
GCF_001591945.1_ASM159194v1_genomic.fna_6:8074-8494 Satlength=421 Nr of Repeats=8 RepeatLength=52 seed=TGTCCCTTAG Num.seqs=7 Similarity=0.863248
0 TGTCCCTTAGATCCTCTCTCTCGGACACTCCTTCTCCTTTTTCCTCAATATT

Consensus:

TGTCCCTTAGATCCTCTCTCTCGGACACTCCTTCTCCTTTTTCCTCAATATT

>Bacillus_Fam_1246_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52 Alignment score = 0.000000
GCF_001591945.1_ASM159194v1_genomic.fna_9:37775-37983 Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TGTCCCTTAG Num.seqs=4 Similarity=0.957265
0 TGTCCCTTAGACGACTTCTCTCGGACACTTCCAACCCCTTCTCCGCGAGAC

Consensus:

TGTCCTTTAGACGACTTCTCTCGGACACTTCCAACCCCTTCTCCCGCGAGAC

>Bacillus_Fam_1247_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001591945.1_ASM159194v1_genomic.fna_11:48233-48493 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=CTATTGGACA Num.seqs=5
Similarity=0.730409
0 CTATTGGACAGATCCTCTCCTCTTTTGGCTCGGACTGTCCTTTAGCGCCCTC

Consensus:

CTATTGGACAGATCCTCTCCTCTTTTGGCTCGGACTGTCCTTTAGCGCCCTC

>Bacillus_Fam_1248_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:512977-513185 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=TATCGAAGAC Num.seqs=4
Similarity=0.679487
0 TATCGAAGACAAATTCCACCGCTTCCACCCTCGTTTTGTCCTCAAGACGCCT

Consensus:

TATCGAAGACAAATTCCACCGCTTCCACCCTCGTTTTGTCCTCAAGACGCCT

>Bacillus_Fam_1249_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:972202-972514 Satlength=313 Nr
of Repeats=6 RepeatLength=52 seed=GGGCACGTAG Num.seqs=6
Similarity=0.717400
0 GGGCACGTAGACGCNTTCTACGTTACCTTGAGGCGGGATATTTACGCTGGAT

Consensus:

GGGCACGTAGACGCNTTCTACGTTACCTTGAGGCGGGATATTTACGCTGGAT

>Bacillus_Fam_1250_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:1021216-1021892 Satlength=677
Nr of Repeats=13 RepeatLength=52 seed=GGGCACGTAG Num.seqs=13
Similarity=0.788955 0
GGGCACGTAGANCACGTCTACGTGACCGAACCGTCAGTTTTTCAGCTGNNTG

Consensus:

GGGCACGTAGANCACGTCTACGTGACCGAACCGTCAGTTTTTCAGCTGNNTG

>Bacillus_Fam_1251_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:1467817-1468025 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=CGGGCACGTA Num.seqs=4
Similarity=0.722222 86
CTATGTGACCTTACACTGCTTTTTCATGCCC GTTCGGGCACGTAGAACACTT

Consensus:

CGGGCACGTAGAACACTTCTATGTGACCTTACACTGCTTTTTCATGCCC GTT

>Bacillus_Fam_1252_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:1863825-1864292 Satlength=468
Nr of Repeats=9 RepeatLength=52 seed=TATTGAAGAC Num.seqs=8
Similarity=0.775641 0
TATTGAAGACAAAATGAGATCACTCCCTTTTAAATTTGTCCCCAATACCCTC

Consensus:

TATTGAAGACAAAATGAGATCACTCCCTTTTAAATTTGTCCCCAATACCCTC

>Bacillus_Fam_1253_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:1939675-1940039 Satlength=365
Nr of Repeats=6 RepeatLength=52 seed=AAGTGTCTCC Num.seqs=5
Similarity=0.843590 0
AAGTGTCTCCAATAAGCTTCATTGGAGACAAAACCCNCTCTTTTTTCACGAG

Consensus:

AAGTGTCTCCAATAAGCTTCATTGGAGACAAAACCCNCTCTTTTTTCACGAG

>Bacillus_Fam_1254_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:2327343-2327760 Satlength=418
Nr of Repeats=8 RepeatLength=52 seed=AAAGTCACGT Num.seqs=7
Similarity=0.738389 0
AAAGTCACGTAGAAACCCTCTACGTGACCGTACCTCCCTTTTNCCTGCTCT

Consensus:

AAAGTCACGTAGAAACCCTCTACGTGACCGTACCTCCCTTTTNCCTGCTCT

>Bacillus_Fam_1255_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:2431592-2432058 Satlength=467
Nr of Repeats=9 RepeatLength=52 seed=CGGATTTTCC Num.seqs=6
Similarity=0.835897 0
CGGATTTTCCCTTTTTCAGACATCACTTAGACGGNCTCTACTTAGTGTCTAAAC

Consensus:

CGGATTTTCCCTTTCAGACATCACTTAGACGGNCTCTACTTAGTGTCTAAAC

>Bacillus_Fam_1256_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:2907285-2907649 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=ATGAGAACTG Num.seqs=7
Similarity=0.755316 0
ATGAGAACTGAAACCANGAAAAGCGCGGCNGTCTTGTCTCATGAAGCGTTC

Consensus:

ATGAGAACTGAAACCANGAAAAGCGCGGCNGTCTTGTCTCATGAAGCGTTC

>Bacillus_Fam_1257_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:3080314-3080988 Satlength=675
Nr of Repeats=13 RepeatLength=52 seed=GACCGAGCAG Num.seqs=11
Similarity=0.820047 0
GACCGAGCAGCTGGAAAAATAGGAAGAAGAGTCGCGTAGAGAGGTTCTANGC

Consensus:

GACCGAGCAGCTGGAAAAATAGGAAGAAGAGTCGCGTAGAGAGGTTCTANGC

>Bacillus_Fam_1258_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:3169529-3169945 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=TAAGAAAGGC Num.seqs=8
Similarity=0.836081 0
TAAGAAAGGCTCTCAAGGACAAAACGCTAGTAAAAATTAATAGAANTGTCTT

Consensus:

TAAGAAAGGCTCTCAAGGACAAAACGCTAGTAAAAATTAATAGAANTGTCTT

>Bacillus_Fam_1259_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:3506345-3506708 Satlength=364
Nr of Repeats=7 RepeatLength=52 seed=TCCATTGCCC Num.seqs=6
Similarity=0.880342 0
TCCATTGCCCCAAAACCGGCTAAATCATCAAATTATGGTCAATGCAGCCCCAT

Consensus:

TCCATTGCCCCAAAACCGGCTAAATCATCAAATTATGGTCAATGCAGCCCCAT

>Bacillus_Fam_1260_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:3527584-3527946 Satlength=363
Nr of Repeats=7 RepeatLength=52 seed=TGTCTGAATG Num.seqs=5
Similarity=0.902564 0
TGTCTGAATGATTATTTTGCAGCCAGAGATCAGTTAGAATCCGTCTAGTTGC

Consensus:

TGTCTGAATGATTATTTTGCAGCCAGAGATCAGTTAGAATCCGTCTAGTTGC

>Bacillus_Fam_1261_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:3645171-3645639 Satlength=469
Nr of Repeats=9 RepeatLength=52 seed=ATGAACCTTT Num.seqs=9
Similarity=0.947293 0
ATGAACCTTTCATAGAGCGCGTCGGAGTAAAAAATCGAGCTCCCGCGTACT

Consensus:

ATGAACCTTTCATAGAGCGCGTCGGAGTAAAAAATCGAGCTCCCGCGTACT

>Bacillus_Fam_1262_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:3709317-3709941 Satlength=625
Nr of Repeats=12 RepeatLength=52 seed=GTTTCATAGAG Num.seqs=12
Similarity=0.770436 0
GTTTCATAGAGCGCGAACNTGAGGGGAAATTCCAAAAACGCGCACTATAAAGA

Consensus:

GTTTCATAGAGCGCGAACNTGAGGGGAAATTCCAAAAACGCGCACTATAAAGA

>Bacillus_Fam_1263_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:3807647-3808011 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=TTTCGGAAAA Num.seqs=7
Similarity=0.824176 0
TTTCGGAAAAGGTGTTTCATAGAAGAGGTCAATGAGCACATGAGGCTGAGTTT

Consensus:

TTTCGGAAAAGGTGTTTCATAGAAGAGGTCAATGAGCACATGAGGCTGAGTTT

>Bacillus_Fam_1264_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:3869085-3869761 Satlength=677
Nr of Repeats=13 RepeatLength=52 seed=ACTATGGGAG Num.seqs=13
Similarity=0.892176 0
ACTATGGGAGGTTCATAGAGCGNGAAATTAGGAAAAAGGAAAGACTCCGCGC

Consensus:

ACTATGGGAGGTTTCATAGAGCGNGAAATTAGGAAAAAGGAAAGACTCCGCGC

>Bacillus_Fam_1265_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:3880946-3881417 Satlength=472

Nr of Repeats=9 RepeatLength=52 seed=TATTGCCCCGA Num.seqs=6

Similarity=0.801709

0

TATTGCCCCGAAGAGAAGAAAAATAAATCCCGCGGTAAAAAGACCGGGCTTC

Consensus:

TATTGCCCCGAAGAGAAGAAAAATAAATCCCGCGGTAAAAAGACCGGGCTTC

>Bacillus_Fam_1266_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:4057906-4058531 Satlength=626

Nr of Repeats=11 RepeatLength=52 seed=AGCGTTTATG Num.seqs=9

Similarity=0.918091

0

AGCGTTTATGAGAACAGAGAGCTAATGATTTGGGTCGGAAGTGTCTCATGA

Consensus:

AGCGTTTATGAGAACAGAGAGCTAATGATTTGGGTCGGAAGTGTCTCATGA

>Bacillus_Fam_1267_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:4191741-4192522 Satlength=782

Nr of Repeats=15 RepeatLength=52 seed=AAAAAAGAGA Num.seqs=13

Similarity=0.833333

0

AAAAAAGAGAGCGCCGGGTAGAATANAGAGCATCTATGCGACCGAGCCCGAG

Consensus:

AAAAAAGAGAGCGCCGGGTAGAATANAGAGCATCTATGCGACCGAGCCCGAG

>Bacillus_Fam_1268_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:4719016-4719328 Satlength=313

Nr of Repeats=6 RepeatLength=52 seed=TCAATGAACA Num.seqs=6

Similarity=0.734382

0

TCAATGAACACGAATCGGCAAAATTTTCAGGCAGGAAGTGTTTCATAGAGAGGT

Consensus:

TCAATGAACACGAATCGGCAAAATTTTCAGGCAGGAAGTGTTTCATAGAGAGGT

>Bacillus_Fam_1269_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:5285435-5285695 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=TCTACGTGCC Num.seqs=5
Similarity=0.846154 0
TCTACGTGCCCCAAGTTCAATAAATTAGTGGGTTTCGGTCGCGTAGAGCCCT

Consensus:

TCTACGTGCCCCAAGTTCAATAAATTAGTGGGTTTCGGTCGCGTAGAGCCCT

>Bacillus_Fam_1270_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:5395730-5396199 Satlength=470
Nr of Repeats=9 RepeatLength=52 seed=TTGACCTTTT Num.seqs=8
Similarity=0.780997 0
TTGACCTTTTCTTTNAAAATCAATTAGTTTTAGGCAATGNACATGGCTTCCA

Consensus:

TTGACCTTTTCTTTNAAAATCAATTAGTTTTAGGCAATGNACATGGCTTCCA

>Bacillus_Fam_1271_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_1:270063-270479 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=CATCCTCTTC Num.seqs=8
Similarity=0.888278
0 CATCCTCTTCAGGTGAAAAAGCCCAATTATTCACCGGAGTGCTCATATTTT

Consensus:

CATCCTCTTCAGGTGAAAAAGCCCAATTATTCACCGGAGTGCTCATATTTT

>Bacillus_Fam_1272_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_1:669107-669471 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=TTATTCCTCT Num.seqs=7
Similarity=0.777778
0 TTATTCCTCTAAAGCAACGCCACACGCGCTCTTCAGGTGAACAAATCGCAT

Consensus:

TTATTCCTCTAAAGCAACGCCACACGCGCTCTTCAGGTGAACAAATCGCAT

>Bacillus_Fam_1273_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_1:2472643-2473059 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=GTATTTACA Num.seqs=8
Similarity=0.934066 0
GTATTTTACACGAAGGGATTTTGAACCGAATGCTTCAGGTGAATAAATTGCG

Consensus:

GTTATTTACACGAAGGGATTTTGAACCGAATGCTTCAGGTGAATAAATTGCG

>Bacillus_Fam_1274_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_3:175232-175492 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=ATTTATTCCC Num.seqs=5
Similarity=0.893082
8 TAAACTGAATTTATTCCCATGAAGCGAGAGGAAAACCGGAGCTTCCGGTGGGA

Consensus:

ATTTATTCCCATGAAGCGAGAGGAAAACCGGAGCTTCCGGTGGATAAACTGA

>Bacillus_Fam_1275_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_3:896857-897117 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=AAAATGGTCA Num.seqs=5
Similarity=0.910256
0 AAAATGGTCACAGAGTGCCAACTAAGACCAAAATGACAAGGGAGCAAGCGG

Consensus:

AAAATGGTCACAGAGTGCCAACTAAGACCAAAATGACAAGGGAGCAAGCGG

>Bacillus_Fam_1276_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_3:1103562-1104238 Satlength=677
Nr of Repeats=13 RepeatLength=52 seed=GGAAGGTAGG Num.seqs=13
Similarity=0.902696 0
GGAAGGTAGGAGAGAGGCAGTCTCATCGCCCGTTCCCAGCTATTTACCATTA

Consensus:

GGAAGGTAGGAGAGAGGCAGTCTCATCGCCCGTTCCCAGCTATTTACCATTA

>Bacillus_Fam_1277_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:243388-244011 Satlength=624 Nr
of Repeats=12 RepeatLength=52 seed=CATAGAGCGA Num.seqs=11
Similarity=0.809324 0
CATAGAGCGAGTCAATGGGACATTTNGCAATTTTCNAGAGCAGCAAATGTCC

Consensus:

CATAGAGCGAGTCAATGGGACATTTNGCAATTTTCNAGAGCAGCAAATGTCC

>Bacillus_Fam_1278_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636335.1_ASM163633v1_genomic.fna_1:698208-698468 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TGATGGACAA Num.seqs=5
Similarity=0.833962
0 TGATGGACAAAACAGTAGATAGAGCGCAAAGCAAAGTCCATCAATCCTGAGA

Consensus:

TGATGGACAAAACAGTAGATAGAGCGCAAAGCAAAGTCCATCAATCCTGAGA

>Bacillus_Fam_1279_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:1609919-1610545 Satlength=627
Nr of Repeats=12 RepeatLength=52 seed=TTCTTCGTT Num.seqs=9
Similarity=0.924501 0
TTCTTCGTTTCTTCATGGGTTTTGTACCATTGATTGCTTCTATGGGACATG

Consensus:

TTCTTCGTTTCTTCATGGGTTTTGTACCATTGATTGCTTCTATGGGACATG

>Bacillus_Fam_1280_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:2312900-2313420 Satlength=521
Nr of Repeats=10 RepeatLength=52 seed=GATTTTTCCT Num.seqs=10
Similarity=0.885470 0
GATTTTTCCTAAAGTACCTTGTTGCGGGCGACATGAGCGCTTCTTGGCTACC

Consensus:

GATTTTTCCTAAAGTACCTTGTTGCGGGCGACATGAGCGCTTCTTGGCTACC

>Bacillus_Fam_1281_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:2486081-2486704 Satlength=624
Nr of Repeats=10 RepeatLength=52 seed=GACTTTTTCG Num.seqs=8
Similarity=0.874542 0
GACTTTTTCGGGAGACATGAGCTAGTCTTGGCGACCGGTTTCACAAGTTGAT

Consensus:

GACTTTTTCGGGAGACATGAGCTAGTCTTGGCGACCGGTTTCACAAGTTGAT

>Bacillus_Fam_1282_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:2726431-2726899 Satlength=469
Nr of Repeats=9 RepeatLength=52 seed=TTCTATGAGA Num.seqs=9
Similarity=0.837607 0
TTCTATGAGACAAAATCGGGGAGCAGACGAGGNGTTTGTCTCATTGGAGCG

Consensus:

TTCTATGAGACAAAAATCGGGGAGCAGACGAGGNGTTTGTCTCATTGGAGCG

>Bacillus_Fam_1283_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:2864058-2864994 Satlength=937
Nr of Repeats=16 RepeatLength=52 seed=GACTCTTTGA Num.seqs=14
Similarity=0.827557 0
GACTCTTTGAGCNGATTTTTTCGGGCGTTGGGTCCTCTATCNGGCTTATTGAN

Consensus:

GACTCTTTGAGCNGATTTTTTCGGGCGTTGGGTCCTCTATCNGGCTTATTGAN

>Bacillus_Fam_1284_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:2901338-2902222 Satlength=885
Nr of Repeats=17 RepeatLength=52 seed=TTTGTCTTC Num.seqs=17
Similarity=0.832579 0
TTTGTCTTCATTCGCTTGATGATGGACTTTTTCTAGAGCGATCGGCTTCGN

Consensus:

TTTGTCTTCATTCGCTTGATGATGGACTTTTTCTAGAGCGATCGGCTTCGN

>Bacillus_Fam_1285_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:2936390-2936910 Satlength=521
Nr of Repeats=10 RepeatLength=52 seed=ATGATGGACA Num.seqs=10
Similarity=0.884331 0
ATGATGGACATTTTCGATAATTTCTCAGCTGCTTTTGGCCTTCATCTCTTCG

Consensus:

ATGATGGACATTTTCGATAATTTCTCAGCTGCTTTTGGCCTTCATCTCTTCG

>Bacillus_Fam_1286_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:3065276-3065640 Satlength=365
Nr of Repeats=7 RepeatLength=52 seed=ATGATGGACA Num.seqs=7
Similarity=0.823600 0
ATGATGGACACTTGGAGCGGATTCTTTTCGCTTTTGTCCATCATCTCTCGC

Consensus:

ATGATGGACACTTGGAGCGGATTCTTTTCGCTTTTGTCCATCATCTCTCGC

>Bacillus_Fam_1287_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636335.1_ASM163633v1_genomic.fna_1:3328615-3328927 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=TTTTGTCCCA Num.seqs=6
Similarity=0.887179 0
TTTTGTCCCATAGAACCCCTCTATGGGACATTTCTCTTGCCTATTCTGATC

Consensus:

TTTTGTCCCATAGAACCCCTCTATGGGACATTTCTCTTGCCTATTCTGATC

>Bacillus_Fam_1288_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:2372700-2373012 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=AGGATTTCAG Num.seqs=6
Similarity=0.871795 0
AGGATTTCAGGAATCAGAACATCAATGTAAATCCCGAAACCAGTTCCATGCA

Consensus:

AGGATTTCAGGAATCAGAACATCAATGTAAATCCCGAAACCAGTTCCATGCA

>Bacillus_Fam_1289_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:2479013-2479325 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=ATTTGGATAT Num.seqs=6
Similarity=0.830769 0
ATTTGGATATTAAGGTCGTGATAAGCGCCTAAACACCCCTCTGTTATACAGT

Consensus:

ATTTGGATATTAAGGTCGTGATAAGCGCCTAAACACCCCTCTGTTATACAGT

>Bacillus_Fam_1290_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:2544842-2545362 Satlength=521
Nr of Repeats=10 RepeatLength=52 seed=TCTCCTTCCC Num.seqs=10
Similarity=0.807827 0
TCTCCTTCCCCAACTCTATTGATGACCGGCATTTTCGGGAAGTACTCTGCCTN

Consensus:

TCTCCTTCCCCAACTCTATTGATGACCGGCATTTTCGGGAAGTACTCTGCCTN

>Bacillus_Fam_1291_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:2589875-2590238 Satlength=364
Nr of Repeats=7 RepeatLength=52 seed=ATTCCCGAAT Num.seqs=6
Similarity=0.808547 0
ATTCCCGAATTCCACTTAATGCACTTGTTTCGGGAATTACTACGGGCTTCTC

Consensus:

ATTCCCGAATTCCACTTAATGCACTTGTTTCGGGAATTACTACGGGCTTCTC

>Bacillus_Fam_1292_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:2600820-2601080 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=ACGGGCACTT Num.seqs=5
Similarity=0.628205 0
ACGGGCACTTTGANCGCACNTTTGTTCCCNCCAACACGCTTTTTTCCAAGCCG

Consensus:

ACGGGCACTTTGANCGCACNTTTGTTCCCNCCAACACGCTTTTTTCCAAGCCG

>Bacillus_Fam_1293_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:2885450-2885866 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=GAATTAGAAT Num.seqs=8
Similarity=0.846154 0
GAATTAGAATCCAAGAGTCATTCTGAAACGGTCTCAACCATGGAAGTTCGG

Consensus:

GAATTAGAATCCAAGAGTCATTCTGAAACGGTCTCAACCATGGAAGTTCGG

>Bacillus_Fam_1294_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:3320349-3320660 Satlength=312
Nr of Repeats=6 RepeatLength=52 seed=AACGCTTAAT Num.seqs=5
Similarity=0.864103 0
AACGCTTAATCACGACAGTATTATCCAGATAACGGTAATTAGGGGCGTGATA

Consensus:

AACGCTTAATCACGACAGTATTATCCAGATAACGGTAATTAGGGGCGTGATA

>Bacillus_Fam_1295_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:3986989-3987509 Satlength=521
Nr of Repeats=10 RepeatLength=52 seed=AGCGGATTTTC Num.seqs=10
Similarity=0.888889 0
AGCGGATTTTCGGGAATTACTTTCCCTTTGCATTTCCCGAAACTTTGTCTCCT

Consensus:

AGCGGATTTTCGGGAATTACTTTCCCTTTGCATTTCCCGAAACTTTGTCTCCT

>Bacillus_Fam_1296_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636345.1_ASM163634v1_genomic.fna_1:4285214-4285526 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=TTACGCCTTA Num.seqs=6
Similarity=0.856410 0
TTACGCCTTAAACACGACTCCAATTCCCAGGTTTTGGTGTTCGTGTCTCGA

Consensus:

TTACGCCTTAAACACGACTCCAATTCCCAGGTTTTGGTGTTCGTGTCTCGA

>Bacillus_Fam_1297_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:4405935-4406559 Satlength=625
Nr of Repeats=12 RepeatLength=52 seed=GTTCTATTTTC Num.seqs=12
Similarity=0.870241 0
GTTCTATTTCCCCAAACCGGCACTCGCCTTCTCTTTTCGGAATTACTTTGCC

Consensus:

GTTCTATTTCCCCAAACCGGCACTCGCCTTCTCTTTTCGGAATTACTTTGCC

>Bacillus_Fam_1298_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:1121864-1122176 Satlength=313
Nr of Repeats=6 RepeatLength=52 seed=TTTTGTCCTT Num.seqs=6
Similarity=0.811966 0
TTTTGTCCTTCATACCACCGATGAAGGACTTTTGACAACGAAAATTCACCAG

Consensus:

TTTTGTCCTTCATACCACCGATGAAGGACTTTTGACAACGAAAATTCACCAG

>Bacillus_Fam_1299_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:2575815-2576335 Satlength=521
Nr of Repeats=10 RepeatLength=52 seed=TGAAGGACTT Num.seqs=10
Similarity=0.852991 0
TGAAGGACTTTTATCACCTTTTATTCTCGCGAAAAGTCCTTCATACCTGCGA

Consensus:

TGAAGGACTTTTATCACCTTTTATTCTCGCGAAAAGTCCTTCATACCTGCGA

>Bacillus_Fam_1300_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:4150616-4151084 Satlength=469
Nr of Repeats=9 RepeatLength=52 seed=GATGAAGGAC Num.seqs=9
Similarity=0.829060 0
GATGAAGGACTATTCTTGCTTTGATTGTGCTCGAATGGTCCATCATCCCCTC

Consensus:

GATGAAGGACTATTCTTGCTTTGATTGTGCTCGAATGGTCCATCATCCCCTC

>Bacillus_Fam_1301_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001636425.1_ASM163642v1_genomic.fna_1:4305654-4306121 Satlength=468

Nr of Repeats=9 RepeatLength=52 seed=AAGTCCTTCA Num.seqs=8

Similarity=0.836081

0

AAGTCCTTCATCGTGGTTATGAAGACCAATAAGAGGTTAATTAGGAAGCGAA

Consensus:

AAGTCCTTCATCGTGGTTATGAAGACCAATAAGAGGTTAATTAGGAAGCGAA

>Bacillus_Fam_1302_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001645705.1_ASM164570v1_genomic.fna_54:62195-62753 Satlength=559 Nr

of Repeats=10 RepeatLength=52 seed=CGGTTCGCATA Num.seqs=8

Similarity=0.845013

0 CGGTTCGCATAGCAAGGTTCTATAAGCCCGGAAACACAGGAAATCCAATGGAA

Consensus:

CGGTTCGCATAGCAAGGTTCTATAAGCCCGGAAACACAGGAAATCCAATGGAA

>Bacillus_Fam_1303_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001645705.1_ASM164570v1_genomic.fna_60:318578-318994 Satlength=417 Nr

of Repeats=8 RepeatLength=52 seed=AGTGAACCGG Num.seqs=8

Similarity=0.891941

0

AGTGAACCGGCGGAAACAGAGTTCAAAGAAGGGCCTATGTTCCCGAAATCG

Consensus:

AGTGAACCGGCGGAAACAGAGTTCAAAGAAGGGCCTATGTTCCCGAAATCG

>Bacillus_Fam_1304_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001648575.1_ASM164857v1_genomic.fna_4:219533-220209 Satlength=677 Nr

of Repeats=13 RepeatLength=52 seed=GCGTGTTCATA Num.seqs=11

Similarity=0.763636

0

GCGTGTTCATAGAGCCCGAATGAAACGCGAANTCGCTGGGGCTTAGTGAAAAC

Consensus:

GCGTGTTCATAGAGCCCGAATGAAACGCGAANTCGCTGGGGCTTAGTGAAAAC

>Bacillus_Fam_1305_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001648575.1_ASM164857v1_genomic.fna_14:26277-26899 Satlength=623 Nr
of Repeats=12 RepeatLength=52 seed=TGGAATTGTC Num.seqs=10
Similarity=0.947578
TGGAATTGTCATCATAGCAATCATGAAGACAATCTCGAGCGGATTTTGTGAG

0

Consensus:

TGGAATTGTCATCATAGCAATCATGAAGACAATCTCGAGCGGATTTTGTGAG

>Bacillus_Fam_1306_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_47:0-207 Satlength=208 Nr of
Repeats=4 RepeatLength=52 seed=CCTTATGAAG Num.seqs=4 Similarity=0.918803
0 CCTTATGAAGACACTTTCGGTCCACTTTCTCTCTCGGATGTGTCTTCATCCA

Consensus:

CCTTATGAAGACACTTTCGGTCCACTTTCTCTCTCGGATGTGTCTTCATCCA

>Bacillus_Fam_1307_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_52:38204-38672 Satlength=469 Nr
of Repeats=9 RepeatLength=52 seed=CGTTTTCCTT Num.seqs=9
Similarity=0.849003
0 CGTTTTCCTTGCTCGCTTCGAAGTTTGCGTGCCATTGCGCCTCTATGACACG

Consensus:

CGTTTTCCTTGCTCGCTTCGAAGTTTGCGTGCCATTGCGCCTCTATGACACG

>Bacillus_Fam_1308_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_59:39775-40244 Satlength=470 Nr
of Repeats=9 RepeatLength=52 seed=CGCGAATTTTC Num.seqs=8
Similarity=0.870879
0 CGCGAATTTCCCTCCCGCTCCTAATTTGGTGTGTCATACTGCTCCTATGACG

Consensus:

CGCGAATTTCCCTCCCGCTCCTAATTTGGTGTGTCATACTGCTCCTATGACG

>Bacillus_Fam_1309_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_60:94014-94277 Satlength=264 Nr
of Repeats=5 RepeatLength=52 seed=TTTCCCTCTC Num.seqs=4
Similarity=0.935897
0 TTTCCCTCTCAACATTGTCTTCATCCACCTTGTGAAGACAGTACCATGCTTG

Consensus:

TTTCCCTCTCAACATTGTCTTCATCCACCTTGTGAAGACAGTACCATGCTTG

>Bacillus_Fam_1310_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_63:225987-226623 Satlength=637 Nr
of Repeats=12 RepeatLength=52 seed=AGATTGTCTT Num.seqs=10
Similarity=0.777239 0
AGATTGTCTTCATCACNCTTATAATGACAATCTTGAAGTATTTTCACTGTG

Consensus:

AGATTGTCTTCATCACNCTTATAATGACAATCTTGAAGTATTTTCACTGTG

>Bacillus_Fam_1311_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_66:89204-89675 Satlength=472 Nr
of Repeats=9 RepeatLength=52 seed=AAGACACTTT Num.seqs=6
Similarity=0.924786
0 AAGACACTTTTGCCGTGTTTTTCCTGCTGACATTGTCTTCAGACCACTGATG

Consensus:

AAGACACTTTTGCCGTGTTTTTCCTGCTGACATTGTCTTCAGACCACTGATG

>Bacillus_Fam_1312_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_37:69494-69702 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=CTCATGAACC Num.seqs=4
Similarity=0.777778
0 CTCATGAACCGCTTATGAGTAAGTAAAATACATGATTAGATTATTTAGTTA

Consensus:

CTCATGAACCGCTTATGAGTAAGTAAAATACATGATTAGATTATTTAGTTA

>Bacillus_Fam_1313_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001887185.1_ASM188718v1_genomic.fna_148:402146-402406 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=AATGTGTCTC Num.seqs=5
Similarity=0.792121 0
AATGTGTCTCAAGAATAGGGTTGGAAACAGATAAACCGGGAATNNCGTTGAA

Consensus:

AATGTGTCTCAAGAATAGGGTTGGAAACAGATAAACCGGGAATNNCGTTGAA

>Bacillus_Fam_1314_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_001887185.1_ASM188718v1_genomic.fna_192:110193-111153 Satlength=961
Nr of Repeats=14 RepeatLength=52 seed=GGTAACCTTT Num.seqs=9
Similarity=0.749288 0
GGTAACCTTTCCGGGGCTTTGGTTACCCGGATCTCATCACAGAGCCNACTTC

Consensus:

GGTAACCTTTCCGGGGCTTTGGTTACCCGGATCTCATCACAGAGCCNACTTC

>Bacillus_Fam_1315_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001887185.1_ASM188718v1_genomic.fna_276:156901-157109 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=TCTTCAAGGT Num.seqs=4
Similarity=0.846154 0
TCTTCAAGGTAATCAAAAGCTCACAAGGTACCCGAGCCGCCGAATTACCT

Consensus:

TCTTCAAGGTAATCAAAAGCTCACAAGGTACCCGAGCCGCCGAATTACCT

>Bacillus_Fam_1316_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_001887185.1_ASM188718v1_genomic.fna_428:41505-41868 Satlength=364 Nr
of Repeats=7 RepeatLength=52 seed=TGGAGACACA Num.seqs=6
Similarity=0.683761
0 TGGAGACACATTTTATTGCTAAAAAGTAAATAATGTGTTTCAGAACCAGNGC

Consensus:

TGGAGACACATTTTATTGCTAAAAAGTAAATAATGTGTTTCAGAACCAGNGC

>Bacillus_Fam_1317_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002009555.1_ASM200955v1_genomic.fna_79:0-258 Satlength=259 Nr of
Repeats=5 RepeatLength=52 seed=TAAGACACAT Num.seqs=4 Similarity=0.709402
0 TAAGACACATAATGTGACCAAACCCCAAAAAATGTGTCTCACCCGCCAGTCT

Consensus:

TAAGACACATAATGTGACCAAACCCCAAAAAATGTGTCTCACCCGCCAGTCT

>Bacillus_Fam_1318_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:2881499-2881761 Satlength=263
Nr of Repeats=5 RepeatLength=52 seed=CGTTGTTTCG Num.seqs=3
Similarity=0.825996 0
CGTTGTTTCGGGCACTATGAACCTCTATAGTTCCAGTCTCTTGCTTCCAT

Consensus:

CGTTGTTTCGGGCACTATGAACCCTCTATAGTTCCCAGTCTCTTGCTTCCAT

>Bacillus_Fam_1319_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:3984598-3985376 Satlength=779
Nr of Repeats=15 RepeatLength=52 seed=CCGTTTGAGC Num.seqs=13
Similarity=0.911900 0
CCGTTTGAGCAGCTCGAAGGAGATAGCGGTCACTATGAAAGCGTCATGGTGA

Consensus:

CCGTTTGAGCAGCTCGAAGGAGATAGCGGTCACTATGAAAGCGTCATGGTGA

>Bacillus_Fam_1320_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:123004-123368 Satlength=365 Nr
of Repeats=7 RepeatLength=52 seed=ACTTCAGACA Num.seqs=7
Similarity=0.857143
0 ACTTCAGACAACTTCTGCNGCCAATTACTTAAACCTGTCCGAACTCTTGCCT

Consensus:

ACTTCAGACAACTTCTGCNGCCAATTACTTAAACCTGTCCGAACTCTTGCCT

>Bacillus_Fam_1321_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:208479-208999 Satlength=521 Nr
of Repeats=10 RepeatLength=52 seed=GAGCAACTTG Num.seqs=8
Similarity=0.878205 0
GAGCAACTTGATCATAGACCTCCTATGATTCACTTCCCTACAATTCATGTGC

Consensus:

GAGCAACTTGATCATAGACCTCCTATGATTCACTTCCCTACAATTCATGTGC

>Bacillus_Fam_1322_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:1309331-1310008 Satlength=678
Nr of Repeats=13 RepeatLength=52 seed=TGTCTGAAGT Num.seqs=12
Similarity=0.897824 0
TGTCTGAAGTTGAGNAGCCTTCGGACAGGTTAGAAGCCTACAGAGTAAAAGC

Consensus:

TGTCTGAAGTTGAGNAGCCTTCGGACAGGTTAGAAGCCTACAGAGTAAAAGC

>Bacillus_Fam_1323_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_002019645.1_ASM201964v1_genomic.fna_1:1511589-1512577 Satlength=989
Nr of Repeats=19 RepeatLength=52 seed=AAGCTGTCCG Num.seqs=19
Similarity=0.906175 0
AAGCTGTCCGAAGAGAGCTCAGGTTGCTCAGGTTNAGTAGA

Consensus:

AAGCTGTCCGAAGAGAGCTCAGGTTGCTCAGGTTNAGTAGA

>Bacillus_Fam_1324_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:2149247-2150387 Satlength=1141
Nr of Repeats=22 RepeatLength=52 seed=TCTGATTCCC Num.seqs=18
Similarity=0.902296 0
TCTGATTCCCTTTTCAGTAGTGNATCGGGGTAGAAAGGGAACGAAAGAGCAAG

Consensus:

TCTGATTCCCTTTTCAGTAGTGNATCGGGGTAGAAAGGGAACGAAAGAGCAAG

>Bacillus_Fam_1325_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:2283102-2283310 Satlength=209
Nr of Repeats=4 RepeatLength=52 seed=AGATTCCCTT Num.seqs=4
Similarity=0.893162 0
AGATTCCCTTACTAGGCAAAAATGAAGTGCAAAGGGAACGAAAGGTAGTCAC

Consensus:

AGATTCCCTTACTAGGCAAAAATGAAGTGCAAAGGGAACGAAAGGTAGTCAC

>Bacillus_Fam_1326_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:3845277-3845745 Satlength=469
Nr of Repeats=9 RepeatLength=52 seed=GAAAGCTGTC Num.seqs=9
Similarity=0.951567 0
GAAAGCTGTCCGAACCTTCACTTGGGTTTCGGAAGTACTTTTCCTTTACGACCAC

Consensus:

GAAAGCTGTCCGAACCTTCACTTGGGTTTCGGAAGTACTTTTCCTTTACGACCAC

>Bacillus_Fam_1327_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:4572662-4573184 Satlength=523
Nr of Repeats=10 RepeatLength=52 seed=ATTCCCTTTG Num.seqs=8
Similarity=0.928571 0
ATTCCCTTTGTTCGAGAAAATACACAGGAAAGGGAACGAAAGGAGCGCTTTG

Consensus:

ATTCCCTTTGTCGGAGAAAATACACAGGAAAGGGAACGAAAGGAGCGCTTTG

>Bacillus_Fam_1328_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:5404130-5406159 Satlength=2030
Nr of Repeats=39 RepeatLength=52 seed=AAGCTGTCTG Num.seqs=38
Similarity=0.813432 0
AAGCTGTCTGAACCTACCCACCTTCGGACAGCTTGACTCCGAAAAACCCAA

Consensus:

AAGCTGTCTGAACCTACCCACCTTCGGACAGCTTGACTCCGAAAAACCCAA

>Bacillus_Fam_1329_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:2317880-2318296 Satlength=417
Nr of Repeats=8 RepeatLength=52 seed=ATTATGGGTA Num.seqs=8
Similarity=0.907509 0
ATTATGGGTAACGATAAAGGCGTGATCGTGCCCTGAACTCGAGAATATAGTG

Consensus:

ATTATGGGTAACGATAAAGGCGTGATCGTGCCCTGAACTCGAGAATATAGTG

>Bacillus_Fam_1330_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_14:10803-11065
Satlength=263 Nr of Repeats=5 RepeatLength=52 seed=GAGTCTGAAC Num.seqs=3
Similarity=0.709402 0
GAGTCTGAACCTNGCGTGAGTTCGGACAGGAATCGTGANTGTGAATGTAAGC

Consensus:

GAGTCTGAACCTNGCGTGAGTTCGGACAGGAATCGTGANTGTGAATGTAAGC

>Bacillus_Fam_1331_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_16:230959-231479
Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=TGTCCAATAG
Num.seqs=10 Similarity=0.801709 0
TGTCCAATAGGATGCCTCTATCGGACATAACTCACTTCCCAAGACTAGATTC

Consensus:

TGTCCAATAGGATGCCTCTATCGGACATAACTCACTTCCCAAGACTAGATTC

>Bacillus_Fam_1332_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_19:76324-76687
Satlength=364 Nr of Repeats=7 RepeatLength=52 seed=ACGGCTCTAT Num.seqs=6
Similarity=0.829060 0
ACGGCTCTATCGAACAAACTATGGGCCTTCACGCTTGGTTTGTCCAATAGG

Consensus:

ACGGCTCTATCGAACAAACTATGGGCCTTCACGCTTGGTTTGTCCAATAGG

>Bacillus_Fam_1333_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_22:326079-326390
Satlength=312 Nr of Repeats=6 RepeatLength=52 seed=CTATTGGACA Num.seqs=5
Similarity=0.933333 0
CTATTGGACAAAATCGCTTCACGGCACTGGCGGTTTGTCTAATACAGGCTTC

Consensus:

CTATTGGACAAAATCGCTTCACGGCACTGGCGGTTTGTCTAATACAGGCTTC

>Bacillus_Fam_1334_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_22:581244-581504
Satlength=261 Nr of Repeats=5 RepeatLength=52 seed=ATCAGAGACC Num.seqs=5
Similarity=0.804938 0
ATCAGAGACCTTTGGACAGCTTCTTCGNTTGATATGGTCATTGACACCTCTC

Consensus:

ATCAGAGACCTTTGGACAGCTTCTTCGNTTGATATGGTCATTGACACCTCTC

>Bacillus_Fam_1335_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_24:146667-146929
Satlength=263 Nr of Repeats=5 RepeatLength=52 seed=TTTTGTCCGA Num.seqs=4
Similarity=0.935897 0
TTTTGTCCGATAGAGACCTCTTATTGGACAAAACCTTTGCTGGCACCGTTTCG

Consensus:

TTTTGTCCGATAGAGACCTCTTATTGGACAAAACCTTTGCTGGCACCGTTTCG

>Bacillus_Fam_1336_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_27:4426-4682
Satlength=257 Nr of Repeats=5 RepeatLength=51 seed=ATAAGTGCCC Num.seqs=4
Similarity=0.786325 0
ATAAGTGCCCGTTCTAGGGTCCCTAGCAAGGAGAGCGGTCATCTAACTCGAG

Consensus:

ATAAGTGCCCGTTCTAGGGTCCCTAGCAAGGAGAGCGGTCATCTAACTCGAG

>Bacillus_Fam_1337_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_27:9518-9884
Satlength=367 Nr of Repeats=7 RepeatLength=52 seed=ACTTCAGACA Num.seqs=5
Similarity=0.761538 0
ACTTCAGACAGAAGAAGGTAAAAGAAGTAAGGGAGAGTCTGAANTNGAAGTG

Consensus:

ACTTCAGACAGAAGAAGGTAAAAGAAGTAAGGGAGAGTCTGAANTNGAAGTG

>Bacillus_Fam_1338_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_32:21776-21984
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TTCTATTGGA Num.seqs=4
Similarity=0.876068 0
TTCTATTGGACATTCTCATCGATACGAACGCACGTTTTGTCCAATAGACGCC

Consensus:

TTCTATTGGACATTCTCATCGATACGAACGCACGTTTTGTCCAATAGACGCC

>Bacillus_Fam_1339_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_18:52517-53042
Satlength=526 Nr of Repeats=5 RepeatLength=52 seed=AAGAGCAAAT Num.seqs=4
Similarity=0.927350 0
AAGAGCAAATCGTTGACGAAACGAGCATTTTGAAAGCTGAACGTCAACGAAT

Consensus:

AAGAGCAAATCGTTGACGAAACGAGCATTTTGAAAGCTGAACGTCAACGAAT

>Bacillus_Fam_1340_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_16:495010-495218

Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=TCGTTACCGT Num.seqs=4
Similarity=0.865226 0
TCGTTACCGTTTTTGGCGTACTCTTCTGTTTTCGGGCACATTAAACTCTTTN

Consensus:

TCGTTACCGTTTTTGGCGTACTCTTCTGTTTTCGGGCACATTAAACTCTTTN

>Bacillus_Fam_1341_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_17:42538-42746
Satlength=209 Nr of Repeats=4 RepeatLength=52 seed=CACCAAGAGC Num.seqs=4
Similarity=0.871795 0
CACCAAGAGCTTTCCTTGGCGCAGTAATATAGGTTTCATCTACTAATAACTG

Consensus:

CACCAAGAGCTTTCCTTGGCGCAGTAATATAGGTTTCATCTACTAATAACTG

>Bacillus_Fam_1342_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:1290871-1291391 Satlength=521 Nr
of Repeats=10 RepeatLength=52 seed=GGTCTTCATA Num.seqs=10
Similarity=0.778917 0
GGTCTTCATAGCACCGATGAAGACCTGAAACAGTTGGAAACTGCTTCGTACA

Consensus:

GGTCTTCATAGCACCGATGAAGACCTGAAACAGTTGGAAACTGCTTCGTACA

>Bacillus_Fam_1343_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:2588049-2588340 Satlength=292 Nr
of Repeats=6 RepeatLength=52 seed=CTCTTCATCT Num.seqs=4
Similarity=0.809748 0
CTCTTCATCTCGCTTATGAAGGGGATTTGGATGAGGTAAGTGCCTTGTTTTT

Consensus:

CTCTTCATCTCGCTTATGAAGGGGATTTGGATGAGGTAAGTGCCTTGTTTTT

>Bacillus_Fam_1344_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:4108755-4109589 Satlength=835 Nr
of Repeats=16 RepeatLength=52 seed=ATGTCGTCAT Num.seqs=14
Similarity=0.767535 0
ATGTCGTCATGAGTGCATGAAGACACAACTCTCCTGGCGAGCGGAAGAAG

Consensus:

ATGTCGTCATGAGTGCATGAAGACACAACTCTCCTGGCGAGCGGAAGAAG

>Bacillus_Fam_1345_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:4353231-4353439 Satlength=209 Nr
of Repeats=4 RepeatLength=52 seed=GGAAAACACA Num.seqs=4
Similarity=0.897436 0
GGAAAACACAGCAAAAGCCGGATAGAAATCCCCTTCATCAAGGCCATGAAGG

Consensus:

GGAAAACACAGCAAAAGCCGGATAGAAATCCCCTTCATCAAGGCCATGAAGG

>Bacillus_Fam_1346_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_10:153192-153608 Satlength=417 Nr
of Repeats=8 RepeatLength=52 seed=GATGAAGACC Num.seqs=8
Similarity=0.677402
0 GATGAAGACCGTTTAAAGGATCCCTCCGNGCCAGAAAAGGTTATCATGGGAGA

Consensus:

GATGAAGACCGTTTAAAGGATCCCTCCGNGCCAGAAAAGGTTATCATGGGAGA

>Bacillus_Fam_1347_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_10:1493463-1493980 Satlength=518
Nr of Repeats=10 RepeatLength=52 seed=ATCTATAAAA Num.seqs=9
Similarity=0.819801 0
ATCTATAAAAATGGTCATCATGTACGTGATGAAAACCGAAATCTGGTATGTG

Consensus:

ATCTATAAAAATGGTCATCATGTACGTGATGAAAACCGAAATCTGGTATGTG

>Bacillus_Fam_1348_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:52363-52884 Satlength=522 Nr of
Repeats=10 RepeatLength=52 seed=CGGTCTTCAT Num.seqs=7
Similarity=0.677249
0 CGGTCTTCATGGCCGGGATGAGAACCGATNTTNCTGATTTCTTTGCGAGAAC

Consensus:

CGGTCTTCATGGCCGGGATGAGAACCGATNTTNCTGATTTCTTTGCGAGAAC

>Bacillus_Fam_1349_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000

GCF_900156875.1_PRJEB18969_genomic.fna_11:147252-147512 Satlength=261 Nr
of Repeats=5 RepeatLength=52 seed=TTGGTTTTCAT Num.seqs=5
Similarity=0.902564
0 TGGTTTTCATAAGCGGAATGAAGACCGTTATTAGGGGCTTTGTCCTGCGTAA

Consensus:

TTGGTTTTCATAAGCGGAATGAAGACCGTTATTAGGGGCTTTGTCCTGCGTAA

>Bacillus_Fam_1350_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_900156875.1_PRJEB18969_genomic.fna_11:295252-297644 Satlength=2393 Nr

of Repeats=46 RepeatLength=52 seed=GATGAAGACC Num.seqs=44

Similarity=0.826120

0

GATGAAGACCAATCCATNGGAAGGAGCGCGGGNAAACGGTCATCATCAAGGG

Consensus:

GATGAAGACCAATCCATNGGAAGGAGCGCGGGNAAACGGTCATCATCAAGGG

>Bacillus_Fam_1351_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_900156875.1_PRJEB18969_genomic.fna_11:372186-372602 Satlength=417 Nr

of Repeats=8 RepeatLength=52 seed=GGTTTTCATA Num.seqs=8

Similarity=0.819632

0 GGTTTTCATAGCTGGAATGAAGACCGAAAGTAACGGTGATAGATCGAGTTTA

Consensus:

GGTTTTCATAGCTGGAATGAAGACCGAAAGTAACGGTGATAGATCGAGTTTA

>Bacillus_Fam_1352_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_900156875.1_PRJEB18969_genomic.fna_11:939998-946134 Satlength=6137 Nr

of Repeats=118 RepeatLength=52 seed=TGAGTCTGAA Num.seqs=118

Similarity=0.789356

0

TGAGTCTGAATCCGAAGGTTATTCGGAATCCAGCAAGAGGAAACCCAGGCAT

Consensus:

TGAGTCTGAATCCGAAGGTTATTCGGAATCCAGCAAGAGGAAACCCAGGCAT

>Bacillus_Fam_1353_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52

Alignment score = 0.000000

GCF_900156875.1_PRJEB18969_genomic.fna_11:1045732-1051088 Satlength=5357

Nr of Repeats=101 RepeatLength=52 seed=TCTTCATAAA Num.seqs=100

Similarity=0.741715

0

TCTTCATAAAGGCAATGAAGACCGTTTGGTTGGTTTTTANAANGNCTTTGG

Consensus:

TCTTCATAAAGGCAATGAAGACCGTTTGGTTGGTTTTTTANAANGNCTTTGG

>Bacillus_Fam_1354_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:1191426-1193454 Satlength=2029
Nr of Repeats=39 RepeatLength=52 seed=TTGGTTTCA Num.seqs=39
Similarity=0.908371 0
TTGGTTTTCATAACGGCGATGATGACCGTTTGGCTGAGTGCTGGCTTGCTTT

Consensus:

TTGGTTTTTCATAACGGCGATGATGACCGTTTGGCTGAGTGCTGGCTTGCTTT

>Bacillus_Fam_1355_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:1294995-1295515 Satlength=521
Nr of Repeats=10 RepeatLength=52 seed=TAAAACTTCA Num.seqs=10
Similarity=0.839316 0
TAAAACTTCATGCTTATGGTCCTCATTCAACGGATGATGACCGTTTGCCTTA

Consensus:

TAAAACTTCATGCTTATGGTCCTCATTCAACGGATGATGACCGTTTGCCTTA

>Bacillus_Fam_1356_52_1 Nr. of seq. 1 Alignment length(with gaps) = 52
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:1698345-1698605 Satlength=261
Nr of Repeats=5 RepeatLength=52 seed=ATGATGACCG Num.seqs=5
Similarity=0.640606 0
ATGATGACCGTTNTTGGTTCATAGAACANAGAACTGGTCTTCATCTGGGCT

Consensus:

ATGATGACCGTTNTTGGTTCATAGAACANAGAACTGGTCTTCATCTGGGCT

>Bacillus_Fam_1357_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_1:64392-64647 Satlength=256 Nr of
Repeats=5 RepeatLength=51 seed=AATACGCAGC Num.seqs=5 Similarity=0.742138
0 AATACGCAGCAATGAAACCGNAAAAATAGTCCTCAATGCCGCACAAATAAA

Consensus:

AATACGCAGCAATGAAACCGNAAAAATAGTCCTCAATGCCGCACAAATAAA

>Bacillus_Fam_1358_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:600241-600496 Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=GGGGTTACTC Num.seqs=5 Similarity=0.823077
0 GGGGTTACTCATGAGAAAAGTGAGAGTAAGCCCGAGAAAAGAGAAATGCNC

Consensus:

GGGGTTACTCATGAGAAAAGTGAGAGTAAGCCCGAGAAAAGAGAAATGCNC

>Bacillus_Fam_1359_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

BACILLUS_PSEUDALCALIPHILUS_genomic.fna_6:120207-120411 Satlength=205 Nr of Repeats=4 RepeatLength=51 seed=CGTTTCTCTG Num.seqs=4 Similarity=0.801816
2 ATCGTTTCTCTCGGGCTTCTACTCTTTTTTCCGCCCCGTAACCCCAAGCATC

Consensus:

CGTTTCTCTCGGGCTTCTACTCTTTTTTCCGCCCCGTAACCCCAAGCATCAT

>Bacillus_Fam_1360_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_000161455.1_ASM16145v1_genomic.fna_1:4028285-4028540 Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=CTAAACAAGA Num.seqs=5
Similarity=0.874510 0

CTAAACAAGACGAGCAAACACAAAACAAACAACATCAATCTGCTCAAGGTA

Consensus:

CTAAACAAGACGAGCAAACACAAAACAAACAACATCAATCTGCTCAAGGTA

>Bacillus_Fam_1361_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_000169195.2_ASM16919v2_genomic.fna_1:2424628-2425463 Satlength=836 Nr of Repeats=16 RepeatLength=52 seed=AAAGACAAAA Num.seqs=14
Similarity=0.612441 0

AAAGACAAAACGNGGNGCCGAGACGAAAGAAATGTCCTTCATAGGGTCATG

Consensus:

AAAGACAAAACGNGGNGCCGAGACGAAAGAAATGTCCTTCATAGGGTCATG

>Bacillus_Fam_1362_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_33:209101-209305 Satlength=205 Nr of Repeats=4 RepeatLength=51 seed=TGAATGAGGA Num.seqs=4
Similarity=0.869281

0 TGAATGAGGACAAAGTAAGCGGGAAAACAGAAACATTGTCCTCGTAGGGCG

Consensus:

TGAATGAGGACAAAGTAAGCGGAAAACAGAAACATTGTCCTCGTAGGGCG

>Bacillus_Fam_1363_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000175075.1_ASM17507v1_genomic.fna_46:49896-50202 Satlength=307 Nr of
Repeats=6 RepeatLength=51 seed=GATGACAAAA Num.seqs=6 Similarity=0.803050
0 GATGACAAAACCTTCAATGAACNAAGGATTTCTGTCATCGGAAAGCTTCAAC

Consensus:

GATGACAAAACCTTCAATGAACNAAGGATTTCTGTCATCGGAAAGCTTCAAC

>Bacillus_Fam_1364_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_129:1421-1931 Satlength=511 Nr of
Repeats=10 RepeatLength=51 seed=TAAAGGACGT Num.seqs=10
Similarity=0.755410
0 TAAAGGACGTTAACGAGTCAATTTAGAGACTAAAGTCCTATAAACAGCTTN

Consensus:

TAAAGGACGTTAACGAGTCAATTTAGAGACTAAAGTCCTATAAACAGCTTN

>Bacillus_Fam_1365_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000181495.1_ASM18149v1_genomic.fna_164:12630-13239 Satlength=610 Nr
of Repeats=12 RepeatLength=51 seed=TATCGTCCTA Num.seqs=11
Similarity=0.749457 0
TATCGTCCTATAGAGGGACTTTAAAGGACTTTAATATTGAATGTTGCNAAA

Consensus:

TATCGTCCTATAGAGGGACTTTAAAGGACTTTAATATTGAATGTTGCNAAA

>Bacillus_Fam_1366_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000242895.2_ASM24289v3_genomic.fna_1:1809966-1810272 Satlength=307 Nr
of Repeats=6 RepeatLength=51 seed=GTGACCAAAA Num.seqs=6
Similarity=0.907625 0
GTGACCAAAAAGAAAAAAGAGAGCTACTTCGGTCACTCCAGAGAATTGGA

Consensus:

GTGACCAAAAAGAAAAAAGAGAGCTACTTCGGTCACTCCAGAGAATTGGA

>Bacillus_Fam_1367_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_000245315.1_ASM24531v1_genomic.fna_55:29067-29424 Satlength=358 Nr of Repeats=7 RepeatLength=51 seed=GCACGCTGAG Num.seqs=7 Similarity=0.886710
0 GCACGCTGAGCCNGCGCTTCGTCAAGAAGAGAAAGCAGCGGCTCAACCGGA

Consensus:

GCACGCTGAGCCNGCGCTTCGTCAAGAAGAGAAAGCAGCGGCTCAACCGGA

>Bacillus_Fam_1368_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_000292245.2_ASM29224v2_genomic.fna_7:20889-21092 Satlength=204 Nr of Repeats=4 RepeatLength=51 seed=CTTATCCTCC Num.seqs=3 Similarity=0.773420
0 CTTATCCTCCGTTTTTCGTACCGTATTTTGGCCAGGGAGAATTTTTCATTC

Consensus:

CTTATCCTCCGTTTTTCGTACCGTATTTTGGCCAGGGAGAATTTTTCATTC

>Bacillus_Fam_1369_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_000292245.2_ASM29224v2_genomic.fna_27:36252-36558 Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=GAAAAAGAAG Num.seqs=6 Similarity=0.839651
0 GAAAAAGAAGCCGAGCTAGCGGAAGTACGGCGTATAAGGAGTCATGAAGTT

Consensus:

GAAAAAGAAGCCGAGCTAGCGGAAGTACGGCGTATAAGGAGTCATGAAGTT

>Bacillus_Fam_1370_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_000292245.2_ASM29224v2_genomic.fna_38:108-363 Satlength=256 Nr of Repeats=5 RepeatLength=51 seed=TTTAAAGGAC Num.seqs=5 Similarity=0.900654
0 TTTAAAGGACAAAAAAGGAAGCCGAAGCTGGAAAGTGTTCCAATAACGAGAG

Consensus:

TTTAAAGGACAAAAAAGGAAGCCGAAGCTGGAAAGTGTTCCAATAACGAGAG

>Bacillus_Fam_1371_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_000292245.2_ASM29224v2_genomic.fna_38:28715-29235 Satlength=521 Nr of Repeats=10 RepeatLength=52 seed=AGTGAAAAGG Num.seqs=10 Similarity=0.711111
0 AGTGAAAAGGGAATCAAAGCCCTCAATGATTCCCAAAGAGCCCCAGAACCA

Consensus:

AGTGAAAAGGGAATCAAAGCCCTCAATGATTCCCAAAGAGCCCCAGAACCA

>Bacillus_Fam_1372_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_100:13250-13504 Satlength=255 Nr of
Repeats=5 RepeatLength=51 seed=AATACGCCGA Num.seqs=4
Similarity=0.869281
0 AATACGCCGAACCTCCCTTTACTCGGCTCTTTTTTCTGCTTCACAGTTCTA

Consensus:

AATACGCCGAACCTCCCTTTACTCGGCTCTTTTTTCTGCTTCACAGTTCTA

>Bacillus_Fam_1373_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_107:6328-6635 Satlength=308 Nr of
Repeats=6 RepeatLength=51 seed=GTGCGTATTC Num.seqs=5 Similarity=0.958170
0 GTGCGTATTCATCTGATTTGGTAATCAAATTTCAACCTGAGCCGAATTACG

Consensus:

GTGCGTATTCATCTGATTTGGTAATCAAATTTCAACCTGAGCCGAATTACG

>Bacillus_Fam_1374_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_122:8353-8558 Satlength=206 Nr of
Repeats=4 RepeatLength=51 seed=TTTTCATTTAC Num.seqs=3 Similarity=0.808279
0 TTTTCATTACCTATTATNGTTTATTCAAACCCTAATTGAGNGAGTTTCCCT

Consensus:

TTTTCATTTACCTATTATNGTTTATTCAAACCCTAATTGAGNGAGTTTCCCT

>Bacillus_Fam_1375_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000307875.1_BABA1.0_genomic.fna_34:35332-35689 Satlength=358 Nr of
Repeats=7 RepeatLength=51 seed=TTGGTCTTCA Num.seqs=7 Similarity=0.875506
0 TTGGTCTTCATCCGCTTAATGAAGACCTTTTTTCCGATTTTCGTTTACACTT

Consensus:

TTGGTCTTCATCCGCTTAATGAAGACCTTTTTTCCGATTTTCGTTTACACTT

>Bacillus_Fam_1376_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000307875.1_BABA1.0_genomic.fna_52:16517-17289 Satlength=773 Nr of
Repeats=5 RepeatLength=51 seed=CGTTACCTTT Num.seqs=4 Similarity=0.747277
0 CGTTACCTTTTCTTCGTATTTTCCCATTTTTGGTCACATAGACCCCTTCTA

Consensus:

CGTTACCTTTTCTTCGTATTTTCCCATTTTGGTCACATAGACCCCTTCTA

>Bacillus_Fam_1377_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000307875.1_BABA1.0_genomic.fna_121:73699-73903 Satlength=205 Nr of
Repeats=4 RepeatLength=51 seed=GTCACGTAGA Num.seqs=4 Similarity=0.873638
0 GTCACGTAGAACCTCTCTACGTGACCTCTCCCATGCTTTTTCTCCAAAATA

Consensus:

GTCACGTAGAACCTCTCTACGTGACCTCTCCCATGCTTTTTCTCCAAAATA

>Bacillus_Fam_1378_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1364253-1364865 Satlength=613 Nr
of Repeats=12 RepeatLength=51 seed=CGCTTTTATC Num.seqs=12
Similarity=0.887502 0
CGCTTTTATCGTCACGTAAATGATTTCAACGCGTTTTGCTGATAATAAAT

Consensus:

CGCTTTTATCGTCACGTAAATGATTTCAACGCGTTTTGCTGATAATAAAT

>Bacillus_Fam_1379_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1553326-1553721 Satlength=396 Nr
of Repeats=4 RepeatLength=51 seed=TCCGTTATTT Num.seqs=3
Similarity=0.694989 0
TCCGTTATTTGTCCAAAACCCTATGCTACAGCTATTTNCCGGACACCAGG

Consensus:

TCCGTTATTTGTCCAAAACCCTATGCTACAGCTATTTNCCGGACACCAGG

>Bacillus_Fam_1380_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_9:47516-47873 Satlength=358 Nr of
Repeats=7 RepeatLength=51 seed=GCTTCAGTTT Num.seqs=7 Similarity=0.841892
0 GCTTCAGTTTCTTCATCCGAAATCATCTCAGCTGTACCTGCAGGCTCTTTT

Consensus:

GCTTCAGTTTCTTCATCCGAAATCATCTCAGCTGTACCTGCAGGCTCTTTT

>Bacillus_Fam_1381_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_5:211104-211479 Satlength=376 Nr
of Repeats=4 RepeatLength=51 seed=ATATTTTTTT Num.seqs=3

Similarity=0.912854

0 ATATTTTTTTGAACGTTCTTCACGTTTGCTAGATCGTTTTTCGCGATCATA

Consensus:

ATATTTTTTTGAACGTTCTTCACGTTTGCTAGATCGTTTTTCGCGATCATA

>Bacillus_Fam_1382_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51

Alignment score = 0.000000

GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:404655-405420

Satlength=766 Nr of Repeats=15 RepeatLength=51 seed=AGTTGTCCAT

Num.seqs=15 Similarity=0.840842

0

AGTTGTCCATTTGCGNGGGCTATTGGACAACTTTTTCNGAAAAACACCAG

Consensus:

AGTTGTCCATTTGCGNGGGCTATTGGACAACTTTTTCNGAAAAACACCAG

>Bacillus_Fam_1383_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51

Alignment score = 0.000000

GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:437106-437412

Satlength=307 Nr of Repeats=6 RepeatLength=51 seed=TTGGACAGCT Num.seqs=6

Similarity=0.864052

0

TTGGACAGCTTCGCGCTATTTTCCAAAAGTTGTCCATTAGACACAAGCTA

Consensus:

TTGGACAGCTTCGCGCTATTTTCCAAAAGTTGTCCATTAGACACAAGCTA

>Bacillus_Fam_1384_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51

Alignment score = 0.000000

GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_30:51081-51439

Satlength=359 Nr of Repeats=7 RepeatLength=51 seed=TTTTCTCTAA Num.seqs=6

Similarity=0.914597

0

TTTTCTCTAATTACGATATTTCTGTCCAATAGGACCTGGCTATTGGACAGG

Consensus:

TTTTCTCTAATTACGATATTTCTGTCCAATAGGACCTGGCTATTGGACAGG

>Bacillus_Fam_1385_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51

Alignment score = 0.000000

GCF_000986785.1_ASM98678v1_genomic.fna_52:2-207 Satlength=206 Nr of

Repeats=4 RepeatLength=51 seed=CTTGGCGCAA Num.seqs=3 Similarity=0.762821

0 CTTGGCGCAAAAAGTTTCCCGAGGNTGGAGAAATTGCGTTAACGCAGGGT

Consensus:

CTTGGCGCAAAAAGTTTCCCGAGGNTGGAGAAATTGCGTTAACGCAGGGT

>Bacillus_Fam_1386_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:3343036-3343241
Satlength=206 Nr of Repeats=4 RepeatLength=51 seed=CTCAGAGACA Num.seqs=3
Similarity=0.773420 0
CTCAGAGACAAAATCCAGGNAAAAAGTAGNGATTTGTCTCTGATCGGGTGT

Consensus:

CTCAGAGACAAAATCCAGGNAAAAAGTAGNGATTTGTCTCTGATCGGGTGT

>Bacillus_Fam_1387_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4007424-4007779
Satlength=356 Nr of Repeats=7 RepeatLength=51 seed=CTTCGGTCGA Num.seqs=5
Similarity=0.848077 0
CTTCGGTCGAATAGAAACGCCCTATTTCGCGCATTTCTGTGATTTTCTTTTN

Consensus:

CTTCGGTCGAATAGAAACGCCCTATTTCGCGCATTTCTGTGATTTTCTTTTN

>Bacillus_Fam_1388_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4072217-4072880
Satlength=664 Nr of Repeats=13 RepeatLength=51 seed=CGCCCCAATT Num.seqs=13 Similarity=0.887410 0
CGCCCCAATTCACCCGAAGAAAAGGAAATACACGTCAANGGTCAATAGAT

Consensus:

CGCCCCAATTCACCCGAAGAAAAGGAAATACACGTCAANGGTCAATAGAT

>Bacillus_Fam_1389_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_001375535.1_Bacillus_niameyensis_genomic.fna_6:4237328-4237736
Satlength=409 Nr of Repeats=8 RepeatLength=51 seed=GGTCGAATAG Num.seqs=6
Similarity=0.775641 0
GGTCGAATAGAAGCGATCAATTGACCGTTGCTGGAAAATCCGCTTTGTTT

Consensus:

GGTCGAATAGAAGCGATCAATTGACCGTTGCTGGAAAATCCGCTTTGTTT

>Bacillus_Fam_1390_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_14:69179-69489 Satlength=311 Nr
of Repeats=6 RepeatLength=52 seed=CTTATACATT Num.seqs=4

Similarity=0.611616

0 CTTATACATTTTTCTTTCTTCCCATGAAAATCTATACGCATCCTCCCTTC

Consensus:

CTTATACATTTTTCTTTCTTCCCATGAAAATCTATACGCATCCTCCCTTC

>Bacillus_Fam_1391_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51

Alignment score = 0.000000

GCF_001591465.1_ASM159146v1_genomic.fna_6:84138-84347 Satlength=210 Nr of

Repeats=4 RepeatLength=52 seed=TTCGGACACA Num.seqs=3 Similarity=0.718107

0 TTCGGACACAGAAAGGGGGAACCCGTGGAATTGAGTCAGAACCCGGNCAAG

Consensus:

TTCGGACACAGAAAGGGGGAACCCGTGGAATTGAGTCAGAACCCGGNCAAG

>Bacillus_Fam_1392_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51

Alignment score = 0.000000

GCF_001591645.1_ASM159164v1_genomic.fna_12:25703-25906 Satlength=204 Nr

of Repeats=4 RepeatLength=51 seed=TAATCGTTCC Num.seqs=3

Similarity=0.557692

0 TAATCGTTCCCGAAAATGCNGTGTANGAGGCTGGNGGTAATGAATAGGGAG

Consensus:

TAATCGTTCCCGAAAATGCNGTGTANGAGGCTGGNGGTAATGAATAGGGAG

>Bacillus_Fam_1393_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51

Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:3673042-3673458 Satlength=417

Nr of Repeats=5 RepeatLength=52 seed=ATAGAGCGCG Num.seqs=3

Similarity=0.524904

ATAGAGCGCGTGTCCAGTAATTTATTGGAAAAGGCGTCCTATGAACCATTC

0

Consensus:

ATAGAGCGCGTGTCCAGTAATTTATTGGAAAAGGCGTCCTATGAACCATTC

>Bacillus_Fam_1394_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51

Alignment score = 0.000000

GCF_001636325.1_ASM163632v1_genomic.fna_1:1408479-1409142 Satlength=664

Nr of Repeats=13 RepeatLength=51 seed=AAAATGGTCC Num.seqs=13

Similarity=0.876655

AAAATGGTCCTAGTTACCAAACCTGGAACCAAAATCAAGAAAGACAGCGTA

0

Consensus:

AAAATGGTCCTAGTTACCAAACCTGGAACCAAAATCAAGAAAGACAGCGTA

>Bacillus_Fam_1395_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_2:1137164-1137571 Satlength=408
Nr of Repeats=8 RepeatLength=51 seed=AACTGTGACC Num.seqs=7
Similarity=0.925303 0
AACTGTGACCAAAAATGGCGGAGAAATCAAAAAACGGTCACAGAGTGTAA

Consensus:

AACTGTGACCAAAAATGGCGGAGAAATCAAAAAACGGTCACAGAGTGTAA

>Bacillus_Fam_1396_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_2:629683-630193 Satlength=511 Nr
of Repeats=10 RepeatLength=51 seed=AAAAAAGTA Num.seqs=10
Similarity=0.933188 0
AAAAAAGTAAAAAACATGTAAAGAGTCTCATAGGAGCATTCAATGGGAC

Consensus:

AAAAAAGTAAAAAACATGTAAAGAGTCTCATAGGAGCATTCAATGGGAC

>Bacillus_Fam_1397_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:4244978-4245368 Satlength=391
Nr of Repeats=8 RepeatLength=51 seed=TAAAAGAGAA Num.seqs=6
Similarity=0.839651 0
TAAAAGAGAACTTAGGATGAATAGCTTCCACAACTGTAAGTGGAAGCATC

Consensus:

TAAAAGAGAACTTAGGATGAATAGCTTCCACAACTGTAAGTGGAAGCATC

>Bacillus_Fam_1398_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:5051740-5052045 Satlength=306
Nr of Repeats=6 RepeatLength=51 seed=GACTTTAGAG Num.seqs=5
Similarity=0.725490 0
GACTTTAGAGNACATTNCTTCCTNATACTGGTAATTAAAGGAGCTAAGATT

Consensus:

GACTTTAGAGNACATTNCTTCCTNATACTGGTAATTAAAGGAGCTAAGATT

>Bacillus_Fam_1399_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:947086-947749 Satlength=664 Nr
of Repeats=13 RepeatLength=51 seed=GGATTTTGGA Num.seqs=13

Similarity=0.922574 0
GGATTTTGAAGAAGGGAAAAGCATGCCCCCAAAGTGGCGTTAGGATACAT

Consensus:

GGATTTTGAAGAAGGGAAAAGCATGCCCCCAAAGTGGCGTTAGGATACAT

>Bacillus_Fam_1400_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:3812725-3813857 Satlength=1133
Nr of Repeats=21 RepeatLength=51 seed=TTCTATTACC Num.seqs=15
Similarity=0.838655 0
TTCTATTACCTCTATCCTGCTTTTGGCGATCACCTTTTCGGCTTCGGGCTT

Consensus:

TTCTATTACCTCTATCCTGCTTTTGGCGATCACCTTTTCGGCTTCGGGCTT

>Bacillus_Fam_1401_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_13:191015-191219
Satlength=205 Nr of Repeats=4 RepeatLength=51 seed=CCATCCGGAA Num.seqs=4
Similarity=0.856209 0
CCATCCGGAAAGTGGTGGAAAGATTTTCATCCCCTGCAAGTTCTACCCCAGTC

Consensus:

CCATCCGGAAAGTGGTGGAAAGATTTTCATCCCCTGCAAGTTCTACCCCAGTC

>Bacillus_Fam_1402_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_20:425714-425918
Satlength=205 Nr of Repeats=4 RepeatLength=51 seed=CATCCTTCAC Num.seqs=4
Similarity=0.825472 0
CATCCTTCACCATGATCACGGGCACTTATCTCCTCTTTGGTTACCTCTTTT

Consensus:

CATCCTTCACCATGATCACGGGCACTTATCTCCTCTTTGGTTACCTCTTTT

>Bacillus_Fam_1403_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_22:4620-4862
Satlength=243 Nr of Repeats=4 RepeatLength=51 seed=TTTGGGGAAC Num.seqs=3
Similarity=0.728632 0
TTTGGGGAACCTATCTCGGCTTTGGTTACCTTTTCCTTGGCTTCGGNTCGA

Consensus:

TTTGGGGAACCTATCTCGGCTTTGGTTACCTTTTCCTTGGCTTCGGNTCGA

>Bacillus_Fam_1404_51_1 Nr. of seq. 1 Alignment length(with gaps) = 51
Alignment score = 0.000000

GCF_900156875.1_PRJEB18969_genomic.fna_11:2558203-2558548 Satlength=346
Nr of Repeats=4 RepeatLength=51 seed=TTCTTCAACA Num.seqs=3

Similarity=0.825708

0

TTCTTCAACAGCCTCTATTGCTTGTGGGACGGATTCTCGGTCATTTCCAC

Consensus:

TTCTTCAACAGCCTCTATTGCTTGTGGGACGGATTCTCGGTCATTTCCAC

>Bacillus_Fam_1405_50_1 Nr. of seq. 1 Alignment length(with gaps) = 50
Alignment score = 0.000000

GCF_000331575.1_ASM33157v1_genomic.fna_4:7266-7566 Satlength=301 Nr of
Repeats=6 RepeatLength=50 seed=CGACTGCCAC Num.seqs=6 Similarity=0.752889

0 CGACTGCCACTATTTGGAAAACAAAATGCACACACACTCATTTACCGCCT

Consensus:

CGACTGCCACTATTTGGAAAACAAAATGCACACACACTCATTTACCGCCT

>Bacillus_Fam_1406_50_1 Nr. of seq. 1 Alignment length(with gaps) = 50
Alignment score = 0.000000

GCF_000751775.1_A1A_genomic.fna_12:25055-25349 Satlength=295 Nr of
Repeats=6 RepeatLength=49 seed=TTTAAAATCA Num.seqs=6 Similarity=0.703111

0 TTTAAAATCAAAGGAATAGATTGTGGTCGGGTNAAATCAAGTAGCTCACT

Consensus:

TTTAAAATCAAAGGAATAGATTGTGGTCGGGTNAAATCAAGTAGCTCACT

>Bacillus_Fam_1407_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000

GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_41:18-465
Satlength=448 Nr of Repeats=7 RepeatLength=48 seed=GCGATGATGC Num.seqs=5

Similarity=0.983333

0

GCGATGATGCCGAGATGCCGCATCAGATGCCACATCAGGTGCAGGGA

Consensus:

GCGATGATGCCGAGATGCCGCATCAGATGCCACATCAGGTGCAGGGA

>Bacillus_Fam_1408_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000

GCF_000299035.1_ASM29903v1_genomic.fna_27:4592-4928 Satlength=337 Nr of Repeats=7 RepeatLength=48 seed=TCAGCCAGAA Num.seqs=7 Similarity=0.952381
0 TCAGCCAGAAAACAACGGAAAAGGATATAAACAAGAAAATAGAGAGTC

Consensus:

TCAGCCAGAAAACAACGGAAAAGGATATAAACAAGAAAATAGAGAGTC

>Bacillus_Fam_1409_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000

GCF_000307855.1_BAZ01.0_genomic.fna_111:42295-42598 Satlength=304 Nr of Repeats=4 RepeatLength=48 seed=GGGATGCCGC Num.seqs=3 Similarity=0.888889
0 GGGATGCCGCTAAATCCGGCTCCTGGTACCCCTCCATAACCTGCTGGT

Consensus:

GGGATGCCGCTAAATCCGGCTCCTGGTACCCCTCCATAACCTGCTGGT

>Bacillus_Fam_1410_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000

GCF_000430785.1_ASM43078v1_genomic.fna_5:99863-100391 Satlength=529 Nr of Repeats=11 RepeatLength=48 seed=AAACCAACAG Num.seqs=11
Similarity=0.825253
0 AAACCAACAGAGTCAGCATCATTGAGCAATGCTGCATAATCATCTTGT

Consensus:

AAACCAACAGAGTCAGCATCATTGAGCAATGCTGCATAATCATCTTGT

>Bacillus_Fam_1411_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000

GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-14515_genome_genomic.fna_27:69414-69702 Satlength=289 Nr of Repeats=6 RepeatLength=48 seed=TCATTTGCTG Num.seqs=6 Similarity=0.962963
0 TCATTTGCTGTCCTGAATACATTGGAGAAGGTATGCTAGAAATATGGCC

Consensus:

TCATTTGCTGTCCTGAATACATTGGAGAAGGTATGCTAGAAATATGGCC

>Bacillus_Fam_1412_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000

GCF_000615945.1_ASM61594v1_genomic.fna_79:12436-12628 Satlength=193 Nr of Repeats=4 RepeatLength=48 seed=AGCCCGATGA Num.seqs=4 Similarity=0.939815
0 AGCCCGATGAGAAATTACTATAGAGCGATTGATCAGCACGTGACCGAT

Consensus:

AGCCCGATGAGAAATTACTATAGAGCGATTGATCAGCACGTGACCGAT

>Bacillus_Fam_1413_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_23:9-231 Satlength=223 Nr of
Repeats=5 RepeatLength=48 seed=GCTTCTTCTG Num.seqs=4 Similarity=0.925926
0 GCTTCTTCTGTTGTTTCCTCTTCTTGGCCTTCTTCATCTACAGCATCC

Consensus:

GCTTCTTCTGTTGTTTCCTCTTCTTGGCCTTCTTCATCTACAGCATCC

>Bacillus_Fam_1414_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000
GCF_000812025.2_ASM81202v2_genomic.fna_60:32692-32932 Satlength=241 Nr of
Repeats=5 RepeatLength=48 seed=GCAAAGAAAAG Num.seqs=5 Similarity=0.904082
0 GCAAAGAAAAGAAGCCGAAGAACAAGCGAAACGAGAGGCTGAAGAACAG

Consensus:

GCAAAGAAAAGAAGCCGAAGAACAAGCGAAACGAGAGGCTGAAGAACAG

>Bacillus_Fam_1415_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000
GCF_001274775.1_ASM127477v1_genomic.fna_3:296300-296492 Satlength=193 Nr
of Repeats=4 RepeatLength=48 seed=GGTGTGATGG Num.seqs=4
Similarity=0.888889
0 GGTGTGATGGGAGCAGAGATGCATCATCAGATGCCGATGGGTCAGCCG

Consensus:

GGTGTGATGGGAGCAGAGATGCATCATCAGATGCCGATGGGTCAGCCG

>Bacillus_Fam_1416_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000
GCF_001278705.1_ASM127870v1_genomic.fna_1:2286101-2286677 Satlength=577
Nr of Repeats=12 RepeatLength=48 seed=TTAGAAAGAA Num.seqs=12
Similarity=0.986111 0
TTAGAAAGAAGCAGAGACAGAAGTTCGGAAGCAGTGTGGACAATGAC

Consensus:

TTAGAAAGAAGCAGAGACAGAAGTTCGGAAGCAGTGTGGACAATGAC

>Bacillus_Fam_1417_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48
Alignment score = 0.000000
GCF_001578185.1_ASM157818v1_genomic.fna_1:5252350-5252542 Satlength=193
Nr of Repeats=4 RepeatLength=48 seed=CGGCCTCCCC Num.seqs=4
Similarity=0.949074 0
CGGCCTCCCCGCGAATCCTCACGTTTAGGTCCGCGGCTGTTTCCATC

Consensus:

CGGCCTCCCCGCGAATCCTCACGTTTAGGTCCGCGGCTGTTTCCATC

>Bacillus_Fam_1418_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48

Alignment score = 0.000000

GCF_001578205.1_ASM157820v1_genomic.fna_1:1115267-1115459 Satlength=193

Nr of Repeats=4 RepeatLength=48 seed=CATCATAAGA Num.seqs=4

Similarity=0.902778

0

CATCATAAGAAGAGCTGCCGCAAGTCACATCGCAGCAAGCACAGATCG

Consensus:

CATCATAAGAAGAGCTGCCGCAAGTCACATCGCAGCAAGCACAGATCG

>Bacillus_Fam_1419_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48

Alignment score = 0.000000

GCF_001590785.1_ASM159078v1_genomic.fna_12:121693-122077 Satlength=385 Nr

of Repeats=8 RepeatLength=48 seed=ATGCCGTGGC Num.seqs=8

Similarity=0.957341

0

ATGCCGTGGCAAAATGGGATGATGCCAATGCCTGGACAGCAGGAAGGA

Consensus:

ATGCCGTGGCAAAATGGGATGATGCCAATGCCTGGACAGCAGGAAGGA

>Bacillus_Fam_1420_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48

Alignment score = 0.000000

GCF_001592005.1_ASM159200v1_genomic.fna_4:110265-110505 Satlength=241 Nr

of Repeats=5 RepeatLength=48 seed=TATAAGAAGG Num.seqs=5

Similarity=0.894444

0 TATAAGAAGGACTACTACTACCATGAGCCTTACAAGAAGCATCACGAG

Consensus:

TATAAGAAGGACTACTACTACCATGAGCCTTACAAGAAGCATCACGAG

>Bacillus_Fam_1421_48_1 Nr. of seq. 1 Alignment length(with gaps) = 48

Alignment score = 0.000000

GCF_900109925.1_IMG-

taxon_2651870116_annotated_assembly_genomic.fna_12:1886-2102

Satlength=217 Nr of Repeats=5 RepeatLength=48 seed=CTGTTCTTC Num.seqs=4

Similarity=0.740741

0

CTGTTCTTCATCCGAACCAGGGCGGTTCTTCTTCCGGCTCATCTC

Consensus:

CTGTTCTTCATCCGAACCAGGGCGGTTCTTCTTCCGGCTCATCTC

>Bacillus_Fam_1422_47_1 Nr. of seq. 1 Alignment length(with gaps) = 47
Alignment score = 0.000000
GCF_001895885.1_ASM189588v1_genomic.fna_2:13546-13781 Satlength=236 Nr of
Repeats=5 RepeatLength=47 seed=AAACACGAGT Num.seqs=5 Similarity=0.971631
0 AAACACGAGTAAGAATATGAATTATTCAGCTACCTTGATTACGTTTA

Consensus:

AAACACGAGTAAGAATATGAATTATTCAGCTACCTTGATTACGTTTA

>Bacillus_Fam_1423_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:4518727-4518952 Satlength=226 Nr
of Repeats=5 RepeatLength=45 seed=TTGTTGATTT Num.seqs=5
Similarity=0.855556 0
TTGTTGATTTCTCTTCTTTTTTACCTTTTTTCATCAGCTGAACCGC

Consensus:

TTGTTGATTTCTCTTCTTTTTTACCTTTTTTCATCAGCTGAACCGC

>Bacillus_Fam_1424_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:5389248-5389428 Satlength=181 Nr
of Repeats=4 RepeatLength=45 seed=CACCATCAAAG Num.seqs=4
Similarity=0.906173 0
CACCATCAAAGTACAACAGGTGGATCTCAATCAAGTGGTGGAGGAG

Consensus:

CACCATCAAAGTACAACAGGTGGATCTCAATCAAGTGGTGGAGGAG

>Bacillus_Fam_1425_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCF_000334155.1_L1_genomic.fna_18:2736-3096 Satlength=361 Nr of Repeats=8
RepeatLength=45 seed=GCCCGAAGCA Num.seqs=6 Similarity=0.871605
0 GCCCGAAGCATTAGGGGTCAGNGCAGAAGTGCCCGAGAGCGTGAGA

Consensus:

GCCCGAAGCATTAGGGGTCAGNGCAGAAGTGCCCGAGAGCGTGAGA

>Bacillus_Fam_1426_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCF_000473245.1_ASM47324v1_genomic.fna_1:550520-550790 Satlength=271 Nr
of Repeats=5 RepeatLength=45 seed=CCGGAGTTTT Num.seqs=4
Similarity=0.624691
0 CCGGAGTATTAACAGAAATAGAATCACACACATCGACATCGACAA

Consensus:

CCGGAGTATTAACAGAAATAGAATCACACACATCGACATCGACAA

>Bacillus_Fam_1427_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

GCF_000712595.1_ASM71259v1_genomic.fna_33:9174-9894 Satlength=721 Nr of
Repeats=16 RepeatLength=45 seed=TCCTTGTTGGT Num.seqs=16
Similarity=0.978519

0 TCCTTGTTGGTCCAGTGGGACCGATAGGCCCTGGTTCCTTGTGA

Consensus:

TCCTTGTTGGTCCAGTGGGACCGATAGGCCCTGGTTCCTTGTGA

>Bacillus_Fam_1428_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

GCF_000712595.1_ASM71259v1_genomic.fna_43:3917-4656 Satlength=740 Nr of
Repeats=5 RepeatLength=45 seed=GAGCAATCTA Num.seqs=3 Similarity=0.980247

0 GAGCAATCTAGTAATTATTGACGGTATCAGCCGTTATCTGAACTT

Consensus:

GAGCAATCTAGTAATTATTGACGGTATCAGCCGTTATCTGAACTT

>Bacillus_Fam_1429_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

GCF_000712615.1_ASM71261v1_genomic.fna_3:111271-111496 Satlength=226 Nr
of Repeats=5 RepeatLength=45 seed=TCTTGAGTTT Num.seqs=5
Similarity=0.857778

0 TCTTGAGTTTGCTGAGATACGTGTTGATTTTGTGACGTTGAGGT

Consensus:

TCTTGAGTTTGCTGAGATACGTGTTGATTTTGTGACGTTGAGGT

>Bacillus_Fam_1430_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

GCF_000712615.1_ASM71261v1_genomic.fna_42:5062-5242 Satlength=181 Nr of
Repeats=4 RepeatLength=45 seed=GGAACAGAAA Num.seqs=4 Similarity=0.901235

0 GGAACAGAAAGACAAGGAATGGGTGAAGGAAATGCAGTTCCAGTA

Consensus:

GGAACAGAAAGACAAGGAATGGGTGAAGGAAATGCAGTTCCAGTA

>Bacillus_Fam_1431_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

GCF_000724485.1_ASM72448v1_genomic.fna_1:2469191-2469371 Satlength=181 Nr of Repeats=4 RepeatLength=45 seed=TGTATCGGTG Num.seqs=4
Similarity=0.777778 0
TGTATCGGTGAAACGGGCATTTGCTTTTCTACTTTAGGAAATTC

Consensus:

TGTATCGGTGAAACGGGCATTTGCTTTTCTACTTTAGGAAATTC

>Bacillus_Fam_1432_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_22:32281-32461
Satlength=181 Nr of Repeats=5 RepeatLength=45 seed=GATAAACCGG Num.seqs=3
Similarity=0.822222 0
GATAAACCGGATGGCGAGAATCCAGATGTAGACAAGCCTGACACG

Consensus:

GATAAACCGGATGGCGAGAATCCAGATGTAGACAAGCCTGACACG

>Bacillus_Fam_1433_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCF_000812025.2_ASM81202v2_genomic.fna_70:2588-3101 Satlength=514 Nr of Repeats=9 RepeatLength=45 seed=TCTGTGCCTT Num.seqs=6 Similarity=0.747160
0 TCTGTGCCTTCCGTTTCCTTCGGTTACCGCTTCTGCTCCTGTGTCG

Consensus:

TCTGTGCCTTCCGTTTCCTTCGGTTACCGCTTCTGCTCCTGTGTCG

>Bacillus_Fam_1434_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_9:41557-41833 Satlength=277 Nr of Repeats=4 RepeatLength=45 seed=TTTTCCTCTT Num.seqs=3 Similarity=0.812346
0 TTTTCCTCTTTAGGAGGAGTTGGATTCTGAAGGCTTNGGAGCCGGT

Consensus:

TTTTCCTCTTTAGGAGGAGTTGGATTCTGAAGGCTTNGGAGCCGGT

>Bacillus_Fam_1435_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_27:20593-20812 Satlength=220 Nr of Repeats=5 RepeatLength=45 seed=CTCATGAAGA Num.seqs=4
Similarity=0.891358
0 CTCATGAAGAAGATCACGACCACGATCACGACCATGAACACGATG

Consensus:

CTCATGAAGAAGATCACGACCACGATCACGACCATGAACACGATG

>Bacillus_Fam_1436_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

GCF_001636315.1_ASM163631v1_genomic.fna_1:2589898-2590303 Satlength=406

Nr of Repeats=8 RepeatLength=45 seed=TCCTCTTCAT Num.seqs=7

Similarity=0.893030

0

TCCTCTTCATCTATAAAAGAGCTCTCTTCTTGGGGAGAACTGGAT

Consensus:

TCCTCTTCATCTATAAAAGAGCTCTCTTCTTGGGGAGAACTGGAT

>Bacillus_Fam_1437_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

GCF_001645555.1_ASM164555v1_genomic.fna_43:255404-255833 Satlength=430 Nr

of Repeats=11 RepeatLength=45 seed=CCATTATTTC Num.seqs=8

Similarity=0.780952

0

CCATTATTTCCTTGCGAGCCTCTTCCGTTGTTCTCTTGCCCATTC

Consensus:

CCATTATTTCCTTGCGAGCCTCTTCCGTTGTTCTCTTGCCCATTC

>Bacillus_Fam_1438_45_1 Nr. of seq. 1 Alignment length(with gaps) = 45
Alignment score = 0.000000

GCF_001896335.1_ASM189633v1_genomic.fna_15:81928-82711 Satlength=784 Nr

of Repeats=7 RepeatLength=45 seed=GCTCCGGTTA Num.seqs=6

Similarity=0.920988

0 GCTCCGGTTACTCCGGTCGCTCCCGTATCTCCCGTTGCACCTGTG

Consensus:

GCTCCGGTTACTCCGGTCGCTCCCGTATCTCCCGTTGCACCTGTG

>Bacillus_Fam_1439_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_7:5367-5580 Satlength=214 Nr of

Repeats=5 RepeatLength=43 seed=AAAACCTTCT Num.seqs=3 Similarity=0.958656

0 AAAACCTTCTAACAAAGATCCAACCCCAACCCCTAGTTACCCA

Consensus:

AAAACCTTCTAACAAAGATCCAACCCCAACCCCTAGTTACCCA

>Bacillus_Fam_1440_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000

GCF_001591445.1_ASM159144v1_genomic.fna_9:156414-156582 Satlength=169 Nr

of Repeats=4 RepeatLength=42 seed=GGCTGGTTAG Num.seqs=4

Similarity=0.801034
0 GGCTGGTTAGATTCGGTTCTTGCTTCTTCGTANATCCAATGAA

Consensus:

GGCTGGTTAGATTCGGTTCTTGCTTCTTCGTANATCCAATGAA

>Bacillus_Fam_1441_43_1 Nr. of seq. 1 Alignment length(with gaps) = 43
Alignment score = 0.000000

GCF_001742425.1_ASM174242v1_genomic.fna_38:12301-12469 Satlength=169 Nr
of Repeats=4 RepeatLength=42 seed=TCAGTTTAA Num.seqs=4
Similarity=0.816537

0 TCAGTTTAAAGCTCGGAGACATCTGTTTTTAAGNTTAGAAACC

Consensus:

TCAGTTTAAAGCTCGGAGACATCTGTTTTTAAGNTTAGAAACC

>Bacillus_Fam_1442_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000011145.1_ASM1114v1_genomic.fna_1:2885595-2885763 Satlength=169 Nr
of Repeats=4 RepeatLength=42 seed=TGATCATCTT Num.seqs=4
Similarity=0.915344

0 TGATCATCTTCCTCGTGACCATGCTCCTCATGGCTATGGTCG

Consensus:

TGATCATCTTCCTCGTGACCATGCTCCTCATGGCTATGGTCG

>Bacillus_Fam_1443_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000017425.1_ASM1742v1_genomic.fna_1:1132359-1132527 Satlength=169 Nr
of Repeats=4 RepeatLength=42 seed=AGGTTTTGT Num.seqs=4
Similarity=0.947090

0 AGGTTTTGTGCTTCAGGTTTAGCTGTTTCGTTGTTTACAGC

Consensus:

AGGTTTTGTGCTTCAGGTTTAGCTGTTTCGTTGTTTACAGC

>Bacillus_Fam_1444_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000017425.1_ASM1742v1_genomic.fna_1:1831558-1831726 Satlength=169 Nr
of Repeats=4 RepeatLength=42 seed=AATCAAGGAA Num.seqs=4
Similarity=0.904762

0 AATCAAGGAAATCAAACGCCGCAAATAGCGGAAACGGAAT

Consensus:

AATCAAGGAAATCAAACGCCGCCAAATAGCGGAAACGGAAAT

>Bacillus_Fam_1445_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000171615.1_ASM17161v1_genomic.fna_94:31227-32096 Satlength=870 Nr of
Repeats=23 RepeatLength=42 seed=TTCTCGTGCG Num.seqs=14
Similarity=0.651723
0 TTCTCGTGCGGTTGCCGCTCCATCCTGTGCGGCTTTTCCCCT

Consensus:

TTCTCGTGCGGTTGCCGCTCCATCCTGTGCGGCTTTTCCCCT

>Bacillus_Fam_1446_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:4299704-4300137 Satlength=434 Nr
of Repeats=6 RepeatLength=42 seed=TAACTTTGAT Num.seqs=4
Similarity=0.820106 0
TAACTTTGATCAAATCGCTCGTAACTCGGGCCGAATCGCGCG

Consensus:

TAACTTTGATCAAATCGCTCGTAACTCGGGCCGAATCGCGCG

>Bacillus_Fam_1447_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000186125.1_Bacillus_BT1B_CT2_V1_genomic.fna_2:24462-24672
Satlength=211 Nr of Repeats=5 RepeatLength=42 seed=TCTCTTTTCA Num.seqs=5
Similarity=0.987302 0
TCTCTTTTCAGCTCATATTCTTCCGTTTCTTCCACTTTC

Consensus:

TCTCTTTTCAGCTCATATTCTTCCGTTTCTTCCACTTTC

>Bacillus_Fam_1448_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000285535.1_ASM28553v1_genomic.fna_1:1108238-1108853 Satlength=616 Nr
of Repeats=5 RepeatLength=42 seed=CTGGACCTAT Num.seqs=4
Similarity=0.920635 0
CTGGACCTATGATGGGTGGGTTTAACCCTCAAGGACCTGGTG

Consensus:

CTGGACCTATGATGGGTGGGTTTAACCCTCAAGGACCTGGTG

>Bacillus_Fam_1449_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000292245.2_ASM29224v2_genomic.fna_35:20426-20996 Satlength=571 Nr of Repeats=4 RepeatLength=42 seed=CTTCTTCAGG Num.seqs=3 Similarity=0.936508
0 CTTCTTCAGGAGTCTCTACTTCCTCTCCTGGTTCTTCTGTTC

Consensus:

CTTCTTCAGGAGTCTCTACTTCCTCTCCTGGTTCTTCTGTTC

>Bacillus_Fam_1450_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000294775.2_ASM29477v2_genomic.fna_1:3171456-3171624 Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=CAGCCTTTTA Num.seqs=4
Similarity=0.894180 0

CAGCCTTTTATCCATCGAGCTGACCTTTTGATCCAGAACGTC

Consensus:

CAGCCTTTTATCCATCGAGCTGACCTTTTGATCCAGAACGTC

>Bacillus_Fam_1451_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000305495.1_BacPsy2.0_genomic.fna_3:23376-23586 Satlength=211 Nr of Repeats=5 RepeatLength=42 seed=ATTGTTAGAG Num.seqs=5 Similarity=0.819697
0 ATTGTTAGAGCTGCGTCGATCATTCGAACAACGACGGCGACG

Consensus:

ATTGTTAGAGCTGCGTCGATCATTCGAACAACGACGGCGACG

>Bacillus_Fam_1452_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000331575.1_ASM33157v1_genomic.fna_1:1325868-1326120 Satlength=253 Nr of Repeats=6 RepeatLength=42 seed=TTCGCTTTCG Num.seqs=6
Similarity=0.794709 0

TTCGCTTTCGGGTTTGCTTTTGGGTCTACCTTCGAATTTCCG

Consensus:

TTCGCTTTCGGGTTTGCTTTTGGGTCTACCTTCGAATTTCCG

>Bacillus_Fam_1453_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000331575.1_ASM33157v1_genomic.fna_3:40144-40312 Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=TCAAGAATCG Num.seqs=4 Similarity=0.931217
0 TCAAGAATCGCGATGAAATGTCCGGTCGTACAATAGACGAGC

Consensus:

TCAAGAATCGCGATGAAATGTCCGGTCGTACAATAGACGAGC

>Bacillus_Fam_1454_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000374345.1_ASM37434v1_genomic.fna_4:87852-88188 Satlength=337 Nr of
Repeats=8 RepeatLength=42 seed=TGCGTGAAGT Num.seqs=8 Similarity=0.794785
0 TGCGTGAAGTATTGCGGTTTCTTGAAGTANAGCGGCTCTGCT

Consensus:

TGCGTGAAGTATTGCGGTTTCTTGAAGTANAGCGGCTCTGCT

>Bacillus_Fam_1455_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_6:25006-25384 Satlength=379 Nr of
Repeats=9 RepeatLength=42 seed=CAACCAAGAG Num.seqs=9 Similarity=0.970018
0 CAACCAAGAGAAGTGGCCCCTGGAGAGGTACCTTCTGAAGCT

Consensus:

CAACCAAGAGAAGTGGCCCCTGGAGAGGTACCTTCTGAAGCT

>Bacillus_Fam_1456_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_11:44641-44941 Satlength=301 Nr of
Repeats=8 RepeatLength=42 seed=GATGATGGTG Num.seqs=6 Similarity=0.862434
0 GATGATGGTGGCCATGCTCATGGTGATGATGCTCACGTTTCAT

Consensus:

GATGATGGTGGCCATGCTCATGGTGATGATGCTCACGTTTCAT

>Bacillus_Fam_1457_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000408885.1_ASM40888v1_genomic.fna_1:3192978-3193251 Satlength=274 Nr
of Repeats=7 RepeatLength=42 seed=AAGCGCTTGT Num.seqs=6
Similarity=0.811640
AAGCGCTTGTGACCTCAACGAAACGTGCGTCCACTTCATCG 0

Consensus:

AAGCGCTTGTGACCTCAACGAAACGTGCGTCCACTTCATCG

>Bacillus_Fam_1458_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000429685.1_ASM42968v1_genomic.fna_11:127207-127375 Satlength=169 Nr
of Repeats=4 RepeatLength=42 seed=TCTCCAGAGT Num.seqs=4
Similarity=0.888889
0 TCTCCAGAGTCATCATCGTTTCCGTCATCCGGATTTCGAATCA

Consensus:

TCTCCAGAGTCATCATCGTTTCCGTCATCCGGATTCTGAATCA

>Bacillus_Fam_1459_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000429705.1_ASM42970v1_genomic.fna_1:1926382-1926520 Satlength=139 Nr of
Repeats=4 RepeatLength=42 seed=TTGTTGTTCT Num.seqs=3
Similarity=0.830688 0
TTGTTGTTCTGGTTGTTATTTGGATCCTGATTGTTCCATTGG

Consensus:

TTGTTGTTCTGGTTGTTATTTGGATCCTGATTGTTCCATTGG

>Bacillus_Fam_1460_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000429725.1_ASM42972v1_genomic.fna_9:71563-71857 Satlength=295 Nr of
Repeats=7 RepeatLength=42 seed=CCGGCGGCGG Num.seqs=7 Similarity=0.869992
0 CCGGCGGCGGGAACAACGGGGCTGACAATGGCGCCAACAACG

Consensus:

CCGGCGGCGGGAACAACGGGGCTGACAATGGCGCCAACAACG

>Bacillus_Fam_1461_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000430785.1_ASM43078v1_genomic.fna_16:70466-70970 Satlength=505 Nr of
Repeats=4 RepeatLength=42 seed=GGAGGATCTT Num.seqs=3 Similarity=0.978836
0 GGAGGATCTTCTCACGCGGAAGGATCGAACACAACAGCCAAT

Consensus:

GGAGGATCTTCTCACGCGGAAGGATCGAACACAACAGCCAAT

>Bacillus_Fam_1462_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000430785.1_ASM43078v1_genomic.fna_27:22202-22412 Satlength=211 Nr of
Repeats=5 RepeatLength=42 seed=CTGTTCAACA Num.seqs=5 Similarity=0.917460
0 CTGTTCAACAGCAATCAGCTCAACAAGAAAAAACTCAGCAGC

Consensus:

CTGTTCAACAGCAATCAGCTCAACAAGAAAAAACTCAGCAGC

>Bacillus_Fam_1463_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000474275.1_Bmar1.0_genomic.fna_50:55500-55668 Satlength=169 Nr of
Repeats=4 RepeatLength=42 seed=TCTGCTCTTC Num.seqs=4 Similarity=0.962963
0 TCTGCTCTTCGACTTTTATAAATCTTTCATTCTCTTATAAC

Consensus:

TCTGCTCTTCGACTTTTATAAATCTTTCATTCTTCTTATAAC

>Bacillus_Fam_1464_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000709935.2_ASM70993v2_genomic.fna_1:258653-258947 Satlength=295 Nr of Repeats=7 RepeatLength=42 seed=CGCTCAGCTT Num.seqs=7
Similarity=0.853364

0 CGCTCAGCTTCTTGTTTAGCAGCAGCCTGTTCTTGAGCTTTT

Consensus:

CGCTCAGCTTCTTGTTTAGCAGCAGCCTGTTCTTGAGCTTTT

>Bacillus_Fam_1465_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000709935.2_ASM70993v2_genomic.fna_13:94783-94999 Satlength=217 Nr of Repeats=5 RepeatLength=42 seed=CAGGTGAAGG Num.seqs=4 Similarity=0.899471

0 CAGGTGAAGGAGCCGGAGAAGGCGAAGGCCAGGGCGGCGGAA

Consensus:

CAGGTGAAGGAGCCGGAGAAGGCGAAGGCCAGGGCGGCGGAA

>Bacillus_Fam_1466_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000712615.1_ASM71261v1_genomic.fna_10:48131-48341 Satlength=211 Nr of Repeats=5 RepeatLength=42 seed=GGATTCGTAC Num.seqs=5 Similarity=0.974603

0 GGATTCGTACACCTTGTTATTTTCGTTTCCACCATTTGGT

Consensus:

GGATTCGTACACCTTGTTATTTTCGTTTCCACCATTTGGT

>Bacillus_Fam_1467_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000724485.1_ASM72448v1_genomic.fna_1:1410335-1410587 Satlength=253 Nr of Repeats=4 RepeatLength=42 seed=AAGAACTTTC Num.seqs=3

Similarity=0.682171

AAGAACTTCTTCCTGCCAAGAAAAAGATTCTCTTGGGAAA

0

Consensus:

AAGAACTTCTTCCTGCCAAGAAAAAGATTCTCTTGGGAAA

>Bacillus_Fam_1468_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_000724485.1_ASM72448v1_genomic.fna_1:2977273-2977777 Satlength=505 Nr
of Repeats=12 RepeatLength=42 seed=TGTTCA GTCT Num.seqs=12
Similarity=0.831841 0
TGTTCA GTCTTGATCGCACCGATTTCTTTCCGCATTTCTGAC

Consensus:

TGTTCA GTCTTGATCGCACCGATTTCTTTCCGCATTTCTGAC

>Bacillus_Fam_1469_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000751775.1_A1A_genomic.fna_90:16-268 Satlength=253 Nr of Repeats=6
RepeatLength=42 seed=TCAAACCGTT Num.seqs=6 Similarity=0.788360
0 TCAAACCGTTTATCCATGCTGTTCA GACGGCCATCCACATCA

Consensus:

TCAAACCGTTTATCCATGCTGTTCA GACGGCCATCCACATCA

>Bacillus_Fam_1470_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_31:29723-29891
Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=AGCCACTTGT Num.seqs=4
Similarity=1.000000 0
AGCCACTTGTAATTTATCGCTCCTTCTTTCACTGGAACGCG

Consensus:

AGCCACTTGTAATTTATCGCTCCTTCTTTCACTGGAACGCG

>Bacillus_Fam_1471_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000769555.1_ASM76955v1_genomic.fna_1:2684106-2684577 Satlength=472 Nr
of Repeats=10 RepeatLength=42 seed=GCTCTTCTTC Num.seqs=7
Similarity=0.879063 0
GCTCTTCTTCTTCCCCTCCCTCAGAATCGGGGCAGTCTCCG

Consensus:

GCTCTTCTTCTTCCCCTCCCTCAGAATCGGGGCAGTCTCCG

>Bacillus_Fam_1472_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000832605.1_ASM83260v1_genomic.fna_2:334361-334613 Satlength=253 Nr
of Repeats=6 RepeatLength=42 seed=GTCAAACGCA Num.seqs=6
Similarity=0.894180
0 GTCAAACGCAAAATGGTGGTAGCCAGCCAGGTGGAAGTGACG

Consensus:

GTCAAACGCAAAATGGTGGTAGCCAGCCAGGTGGAAGTGACG

>Bacillus_Fam_1473_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000934845.1_ASM93484v1_genomic.fna_23:28230-28440 Satlength=211 Nr of
Repeats=5 RepeatLength=42 seed=GGAGGACCGG Num.seqs=5 Similarity=0.787302
0 GGAGGACCGGGTGGNTTTCAGGCANTCCAGGTGGNTTCCCA

Consensus:

GGAGGACCGGGTGGNTTTCAGGCANTCCAGGTGGNTTCCCA

>Bacillus_Fam_1474_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_000948175.1_BFA_2_A_genomic.fna_157:17151-17403 Satlength=253 Nr of
Repeats=6 RepeatLength=42 seed=GATGTGGGAG Num.seqs=6 Similarity=0.908995
0 GATGTGGGAGGCCTAAAACAAAATGTCGAAATGCTAAAAGAC

Consensus:

GATGTGGGAGGCCTAAAACAAAATGTCGAAATGCTAAAAGAC

>Bacillus_Fam_1475_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001278705.1_ASM127870v1_genomic.fna_1:1934684-1934978 Satlength=295
Nr of Repeats=7 RepeatLength=42 seed=CCTGCTACGT Num.seqs=7
Similarity=0.918367 0
CCTGCTACGTTTGGCTGTCCGTGATACGGATTTTCTGATGCG

Consensus:

CCTGCTACGTTTGGCTGTCCGTGATACGGATTTTCTGATGCG

>Bacillus_Fam_1476_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001278705.1_ASM127870v1_genomic.fna_1:3048777-3049027 Satlength=251
Nr of Repeats=6 RepeatLength=42 seed=GGAATTGCAC Num.seqs=4
Similarity=0.809524 0
GGAATTGCACCGATAACAACGATAATTGCACCGTTGACCTTG

Consensus:

GGAATTGCACCGATAACAACGATAATTGCACCGTTGACCTTG

>Bacillus_Fam_1477_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_24:439598-439808 Satlength=211 Nr
of Repeats=5 RepeatLength=42 seed=GCTTTCGTTT Num.seqs=5

Similarity=0.844444 0
GCTTTCGTTTGTGATGCGTAGAGTATCTCGAATCTTCCTCGT

Consensus:

GCTTTCGTTTGTGATGCGTAGAGTATCTCGAATCTTCCTCGT

>Bacillus_Fam_1478_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001439635.1_ASM143963v1_genomic.fna_173:188835-189045 Satlength=211
Nr of Repeats=4 RepeatLength=42 seed=CAGGAGTCGG Num.seqs=3
Similarity=0.873016 0
CAGGAGTCGGACAATTAGTTGACGGACAAAAACAGCGGTTG

Consensus:

CAGGAGTCGGACAATTAGTTGACGGACAAAAACAGCGGTTG

>Bacillus_Fam_1479_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001484965.1_ASM148496v1_genomic.fna_5:164270-164606 Satlength=337 Nr
of Repeats=7 RepeatLength=42 seed=GAGCTTCAAT Num.seqs=6
Similarity=0.928042
0 GAGCTTCAATCCGACAAGAGGAGCGCTCATTCGGACAGGAGG

Consensus:

GAGCTTCAATCCGACAAGAGGAGCGCTCATTCGGACAGGAGG

>Bacillus_Fam_1480_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001484965.1_ASM148496v1_genomic.fna_6:187378-187747 Satlength=370 Nr
of Repeats=9 RepeatLength=42 seed=TGATCGGTAA Num.seqs=6
Similarity=0.904762
0 TGATCGGTAAATCCTCTGACATGAGCGATAACCATCTCTCACT

Consensus:

TGATCGGTAAATCCTCTGACATGAGCGATAACCATCTCTCACT

>Bacillus_Fam_1481_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001578185.1_ASM157818v1_genomic.fna_1:1320901-1321126 Satlength=226
Nr of Repeats=4 RepeatLength=42 seed=ATTTCTGCTA Num.seqs=3
Similarity=0.894180 0
ATTTCTGCTAGTGC GCCTTTGGTTTCTGCATGTAGATCTCCG

Consensus:

ATTTCTGCTAGTGC GCCTTTGGTTTCTGCATGTAGATCTCCG

>Bacillus_Fam_1482_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001587375.1_ASM158737v1_genomic.fna_134:11775-12027 Satlength=253 Nr
of Repeats=6 RepeatLength=42 seed=TTGAAGTCGA Num.seqs=6
Similarity=0.936508
0 TTGAAGTCGACAAACGGTTTGATGCTGTTGATCAAAAATTTA

Consensus:

TTGAAGTCGACAAACGGTTTGATGCTGTTGATCAAAAATTTA

>Bacillus_Fam_1483_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_25:20219-20387 Satlength=169 Nr
of Repeats=4 RepeatLength=42 seed=TTATTTAACA Num.seqs=4
Similarity=0.941799
0 TTATTTAACAGGTAGCAGAATTAACATAACAGAGTTTCGATT

Consensus:

TTATTTAACAGGTAGCAGAATTAACATAACAGAGTTTCGATT

>Bacillus_Fam_1484_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_72:22227-22647 Satlength=421 Nr
of Repeats=10 RepeatLength=42 seed=GTTGGCCGAT Num.seqs=10
Similarity=0.779189
GTTGGCCGATATATCGATTGTGGTGGCGCAATAACATGCTCA

0

Consensus:

GTTGGCCGATATATCGATTGTGGTGGCGCAATAACATGCTCA

>Bacillus_Fam_1485_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_137:8995-9163 Satlength=169 Nr of
Repeats=4 RepeatLength=42 seed=AAGTGCGTCA Num.seqs=4 Similarity=0.822997
0 AAGTGCGTCAATTACTTATCCAGCTGCGTCAAAAAGTTCGCC

Consensus:

AAGTGCGTCAATTACTTATCCAGCTGCGTCAAAAAGTTCGCC

>Bacillus_Fam_1486_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001591445.1_ASM159144v1_genomic.fna_22:81979-82189 Satlength=211 Nr
of Repeats=5 RepeatLength=42 seed=TTTGATAAAA Num.seqs=3

Similarity=0.957672

0 TTTGATAAAATTGAAACTCGACTTAATAATATGGATCAGCGG

Consensus:

TTTGATAAAATTGAAACTCGACTTAATAATATGGATCAGCGG

>Bacillus_Fam_1487_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42

Alignment score = 0.000000

GCF_001591585.1_ASM159158v1_genomic.fna_13:66350-66497 Satlength=148 Nr

of Repeats=4 RepeatLength=42 seed=AGAAACGCCA Num.seqs=3

Similarity=0.809524

0 AGAAACGCCAGGAGATAACGAAGAACTCCTGGAGATAATGA

Consensus:

AGAAACGCCAGGAGATAACGAAGAACTCCTGGAGATAATGA

>Bacillus_Fam_1488_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42

Alignment score = 0.000000

GCF_001591665.1_ASM159166v1_genomic.fna_15:56816-56984 Satlength=169 Nr

of Repeats=5 RepeatLength=42 seed=GCGAATTTCC Num.seqs=3

Similarity=0.542929

0 GCGAATTTCCGNGCCCAATGNGCGAATTATCGNACCTTACTN

Consensus:

GCGAATTTCCGNGCCCAATGNGCGAATTATCGNACCTTACTN

>Bacillus_Fam_1489_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42

Alignment score = 0.000000

GCF_001592005.1_ASM159200v1_genomic.fna_21:10147-10315 Satlength=169 Nr

of Repeats=4 RepeatLength=42 seed=GTGATCATTC Num.seqs=4

Similarity=0.915344

0 GTGATCATTCGCGCGCGGTTTGAAAATCATTGGTTGATGAC

Consensus:

GTGATCATTCGCGCGCGGTTTGAAAATCATTGGTTGATGAC

>Bacillus_Fam_1490_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42

Alignment score = 0.000000

GCF_001636335.1_ASM163633v1_genomic.fna_1:2763111-2763578 Satlength=468

Nr of Repeats=7 RepeatLength=42 seed=TATTCGCCGT Num.seqs=5

Similarity=0.638636

TATTCGCCGTCTNCTCNATTTATTGGACATTANCNGCACTT

0

Consensus:

TATTCGCCGTTCTNCTCNATTTATTGGACATTANCNGCACTT

>Bacillus_Fam_1491_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:2163616-2163826 Satlength=211
Nr of Repeats=5 RepeatLength=42 seed=ACATATCTAT Num.seqs=5
Similarity=0.923810 0
ACATATCTATGCTGATAAAAGGCAATTACCCCTTTAAGTAG

Consensus:

ACATATCTATGCTGATAAAAGGCAATTACCCCTTTAAGTAG

>Bacillus_Fam_1492_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:3182234-3182381 Satlength=148
Nr of Repeats=4 RepeatLength=42 seed=CTCGCCAATT Num.seqs=3
Similarity=0.772727 0
CTCGCCAATTCGGCACTTTTACTCGCGAGTTTCTGCTGTTTA

Consensus:

CTCGCCAATTCGGCACTTTTACTCGCGAGTTTCTGCTGTTTA

>Bacillus_Fam_1493_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:3510154-3511004 Satlength=851
Nr of Repeats=19 RepeatLength=42 seed=TTTTTCGGCC Num.seqs=12
Similarity=0.854738 18
TTTCGACCTGCATCCACTTTTTTTTCGGCCTGCACTCAACTTAA

Consensus:

TTTTTCGGCCTGCACTCAACTTAATTCGACCTGCATCCACTT

>Bacillus_Fam_1494_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_001645705.1_ASM164570v1_genomic.fna_60:510572-511860 Satlength=1289
Nr of Repeats=31 RepeatLength=42 seed=GTTGCGCAAT Num.seqs=25
Similarity=0.780465 0
GTTGCGCAATANGGTANTGTTTTAGCGCAATTCCGTGTGNAA

Consensus:

GTTGCGCAATANGGTANTGTTTTAGCGCAATTCCGTGTGNAA

>Bacillus_Fam_1495_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_001654695.1_ASM165469v1_genomic.fna_17:33252-33504 Satlength=253 Nr of Repeats=6 RepeatLength=42 seed=TCGTAGCATT Num.seqs=6 Similarity=0.881481

0 TCGTAGCATTTTTTCTTCTTACAGCAAAAATCTACGTGATCG

Consensus:

TCGTAGCATTTTTTCTTCTTACAGCAAAAATCTACGTGATCG

>Bacillus_Fam_1496_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000

GCF_001712755.1_ASM171275v1_genomic.fna_35:220736-221801 Satlength=1066 Nr of Repeats=19 RepeatLength=42 seed=TTTGGTCCCA Num.seqs=16

Similarity=0.741534 0

TTTGGTCCCATATATGCTGGCATTGTTTGTGGGAAGTTTGCA

Consensus:

TTTGGTCCCATATATGCTGGCATTGTTTGTGGGAAGTTTGCA

>Bacillus_Fam_1497_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000

GCF_001742425.1_ASM174242v1_genomic.fna_13:64716-64926 Satlength=211 Nr of Repeats=5 RepeatLength=42 seed=GAAGTAGAAG Num.seqs=5

Similarity=0.761905

0 GAAGTAGAAGATCTAAAAGCAGGTCAAACGAAGTTAACAACG

Consensus:

GAAGTAGAAGATCTAAAAGCAGGTCAAACGAAGTTAACAACG

>Bacillus_Fam_1498_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000

GCF_001742425.1_ASM174242v1_genomic.fna_37:154-322 Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=TTCTTCTTCA Num.seqs=4 Similarity=0.874031

0 TTCTTCTTCAGCAACGGTGTTAACTTCATCCTCAGGAAGGTA

Consensus:

TTCTTCTTCAGCAACGGTGTTAACTTCATCCTCAGGAAGGTA

>Bacillus_Fam_1499_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000

GCF_001877785.1_PlanoSAMM_genomic.fna_72:16191-16527 Satlength=337 Nr of Repeats=8 RepeatLength=42 seed=TACTTACTTG Num.seqs=8 Similarity=0.969388

0 TACTTACTTGTTGACCATTCTCCACTCTTCCAAACGTTCGT

Consensus:

TACTTACTTGTGACCATCTCCACTCTTTCCAAACGTTTCGT

>Bacillus_Fam_1500_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_002019635.1_ASM201963v1_genomic.fna_1:836663-836873 Satlength=211 Nr
of Repeats=5 RepeatLength=42 seed=AGTTCTTTTCG Num.seqs=5
Similarity=0.898413
0 AGTTCTTTTCGTGTCTGCTTTTAATAGCCGGACGTCTCCTTTT

Consensus:

AGTTCTTTTCGTGTCTGCTTTTAATAGCCGGACGTCTCCTTTT

>Bacillus_Fam_1501_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:2650891-2651059 Satlength=169
Nr of Repeats=4 RepeatLength=42 seed=GTCACCTACA Num.seqs=4
Similarity=0.873016
GTCACCTACATTGGTTTTCAATTCACCAACATCGGTTGTCAG

Consensus:

GTCACCTACATTGGTTTTCAATTCACCAACATCGGTTGTCAG

>Bacillus_Fam_1502_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_900103955.1_IMG-
taxon_2617270767_annotated_assembly_genomic.fna_4:117-426 Satlength=310
Nr of Repeats=4 RepeatLength=42 seed=TTTACTCCGA Num.seqs=3
Similarity=0.788360
TTTACTCCGATCCTCTTATACTTTACTAACAACCACCTATAC

Consensus:

TTTACTCCGATCCTCTTATACTTTACTAACAACCACCTATAC

>Bacillus_Fam_1503_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_22:838320-838572
Satlength=253 Nr of Repeats=6 RepeatLength=42 seed=GCTACTGAAG Num.seqs=6
Similarity=0.904762
GCTACTGAAGACACTCATTCTCATGACGATGAAGAGAGTCAT

Consensus:

GCTACTGAAGACACTCATTCTCATGACGATGAAGAGAGTCAT

>Bacillus_Fam_1504_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_12:79980-80484
Satlength=505 Nr of Repeats=12 RepeatLength=42 seed=CGGAAGACGG
Num.seqs=12 Similarity=0.923040 0
CGGAAGACGGGGAGAACGCCGAAGGAGAAGCGCCAAGTCCGC

Consensus:

CGGAAGACGGGGAGAACGCCGAAGGAGAAGCGCCAAGTCCGC

>Bacillus_Fam_1505_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_35:69303-69513
Satlength=211 Nr of Repeats=5 RepeatLength=42 seed=AGAGCAGTGC Num.seqs=5
Similarity=0.923810 0
AGAGCAGTGCACAGCGCTGCGTCGTGCGAAGCACAAAAAAG

Consensus:

AGAGCAGTGCACAGCGCTGCGTCGTGCGAAGCACAAAAAAG

>Bacillus_Fam_1506_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_42:1093335-1093503
Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=GCCGAATCCT Num.seqs=4
Similarity=0.925926 0
GCCGAATCCTGGAGTCGCATACGGAGAACTGGACGAACACG

Consensus:

GCCGAATCCTGGAGTCGCATACGGAGAACTGGACGAACACG

>Bacillus_Fam_1507_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000
GCF_900111815.1_PRJEB17078_genomic.fna_1:571953-572162 Satlength=210 Nr
of Repeats=5 RepeatLength=42 seed=ATCAGCCAAC Num.seqs=4
Similarity=0.968254
0 ATCAGCCAACCTTCGGGCGAGAATCAACCAAGCTTGGCGAAAA

Consensus:

ATCAGCCAACCTTCGGGCGAGAATCAACCAAGCTTGGCGAAAA

>Bacillus_Fam_1508_42_1 Nr. of seq. 1 Alignment length(with gaps) = 42
Alignment score = 0.000000

GCF_900142675.1_IMG-
taxon_2654588196_annotated_assembly_genomic.fna_9:331825-331993
Satlength=169 Nr of Repeats=4 RepeatLength=42 seed=GAAAAGCGTT Num.seqs=4
Similarity=0.931217 0
GAAAAGCGTTTTGACGGTTTAGAAGGGCGTATTGATGGGCTA

Consensus:

GAAAAGCGTTTTGACGGTTTAGAAGGGCGTATTGATGGGCTA

>Bacillus_Fam_1509_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_000285535.1_ASM28553v1_genomic.fna_2:783130-783602 Satlength=473 Nr
of Repeats=11 RepeatLength=41 seed=TTTGCCTCTT Num.seqs=9
Similarity=0.820106
0 TTTGCCTCTTCTGATGAGNGATTTGCACCGGTTTGGTGGCA

Consensus:

TTTGCCTCTTCTGATGAGNGATTTGCACCGGTTTGGTGGCA

>Bacillus_Fam_1510_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1704740-1704945 Satlength=206 Nr
of Repeats=4 RepeatLength=41 seed=AATATTGGAA Num.seqs=3
Similarity=0.869919 0
AATATTGGAATTTGCTTCTGAAAATTTAGGGTTAGTTCCC

Consensus:

AATATTGGAATTTGCTTCTGAAAATTTAGGGTTAGTTCCC

>Bacillus_Fam_1511_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_7:121779-122039 Satlength=261 Nr
of Repeats=6 RepeatLength=40 seed=TATACGAGAG Num.seqs=4
Similarity=0.794038
0 TATACGAGAGGTGGAGCTGCTATAAGTGAGTGGCACCTGTC

Consensus:

TATACGAGAGGTGGAGCTGCTATAAGTGAGTGGCACCTGTC

>Bacillus_Fam_1512_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_000401235.1_BacNeaAAU1_genomic.fna_215:29479-29643 Satlength=165 Nr
of Repeats=4 RepeatLength=41 seed=GATTTATCAG Num.seqs=4
Similarity=0.934959
0 GATTTATCAGCCAAAACCTCACTCTTTTCAGCCAAAACCTCC

Consensus:

GATTTATCAGCCAAAACTCACTCTTTTCAGCCAACTTCC

>Bacillus_Fam_1513_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000

GCF_000429705.1_ASM42970v1_genomic.fna_2:114683-114847 Satlength=165 Nr
of Repeats=5 RepeatLength=41 seed=TCGATCGATA Num.seqs=3
Similarity=0.956640

0 TCGATCGATAAATCTCAAAGTCGATGAATAAACCAGGCAAC

Consensus:

TCGATCGATAAATCTCAAAGTCGATGAATAAACCAGGCAAC

>Bacillus_Fam_1514_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000

GCF_000429705.1_ASM42970v1_genomic.fna_6:23293-23457 Satlength=165 Nr of
Repeats=4 RepeatLength=41 seed=TTTATCAATC Num.seqs=4 Similarity=0.853659

0 TTTATCAATCACTTTCCCCTCGTTATCCATCACTTTCACAA

Consensus:

TTTATCAATCACTTTCCCCTCGTTATCCATCACTTTCACAA

>Bacillus_Fam_1515_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000

GCF_000429725.1_ASM42972v1_genomic.fna_2:355518-356110 Satlength=593 Nr
of Repeats=5 RepeatLength=41 seed=TGGACAATTC Num.seqs=3
Similarity=0.869919

0 TGGACAATTCGGCGGGATTGTGACCAAGCGGCGGCAAGTC

Consensus:

TGGACAATTCGGCGGGATTGTGACCAAGCGGCGGCAAGTC

>Bacillus_Fam_1516_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000

GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_1:2086005-2086495 Satlength=491 Nr of Repeats=12
RepeatLength=41 seed=TTGCGGGCCG Num.seqs=10 Similarity=0.9407 0
TTGCGGGCCGACCTAACCCTTTACATGCCGATTTCTTATA

Consensus:

TTGCGGGCCGACCTAACCCTTTACATGCCGATTTCTTATA

>Bacillus_Fam_1517_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_1:2113011-2113379 Satlength=369 Nr of Repeats=9
RepeatLength=41 seed=CACTTTTCAC Num.seqs=8 Similarity=0.907085 0
CACTTTTCACACCAAATCGAAGTTTGCGGGCCGGTTCAAA

Consensus:

CACTTTTCACACCAAATCGAAGTTTGCGGGCCGGTTCAAA

>Bacillus_Fam_1518_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_1:175979-176594 Satlength=616 Nr
of Repeats=15 RepeatLength=41 seed=AAAAAGTGAC Num.seqs=15
Similarity=0.995664 0
AAAAAGTGACCGCATTATCACCTGTTTTGACTGAATAAACG

Consensus:

AAAAAGTGACCGCATTATCACCTGTTTTGACTGAATAAACG

>Bacillus_Fam_1519_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:206866-207071 Satlength=206 Nr
of Repeats=5 RepeatLength=41 seed=AATTCGTCCCT Num.seqs=5
Similarity=0.752381 0
AATTCGTCCCTACATGGNAANAATTCGACCGTAACCGGCAAN

Consensus:

AATTCGTCCCTACATGGNAANAATTCGACCGTAACCGGCAAN

>Bacillus_Fam_1520_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:3549779-3549982 Satlength=204
Nr of Repeats=5 RepeatLength=41 seed=CTGAAGGTCTG Num.seqs=3
Similarity=0.913279 0
CTGAAGGTCTGATTTATTCCGACCCACGGACGAATTCATTCA

Consensus:

CTGAAGGTCTGATTTATTCCGACCCACGGACGAATTCATTCA

>Bacillus_Fam_1521_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_1:591647-591811 Satlength=165 Nr
of Repeats=4 RepeatLength=41 seed=GAGACGCAAA Num.seqs=4
Similarity=0.967480
0 GAGACGCAAAAGTAGTTGCAGCTTACGCAAAAAACAGTGGA

Consensus:

GAGACGCAAAAGTAGTTGCAGCTTACGCAAAAACAGTGGA

>Bacillus_Fam_1522_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_3:885452-885657 Satlength=206 Nr
of Repeats=5 RepeatLength=41 seed=TAAATATTTG Num.seqs=5
Similarity=0.930159
0 TAAATATTTGCGTCAGCCTCAGTGATTTAAGCGTCACCATT

Consensus:

TAAATATTTGCGTCAGCCTCAGTGATTTAAGCGTCACCATT

>Bacillus_Fam_1523_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_2:321955-322365 Satlength=411 Nr
of Repeats=10 RepeatLength=41 seed=TGCATATATT Num.seqs=10
Similarity=0.947245 0
TGCATATATTGCGCGTCCTCAAGCAGATATTGGACAAAACC

Consensus:

TGCATATATTGCGCGTCCTCAAGCAGATATTGGACAAAACC

>Bacillus_Fam_1524_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:1284454-1284618 Satlength=165
Nr of Repeats=4 RepeatLength=41 seed=AGGGAAGCAG Num.seqs=4
Similarity=0.983740 0
AGGGAAGCAGGACGAATAAATTCGCGGACGGACGGAAAAAG

Consensus:

AGGGAAGCAGGACGAATAAATTCGCGGACGGACGGAAAAAG

>Bacillus_Fam_1525_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:3245887-3246338 Satlength=452
Nr of Repeats=13 RepeatLength=41 seed=GGACGAATTC Num.seqs=9
Similarity=0.881662 0
GGACGAATTCCTCTCGACGGTAGGTCTGAATTAAACCTGTTTG

Consensus:

GGACGAATTCCTCTCGACGGTAGGTCTGAATTAAACCTGTTTG

>Bacillus_Fam_1526_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:3591693-3592229 Satlength=537
Nr of Repeats=13 RepeatLength=41 seed=GGACGGATTA Num.seqs=10
Similarity=0.819332 0
GGACGGATTATTTTCATCCCAGGTCGGATTCCACGCGCTGTC

Consensus:

GGACGGATTATTTTCATCCCAGGTCGGATTCCACGCGCTGTC

>Bacillus_Fam_1527_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:3945848-3946297 Satlength=450
Nr of Repeats=11 RepeatLength=41 seed=TTCGACCTAA Num.seqs=7
Similarity=0.724622 0
TTCGACCTAAACTCCATTTTTTTCCGGCCCACTATCGATTAA

Consensus:

TTCGACCTAAACTCCATTTTTTTCCGGCCCACTATCGATTAA

>Bacillus_Fam_1528_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:4091702-4091905 Satlength=204
Nr of Repeats=5 RepeatLength=41 seed=GATATAATTC Num.seqs=3
Similarity=0.738095 0
GATATAATTCAGTTTCGGCGATATATTGCCGGTTTTTCGTA

Consensus:

GATATAATTCAGTTTCGGCGATATATTGCCGGTTTTTCGTA

>Bacillus_Fam_1529_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:4831063-4831779 Satlength=717
Nr of Repeats=18 RepeatLength=41 seed=ATATTCCGGC Num.seqs=15
Similarity=0.847309 0
ATATTCCGGCCTTACCCGCTGGTTTCCGGCCTGCTTCATCG

Consensus:

ATATTCCGGCCTTACCCGCTGGTTTCCGGCCTGCTTCATCG

>Bacillus_Fam_1530_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:4869499-4869784 Satlength=286
Nr of Repeats=7 RepeatLength=41 seed=ATTGGGTCGA Num.seqs=5
Similarity=0.834146 0
ATTGGGTCGATTATCTCCTGTTAGGACGATTTATCCCCGC

Consensus:

ATTGGGTCGATTTATCTCCTGTTAGGACGATTTATCCCCGC

>Bacillus_Fam_1531_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001645705.1_ASM164570v1_genomic.fna_57:5429-5921 Satlength=493 Nr of
Repeats=12 RepeatLength=41 seed=GTAAGGAAGT Num.seqs=12
Similarity=0.907366
0 GTAAGGAAGTCGCGCAATCCCCAGGAAAGAAGCGCAATGCA

Consensus:

GTAAGGAAGTCGCGCAATCCCCAGGAAAGAAGCGCAATGCA

>Bacillus_Fam_1532_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_3:67197-67361 Satlength=165 Nr of
Repeats=4 RepeatLength=41 seed=AAAAGTAGCG Num.seqs=4 Similarity=0.902439
0 AAAAGTAGCGGATAAAACCCAAAAGTTGTTGGATAAATCCC

Consensus:

AAAAGTAGCGGATAAAACCCAAAAGTTGTTGGATAAATCCC

>Bacillus_Fam_1533_41_1 Nr. of seq. 1 Alignment length(with gaps) = 41
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:1580930-1581300 Satlength=371
Nr of Repeats=5 RepeatLength=41 seed=TTCTCGTGCT Num.seqs=4
Similarity=1.000000
TTCTCGTGCTTCAAATGGAAGCATGAGAACCGTCCCACTGC

0

Consensus:

TTCTCGTGCTTCAAATGGAAGCATGAGAACCGTCCCACTGC

>Bacillus_Fam_1534_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_3:56177-56333 Satlength=157 Nr of
Repeats=4 RepeatLength=39 seed=CATGAAGAAG Num.seqs=4 Similarity=0.905556
0 CATGAAGAAGACGAACATGAGCATCACGAGCATGAGGGGC

Consensus:

CATGAAGAAGACGAACATGAGCATCACGAGCATGAGGGGC

>Bacillus_Fam_1535_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000

GCF_000285535.1_ASM28553v1_genomic.fna_3:14224-14505 Satlength=282 Nr of Repeats=7 RepeatLength=40 seed=GATTTGCGTC Num.seqs=6 Similarity=0.797778
0 GATTTGCGTCTGCATTTTCGTTTTTTGCGTCGCACCCGGCA

Consensus:

GATTTGCGTCTGCATTTTCGTTTTTTGCGTCGCACCCGGCA

>Bacillus_Fam_1536_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000

GCF_000429705.1_ASM42970v1_genomic.fna_1:1910664-1910961 Satlength=298 Nr of Repeats=6 RepeatLength=40 seed=ATCCACTTAT Num.seqs=5
Similarity=0.883333

0

ATCCACTTATTTTAACTTTGTCCGAGTTATTGGCAGATTG

Consensus:

ATCCACTTATTTTAACTTTGTCCGAGTTATTGGCAGATTG

>Bacillus_Fam_1537_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_83:95603-96081 Satlength=479 Nr of Repeats=12 RepeatLength=40 seed=ACGCATAAAT Num.seqs=8
Similarity=0.858333

0 ACGCATAAATCCTGGAACCGATGCAAATAACTTGGATCCG

Consensus:

ACGCATAAATCCTGGAACCGATGCAAATAACTTGGATCCG

>Bacillus_Fam_1538_40_1 Nr. of seq. 1 Alignment length(with gaps) = 40
Alignment score = 0.000000

GCF_001712755.1_ASM171275v1_genomic.fna_36:70380-70659 Satlength=280 Nr of Repeats=7 RepeatLength=40 seed=ATTTTAAATT Num.seqs=6
Similarity=0.922222

0 ATTTTAAATTGCGATTACACGAATTTATTTGCCATTTCCC

Consensus:

ATTTTAAATTGCGATTACACGAATTTATTTGCCATTTCCC

>Bacillus_Fam_1539_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000

GCF_000008505.1_ASM850v1_genomic.fna_1:2312216-2312489 Satlength=274 Nr of Repeats=7 RepeatLength=39 seed=TTATCTTAG Num.seqs=7
Similarity=0.960928

0 TTATCTTAGATTTCCACCAATCGTCATCACAATTGTGC

Consensus:

TTATCTTTAGATTTCCACCAATCGTCATCACAATTGTGC

>Bacillus_Fam_1540_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000025825.1_ASM2582v1_genomic.fna_1:2728911-2729106 Satlength=196 Nr
of Repeats=5 RepeatLength=39 seed=TCTTCTTTTG Num.seqs=5
Similarity=0.842735
0 TCTTCTTTTGCCGCTTGCTCCTCAGCTTTTCGTTTTGCT

Consensus:

TCTTCTTTTGCCGCTTGCTCCTCAGCTTTTCGTTTTGCT

>Bacillus_Fam_1541_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000025825.1_ASM2582v1_genomic.fna_8:158379-158808 Satlength=430 Nr of
Repeats=11 RepeatLength=39 seed=TTTCATGCCTT Num.seqs=11
Similarity=0.987568
0 TTTCATGCCTTCCATATCATGAGAAGTGTGCTCGTCCATA

Consensus:

TTTCATGCCTTCCATATCATGAGAAGTGTGCTCGTCCATA

>Bacillus_Fam_1542_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_2:34085-34280
Satlength=196 Nr of Repeats=5 RepeatLength=39 seed=CGCCTGGATT Num.seqs=5
Similarity=0.931624 0
CGCCTGGATTGCCCCGGATCTTCAGGATCCGGCTCCTCTC

Consensus:

CGCCTGGATTGCCCCGGATCTTCAGGATCCGGCTCCTCTC

>Bacillus_Fam_1543_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000242895.2_ASM24289v3_genomic.fna_1:3783533-3783728 Satlength=196 Nr
of Repeats=5 RepeatLength=39 seed=TCTGGTAATT Num.seqs=5
Similarity=1.000000 0
TCTGGTAATTTGTTAGTTGCTTCCTCTTCATGTGCAAGC

Consensus:

TCTGGTAATTTGTTAGTTGCTTCCTCTTCATGTGCAAGC

>Bacillus_Fam_1544_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000

GCF_000285535.1_ASM28553v1_genomic.fna_2:942459-942748 Satlength=290 Nr of Repeats=5 RepeatLength=39 seed=GCGCTTTTCT Num.seqs=3 Similarity=0.977208
0 GCGCTTTTCTTATGCTTGTCGCCGATAAACAGGCGCCTT

Consensus:

GCGCTTTTCTTATGCTTGTCGCCGATAAACAGGCGCCTT

>Bacillus_Fam_1545_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000299035.1_ASM29903v1_genomic.fna_14:15269-15464 Satlength=196 Nr of Repeats=5 RepeatLength=39 seed=TTACCATTAT Num.seqs=5 Similarity=0.952137
0 TTACCATTATCAGAGCCACTGCCATTGTTTCGTGTTGTTA

Consensus:

TTACCATTATCAGAGCCACTGCCATTGTTTCGTGTTGTTA

>Bacillus_Fam_1546_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000305495.1_BacPsy2.0_genomic.fna_84:16859-17291 Satlength=433 Nr of Repeats=7 RepeatLength=39 seed=CTTTTCCTGA Num.seqs=5 Similarity=0.890598
0 CTTTTCCTGAAGTCTACGGATCCTGTGTAGTATGGTGCG

Consensus:

CTTTTCCTGAAGTCTACGGATCCTGTGTAGTATGGTGCG

>Bacillus_Fam_1547_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000321185.1_ASM32118v1_genomic.fna_73:12532-12802 Satlength=271 Nr of Repeats=7 RepeatLength=39 seed=GCTGGTTGCT Num.seqs=6 Similarity=0.949858
0 GCTGGTTGCTGCTGCATGCCACCCATCGGTTGTTGGTAC

Consensus:

GCTGGTTGCTGCTGCATGCCACCCATCGGTTGTTGGTAC

>Bacillus_Fam_1548_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:892265-892616 Satlength=352 Nr of Repeats=9 RepeatLength=39 seed=CTCCGTATCC Num.seqs=9 Similarity=0.798670
0 CTCCGTATCCAGGCATTGCTCCATAGCCCGCTGGGGCTG

Consensus:

CTCCGTATCCAGGCATTGCTCCATAGCCCGCTGGGGCTG

>Bacillus_Fam_1549_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:893092-893287 Satlength=196 Nr
of Repeats=5 RepeatLength=39 seed=AAACCTGGCT Num.seqs=5
Similarity=0.911111
0 AAACCTGGCTGAGCGCCATAAGGAACTCCTGCTGCGGCG

Consensus:

AAACCTGGCTGAGCGCCATAAGGAACTCCTGCTGCGGCG

>Bacillus_Fam_1550_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1527350-1527623 Satlength=274 Nr
of Repeats=7 RepeatLength=39 seed=CAAAGTCTCA Num.seqs=5
Similarity=0.829060 0
CAAAGTCTCATAGCATGCTGATCATTGACTACATCAATG

Consensus:

CAAAGTCTCATAGCATGCTGATCATTGACTACATCAATG

>Bacillus_Fam_1551_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000430785.1_ASM43078v1_genomic.fna_125:5214-5682 Satlength=469 Nr of
Repeats=4 RepeatLength=39 seed=TTACCTACT Num.seqs=3 Similarity=0.954416
0 TTACCTACTCTTTGCTTCATTGCAGTTAAGTCCGTCAA

Consensus:

TTACCTACTCTTTGCTTCATTGCAGTTAAGTCCGTCAA

>Bacillus_Fam_1552_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000474275.1_Bmar1.0_genomic.fna_3:53101-53257 Satlength=157 Nr of
Repeats=4 RepeatLength=39 seed=CTCAAGCAAA Num.seqs=4 Similarity=0.925926
0 CTCAAGCAAATCAGTCAATGATGCCAATGAATATAGGGC

Consensus:

CTCAAGCAAATCAGTCAATGATGCCAATGAATATAGGGC

>Bacillus_Fam_1553_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_22:379727-380150 Satlength=424 Nr of Repeats=11
RepeatLength=39 seed=AGGATATTGA Num.seqs=9 Similarity=0.882241 0
AGGATATTGACCAGGGCCTCCTTGGGGCGGCAGTCC

Consensus:

AGGATATTGACCAGGGCCTCCTCCTTGGGGCGGCAGTCC

>Bacillus_Fam_1554_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000526655.1_ASM52665v1_genomic.fna_57:9993-10290 Satlength=298 Nr of
Repeats=7 RepeatLength=39 seed=GGAATGGGAA Num.seqs=5 Similarity=0.952137
0 GGAATGGGAACAGGAGGCTATCCCGGCGGAGGATTCCA

Consensus:

GGAATGGGAACAGGAGGCTATCCCGGCGGAGGATTCCA

>Bacillus_Fam_1555_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000612665.1_FF4_genomic.fna_72:73187-73343 Satlength=157 Nr of
Repeats=4 RepeatLength=39 seed=GGGGGCCTGT Num.seqs=4 Similarity=0.891738
0 GGGGGCCTGTCCCCCGCTGTTTTAACGCATTACTCCGCC

Consensus:

GGGGGCCTGTCCCCCGCTGTTTTAACGCATTACTCCGCC

>Bacillus_Fam_1556_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000615945.1_ASM61594v1_genomic.fna_21:1342-1537 Satlength=196 Nr of
Repeats=5 RepeatLength=39 seed=AGAATCAACA Num.seqs=5 Similarity=0.805128
0 AGAATCAACAGAAGAAATTCAAGCAGTAGCAGAGGAAGT

Consensus:

AGAATCAACAGAAGAAATTCAAGCAGTAGCAGAGGAAGT

>Bacillus_Fam_1557_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_1:262817-263012 Satlength=196 Nr
of Repeats=5 RepeatLength=39 seed=TCTTTCTTCT Num.seqs=5
Similarity=0.917949
0 TCTTTCTTCTCTTCAGAAGAACCACTTGTTGATTCTCT

Consensus:

TCTTTCTTCTCTTCAGAAGAACCACTTGTTGATTCTCT

>Bacillus_Fam_1558_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000

GCF_000712595.1_ASM71259v1_genomic.fna_4:298794-298989 Satlength=196 Nr
of Repeats=5 RepeatLength=39 seed=TTTTCTTCAG Num.seqs=5
Similarity=0.840650
0 TTTTCTTCAGGAGCTACAGTTTCGTTACCTGTTTCAGGT

Consensus:

TTTTCTTCAGGAGCTACAGTTTCGTTACCTGTTTCAGGT

>Bacillus_Fam_1559_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_8:89072-89945 Satlength=874 Nr of
Repeats=24 RepeatLength=39 seed=GCAGGTAAAG Num.seqs=16
Similarity=0.991453
0 GCAGGTAAAGGTGGCGCAGGAGCAGGCGAAGGTCCAGGA

Consensus:

GCAGGTAAAGGTGGCGCAGGAGCAGGCGAAGGTCCAGGA

>Bacillus_Fam_1560_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_52:17519-17675 Satlength=157 Nr of
Repeats=4 RepeatLength=39 seed=CAAAACCACC Num.seqs=4 Similarity=0.811966
0 CAAAACCACCAGTAGACCCACCAACAGATCCAGGAGATA

Consensus:

CAAAACCACCAGTAGACCCACCAACAGATCCAGGAGATA

>Bacillus_Fam_1561_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000769555.1_ASM76955v1_genomic.fna_1:2858012-2858741 Satlength=730 Nr
of Repeats=19 RepeatLength=39 seed=TCTGCTGCGG Num.seqs=18
Similarity=0.988604 0
TCTGCTGCGGGAACGGTGTGTCCGGTGATGCGTCCGTCT

Consensus:

TCTGCTGCGGGAACGGTGTGTCCGGTGATGCGTCCGTCT

>Bacillus_Fam_1562_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000829555.1_ASM82955v1_genomic.fna_11:1052056-1052221 Satlength=166
Nr of Repeats=4 RepeatLength=39 seed=GGCATATTTG Num.seqs=3
Similarity=0.954416 0
GGCATATTTGGCATCGGTTTCATTCGGCATTGGCATGTTC

Consensus:

GGCATATTTGGCATCGGTTTCATTCGGCATTGGCATGTTC

>Bacillus_Fam_1563_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_000831065.1_ASM83106v1_genomic.fna_1:809013-809169 Satlength=157 Nr
of Repeats=4 RepeatLength=39 seed=CAAAGATAGA Num.seqs=4
Similarity=0.931624
0 CAAAGATAGAAGAGAAGAAACTGAAGATAAAGAAACAG

Consensus:

CAAAGATAGAAGAGAAGAAACTGAAGATAAAGAAACAG

>Bacillus_Fam_1564_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:4517711-4518605 Satlength=895
Nr of Repeats=23 RepeatLength=39 seed=CCTTGACCTC Num.seqs=22
Similarity=0.957968 0
CCTTGACCTCCCGGCATCATCGGAAATCCTCCAGGCTGA

Consensus:

CCTTGACCTCCCGGCATCATCGGAAATCCTCCAGGCTGA

>Bacillus_Fam_1565_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001274935.1_ASM127493v1_genomic.fna_27:120842-121037 Satlength=196 Nr
of Repeats=4 RepeatLength=39 seed=AGATCTGGTC Num.seqs=3
Similarity=0.863248 0
AGATCTGGTCGTTCTCGTAGATCCCGCGTTCTGGAGGC

Consensus:

AGATCTGGTCGTTCTCGTAGATCCCGCGTTCTGGAGGC

>Bacillus_Fam_1566_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001274935.1_ASM127493v1_genomic.fna_27:368943-369780 Satlength=838 Nr
of Repeats=20 RepeatLength=39 seed=CCTGGCATCA Num.seqs=13
Similarity=0.903134 0
CCTGGCATCATTGGCTGGCCGCTCATTCCTTGACCCATT

Consensus:

CCTGGCATCATTGGCTGGCCGCTCATTCCTTGACCCATT

>Bacillus_Fam_1567_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000

GCF_001274935.1_ASM127493v1_genomic.fna_36:331062-331251 Satlength=190 Nr of Repeats=5 RepeatLength=39 seed=TGATCATGAC Num.seqs=4
Similarity=0.931624 0
TGATCATGACTATGACTGTGACCTTCGTGACTGTGTTTCG

Consensus:

TGATCATGACTATGACTGTGACCTTCGTGACTGTGTTTCG

>Bacillus_Fam_1568_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001315085.1_ASM131508v1_genomic.fna_47:6-162 Satlength=157 Nr of Repeats=4 RepeatLength=39 seed=GGATGGGGAA Num.seqs=4 Similarity=0.863248
0 GGATGGGGAAGCGGATTCCCACAAACACCAGGCCAAAGC

Consensus:

GGATGGGGAAGCGGATTCCCACAAACACCAGGCCAAAGC

>Bacillus_Fam_1569_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:2191867-2192027 Satlength=161
Nr of Repeats=4 RepeatLength=40 seed=CAAATAAAAT Num.seqs=4
Similarity=0.566667 0
CAAATAAAATGAGAGTTTCGCAAAAATAAAGCGTTCTTG

Consensus:

CAAATAAAATGAGAGTTTCGCAAAAATAAAGCGTTCTTG

>Bacillus_Fam_1570_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001578205.1_ASM157820v1_genomic.fna_2:10302-10458 Satlength=157 Nr of Repeats=4 RepeatLength=39 seed=AAGCTGTAGA Num.seqs=4 Similarity=0.931624
0 AAGCTGTAGAGAAGCAGGAACCGGCCAAGGAAGCAGCAC

Consensus:

AAGCTGTAGAGAAGCAGGAACCGGCCAAGGAAGCAGCAC

>Bacillus_Fam_1571_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001591945.1_ASM159194v1_genomic.fna_7:147123-147357 Satlength=235 Nr of Repeats=6 RepeatLength=39 seed=TGCATTGGCA Num.seqs=6
Similarity=0.938462
0 TGCATTGGCATTTGACCTTGATCTGGCATATATGGTTGC

Consensus:

TGCATTGGCATTTCGACCTTGATCTGGCATATATGGTTGC

>Bacillus_Fam_1572_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_1:545978-546593 Satlength=616 Nr
of Repeats=16 RepeatLength=39 seed=TTCTGCGAGA Num.seqs=13
Similarity=0.914092 0
TTCTGCGAGAACGGCATGATCTGCGCGTGCCTCTCGTGC

Consensus:

TTCTGCGAGAACGGCATGATCTGCGCGTGCCTCTCGTGC

>Bacillus_Fam_1573_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:1653655-1653811 Satlength=157
Nr of Repeats=4 RepeatLength=39 seed=TTTGTGTTTG Num.seqs=4
Similarity=0.811966 0
TTTGTGTTTGCGTTTGAGCTGGTTGCTTTTCTACCGGCT

Consensus:

TTTGTGTTTGCGTTTGAGCTGGTTGCTTTTCTACCGGCT

>Bacillus_Fam_1574_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_7:93822-93969 Satlength=148 Nr of
Repeats=4 RepeatLength=39 seed=GCTTTAGAGT Num.seqs=3 Similarity=0.886040
0 GCTTTAGAGTTGAATCTGTATCAGAATTATTTGAATCGT

Consensus:

GCTTTAGAGTTGAATCTGTATCAGAATTATTTGAATCGT

>Bacillus_Fam_1575_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_13:255755-256136 Satlength=382 Nr
of Repeats=11 RepeatLength=39 seed=CAACAACTGG Num.seqs=7
Similarity=0.882784 0
CAACAACTGGTGAGACAACTGGAGGAACAACCGGCAGCA

Consensus:

CAACAACTGGTGAGACAACTGGAGGAACAACCGGCAGCA

>Bacillus_Fam_1576_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:2847050-2847845 Satlength=796
Nr of Repeats=9 RepeatLength=39 seed=TGTGGTGCCA Num.seqs=6

Similarity=0.977208 0
TGTGGTGCCATTTGATGCGGTTGATACGGCATCGCCTGC

Consensus:

TGTGGTGCCATTTGATGCGGTTGATACGGCATCGCCTGC

>Bacillus_Fam_1577_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_002019635.1_ASM201963v1_genomic.fna_1:1500315-1500474 Satlength=160
Nr of Repeats=4 RepeatLength=39 seed=CATGTTCTTC Num.seqs=3
Similarity=0.954416 0
CATGTTCTTCTTCATGAGCAGCCTCAGTTTCATCATGTG

Consensus:

CATGTTCTTCTTCATGAGCAGCCTCAGTTTCATCATGTG

>Bacillus_Fam_1578_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_002019635.1_ASM201963v1_genomic.fna_1:2134773-2135010 Satlength=238
Nr of Repeats=6 RepeatLength=39 seed=AAAACAACAA Num.seqs=5
Similarity=0.833333 0
AAAACAACAACAAGAGCAGCAACAGCAGCAGGCCCAACA

Consensus:

AAAACAACAACAAGAGCAGCAACAGCAGCAGGCCCAACA

>Bacillus_Fam_1579_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:1404723-1404996 Satlength=274
Nr of Repeats=7 RepeatLength=39 seed=TCTTCTTCCT Num.seqs=7
Similarity=0.916972 0
TCTTCTTCCTCATGGGCATGTTTCATCGTCAGCGTGNTGC

Consensus:

TCTTCTTCCTCATGGGCATGTTTCATCGTCAGCGTGNTGC

>Bacillus_Fam_1580_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_900093775.1_EVONIK_BGLY_genomic.fna_1:3164589-3164784 Satlength=196
Nr of Repeats=5 RepeatLength=39 seed=GCTTTCTTCC Num.seqs=5
Similarity=0.883761 0
GCTTTCTTCCATTCTCGGTTCCGCTTTTGCGTCCCTGCT

Consensus:

GCTTTCTTCCATTCTCGGTTCCGCTTTTGCGTCCCTGCT

>Bacillus_Fam_1581_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_900098925.1_PRJEB15625_genomic.fna_15:229366-229608 Satlength=243 Nr
of Repeats=5 RepeatLength=39 seed=CACGGCTGGC Num.seqs=3
Similarity=0.886040
0 CACGGCTGGCCGGGTCAAGGCGGGTCTGGCTCCGGCGGG

Consensus:

CACGGCTGGCCGGGTCAAGGCGGGTCTGGCTCCGGCGGG

>Bacillus_Fam_1582_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_900098925.1_PRJEB15625_genomic.fna_16:204771-204963 Satlength=193 Nr
of Repeats=5 RepeatLength=39 seed=CCCTGCATAT Num.seqs=4
Similarity=0.943020
0 CCCTGCATATGATGTCCGTGTCCCATATCCGGCATGTTT

Consensus:

CCCTGCATATGATGTCCGTGTCCCATATCCGGCATGTTT

>Bacillus_Fam_1583_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_900103955.1_IMG-
taxon_2617270767_annotated_assembly_genomic.fna_20:6914-7262
Satlength=349 Nr of Repeats=8 RepeatLength=39 seed=CGTTCGGCTT Num.seqs=6
Similarity=0.835897 0
CGTTCGGCTTCTTCCGCAGCAATGCGCTCTTCCTCCTCA

Consensus:

CGTTCGGCTTCTTCCGCAGCAATGCGCTCTTCCTCCTCA

>Bacillus_Fam_1584_39_1 Nr. of seq. 1 Alignment length(with gaps) = 39
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_13:10452-10608
Satlength=157 Nr of Repeats=4 RepeatLength=39 seed=TATCAACCAG Num.seqs=4
Similarity=0.960114 0
TATCAACCAGCACCGTTTCCACAAGGTGGTCAAATGGGA

Consensus:

TATCAACCAGCACCGTTTCCACAAGGTGGTCAAATGGGA

>Bacillus_Fam_1585_38_1 Nr. of seq. 1 Alignment length(with gaps) = 38
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_37:151112-151470
Satlength=359 Nr of Repeats=5 RepeatLength=38 seed=TTTGCTTCGT Num.seqs=3
Similarity=1.000000 0
TTTGCTTCGTAGTCTTCCCTGTTTCTTCCTCTGCCAGC

Consensus:

TTTGCTTCGTAGTCTTCCCTGTTTCTTCCTCTGCCAGC

>Bacillus_Fam_1586_37_1 Nr. of seq. 1 Alignment length(with gaps) = 37
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:174812-175053 Satlength=242 Nr
of Repeats=6 RepeatLength=37 seed=GAAATCGGCC Num.seqs=4
Similarity=0.861862
0 GAAATCGGCCTTATTGCACGTTATCGGGCTTGTTGCA

Consensus:

GAAATCGGCCTTATTGCACGTTATCGGGCTTGTTGCA

>Bacillus_Fam_1587_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000007825.1_ASM782v1_genomic.fna_1:2019353-2019731 Satlength=379 Nr
of Repeats=13 RepeatLength=36 seed=AAAACCTGAT Num.seqs=8
Similarity=0.898148
0 AAAACCTGATACGGGAGGAAATCCAGACACAGGAGG

Consensus:

AAAACCTGATACGGGAGGAAATCCAGACACAGGAGG

>Bacillus_Fam_1588_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000011145.1_ASM1114v1_genomic.fna_1:1314924-1315176 Satlength=253 Nr
of Repeats=7 RepeatLength=36 seed=ATGGATCAAAA Num.seqs=7
Similarity=0.961199
0 ATGGATCAAAAACGTGCATCCGCAGCAATGGCCGCAA

Consensus:

ATGGATCAAAAACGTGCATCCGCAGCAATGGCCGCAA

>Bacillus_Fam_1589_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000262045.1_KCTC_13613_01_genomic.fna_39:441056-441350 Satlength=295
Nr of Repeats=8 RepeatLength=36 seed=TTTTGTGAGA Num.seqs=6

Similarity=0.886420

0

TTTTGTGAGAACGTGATTTTTTATGGCTGCGGGATT

Consensus:

TTTTGTGAGAACGTGATTTTTTATGGCTGCGGGATT

>Bacillus_Fam_1590_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000285535.1_ASM28553v1_genomic.fna_4:98805-98913 Satlength=109 Nr of
Repeats=5 RepeatLength=36 seed=ATGCAGGGTA Num.seqs=3 Similarity=0.925926

0 ATGCAGGGTATGCAGGGTAGAGCTGGCCTGGGGGGT

Consensus:

ATGCAGGGTATGCAGGGTAGAGCTGGCCTGGGGGGT

>Bacillus_Fam_1591_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000305495.1_BacPsy2.0_genomic.fna_193:33-213 Satlength=181 Nr of
Repeats=5 RepeatLength=36 seed=ACAGGTGATA Num.seqs=5 Similarity=0.796296

0 ACAGGTGATACCGGGGCNACCGGAGTAACNGGAGCA

Consensus:

ACAGGTGATACCGGGGCNACCGGAGTAACNGGAGCA

>Bacillus_Fam_1592_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000307875.1_BABA1.0_genomic.fna_146:993-1137 Satlength=145 Nr of
Repeats=4 RepeatLength=36 seed=AAAAGGGAAT Num.seqs=4 Similarity=0.919753

0 AAAAGGGAATTGGAAGTGCAGTCAGAACAACAGAGA

Consensus:

AAAAGGGAATTGGAAGTGCAGTCAGAACAACAGAGA

>Bacillus_Fam_1593_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000321185.1_ASM32118v1_genomic.fna_87:51026-51170 Satlength=145 Nr of
Repeats=4 RepeatLength=36 seed=CTTCTGGTTT Num.seqs=4 Similarity=0.944444

0 CTTCTGGTTTATTGTTATCAACAACCTGGTTGATCTG

Consensus:

CTTCTGGTTTATTGTTATCAACAACCTGGTTGATCTG

>Bacillus_Fam_1594_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000331575.1_ASM33157v1_genomic.fna_1:1603161-1603305 Satlength=145 Nr of Repeats=4 RepeatLength=36 seed=TCGCTTTGAT Num.seqs=4
Similarity=0.827160 0

TCGCTTTGATTTTGGTTTTGGGACAAGCCCTCGTCC

Consensus:

TCGCTTTGATTTTGGTTTTGGGACAAGCCCTCGTCC

>Bacillus_Fam_1595_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000374565.1_ASM37456v1_genomic.fna_18:1732-1914 Satlength=183 Nr of Repeats=5 RepeatLength=36 seed=TTTTCATCCA Num.seqs=3 Similarity=0.950617
0 TTTTCATCCAAAGGGCAGCCGAAAAGCAAACCAGG

Consensus:

TTTTCATCCAAAGGGCAGCCGAAAAGCAAACCAGG

>Bacillus_Fam_1596_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000380245.2_ASM38024v2_genomic.fna_12:377405-377621 Satlength=217 Nr of Repeats=6 RepeatLength=36 seed=CAGACATATC Num.seqs=6
Similarity=0.967901
0 CAGACATATCAACCAAATCAAATGACGATGCCACAA

Consensus:

CAGACATATCAACCAAATCAAATGACGATGCCACAA

>Bacillus_Fam_1597_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000401235.1_BacNeaAAU1_genomic.fna_112:56318-56642 Satlength=325 Nr of Repeats=9 RepeatLength=36 seed=CTATCTCTTC Num.seqs=9
Similarity=0.787287
0 CTATCTCTTCAGTTACTTCGACTTCTGGAGTTACAG

Consensus:

CTATCTCTTCAGTTACTTCGACTTCTGGAGTTACAG

>Bacillus_Fam_1598_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36

Alignment score = 0.000000

GCF_000430785.1_ASM43078v1_genomic.fna_4:125493-125637 Satlength=145 Nr of Repeats=4 RepeatLength=36 seed=CCGCTTCCTG Num.seqs=4
Similarity=0.981481
0 CCGCTTCCTGGAGCATCTGGTTGATTCCTTCTTG

Consensus:

CCGCTTCCTGGAGCATCTGGTTGATTCCTTCTTGG

>Bacillus_Fam_1599_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000496285.1_ASM49628v1_genomic.fna_1:1885990-1886788 Satlength=799 Nr
of Repeats=13 RepeatLength=36 seed=CTTCTGCAAC Num.seqs=11
Similarity=0.955556 0
CTTCTGCAACTGGTTGTTCTTCAGCGACTGGCCCTT

Consensus:

CTTCTGCAACTGGTTGTTCTTCAGCGACTGGCCCTT

>Bacillus_Fam_1600_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000612625.1_JCE_genomic.fna_1:141216-141576 Satlength=361 Nr of
Repeats=10 RepeatLength=36 seed=GGGCGGATTC Num.seqs=10
Similarity=0.758674
0 GGGCGGATTCCCTGGTCANGGTGGNCATGGNGGAAT

Consensus:

GGGCGGATTCCCTGGTCANGGTGGNCATGGNGGAAT

>Bacillus_Fam_1601_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000612625.1_JCE_genomic.fna_1:153492-153708 Satlength=217 Nr of
Repeats=6 RepeatLength=36 seed=TCCAAAGGCA Num.seqs=6 Similarity=0.906173
0 TCCAAAGGCAGTGGTGGATCGAAAGGAAGTCATGGC

Consensus:

TCCAAAGGCAGTGGTGGATCGAAAGGAAGTCATGGC

>Bacillus_Fam_1602_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000612625.1_JCE_genomic.fna_6:65616-65796 Satlength=181 Nr of
Repeats=5 RepeatLength=36 seed=CTGTTATTTC Num.seqs=5 Similarity=0.837037
0 CTGTTATTTCCGCCACTTCGACTACGTCATCTACAC

Consensus:

CTGTTATTTCCGCCACTTCGACTACGTCATCTACAC

>Bacillus_Fam_1603_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000621445.1_ASM62144v1_genomic.fna_3:309868-310012 Satlength=145 Nr
of Repeats=4 RepeatLength=36 seed=GTGTCATCCC Num.seqs=4

Similarity=0.888889
0 GTGTCATCCCCAGTACCTGGACTTCCTCCATTATCC

Consensus:

GTGTCATCCCCAGTACCTGGACTTCCTCCATTATCC

>Bacillus_Fam_1604_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000706725.1_ASM70672v1_genomic.fna_1:3481500-3481644 Satlength=145 Nr
of Repeats=4 RepeatLength=36 seed=GTTTCTTCCT Num.seqs=4
Similarity=0.932099 0
GTTTCTTCCTCTACTGCTTCTTCCGGCGCTTCTGAA

Consensus:

GTTTCTTCCTCTACTGCTTCTTCCGGCGCTTCTGAA

>Bacillus_Fam_1605_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_6:44543-44699 Satlength=157 Nr of
Repeats=4 RepeatLength=36 seed=ACTAGCTCTT Num.seqs=3 Similarity=0.950617
0 ACTAGCTCTTCTTCAAATGCTTCCTCTGTTTCCGCA

Consensus:

ACTAGCTCTTCTTCAAATGCTTCCTCTGTTTCCGCA

>Bacillus_Fam_1606_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000724485.1_ASM72448v1_genomic.fna_1:1629403-1629607 Satlength=205 Nr
of Repeats=4 RepeatLength=36 seed=GCTTCAAGAA Num.seqs=3
Similarity=0.827160 0
GCTTCAAGAAACACCATTTGTGACTGCTGTGACAAGT

Consensus:

GCTTCAAGAAACACCATTTGTGACTGCTGTGACAAGT

>Bacillus_Fam_1607_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000742675.1_ASM74267v1_genomic.fna_1:639619-639763 Satlength=145 Nr
of Repeats=4 RepeatLength=36 seed=TGCAGCAGCA Num.seqs=4
Similarity=0.888889
0 TGCAGCAGCAGGAAGCACGGAAGCATGAGGAGACGT

Consensus:

TGCAGCAGCAGGAAGCACGGAAGCATGAGGAGACGT

>Bacillus_Fam_1608_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_79:5447-5843 Satlength=397 Nr of
Repeats=11 RepeatLength=36 seed=ACAAGCATGA Num.seqs=7
Similarity=0.715507
0 ACAAGCATGATGACTGTAATAAACGAGACAGAAACG

Consensus:

ACAAGCATGATGACTGTAATAAACGAGACAGAAACG

>Bacillus_Fam_1609_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000812025.2_ASM81202v2_genomic.fna_59:10582-10798 Satlength=217 Nr of
Repeats=6 RepeatLength=36 seed=CGATGCATGC Num.seqs=6 Similarity=0.846914
0 CGATGCATGCTCAGCCAATGATGTACCCAGACAATG

Consensus:

CGATGCATGCTCAGCCAATGATGTACCCAGACAATG

>Bacillus_Fam_1610_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000812025.2_ASM81202v2_genomic.fna_69:27049-27229 Satlength=181 Nr of
Repeats=4 RepeatLength=36 seed=CGAAGAAACC Num.seqs=3 Similarity=0.827160
0 CGAAGAAACCAGACGGATACAAAAGGATGACGATT

Consensus:

CGAAGAAACCAGACGGATACAAAAGGATGACGATT

>Bacillus_Fam_1611_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_55:48259-48403 Satlength=145 Nr of
Repeats=4 RepeatLength=36 seed=TCTTCTTCGG Num.seqs=4 Similarity=0.796296
0 TCTTCTTCGGAGTGAGCGGCTTCTTCGTCATGGTGC

Consensus:

TCTTCTTCGGAGTGAGCGGCTTCTTCGTCATGGTGC

>Bacillus_Fam_1612_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000832605.1_ASM83260v1_genomic.fna_1:2585613-2585757 Satlength=145 Nr
of Repeats=4 RepeatLength=36 seed=GAACCGAAAA Num.seqs=4
Similarity=0.956790
GAACCGAAAAACAGAAAAGCCAGATGGTAAACCAGAA

0

Consensus:

GAACCGAAAACAGAAAAGCCAGATGGTAAACCAGAA

>Bacillus_Fam_1613_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000972245.2_ASM97224v2_genomic.fna_1:2081436-2082147 Satlength=712 Nr
of Repeats=20 RepeatLength=36 seed=GTAGGTCCAG Num.seqs=19
Similarity=0.891705 0
GTAGGTCCAGTCGGTCCAAGGTCGCCGGTAGCACCT

Consensus:

GTAGGTCCAGTCGGTCCAAGGTCGCCGGTAGCACCT

>Bacillus_Fam_1614_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_8:166666-166882 Satlength=217 Nr
of Repeats=6 RepeatLength=36 seed=TTTTCCTCCG Num.seqs=6
Similarity=0.930864
0 TTTTCCTCCGGCTCCTGTTCCAGGACGAAATCCGGC

Consensus:

TTTTCCTCCGGCTCCTGTTCCAGGACGAAATCCGGC

>Bacillus_Fam_1615_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_101:89652-90012 Satlength=361 Nr
of Repeats=10 RepeatLength=36 seed=CCGCAAATGG Num.seqs=10
Similarity=0.847737 0
CCGCAAATGGGCTATGGCCCGCAAGCTGGATTTCGCC

Consensus:

CCGCAAATGGGCTATGGCCCGCAAGCTGGATTTCGCC

>Bacillus_Fam_1616_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:1088058-1088238 Satlength=181
Nr of Repeats=5 RepeatLength=36 seed=GGAGGAGGTC Num.seqs=5
Similarity=0.933333 0
GGAGGAGGTCAACCGCCGCGGCGACCAACCAAGGG

Consensus:

GGAGGAGGTCAACCGCCGCGGCGACCAACCAAGGG

>Bacillus_Fam_1617_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_105:131730-131874 Satlength=145
Nr of Repeats=4 RepeatLength=36 seed=GAAGATGATC Num.seqs=4
Similarity=0.808642 0
GAAGATGATCAATCGGACACCGATGACACAGAAGGG

Consensus:

GAAGATGATCAATCGGACACCGATGACACAGAAGGG

>Bacillus_Fam_1618_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001578185.1_ASM157818v1_genomic.fna_1:1776217-1776385 Satlength=169
Nr of Repeats=5 RepeatLength=36 seed=CAATGGGACG Num.seqs=4
Similarity=0.944444 0
CAATGGGACGGACATGGCGGAGGTCATGGTGGCGGT

Consensus:

CAATGGGACGGACATGGCGGAGGTCATGGTGGCGGT

>Bacillus_Fam_1619_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001590785.1_ASM159078v1_genomic.fna_23:164317-164461 Satlength=145 Nr
of Repeats=4 RepeatLength=36 seed=TTTCCTCGCC Num.seqs=4
Similarity=0.870370 0
TTTCCTCGCCTCCGTCATTTTCTTCCGAGACTCTG

Consensus:

TTTCCTCGCCTCCGTCATTTTCTTCCGAGACTCTG

>Bacillus_Fam_1620_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001590785.1_ASM159078v1_genomic.fna_23:392091-392217 Satlength=127 Nr
of Repeats=4 RepeatLength=36 seed=TCTTCGCCTT Num.seqs=3
Similarity=0.925926 0
TCTTCGCCTTCGACTGGTTCTTCTCCCTCAACTGGC

Consensus:

TCTTCGCCTTCGACTGGTTCTTCTCCCTCAACTGGC

>Bacillus_Fam_1621_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001591445.1_ASM159144v1_genomic.fna_59:421-646 Satlength=226 Nr of
Repeats=4 RepeatLength=36 seed=TGTTGGTGCT Num.seqs=3 Similarity=0.864198
0 TGTTGGTGCTTTTGNGCTTGTCAGGTTTCGATAC

Consensus:

TGTTGGTGCTTTTGNGCTTGTCCCAGGTTTCGATAC

>Bacillus_Fam_1622_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001591625.1_ASM159162v1_genomic.fna_26:7794-8010 Satlength=217 Nr of
Repeats=6 RepeatLength=36 seed=AGAGAAAATA Num.seqs=6 Similarity=0.871605
0 AGAGAAAATAACAAGAACAAGCAAACCAACAGGCA

Consensus:

AGAGAAAATAACAAGAACAAGCAAACCAACAGGCA

>Bacillus_Fam_1623_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001591665.1_ASM159166v1_genomic.fna_83:5099-5375 Satlength=277 Nr of
Repeats=8 RepeatLength=36 seed=TTCTTCTGTT Num.seqs=7 Similarity=0.846561
0 TTCTTCTGTTACAACCTTCAGTAGNTTCGTTAGTTGC

Consensus:

TTCTTCTGTTACAACCTTCAGTAGNTTCGTTAGTTGC

>Bacillus_Fam_1624_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_2:690522-690702 Satlength=181 Nr
of Repeats=5 RepeatLength=36 seed=GGTCTTTTAA Num.seqs=5
Similarity=0.948148
0 GGTCTTTTAAATTGGTTCTTCACTAGGTTGTTTAGCT

Consensus:

GGTCTTTTAAATTGGTTCTTCACTAGGTTGTTTAGCT

>Bacillus_Fam_1625_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:4287145-4287451 Satlength=307
Nr of Repeats=8 RepeatLength=36 seed=TTAGCGGCAT Num.seqs=6
Similarity=0.856790
0 TTAGCGGCATTTCCGCCATTGGCTGCGTCGCCTCCG

Consensus:

TTAGCGGCATTTCCGCCATTGGCTGCGTCGCCTCCG

>Bacillus_Fam_1626_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:4311548-4311809 Satlength=262
Nr of Repeats=6 RepeatLength=36 seed=ATCCGGGACA Num.seqs=4

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Similarity=0.938272
ATCCGGGACATCCAGGGTATGGCGGCATGACTGGTT

*****
Consensus:

ATCCGGGACATCCAGGGTATGGCGGCATGACTGGTT

>Bacillus_Fam_1627_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001645555.1_ASM164555v1_genomic.fna_12:311932-312166 Satlength=235 Nr
of Repeats=7 RepeatLength=36 seed=GTTACTCCCG Num.seqs=6
Similarity=0.911111
GTTACTCCCGGTGATCCCGTTAAACCAGTTGCACCT

*****
Consensus:

GTTACTCCCGGTGATCCCGTTAAACCAGTTGCACCT

>Bacillus_Fam_1628_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_35:221909-222269 Satlength=361 Nr
of Repeats=10 RepeatLength=36 seed=TTTCCTGTTG Num.seqs=10
Similarity=0.819753
TTTCCTGTTGATACTGGTGATACTTGCATATTTGGT

*****
Consensus:

TTTCCTGTTGATACTGGTGATACTTGCATATTTGGT

>Bacillus_Fam_1629_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:2358432-2358672 Satlength=241
Nr of Repeats=6 RepeatLength=36 seed=CAGGAGCACC Num.seqs=4
Similarity=0.962963
CAGGAGCACCGGGAGCAGCAGCTGGA ACTCCATATC

*****
Consensus:

CAGGAGCACCGGGAGCAGCAGCTGGA ACTCCATATC

>Bacillus_Fam_1630_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_002019765.1_ASM201976v1_genomic.fna_1:651174-652542 Satlength=1369 Nr
of Repeats=42 RepeatLength=36 seed=AGGAGAAACA Num.seqs=30
Similarity=0.903293
AGGAGAAACAGGGGCGACTGGTAGTCAAGGAGTTCA

*****
Consensus:

```

AGGAGAAACAGGGGCGACTGGTAGTCAAGGAGTTCA

>Bacillus_Fam_1631_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_900098925.1_PRJEB15625_genomic.fna_16:204570-204750 Satlength=181 Nr
of Repeats=5 RepeatLength=36 seed=GGCATCATTC Num.seqs=5
Similarity=0.925926
0 GGCATCATTCCTCGGCATGCCTCCTTGCAATTTGTCCC

Consensus:

GGCATCATTCCTCGGCATGCCTCCTTGCAATTTGTCCC

>Bacillus_Fam_1632_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_900104555.1_IMG-taxon_2651870172_annotated_assembly_genomic.fna_17:0-
143 Satlength=144 Nr of Repeats=4 RepeatLength=36 seed=CAGGTCCAAA
Num.seqs=4 Similarity=0.876543 0
CAGGTCCAAAAGGAAAAGAAGGCCACCCGGTCCAG

Consensus:

CAGGTCCAAAAGGAAAAGAAGGCCACCCGGTCCAG

>Bacillus_Fam_1633_36_1 Nr. of seq. 1 Alignment length(with gaps) = 36
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_20:439434-439668
Satlength=235 Nr of Repeats=6 RepeatLength=36 seed=CTCCTGGTAC Num.seqs=5
Similarity=0.881481 0
CTCCTGGTACTGGATTAAATCCTGGCATGGGTTATG

Consensus:

CTCCTGGTACTGGATTAAATCCTGGCATGGGTTATG

>Bacillus_Fam_1634_34_1 Nr. of seq. 1 Alignment length(with gaps) = 34
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:633923-634127
Satlength=205 Nr of Repeats=6 RepeatLength=34 seed=AACGTTTGAT Num.seqs=4
Similarity=0.676698 0
AACGTTTGATTGACTTCAGCGTTCTACTAACTA

Consensus:

AACGTTTGATTGACTTCAGCGTTCTACTAACTA

>Bacillus_Fam_1635_34_1 Nr. of seq. 1 Alignment length(with gaps) = 34
Alignment score = 0.000000

GCF_900111815.1_PRJEB17078_genomic.fna_1:193561-194089 Satlength=529 Nr of Repeats=4 RepeatLength=34 seed=GGGGGTCAGG Num.seqs=3 Similarity=0.895425

0 GGGGGTCAGGCACGCTTTAATGATTACCGCACT

Consensus:

GGGGGTCAGGCACGCTTTAATGATTACCGCACT

>Bacillus_Fam_1636_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33

Alignment score = 0.000000

BACILLUS_PSEUDALCALIPHILUS_genomic.fna_5:362967-363159 Satlength=193 Nr of Repeats=6 RepeatLength=33 seed=GGAATGATGC Num.seqs=5 Similarity=0.862626

0 GGAATGATGCCAATGCCAGGTCAAAACGGAAAT

Consensus:

GGAATGATGCCAATGCCAGGTCAAAACGGAAAT

>Bacillus_Fam_1637_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33

Alignment score = 0.000000

GCF_000009825.1_ASM982v1_genomic.fna_1:3221981-3222245 Satlength=265 Nr of Repeats=8 RepeatLength=33 seed=GAACAAGAGC Num.seqs=8 Similarity=0.911977

0 GAACAAGAGCCTGAAACTGACGCTAGCACAGAC

Consensus:

GAACAAGAGCCTGAAACTGACGCTAGCACAGAC

>Bacillus_Fam_1638_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33

Alignment score = 0.000000

GCF_000380245.2_ASM38024v2_genomic.fna_12:1180413-1180611 Satlength=199 Nr of Repeats=6 RepeatLength=33 seed=AACAAATCCG Num.seqs=6 Similarity=0.973064

AACAAATCCGCCGTCAACAGGAGGAAATGAATC

0

Consensus:

AACAAATCCGCCGTCAACAGGAGGAAATGAATC

>Bacillus_Fam_1639_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33

Alignment score = 0.000000

GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-14515_genome_genomic.fna_1:1765976-1769141 Satlength=3166 Nr of Repeats=101 RepeatLength=33 seed=GGCATGCCTC Num.seqs=70 Similarity=0.84

0 GGCATGCCTCCTTGGTTGACCTCCCAATCCC

Consensus:

GGCATGCCTCCACTTG GTTGACCTCCCAATCCC

>Bacillus_Fam_1640_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000
GCF_000612805.1_FF3_genomic.fna_3:320276-320474 Satlength=199 Nr of
Repeats=6 RepeatLength=33 seed=TAGAGCATAG Num.seqs=6 Similarity=0.843771
0 TAGAGCATAGATTAGAAGGCAAAATAGAAGAAC

Consensus:

TAGAGCATAGATTAGAAGGCAAAATAGAAGAAC

>Bacillus_Fam_1641_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_2:456487-456652 Satlength=166 Nr
of Repeats=5 RepeatLength=33 seed=ATTGTTGGAA Num.seqs=5
Similarity=0.919192
0 ATTGTTGGAAGTCTAAGGATAAACATCATTCTG

Consensus:

ATTGTTGGAAGTCTAAGGATAAACATCATTCTG

>Bacillus_Fam_1642_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_56:326201-326366
Satlength=166 Nr of Repeats=5 RepeatLength=33 seed=CAACTAACAG Num.seqs=5
Similarity=0.854545 0
CAACTAACAGAAACGAAAGATAA CTTACAGTCA

Consensus:

CAACTAACAGAAACGAAAGATAA CTTACAGTCA

>Bacillus_Fam_1643_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000
GCF_000775975.1_ASM77597v1_genomic.fna_1:1324054-1324219 Satlength=166 Nr
of Repeats=5 RepeatLength=33 seed=ATCAGCATGA Num.seqs=5
Similarity=0.919192 0
ATCAGCATGACCTTCTTGCTTAGGAGCAGGGAA

Consensus:

ATCAGCATGACCTTCTTGCTTAGGAGCAGGGAA

>Bacillus_Fam_1644_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000

GCF_000787375.1_ASM78737v1_genomic.fna_14:44934-45126 Satlength=193 Nr of Repeats=5 RepeatLength=33 seed=AAAAGAAGAA Num.seqs=4 Similarity=0.872054
0 AAAAGAAGAAAGCTTGTCTCGCAGCGAGAAAAGCA

Consensus:

AAAAGAAGAAAGCTTGTCTCGCAGCGAGAAAAGCA

>Bacillus_Fam_1645_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000

GCF_001243895.1_Bacillus_testis_genomic.fna_9:2298830-2299094
Satlength=265 Nr of Repeats=8 RepeatLength=33 seed=GGTTGGTTTT Num.seqs=8
Similarity=0.888889 0
GGTTGGTTTTGTTCTGGTGTGTTGTCCACTTCC

Consensus:

GGTTGGTTTTGTTCTGGTGTGTTGTCCACTTCC

>Bacillus_Fam_1646_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000

GCF_001587375.1_ASM158737v1_genomic.fna_152:5556-5678 Satlength=123 Nr of Repeats=4 RepeatLength=33 seed=AGTGTTTAC Num.seqs=3 Similarity=0.688889
0 AGTGTTTACTAACTTNTTCATCTAATTCAGTT

Consensus:

AGTGTTTACTAACTTNTTCATCTAATTCAGTT

>Bacillus_Fam_1647_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000

GCF_001636325.1_ASM163632v1_genomic.fna_2:478165-478297 Satlength=133 Nr of Repeats=4 RepeatLength=33 seed=TAAGTTTGAT Num.seqs=4
Similarity=0.939394
0 TAAGTTTGATGGAAAGCTTGAGGATTTAAGCAA

Consensus:

TAAGTTTGATGGAAAGCTTGAGGATTTAAGCAA

>Bacillus_Fam_1648_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000

GCF_001636335.1_ASM163633v1_genomic.fna_1:2556735-2556966 Satlength=232
Nr of Repeats=7 RepeatLength=33 seed=GTAAACCTT Num.seqs=7
Similarity=0.896104 0
GTAAACCTTGGTTCATTTCAATTCCTTACTTCC

Consensus:

GTAAACCTTGGTTCATTTCAATTTCTTACTTCC

>Bacillus_Fam_1649_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000
GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_4:325661-325793
Satlength=133 Nr of Repeats=4 RepeatLength=33 seed=CTGACGTACA Num.seqs=4
Similarity=0.684921 0
CTGACGTACAAGCGGAAATGCAAGAGTTAAGAA

Consensus:

CTGACGTACAAGCGGAAATGCAAGAGTTAAGAA

>Bacillus_Fam_1650_33_1 Nr. of seq. 1 Alignment length(with gaps) = 33
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:2936055-2936187 Satlength=133 Nr
of Repeats=4 RepeatLength=33 seed=ATTTTCATCTT Num.seqs=4
Similarity=0.912458 0
ATTTTCATCTTTTAAGTCCACTCTCACTACCGAG

Consensus:

ATTTTCATCTTTTAAGTCCACTCTCACTACCGAG

>Bacillus_Fam_1651_32_1 Nr. of seq. 1 Alignment length(with gaps) = 32
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:759687-760190 Satlength=504 Nr
of Repeats=16 RepeatLength=32 seed=CAGTTGTACA Num.seqs=10
Similarity=0.856481 0
CAGTTGTACAAGAACCCCTGTTTGCCAACCTGT

Consensus:

CAGTTGTACAAGAACCCCTGTTTGCCAACCTGT

>Bacillus_Fam_1652_31_1 Nr. of seq. 1 Alignment length(with gaps) = 31
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:6822-6946 Satlength=125 Nr of
Repeats=4 RepeatLength=31 seed=TAGAATATAT Num.seqs=4 Similarity=0.913979
0 TAGAATATATGAGAAAACGTTAATTCCGTTG

Consensus:

TAGAATATATGAGAAAACGTTAATTCCGTTG

>Bacillus_Fam_1653_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000

GCF_000008505.1_ASM850v1_genomic.fna_1:4693242-4693602 Satlength=361 Nr of Repeats=12 RepeatLength=30 seed=GGATCTTCCG Num.seqs=12
Similarity=0.934680
GGATCTTCCGTTTCACTTCTGGTTCTTTC

0

Consensus:

GGATCTTCCGTTTCACTTCTGGTTCTTTC

>Bacillus_Fam_1654_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000025825.1_ASM2582v1_genomic.fna_7:66068-66788 Satlength=721 Nr of Repeats=24 RepeatLength=30 seed=CTTCATCCTA Num.seqs=24
Similarity=0.882770
0 CTTCATCCTATCGTGAGGCCGATCTCGAGA

Consensus:

CTTCATCCTATCGTGAGGCCGATCTCGAGA

>Bacillus_Fam_1655_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000245315.1_ASM24531v1_genomic.fna_45:128844-129054 Satlength=211 Nr of Repeats=6 RepeatLength=30 seed=ATGCAAGGCG Num.seqs=5
Similarity=0.866667
0 ATGCAAGGCGGAGGCTACCCGGGCTACGGT

Consensus:

ATGCAAGGCGGAGGCTACCCGGGCTACGGT

>Bacillus_Fam_1656_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:32436-32556 Satlength=121 Nr of Repeats=4 RepeatLength=30 seed=ATATTTTCGGT Num.seqs=4 Similarity=0.933333
0 ATATTTTCGGTTAGCTTTTCAACATAATGGG

Consensus:

ATATTTTCGGTTAGCTTTTCAACATAATGGG

>Bacillus_Fam_1657_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000429685.1_ASM42968v1_genomic.fna_3:302688-302835 Satlength=148 Nr of Repeats=5 RepeatLength=30 seed=TGCATGCCCT Num.seqs=4
Similarity=0.933333
0 TGCATGCCCTGCACATTGTTGGGTGGATAC

Consensus:

TGCATGCCCTGCACATTGTTGGGTGGATAC

>Bacillus_Fam_1658_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_15:76408-77458 Satlength=1051 Nr
of Repeats=27 RepeatLength=30 seed=TAATCAAAGA Num.seqs=20
Similarity=0.587214 0
TAANCAAAGAGCCTATGAGTCCAACAGGAG

Consensus:

TAANCAAAGAGCCTATGAGTCCAACAGGAG

>Bacillus_Fam_1659_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_18:57595-57835 Satlength=241 Nr of
Repeats=8 RepeatLength=30 seed=TTTTGTCCAT Num.seqs=8 Similarity=0.898413
0 TTTTGTCCATCCGGCTTCTGCTCTTCTGGA

Consensus:

TTTTGTCCATCCGGCTTCTGCTCTTCTGGA

>Bacillus_Fam_1660_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_26:20583-20787 Satlength=205 Nr of
Repeats=7 RepeatLength=30 seed=AAGAAAAAAG Num.seqs=6 Similarity=0.896296
0 AAGAAAAAAGCTGAAGACGACGCAGCAGCC

Consensus:

AAGAAAAAAGCTGAAGACGACGCAGCAGCC

>Bacillus_Fam_1661_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000832605.1_ASM83260v1_genomic.fna_1:3770138-3770468 Satlength=331 Nr
of Repeats=11 RepeatLength=30 seed=TTACCTGTTC Num.seqs=11
Similarity=0.936970 0
TTACCTGTTCAGGGTCTGGGTTTCCTCCA

Consensus:

TTACCTGTTCAGGGTCTGGGTTTCCTCCA

>Bacillus_Fam_1662_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_16:91585-91696 Satlength=112 Nr of
Repeats=4 RepeatLength=30 seed=CCAGCCAAGC Num.seqs=3 Similarity=0.911111
0 CCAGCCAAGCAGCAGCCTGCAGCTCCTGCA

Consensus:

CCAGCCAAGCAGCAGCCTGCAGCTCCTGCA

>Bacillus_Fam_1663_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:3266495-3266615 Satlength=121
Nr of Repeats=4 RepeatLength=30 seed=TTTCTTCAG Num.seqs=4
Similarity=0.711111 0
TTTCTTCAGCTATTGCTTTGCCTTTGCC

Consensus:

TTTCTTCAGCTATTGCTTTGCCTTTGCC

>Bacillus_Fam_1664_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:3552762-3553117 Satlength=356
Nr of Repeats=12 RepeatLength=30 seed=GATGAGCTTT Num.seqs=11
Similarity=0.772121 0
GATGAGCTTTCTGTTGTACTACTTTCNTCT

Consensus:

GATGAGCTTTCTGTTGTACTACTTTCNTCT

>Bacillus_Fam_1665_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_001315065.1_ASM131506v1_genomic.fna_25:60788-60956 Satlength=169 Nr
of Repeats=5 RepeatLength=30 seed=GAGGAAGATC Num.seqs=3
Similarity=0.970370
0 GAGGAAGATCACGATCACGAACATGGACAT

Consensus:

GAGGAAGATCACGATCACGAACATGGACAT

>Bacillus_Fam_1666_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_001578185.1_ASM157818v1_genomic.fna_1:1359899-1360049 Satlength=151
Nr of Repeats=4 RepeatLength=30 seed=TATGGCGGTC Num.seqs=3
Similarity=0.881481 0
TATGGCGGTCATTCTGGATATGGTATGGGC

Consensus:

TATGGCGGTCATTCTGGATATGGTATGGGC

>Bacillus_Fam_1667_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_001591585.1_ASM159158v1_genomic.fna_4:226-586 Satlength=361 Nr of
Repeats=11 RepeatLength=30 seed=CTTGTTTCGC Num.seqs=10
Similarity=0.853827
0 CTTGTTTCGCTTTTTCCTTCACTAATGCTG

Consensus:

CTTGTTTCGCTTTTTCCTTCACTAATGCTG

>Bacillus_Fam_1668_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_001591625.1_ASM159162v1_genomic.fna_70:12964-13156 Satlength=193 Nr
of Repeats=5 RepeatLength=30 seed=CACCATTGTC Num.seqs=4
Similarity=0.874074
0 CACCATTGTCATGATGGACATAAACCTTGC

Consensus:

CACCATTGTCATGATGGACATAAACCTTGC

>Bacillus_Fam_1669_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:3346551-3346701 Satlength=151
Nr of Repeats=5 RepeatLength=30 seed=TCTTTGATCG Num.seqs=5
Similarity=0.776344
TCTTTGATCGGTGCNTGATACTTCGGCTGT 0

Consensus:

TCTTTGATCGGTGCNTGATACTTCGGCTGT

>Bacillus_Fam_1670_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_001742425.1_ASM174242v1_genomic.fna_11:173420-173555 Satlength=136 Nr
of Repeats=5 RepeatLength=30 seed=TACTACTTCT Num.seqs=4
Similarity=0.948148
TACTACTTCTTCAGCTGCCGCTTCTTCAGT 0

Consensus:

TACTACTTCTTCAGCTGCCGCTTCTTCAGT

>Bacillus_Fam_1671_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_002019595.1_ASM201959v1_genomic.fna_1:1449566-1449722 Satlength=157
Nr of Repeats=5 RepeatLength=30 seed=CCAGGACCAG Num.seqs=4
Similarity=0.955556
CCAGGACCAGGCATGATGCCAGGAGGAATG 0

Consensus:

CCAGGACCAGGCATGATGCCAGGAGGAATG

>Bacillus_Fam_1672_30_1 Nr. of seq. 1 Alignment length(with gaps) = 30
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:1860072-1860222 Satlength=151 Nr
of Repeats=5 RepeatLength=30 seed=CCACCTTGTG Num.seqs=5
Similarity=0.763441 0
CCACCTTGTGTTGCTTTGGCTGCTGTGCT

Consensus:

CCACCTTGTGTTGCTTTGGCTGCTGTGCT

>Bacillus_Fam_1673_29_1 Nr. of seq. 1 Alignment length(with gaps) = 29
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:32194-32368 Satlength=175 Nr of
Repeats=6 RepeatLength=29 seed=TTGCGGTAAT Num.seqs=6 Similarity=0.898851
0 TTGCGGTAATAAACTTCTAATACCCCTT

Consensus:

TTGCGGTAATAAACTTCTAATACCCCTT

>Bacillus_Fam_1674_28_1 Nr. of seq. 1 Alignment length(with gaps) = 28
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:2184233-2184341 Satlength=109
Nr of Repeats=4 RepeatLength=27 seed=TTGGCATTA Num.seqs=4
Similarity=0.769841 0
TTGGCATTAACGGCATTGATTTGCGN

Consensus:

TTGGCATTAACGGCATTGATTTGCGN

>Bacillus_Fam_1675_28_1 Nr. of seq. 1 Alignment length(with gaps) = 28
Alignment score = 0.000000
GCF_002019705.1_ASM201970v1_genomic.fna_1:3847148-3847274 Satlength=127
Nr of Repeats=6 RepeatLength=27 seed=CCAGTAACGC Num.seqs=4
Similarity=0.714286 0
CCAGTAACGCCAGTAACACCTGTNTAAG

Consensus:

CCAGTAACGCCAGTAACACCTGTNTAAG

>Bacillus_Fam_1676_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
BACILLUS_PSEUDALCALIPHILUS_genomic.fna_2:129576-130332 Satlength=757 Nr of
Repeats=20 RepeatLength=27 seed=GGACCAACAG Num.seqs=15
Similarity=0.854203 0
GGACCAACAGGNGAGCAAGGGATCCAA

Consensus:

GGACCAACAGGNGAGCAAGGGATCCAA

>Bacillus_Fam_1677_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_000177235.2_ASM17723v2_genomic.fna_1:1354085-1354274 Satlength=190 Nr
of Repeats=7 RepeatLength=27 seed=GGAGATGACG Num.seqs=5
Similarity=0.695556 0
GGAGATGACGGCGAAACNCCAGGCACA

Consensus:

GGAGATGACGGCGAAACNCCAGGCACA

>Bacillus_Fam_1678_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_27:57375-57516 Satlength=142 Nr of Repeats=5
RepeatLength=27 seed=CCACCATATC Num.seqs=3 Similarity=0.769547 0
CCACCATATCCATGATGGTACGGGTAA

Consensus:

CCACCATATCCATGATGGTACGGGTAA

>Bacillus_Fam_1679_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_000507145.1_KCTC_13622_01_genomic.fna_39:156813-156975 Satlength=163
Nr of Repeats=6 RepeatLength=27 seed=CCATACATGC Num.seqs=6
Similarity=0.947325 0
CCATACATGCCGGATCCTGGGAAACCC

Consensus:

CCATACATGCCGGATCCTGGGAAACCC

>Bacillus_Fam_1680_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_000621445.1_ASM62144v1_genomic.fna_1:408565-408724 Satlength=160 Nr
of Repeats=6 RepeatLength=27 seed=TCTTCTTCTC Num.seqs=5
Similarity=0.841667
0 TCTTCTTCTCCTCCCGGTGGCAACTCT

Consensus:

TCTTCTTCTCCTCCCGGTGGCAACTCT

>Bacillus_Fam_1681_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27

Alignment score = 0.000000

GCF_000712615.1_ASM71261v1_genomic.fna_26:13505-13964 Satlength=460 Nr of

Repeats=17 RepeatLength=27 seed=CCTGGTCCGA Num.seqs=17

Similarity=1.000000

0 CCTGGTCCGAATGGAGATACGTTTGGC

Consensus:

CCTGGTCCGAATGGAGATACGTTTGGC

>Bacillus_Fam_1682_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27

Alignment score = 0.000000

GCF_000829555.1_ASM82955v1_genomic.fna_1:540159-540303 Satlength=145 Nr

of Repeats=6 RepeatLength=27 seed=CCCGGTTCTC Num.seqs=4

Similarity=0.917695

0 CCCGGTTCTCCTGGCTCTCCCGTTTA

Consensus:

CCCGGTTCTCCTGGCTCTCCCGTTTA

>Bacillus_Fam_1683_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27

Alignment score = 0.000000

GCF_001274775.1_ASM127477v1_genomic.fna_3:360890-361097 Satlength=208 Nr

of Repeats=9 RepeatLength=27 seed=CACAGGGGCC Num.seqs=7

Similarity=0.727219

0 CACAGGGGCCACAAGGGTTGACGGGN

Consensus:

CACAGGGGCCACAAGGGTTGACGGGN

>Bacillus_Fam_1684_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27

Alignment score = 0.000000

GCF_001315065.1_ASM131506v1_genomic.fna_30:1799-1955 Satlength=157 Nr of

Repeats=6 RepeatLength=27 seed=CCAGAGCCTC Num.seqs=5 Similarity=0.930864

0 CCAGAGCCTCCTTCTCCGTCTCCAGTG

Consensus:

CCAGAGCCTCCTTCTCCGTCTCCAGTG

>Bacillus_Fam_1685_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001439635.1_ASM143963v1_genomic.fna_165:21253-21388 Satlength=136 Nr
of Repeats=4 RepeatLength=27 seed=TTTCTGAAAT Num.seqs=3
Similarity=0.595238
0 TTTCTGAAATTGCTNCCACTTCTTGAN

Consensus:

TTTCTGAAATTGCTNCCACTTCTTGAN

>Bacillus_Fam_1686_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001578185.1_ASM157818v1_genomic.fna_1:2745149-2745257 Satlength=109
Nr of Repeats=6 RepeatLength=27 seed=TGAAGCTGTT Num.seqs=4
Similarity=0.909465 0
TGAAGCTGTTGAAGCTGTTGATGCTCT

Consensus:

TGAAGCTGTTGAAGCTGTTGATGCTCT

>Bacillus_Fam_1687_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001591625.1_ASM159162v1_genomic.fna_178:4262-4433 Satlength=172 Nr of
Repeats=6 RepeatLength=27 seed=GAGGTCCTTG Num.seqs=4 Similarity=0.901235
0 GAGGTCCTTGAGGCCAGTTGCTCCCT

Consensus:

GAGGTCCTTGAGGCCAGTTGCTCCCT

>Bacillus_Fam_1688_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_2:1328784-1328973 Satlength=190
Nr of Repeats=7 RepeatLength=27 seed=AGCAAAAACC Num.seqs=5
Similarity=0.743210 0
AGCAAAAACCGTTGCAGCCTATTCAAC

Consensus:

AGCAAAAACCGTTGCAGCCTATTCAAC

>Bacillus_Fam_1689_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_2:151590-151686 Satlength=97 Nr
of Repeats=4 RepeatLength=27 seed=GGTTCTACTG Num.seqs=3
Similarity=0.934156
0 GGTTCTACTGGTTCAACAGGAACATCA

Consensus:

GGTTCTACTGGTTCAACAGGAACATCA

>Bacillus_Fam_1690_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:3248002-3248306 Satlength=305
Nr of Repeats=10 RepeatLength=27 seed=AACTGCTTGA Num.seqs=9
Similarity=0.950617 0
AACTGCTTGATGAGCTCTCGCATGAGG

Consensus:

AACTGCTTGATGAGCTCTCGCATGAGG

>Bacillus_Fam_1691_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_8:6481-6859 Satlength=379 Nr of
Repeats=13 RepeatLength=27 seed=CCTTCTGGTC Num.seqs=12
Similarity=0.976057
0 CCTTCTGGTCCCGCTGGTCCTATTGCT

Consensus:

CCTTCTGGTCCCGCTGGTCCTATTGCT

>Bacillus_Fam_1692_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_36:39981-40521 Satlength=541 Nr
of Repeats=20 RepeatLength=27 seed=CCTGCATTTC Num.seqs=20
Similarity=0.893437 0
CCTGCATTTCCTGTTCTTTCTGCTCTG

Consensus:

CCTGCATTTCCTGTTCTTTCTGCTCTG

>Bacillus_Fam_1693_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_001887185.1_ASM188718v1_genomic.fna_197:67384-67492 Satlength=109 Nr
of Repeats=4 RepeatLength=27 seed=GCCAATTTTA Num.seqs=4
Similarity=0.975309
0 GCCAATTTTACTAGGTAAAATTCTACT

Consensus:

GCCAATTTTACTAGGTAAAATTCTACT

>Bacillus_Fam_1694_27_1 Nr. of seq. 1 Alignment length(with gaps) = 27
Alignment score = 0.000000
GCF_002019605.1_ASM201960v1_genomic.fna_1:2443028-2443136 Satlength=109
Nr of Repeats=4 RepeatLength=27 seed=TCATGTCCAT Num.seqs=4
Similarity=0.942387 0
TCATGTCCATGCTCTTCATGCTCGTGA

Consensus:

TCATGTCCATGCTCTTCATGCTCGTGA

>Bacillus_Fam_1695_26_1 Nr. of seq. 1 Alignment length(with gaps) = 26
Alignment score = 0.000000
GCF_001877785.1_PlanoSAMM_genomic.fna_128:141796-141971 Satlength=176 Nr
of Repeats=7 RepeatLength=25 seed=TGTACCAGGT Num.seqs=7
Similarity=0.567460
0 TGTACCAGGTACAANACCNCAACTNN

Consensus:

TGTACCAGGTACAANACCNCAACTNN

>Bacillus_Fam_1696_25_1 Nr. of seq. 1 Alignment length(with gaps) = 25
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:37610-37783 Satlength=174 Nr of
Repeats=7 RepeatLength=25 seed=TACTACCCTA Num.seqs=5 Similarity=0.957333
0 TACTACCCTATGGTAAAATATGTAA

Consensus:

TACTACCCTATGGTAAAATATGTAA

>Bacillus_Fam_1697_25_1 Nr. of seq. 1 Alignment length(with gaps) = 25
Alignment score = 0.000000
GCF_001877785.1_PlanoSAMM_genomic.fna_117:71061-71186 Satlength=126 Nr of
Repeats=5 RepeatLength=25 seed=TGTACCTGGT Num.seqs=5 Similarity=0.553086
0 TGTACCTGGTACATGANCCNGTNNT

Consensus:

TGTACCTGGTACATGANCCNGTNNT

>Bacillus_Fam_1698_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:1443980-1444148 Satlength=169 Nr
of Repeats=7 RepeatLength=24 seed=TGGAGTTGGA Num.seqs=7
Similarity=1.000000 0
TGGAGTTGGAGGATTCGGCGGACC

Consensus:

TGGAGTTGGAGGATTCGGCGGACC

>Bacillus_Fam_1699_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000186125.1_Bacillus_BT1B_CT2_V1_genomic.fna_1:1895116-1895212
Satlength=97 Nr of Repeats=4 RepeatLength=24 seed=GGGACACAGC Num.seqs=4
Similarity=0.826923 0
GGGACACAGCTGTTGGAGCTGTGC

Consensus:

GGGACACAGCTGTTGGAGCTGTGC

>Bacillus_Fam_1700_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000245335.1_ASM24533v1_genomic.fna_8:553929-554097 Satlength=169 Nr
of Repeats=7 RepeatLength=24 seed=CCTCCGCCAA Num.seqs=7
Similarity=0.756614
0 CCTCCGCCAATACCAGGCACGGCG

Consensus:

CCTCCGCCAATACCAGGCACGGCG

>Bacillus_Fam_1701_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000307855.1_BAZO1.0_genomic.fna_16:13575-13719 Satlength=145 Nr of
Repeats=6 RepeatLength=24 seed=GGAGGATTTT Num.seqs=6 Similarity=0.900000
0 GGAGGATTTTGCGCAGGCAGGTGC

Consensus:

GGAGGATTTTGCGCAGGCAGGTGC

>Bacillus_Fam_1702_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:75628-75724 Satlength=97 Nr of
Repeats=4 RepeatLength=24 seed=ACTGTTTTTC Num.seqs=4 Similarity=0.907407
0 ACTGTTTTTCGTTCTGCTATTTAC

Consensus:

ACTGTTTTTCGTTCTGCTATTTAC

>Bacillus_Fam_1703_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_3:126837-127053 Satlength=217 Nr
of Repeats=9 RepeatLength=24 seed=GACCAAAACA Num.seqs=9

Similarity=0.833333
0 GACCAAAACACAATACAGAAGTTG

Consensus:

GACCAAAACACAATACAGAAGTTG

>Bacillus_Fam_1704_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000374565.1_ASM37456v1_genomic.fna_6:153087-153207 Satlength=121 Nr
of Repeats=5 RepeatLength=24 seed=CCGGGTGAAG Num.seqs=5
Similarity=0.922222
0 CCGGGTGAAGGGCCAGGAGAAAAC

Consensus:

CCGGGTGAAGGGCCAGGAGAAAAC

>Bacillus_Fam_1705_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000496285.1_ASM49628v1_genomic.fna_1:3406349-3406469 Satlength=121 Nr
of Repeats=5 RepeatLength=24 seed=AGTGTCTTTT Num.seqs=5
Similarity=0.922222
AGTGTCTTTTGTTCCTCTCAGAGTT 0

Consensus:

AGTGTCTTTTGTTCCTCTCAGAGTT

>Bacillus_Fam_1706_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_1:918376-919127 Satlength=752 Nr of Repeats=28
RepeatLength=24 seed=TCGGCACTTT Num.seqs=18 Similarity=0.714597 0
TCGGCACTTTCATCTNCACTTTTCG

Consensus:

TCGGCACTTTCATCTNCACTTTTCG

>Bacillus_Fam_1707_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000612625.1_JCE_genomic.fna_19:40197-40437 Satlength=241 Nr of
Repeats=10 RepeatLength=24 seed=TCCTCCAGTG Num.seqs=10
Similarity=0.944444
0 TCCTCCAGTGCTGCCTCCGTTGTC

Consensus:

TCCTCCAGTGCTGCCTCCGTTGTC

>Bacillus_Fam_1708_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_3:200804-201365 Satlength=562 Nr
of Repeats=23 RepeatLength=24 seed=TTACCTTGGC Num.seqs=20
Similarity=0.994444
TTACCTTGGCCACCACCTTGGTCG

0

Consensus:

TTACCTTGGCCACCACCTTGGTCG

>Bacillus_Fam_1709_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000712595.1_ASM71259v1_genomic.fna_14:27323-27635 Satlength=313 Nr of
Repeats=13 RepeatLength=24 seed=TTGTACTTGC Num.seqs=13
Similarity=0.921652
0 TTGTACTTGCTCCTGCACCGGCTC

Consensus:

TTGTACTTGCTCCTGCACCGGCTC

>Bacillus_Fam_1710_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000712615.1_ASM71261v1_genomic.fna_12:99179-99620 Satlength=442 Nr of
Repeats=18 RepeatLength=24 seed=CCATGATGAT Num.seqs=17
Similarity=1.000000
0 CCATGATGATTGTGATGGTGTCCG

Consensus:

CCATGATGATTGTGATGGTGTCCG

>Bacillus_Fam_1711_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000724485.1_ASM72448v1_genomic.fna_1:2088487-2088577 Satlength=91 Nr
of Repeats=4 RepeatLength=24 seed=CCTGGTCCAT Num.seqs=3
Similarity=0.962963
0 CCTGGTCCATAACCAGGGCCCATA

Consensus:

CCTGGTCCATAACCAGGGCCCATA

>Bacillus_Fam_1712_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000

GCF_000724485.1_ASM72448v1_genomic.fna_1:2102157-2102379 Satlength=223 Nr
of Repeats=8 RepeatLength=24 seed=CGGTACTGGC Num.seqs=7
Similarity=0.915344 0
CGGTACTGGCGCCGGTGGCAACGG

Consensus:

CGGTACTGGCGCCGGTGGCAACGG

>Bacillus_Fam_1713_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_000775975.1_ASM77597v1_genomic.fna_1:3273312-3273480 Satlength=169 Nr
of Repeats=6 RepeatLength=24 seed=TGATTCATAT Num.seqs=5
Similarity=0.777778 0
TGATTCATATGCGCTTGTTGCGGC

Consensus:

TGATTCATATGCGCTTGTTGCGGC

>Bacillus_Fam_1714_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001274935.1_ASM127493v1_genomic.fna_1:6173-6293 Satlength=121 Nr of
Repeats=5 RepeatLength=24 seed=GGTGGCGTTG Num.seqs=5 Similarity=0.866667
0 GGTGGCGTTGTACCTCCATCTCCG

Consensus:

GGTGGCGTTGTACCTCCATCTCCG

>Bacillus_Fam_1715_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:3031878-3031998 Satlength=121
Nr of Repeats=5 RepeatLength=24 seed=GTTTGTGCTG Num.seqs=5
Similarity=0.933333 0
GTTTGTGCTGGCTTTTGAGTCTGA

Consensus:

GTTTGTGCTGGCTTTTGAGTCTGA

>Bacillus_Fam_1716_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:560318-560419 Satlength=102 Nr
of Repeats=5 RepeatLength=20 seed=GGCTAATAGA Num.seqs=4
Similarity=0.528935 0
GGCTAATAGANCGAAAGTGATAAC

Consensus:

GGCTAATAGANCGAAAGTGATAAC

>Bacillus_Fam_1717_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001578185.1_ASM157818v1_genomic.fna_1:4072028-4072112 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=TTCACGAGTA Num.seqs=4
Similarity=0.583333 0
TTCACGAGTAAATGACCCAATNAN

Consensus:

TTCACGAGTAAATGACCCAATNAN

>Bacillus_Fam_1718_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001591445.1_ASM159144v1_genomic.fna_22:102672-102756 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=ATTCCGCCAA Num.seqs=4
Similarity=0.546296
0 ATTCCGCCAACTATTGGAGTTNGG

Consensus:

ATTCCGCCAACTATTGGAGTTNGG

>Bacillus_Fam_1719_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001591585.1_ASM159158v1_genomic.fna_10:33080-33226 Satlength=147 Nr
of Repeats=7 RepeatLength=21 seed=ATATCAGCCA Num.seqs=6
Similarity=0.616204
0 ATATCAGCCAANGTAACGGGGAGC

Consensus:

ATATCAGCCAANGTAACGGGGAGC

>Bacillus_Fam_1720_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:5656908-5657010 Satlength=103
Nr of Repeats=5 RepeatLength=24 seed=TTTCAATTTC Num.seqs=3
Similarity=0.925926 0
TTTCAATTTC AATTCGTCTTCTTC

Consensus:

TTTCAATTTC AATTCGTCTTCTTC

>Bacillus_Fam_1721_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000

GCF_001645685.2_ASM164568v2_genomic.fna_1:664949-665049 Satlength=101 Nr
of Repeats=4 RepeatLength=24 seed=TTGCAGTACG Num.seqs=3
Similarity=0.962963
0 TTGCAGTACGCTAGAGTACTCCAG

Consensus:

TTGCAGTACGCTAGAGTACTCCAG

>Bacillus_Fam_1722_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001654695.1_ASM165469v1_genomic.fna_23:346230-346323 Satlength=94 Nr
of Repeats=4 RepeatLength=24 seed=GAAAAACAGC Num.seqs=3
Similarity=0.888889
0 GAAAAACAGCCTGCAACAGAAGAA

Consensus:

GAAAAACAGCCTGCAACAGAAGAA

>Bacillus_Fam_1723_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001654695.1_ASM165469v1_genomic.fna_34:84196-84424 Satlength=229 Nr
of Repeats=6 RepeatLength=21 seed=TGGTTCAATC Num.seqs=4
Similarity=0.527778
0 TGGTTCAATCNCCTCGNTCTTCAA

Consensus:

TGGTTCAATCNCCTCGNTCTTCAA

>Bacillus_Fam_1724_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_1:111413-111521 Satlength=109 Nr
of Repeats=5 RepeatLength=24 seed=GTGCCGTCAC Num.seqs=3
Similarity=0.925926
0 GTGCCGTCACCAGTACCAGTACCC

Consensus:

GTGCCGTCACCAGTACCAGTACCC

>Bacillus_Fam_1725_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001742425.1_ASM174242v1_genomic.fna_18:1219-1339 Satlength=121 Nr of
Repeats=5 RepeatLength=24 seed=GAAGAACCAA Num.seqs=5 Similarity=0.772222
0 GAAGAACCAACAACAGAACAACCT

Consensus:

GAAGAACCAACAACAGAACAACCT

>Bacillus_Fam_1726_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_001742425.1_ASM174242v1_genomic.fna_33:4678-4870 Satlength=193 Nr of
Repeats=8 RepeatLength=24 seed=AAACCAAGTG Num.seqs=8 Similarity=0.847222
0 AAACCAAGTGAAATAGACGAGACA

Consensus:

AAACCAAGTGAAATAGACGAGACA

>Bacillus_Fam_1727_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:4130416-4130536 Satlength=121
Nr of Repeats=5 RepeatLength=24 seed=TTATTACCTG Num.seqs=5
Similarity=0.855556 0
TTATTACCTGGTTTCTCGCCCGGT

Consensus:

TTATTACCTGGTTTCTCGCCCGGT

>Bacillus_Fam_1728_24_1 Nr. of seq. 1 Alignment length(with gaps) = 24
Alignment score = 0.000000
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_23:96772-97084
Satlength=313 Nr of Repeats=13 RepeatLength=24 seed=CGACCATCAG
Num.seqs=13 Similarity=0.881054 0
CGACCATCAGGTCAAGGCCAACAA

Consensus:

CGACCATCAGGTCAAGGCCAACAA

>Bacillus_Fam_1729_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_000171615.1_ASM17161v1_genomic.fna_93:12659-12804 Satlength=146 Nr of
Repeats=5 RepeatLength=21 seed=GTGCACGCAA Num.seqs=4 Similarity=0.719807
0 GTGCACGCAAGAAGNCCGAAAAA

Consensus:

GTGCACGCAAGAAGNCCGAAAAA

>Bacillus_Fam_1730_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_000186145.1_Bacillus_sp_2_A_57_CT2_V1_genomic.fna_6:213928-214012
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TTGGCCGGTA Num.seqs=4

Similarity=0.396368
TTGGCCGGTAATTTNCATTNAAA

0

Consensus:

TTGGCCGGTAATTTNCATTNAAA

>Bacillus_Fam_1731_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_000305495.1_BacPsy2.0_genomic.fna_90:7041-7359 Satlength=319 Nr of
Repeats=7 RepeatLength=21 seed=ATTCGGCCCT Num.seqs=6 Similarity=0.508213
0 ATTCGGCCCTTANTCTCCATCNN

Consensus:

ATTCGGCCCTTANTCTCCATCNN

>Bacillus_Fam_1732_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:173707-173821 Satlength=115 Nr
of Repeats=5 RepeatLength=23 seed=TACATGTAAA Num.seqs=4
Similarity=0.876157
0 TACATGTAAAATCATATTTTCGA

Consensus:

TACATGTAAAATCATATTTTCGA

>Bacillus_Fam_1733_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_5:604719-605171 Satlength=453 Nr
of Repeats=6 RepeatLength=21 seed=TACATCCAAC Num.seqs=4
Similarity=0.555556
0 TACATCCAACAATTAGAGCAATT

Consensus:

TACATCCAACAATTAGAGCAATT

>Bacillus_Fam_1734_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_90:13367-13451 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=GGTGATAAAAT Num.seqs=4 Similarity=0.572464
0 GGTGATAAAATAAATACCACTCTT

Consensus:

GGTGATAAAATAAATACCACTCTT

>Bacillus_Fam_1735_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_135:8975-9359 Satlength=385 Nr of
Repeats=11 RepeatLength=21 seed=GTTGAACAGA Num.seqs=8
Similarity=0.610766
0 GTTGAACAGAANNATCAAGTTGA

Consensus:

GTTGAACAGAANNATCAAGTTGA

>Bacillus_Fam_1736_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_001591825.1_ASM159182v1_genomic.fna_26:22973-23057 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=AATCCAGCCG Num.seqs=4 Similarity=0.507246
0 AATCCAGCCGANAATACGAAANG

Consensus:

AATCCAGCCGANAATACGAAANG

>Bacillus_Fam_1737_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:1929121-1929205 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=TTCCGCGATA Num.seqs=4
Similarity=0.518519 0
TTCCGCGATAACTNGCTNCATGN

Consensus:

TTCCGCGATAACTNGCTNCATGN

>Bacillus_Fam_1738_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:4339164-4339477 Satlength=314
Nr of Repeats=15 RepeatLength=21 seed=TTTTCCGGCC Num.seqs=10
Similarity=0.686634 0
TTTTCCGGCCGGTCGACTCGACT

Consensus:

TTTTCCGGCCGGTCGACTCGACT

>Bacillus_Fam_1739_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_37:34288-34763 Satlength=476 Nr
of Repeats=16 RepeatLength=20 seed=AATCGCAATT Num.seqs=12
Similarity=0.595749 0
AATCGCAATAAAATCNAAGNNN

Consensus:

AATCGCAAATAAAATCNAAGNNN

>Bacillus_Fam_1740_23_1 Nr. of seq. 1 Alignment length(with gaps) = 23
Alignment score = 0.000000

GCF_900111815.1_PRJEB17078_genomic.fna_1:496274-496585 Satlength=312 Nr
of Repeats=11 RepeatLength=21 seed=AAATCAACCA Num.seqs=8
Similarity=0.576605

0 AAATCAACCAACTNATGAGTGAG

Consensus:

AAATCAACCAACTNATGAGTGAG

>Bacillus_Fam_1741_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_31:195679-195783 Satlength=105 Nr
of Repeats=4 RepeatLength=21 seed=TATTTTCCGT Num.seqs=3
Similarity=0.521739

0 TATTTTCCGTTACNGNTATATT

Consensus:

TATTTTCCGTTACNGNTATATT

>Bacillus_Fam_1742_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000

GCF_000175075.1_ASM17507v1_genomic.fna_32:57067-57168 Satlength=102 Nr of
Repeats=5 RepeatLength=20 seed=TTTCTTGATA Num.seqs=4 Similarity=0.589646
0 TTTCTTGATATATCTTGCAANA

Consensus:

TTTCTTGATATATCTTGCAANA

>Bacillus_Fam_1743_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000

GCF_000242895.2_ASM24289v3_genomic.fna_1:4424659-4424743 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=TTTATCGGCC Num.seqs=4
Similarity=0.641304

0 TTTATCGGCCGCTTTTGATAAT

Consensus:

TTTATCGGCCGCTTTTGATAAT

>Bacillus_Fam_1744_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_000307875.1_BABA1.0_genomic.fna_135:3379-3463 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTTATTTGCG Num.seqs=4 Similarity=0.525463
19 ATTTGCGAAACTAGCCACATTT

Consensus:

TTTATTTGCGAAACTAGCCACA

>Bacillus_Fam_1745_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_000311725.1_ASM31172v1_genomic.fna_2:350998-351082 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=ATTGCGGGCG Num.seqs=4 Similarity=0.601010
0 ATTGCGGGCGTTCTANGCCATA

Consensus:

ATTGCGGGCGTTCTANGCCATA

>Bacillus_Fam_1746_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:23784-24242 Satlength=459 Nr of
Repeats=13 RepeatLength=22 seed=GATACCTTAT Num.seqs=8
Similarity=0.902597
0 GATACCTTATGAGTACGGAAAT

Consensus:

GATACCTTATGAGTACGGAAAT

>Bacillus_Fam_1747_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_000429685.1_ASM42968v1_genomic.fna_13:95209-95355 Satlength=147 Nr of
Repeats=6 RepeatLength=21 seed=GAGGAGAAAA Num.seqs=4 Similarity=0.606061
0 GAGGAGAAGAAANAGCGGAGCN

Consensus:

GAGGAGAAGAAANAGCGGAGCN

>Bacillus_Fam_1748_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_000429705.1_ASM42970v1_genomic.fna_3:352016-352120 Satlength=105 Nr
of Repeats=5 RepeatLength=21 seed=TATAATGAAT Num.seqs=4
Similarity=0.637626
0 TATAATGAATTCCTCAACNATA

Consensus:

TATAATGAATTCCTCAACNATA

>Bacillus_Fam_1749_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_5:35642-35726 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TAATCCTGAT Num.seqs=4 Similarity=0.543981
0 TAATCCTGATTTCGCTGCATT

Consensus:

TAATCCTGATTTCGCTGCATT

>Bacillus_Fam_1750_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_5:81208-81561 Satlength=354 Nr of
Repeats=5 RepeatLength=21 seed=CAATAATTGA Num.seqs=4 Similarity=0.757576
0 CAATAATTGATGCAATCAACTT

Consensus:

CAATAATTGATGCAATCAACTT

>Bacillus_Fam_1751_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_1:26204-26330 Satlength=127 Nr of
Repeats=6 RepeatLength=21 seed=TTTTCTTAAC Num.seqs=6 Similarity=0.546377
0 TTTACTTAACAGAGCTTCGGAA

Consensus:

TTTACTTAACAGAGCTTCGGAA

>Bacillus_Fam_1752_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_10:28205-28351 Satlength=147 Nr
of Repeats=6 RepeatLength=21 seed=TGGTGCAACC Num.seqs=4
Similarity=0.513285
0 TGGTGCAACACCACCGCAAAAN

Consensus:

TGGTGCAACACCACCGCAAAAN

>Bacillus_Fam_1753_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_001591445.1_ASM159144v1_genomic.fna_16:43521-43605 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TCTATTGGCG Num.seqs=4 Similarity=0.717172
0 TCTATTGGCGAATTTACCTAN

Consensus:

TCTATTGGCGAATTTTCACCTAN

>Bacillus_Fam_1754_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:454483-454588 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=TTTGATAGGA Num.seqs=5
Similarity=0.542029
0 TTTGATAGGAAAGCTGNTTANN

Consensus:

TTTGATAGGAAAGCTGNTTANN

>Bacillus_Fam_1755_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:4479552-4479636 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=TTTACCCGAT Num.seqs=4
Similarity=0.631313 0
TTTACCCGATTANACGCATANT

Consensus:

TTTACCCGATTANACGCATANT

>Bacillus_Fam_1756_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_37:29313-29417 Satlength=105 Nr
of Repeats=5 RepeatLength=21 seed=TTTAATTGCA Num.seqs=4
Similarity=0.585859
0 TTTAATTGCAGATATAGCATAN

Consensus:

TTTAATTGCAGATATAGCATAN

>Bacillus_Fam_1757_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:3363210-3363336 Satlength=127
Nr of Repeats=6 RepeatLength=21 seed=ATTCGTCCAG Num.seqs=6
Similarity=0.657071 0
ATTCGTCCGAAATCCGCCTTCN

Consensus:

ATTCGTCCGAAATCCGCCTTCN

>Bacillus_Fam_1758_22_1 Nr. of seq. 1 Alignment length(with gaps) = 22
Alignment score = 0.000000
GCF_900104555.1_IMG-
taxon_2651870172_annotated_assembly_genomic.fna_19:64922-65582
Satlength=661 Nr of Repeats=20 RepeatLength=21 seed=TCGCGGGATT
Num.seqs=14 Similarity=0.665668 0
TCGCGGGATTNCCATGCTCTTT

Consensus:

TCGCGGGATTNCCATGCTCTTT

>Bacillus_Fam_1759_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000153365.1_ASM15336v1_genomic.fna_17:503213-503318 Satlength=106 Nr
of Repeats=4 RepeatLength=21 seed=TCAAACCTTT Num.seqs=3
Similarity=0.788360
0 TCAAACCTTTTATCAACAGCA

Consensus:

TCAAACCTTTTATCAACAGCA

>Bacillus_Fam_1760_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:1878049-1878322 Satlength=274 Nr
of Repeats=12 RepeatLength=21 seed=GGTGGCACAA Num.seqs=11
Similarity=0.866089 0
GGTGGCACAAACCCAGGC

Consensus:

GGTGGCACAAACCCAGGC

>Bacillus_Fam_1761_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000171615.1_ASM17161v1_genomic.fna_106:18545-18854 Satlength=310 Nr
of Repeats=10 RepeatLength=21 seed=CCGCACGAGA Num.seqs=7
Similarity=0.617605
0 CCGCACGAGAAGAAGGTCCNC

Consensus:

CCGCACGAGAAGAAGGTCCNC

>Bacillus_Fam_1762_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000245315.1_ASM24531v1_genomic.fna_45:163118-163205 Satlength=88 Nr
of Repeats=4 RepeatLength=21 seed=GCCGGGCACA Num.seqs=3

Similarity=1.000000
0 GCCGGGCACACCGCCGCCGAA

Consensus:

GCCGGGCACACCGCCGCCGAA

>Bacillus_Fam_1763_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000290995.1_Baci_cere_AND1407_G13175_V1_genomic.fna_1:1730757-1730841
Satlength=85 Nr of Repeats=4 RepeatLength=21 seed=TCTTTTTTTTG Num.seqs=4
Similarity=0.957672 0
TCTTTTTTTGGCTCACAATCC

Consensus:

TCTTTTTTTGGCTCACAATCC

>Bacillus_Fam_1764_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:475624-475876 Satlength=253 Nr
of Repeats=12 RepeatLength=21 seed=TTACCCATAT Num.seqs=12
Similarity=0.735308 0
TTACCCATATATCTGNGCACT

Consensus:

TTACCCATATATCTGNGCACT

>Bacillus_Fam_1765_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_2:594953-595079 Satlength=127 Nr
of Repeats=5 RepeatLength=21 seed=TTCTTCCGT Num.seqs=4
Similarity=0.862434
0 TTCCTTCCGTGGTAACGTGGA

Consensus:

TTCCTTCCGTGGTAACGTGGA

>Bacillus_Fam_1766_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:107598-107787 Satlength=190 Nr
of Repeats=7 RepeatLength=21 seed=AATCGAGTGC Num.seqs=5
Similarity=0.911111
0 AATCGAGTGCTTTTCTCGCGG

Consensus:

AATCGAGTGCTTTTCTCGCGG

>Bacillus_Fam_1767_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:141893-142040 Satlength=148 Nr
of Repeats=7 RepeatLength=21 seed=TTTACCCATA Num.seqs=7
Similarity=0.687590
0 TTTACCCATATGAATTAGCTA

Consensus:

TTTACCCATATGAATTAGCTA

>Bacillus_Fam_1768_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:228625-228873 Satlength=249 Nr
of Repeats=10 RepeatLength=21 seed=TACCCACATA Num.seqs=9
Similarity=0.669082
0 TACCCACATAAAATGCGGATT

Consensus:

TACCCACATAAAATGCGGATT

>Bacillus_Fam_1769_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000334155.1_L1_genomic.fna_69:26716-27262 Satlength=547 Nr of
Repeats=26 RepeatLength=21 seed=CATGAAGAAG Num.seqs=26
Similarity=0.867936
0 CATGAAGAAGAAGAACATGGA

Consensus:

CATGAAGAAGAAGAACATGGA

>Bacillus_Fam_1770_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000401235.1_BacNeaAAU1_genomic.fna_109:50519-50812 Satlength=294 Nr
of Repeats=14 RepeatLength=21 seed=TTGGCTGATA Num.seqs=13
Similarity=0.808081
TTGGCTGATATCGGTGTTGGA

0

Consensus:

TTGGCTGATATCGGTGTTGGA

>Bacillus_Fam_1771_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000

GCF_000429705.1_ASM42970v1_genomic.fna_1:164813-164917 Satlength=105 Nr
of Repeats=5 RepeatLength=21 seed=TATAATGAAT Num.seqs=4
Similarity=0.498843
0 TATAATGAATCTCGAANCATT

Consensus:

TATAATGAATCTCGAANCATT

>Bacillus_Fam_1772_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000429705.1_ASM42970v1_genomic.fna_1:212906-213009 Satlength=104 Nr
of Repeats=5 RepeatLength=21 seed=AAAGTGATGG Num.seqs=3
Similarity=0.682540
0 AAAGTGATTGATAANNGGATN

Consensus:

AAAGTGATTGATAANNGGATN

>Bacillus_Fam_1773_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000429705.1_ASM42970v1_genomic.fna_1:1695051-1695135 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=TTAAACAGGT Num.seqs=4
Similarity=0.693122
0 TTAAACAGGTTAGGCTCTCAT

Consensus:

TTAAACAGGTTAGGCTCTCAT

>Bacillus_Fam_1774_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000429705.1_ASM42970v1_genomic.fna_2:604162-604246 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TAATTCTACC Num.seqs=4 Similarity=0.520833
0 TAATTCTACCTAAAAAGNCAT

Consensus:

TAATTCTACCTAAAAAGNCAT

>Bacillus_Fam_1775_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_7:272233-272397 Satlength=165 Nr
of Repeats=5 RepeatLength=21 seed=GAGCAAAAAA Num.seqs=3
Similarity=0.416667
0 GAGCAAAAAAGNACCNTGCNG

Consensus:

GAGCAAAAAAGNACCNTGCNG

>Bacillus_Fam_1776_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_14:8047-8192 Satlength=146 Nr of
Repeats=7 RepeatLength=21 seed=TTTTTGCTCA Num.seqs=5 Similarity=0.525333
0 TTTTTGCTCANCACACCNATN

Consensus:

TTTTTGCTCANCACACCNATN

>Bacillus_Fam_1777_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000430785.1_ASM43078v1_genomic.fna_3:131543-131690 Satlength=148 Nr
of Repeats=7 RepeatLength=21 seed=TGCCACAAGG Num.seqs=7
Similarity=0.945578
0 TGCCACAAGGAATGCATCAAG

Consensus:

TGCCACAAGGAATGCATCAAG

>Bacillus_Fam_1778_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000474275.1_Bmar1.0_genomic.fna_20:6145-6290 Satlength=146 Nr of
Repeats=4 RepeatLength=21 seed=ACTGACGCAA Num.seqs=3 Similarity=1.000000
0 ACTGACGCAATAGCGTCTGGA

Consensus:

ACTGACGCAATAGCGTCTGGA

>Bacillus_Fam_1779_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000496285.1_ASM49628v1_genomic.fna_1:2486611-2486716 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=TTGGATCTTT Num.seqs=5
Similarity=0.898413
TTGGATCTTTCGGATCTGTGC 0

Consensus:

TTGGATCTTTCGGATCTGTGC

>Bacillus_Fam_1780_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000504145.1_SOAPdenovo_for_version2.04_of_Bacillus_sp._FJAT-
14515_genome_genomic.fna_1:1809470-1809638 Satlength=169 Nr of Repeats=8

RepeatLength=21 seed=CTTCTTGGGA Num.seqs=8 Similarity=0.895692 0
CTTCTTGGGACCGTCATCCGG

Consensus:

CTTCTTGGGACCGTCATCCGG

>Bacillus_Fam_1781_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000508325.1_BAVI_1_genomic.fna_92:129782-130070 Satlength=289 Nr of
Repeats=4 RepeatLength=21 seed=AAGTGACCGG Num.seqs=3 Similarity=0.628019
0 AAGTGACCGGTATTTNNACNA

Consensus:

AAGTGACCGGTATTTNNACNA

>Bacillus_Fam_1782_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000526655.1_ASM52665v1_genomic.fna_1:7-112 Satlength=106 Nr of
Repeats=5 RepeatLength=21 seed=GAAGTGCAGAC Num.seqs=5 Similarity=0.847619
0 GAAGTGCAGACGGTTGCGAGAA

Consensus:

GAAGTGCAGACGGTTGCGAGAA

>Bacillus_Fam_1783_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000612625.1_JCE_genomic.fna_8:31125-31331 Satlength=207 Nr of
Repeats=5 RepeatLength=21 seed=GGATCATTTT Num.seqs=3 Similarity=0.509259
0 GGATCATTTTCCAATATCNTT

Consensus:

GGATCATTTTCCAATATCNTT

>Bacillus_Fam_1784_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000612665.1_FF4_genomic.fna_12:2775-2932 Satlength=158 Nr of
Repeats=4 RepeatLength=21 seed=AATTTGTAGA Num.seqs=3 Similarity=0.788360
0 AATTTGTAGATATCTAGACCA

Consensus:

AATTTGTAGATATCTAGACCA

>Bacillus_Fam_1785_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000

GCF_000612665.1_FF4_genomic.fna_25:19828-19954 Satlength=127 Nr of
Repeats=6 RepeatLength=21 seed=CAGCCAGCAC Num.seqs=6 Similarity=0.957672
0 CAGCCAGCACCGCAGCAGGCA

Consensus:

CAGCCAGCACCGCAGCAGGCA

>Bacillus_Fam_1786_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000612805.1_FF3_genomic.fna_6:195760-195886 Satlength=127 Nr of
Repeats=5 RepeatLength=21 seed=CCTGGGAAAA Num.seqs=4 Similarity=0.798942
0 CCTGGGAAAAACGGACCCACA

Consensus:

CCTGGGAAAAACGGACCCACA

>Bacillus_Fam_1787_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000709935.2_ASM70993v2_genomic.fna_5:763265-763757 Satlength=493 Nr
of Repeats=5 RepeatLength=21 seed=TTTGGATTGT Num.seqs=3
Similarity=1.000000
0 TTTGGATTGTTACACGCCGCA

Consensus:

TTTGGATTGTTACACGCCGCA

>Bacillus_Fam_1788_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000724485.1_ASM72448v1_genomic.fna_1:2060503-2060703 Satlength=201 Nr
of Repeats=4 RepeatLength=21 seed=AACGGGAGTA Num.seqs=3
Similarity=0.681818
AACGGGAGTAAANTCCTCCTG 0

Consensus:

AACGGGAGTAAANTCCTCCTG

>Bacillus_Fam_1789_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000751775.1_A1A_genomic.fna_84:23149-23297 Satlength=149 Nr of
Repeats=6 RepeatLength=21 seed=ATTCAACAGT Num.seqs=4 Similarity=0.502645
0 ATTCAACAGTAGATTACGAGT

Consensus:

ATTCAACAGTAGATTACGAGT

>Bacillus_Fam_1790_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000751775.1_A1A_genomic.fna_102:29051-29177 Satlength=127 Nr of
Repeats=5 RepeatLength=21 seed=ATGGACAAGC Num.seqs=4 Similarity=0.936508
0 ATGGACAAGCTTGAATCCCGA

Consensus:

ATGGACAAGCTTGAATCCCGA

>Bacillus_Fam_1791_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:391259-391490
Satlength=232 Nr of Repeats=11 RepeatLength=21 seed=TACGAGAGTA
Num.seqs=11 Similarity=0.611331 0
TACGAGAGTAAACCTGNGTTA

Consensus:

TACGAGAGTAAACCTGNGTTA

>Bacillus_Fam_1792_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_11:573150-573648
Satlength=499 Nr of Repeats=18 RepeatLength=21 seed=TCTACAAATT
Num.seqs=12 Similarity=0.615200 0
TCTACAAATTCAGGNCCGTAT

Consensus:

TCTACAAATTCAGGNCCGTAT

>Bacillus_Fam_1793_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_23:26534-26639
Satlength=106 Nr of Repeats=4 RepeatLength=21 seed=TGTTTCTACA Num.seqs=3
Similarity=0.957672 0
TGTTTCTACAAATTAAAGATG

Consensus:

TGTTTCTACAAATTAAAGATG

>Bacillus_Fam_1794_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_30:64121-64390
Satlength=270 Nr of Repeats=11 RepeatLength=21 seed=TTTTGTAGAT
Num.seqs=9 Similarity=0.602623
0 TTTTGTAGANTNAGCACTTAA

Consensus:

TTTTGTAGANTNAGCACTTAA

>Bacillus_Fam_1795_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_12:197233-197359
Satlength=127 Nr of Repeats=6 RepeatLength=21 seed=TACTGTTGAA Num.seqs=6
Similarity=0.624074 0
TACTGTTGAAGTTTCATCTTT

Consensus:

TACTGTTGAAGTTTCATCTTT

>Bacillus_Fam_1796_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_45:59415-59652
Satlength=238 Nr of Repeats=9 RepeatLength=20 seed=AACTTCGGAA Num.seqs=6
Similarity=0.503535 0
AACTTCGGAAATNATAGCNTC

Consensus:

AACTTCGGAAATNATAGCNTC

>Bacillus_Fam_1797_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_150:11338-11443 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=AGTCCAAAAC Num.seqs=3
Similarity=0.682540
0 AGTCCAAAACNCATGGAAAT

Consensus:

AGTCCAAAACNCATGGAAAT

>Bacillus_Fam_1798_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_158:119179-119305 Satlength=127 Nr
of Repeats=5 RepeatLength=21 seed=CTGTTCTACA Num.seqs=4
Similarity=0.777778 0
CTGTTCTACAGCTTCGACAAG

Consensus:

CTGTTCTACAGCTTCGACAAG

>Bacillus_Fam_1799_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000812025.2_ASM81202v2_genomic.fna_59:9522-9690 Satlength=169 Nr of
Repeats=8 RepeatLength=21 seed=AAGGAACAGC Num.seqs=6 Similarity=0.671212
0 AAGGAACAGCCGAAACAAGTA

Consensus:

AAGGAACAGCCGAAACAAGTA

>Bacillus_Fam_1800_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_110:11398-11482 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=AGAGATTAT Num.seqs=4 Similarity=0.875000
0 AGAGATTATCTCCAGTTAAG

Consensus:

AGAGATTATCTCCAGTTAAG

>Bacillus_Fam_1801_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_129:71964-72048 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=ATTCCGCGAA Num.seqs=4 Similarity=0.587302
0 ATTCCGCGAAAAATTCTTTA

Consensus:

ATTCCGCGAAAAATTCTTTA

>Bacillus_Fam_1802_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000813125.1_ASM81312v1_genomic.fna_142:7599-7683 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=TTTTTCTACG Num.seqs=4 Similarity=0.586957
0 TTTTCTACGGTTGGCAGCAN

Consensus:

TTTTTCTACGGTTGGCAGCAN

>Bacillus_Fam_1803_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000831065.1_ASM83106v1_genomic.fna_1:1513435-1513582 Satlength=148 Nr
of Repeats=7 RepeatLength=21 seed=AAAACCAGAA Num.seqs=7
Similarity=0.897203
AAAACCAGAAAGCGAAGGTGG 0

Consensus:

AAAACCAGAAGGCGAAGGTGG

>Bacillus_Fam_1804_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000832605.1_ASM83260v1_genomic.fna_1:783460-783565 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=AGACTAAGCT Num.seqs=5
Similarity=1.000000
0 AGACTAAGCTGATACTTAATG

Consensus:

AGACTAAGCTGATACTTAATG

>Bacillus_Fam_1805_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000948175.1_BFA_2_A_genomic.fna_39:29576-29984 Satlength=409 Nr of
Repeats=4 RepeatLength=21 seed=GGTTGGATCG Num.seqs=3 Similarity=0.915344
0 GGTTGGATCGGGTTGAAGAGC

Consensus:

GGTTGGATCGGGTTGAAGAGC

>Bacillus_Fam_1806_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_000986785.1_ASM98678v1_genomic.fna_38:8628-8733 Satlength=106 Nr of
Repeats=5 RepeatLength=21 seed=TTGGAAAATA Num.seqs=5 Similarity=0.476812
0 TTGGAAAATAAACTTNCTNTN

Consensus:

TTGGAAAATAAACTTNCTNTN

>Bacillus_Fam_1807_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001273755.1_ASM127375v1_genomic.fna_17:3548301-3548609 Satlength=309
Nr of Repeats=13 RepeatLength=21 seed=GACGAATTAT Num.seqs=8
Similarity=0.615823 0
GACGAATTATCTTCTCTCAAG

Consensus:

GACGAATTATCTTCTCTCAAG

>Bacillus_Fam_1808_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001278705.1_ASM127870v1_genomic.fna_1:21006-21130 Satlength=125 Nr of
Repeats=6 RepeatLength=21 seed=GGCACATAAA Num.seqs=4 Similarity=0.586957
0 GGCACATAAACTACGTCGAGT

Consensus:

GGCACATAAACTACGTCGAGT

>Bacillus_Fam_1809_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000

GCF_001278705.1_ASM127870v1_genomic.fna_1:3026647-3026771 Satlength=125

Nr of Repeats=6 RepeatLength=21 seed=TTATGCGCGA Num.seqs=4

Similarity=0.693122

0

TTATGCGCGATCTTCCCTCGG

Consensus:

TTATGCGCGATCTTCCCTCGG

>Bacillus_Fam_1810_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000

GCF_001315065.1_ASM131506v1_genomic.fna_5:75663-75783 Satlength=121 Nr of

Repeats=4 RepeatLength=21 seed=AACAAGCACA Num.seqs=3 Similarity=0.601010

0 AACAAGCACAGCANGCAATTC

Consensus:

AACAAGCACAGCANGCAATTC

>Bacillus_Fam_1811_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000

GCF_001315165.1_ASM131516v1_genomic.fna_94:3047-3130 Satlength=84 Nr of

Repeats=4 RepeatLength=21 seed=TTTGCGAATA Num.seqs=3 Similarity=0.646465

0 TTTGCGAATAAACCATNNATT

Consensus:

TTTGCGAATAAACCATNNATT

>Bacillus_Fam_1812_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000

GCF_001420595.1_ASM142059v1_genomic.fna_11:777561-777645 Satlength=85 Nr

of Repeats=4 RepeatLength=21 seed=TGCTAGATAA Num.seqs=4

Similarity=0.642677

0 TGCTAGATAAATAGCTACAAT

Consensus:

TGCTAGATAAATAGCTACAAT

>Bacillus_Fam_1813_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000

GCF_001420715.1_ASM142071v1_genomic.fna_22:401748-401832 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=GCGGGATTAT Num.seqs=4
Similarity=0.703704
0 GCGGGATTATAGTAAAAATTC

Consensus:

GCGGGATTATAGTAAAAATTC

>Bacillus_Fam_1814_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001439635.1_ASM143963v1_genomic.fna_162:47575-47699 Satlength=125 Nr
of Repeats=5 RepeatLength=21 seed=TAATAGACAA Num.seqs=3
Similarity=0.537778
0 TAATAGACAAAATACTTNGGN

Consensus:

TAATAGACAAAATACTTNGGN

>Bacillus_Fam_1815_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_90:1-81 Satlength=81 Nr of
Repeats=4 RepeatLength=20 seed=CGACGCAAAT Num.seqs=4 Similarity=0.671958
0 CGACGCAAATAATCCAGTAAT

Consensus:

CGACGCAAATAATCCAGTAAT

>Bacillus_Fam_1816_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_105:333431-333536 Satlength=106
Nr of Repeats=5 RepeatLength=21 seed=TAGGGCACAA Num.seqs=5
Similarity=0.574603
TAGGGCACAAATTANTTCCANN 0

Consensus:

TAGGGCACAAATTANTTCCANN

>Bacillus_Fam_1817_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001439915.1_ASM143991v1_genomic.fna_122:184310-184415 Satlength=106
Nr of Repeats=5 RepeatLength=21 seed=ACCTCCTAGT Num.seqs=5
Similarity=0.961905
ACCTCCTAGTCCAACAGGAAA 0

Consensus:

ACCTCCTAGTCCAACAGGAAA

>Bacillus_Fam_1818_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001484965.1_ASM148496v1_genomic.fna_38:7986-8153 Satlength=168 Nr of
Repeats=7 RepeatLength=21 seed=GCGAGAATCC Num.seqs=6 Similarity=0.788889
0 GCGAGAATCCAGACAAGAGGA

Consensus:

GCGAGAATCCAGACAAGAGGA

>Bacillus_Fam_1819_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001584325.1_ASM158432v1_genomic.fna_23:115575-115659 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=GTCCTCCAAT Num.seqs=4
Similarity=0.814394
0 GTCCTCCAATGCTTCAACTCT

Consensus:

GTCCTCCAATGCTTCAACTCT

>Bacillus_Fam_1820_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001590785.1_ASM159078v1_genomic.fna_16:23682-23806 Satlength=125 Nr
of Repeats=6 RepeatLength=21 seed=GGAAGCGGAG Num.seqs=5
Similarity=0.898413
0 GGAAGCGGAGACGGAGATAGC

Consensus:

GGAAGCGGAGACGGAGATAGC

>Bacillus_Fam_1821_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_6:69823-70055 Satlength=233 Nr of
Repeats=10 RepeatLength=21 seed=GTTGCACCAG Num.seqs=6
Similarity=0.729101
0 GTTGCACCAGTTTGTACGGT

Consensus:

GTTGCACCAGTTTGTACGGT

>Bacillus_Fam_1822_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_57:20937-21147 Satlength=211 Nr
of Repeats=9 RepeatLength=21 seed=TGGCACAAAA Num.seqs=8

Similarity=0.649327
0 TGGCACAAAAGGATGTTGGGT

Consensus:

TGGCACAAAAGGATGTTGGGT

>Bacillus_Fam_1823_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_130:10418-10565 Satlength=148 Nr
of Repeats=7 RepeatLength=21 seed=TTGACGCACT Num.seqs=7
Similarity=0.576950
0 TTGACGCACTTGNAATTAA

Consensus:

TTGACGCACTTGNAATTAA

>Bacillus_Fam_1824_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591425.1_ASM159142v1_genomic.fna_153:1987-2338 Satlength=352 Nr of
Repeats=11 RepeatLength=21 seed=TTTATGTGGG Num.seqs=7
Similarity=0.476190
0 TTTATGTGTGCCNGTGAANCN

Consensus:

TTTATGTGTGCCNGTGAANCN

>Bacillus_Fam_1825_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591445.1_ASM159144v1_genomic.fna_5:214153-214237 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=CCGAAACCTG Num.seqs=4
Similarity=0.904762
0 CCGAAACCTGGGCCTCCTGGG

Consensus:

CCGAAACCTGGGCCTCCTGGG

>Bacillus_Fam_1826_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591465.1_ASM159146v1_genomic.fna_19:29474-29577 Satlength=104 Nr
of Repeats=5 RepeatLength=21 seed=TGCAAATAGA Num.seqs=3
Similarity=0.497585
0 TGCAAATAGAANGCANGAATN

Consensus:

TGCAAATAGAANGCANGAATN

>Bacillus_Fam_1827_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591465.1_ASM159146v1_genomic.fna_20:25050-25133 Satlength=84 Nr of
Repeats=4 RepeatLength=21 seed=TTTGGCCGGT Num.seqs=3 Similarity=0.585859
0 TTTGGCCGGTAAATTATGCAN

Consensus:

TTTGGCCGGTAAATTATGCAN

>Bacillus_Fam_1828_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591565.1_ASM159156v1_genomic.fna_44:15843-15969 Satlength=127 Nr
of Repeats=4 RepeatLength=21 seed=GAAGCTCTTC Num.seqs=3
Similarity=0.746032
0 GAAGCTCTTCGGACTGCGTTT

Consensus:

GAAGCTCTTCGGACTGCGTTT

>Bacillus_Fam_1829_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591585.1_ASM159158v1_genomic.fna_5:250479-251099 Satlength=621 Nr
of Repeats=9 RepeatLength=21 seed=TATCAGCCAA Num.seqs=8
Similarity=0.826028
0 TATCAGCCAAACTCGAGGGCT

Consensus:

TATCAGCCAAACTCGAGGGCT

>Bacillus_Fam_1830_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591665.1_ASM159166v1_genomic.fna_56:43606-43761 Satlength=156 Nr
of Repeats=5 RepeatLength=21 seed=AAATAGGTAG Num.seqs=4
Similarity=0.756614
0 AAATAGGTAGTAAGTGACCAT

Consensus:

AAATAGGTAGTAAGTGACCAT

>Bacillus_Fam_1831_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001591805.1_ASM159180v1_genomic.fna_38:45950-46055 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=TTTTGTTGAA Num.seqs=5

Similarity=0.703030
0 TTTTGTTGAATGGCACCTGGT

Consensus:

TTTTGTTGAATGGCACCTGGT

>Bacillus_Fam_1832_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001592005.1_ASM159200v1_genomic.fna_23:5049-5133 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=CGCCTTGACG Num.seqs=4 Similarity=0.915344
0 CGCCTTGACGGACTAGACCAA

Consensus:

CGCCTTGACGGACTAGACCAA

>Bacillus_Fam_1833_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:2331927-2332076 Satlength=150
Nr of Repeats=6 RepeatLength=21 seed=TTAGCGATTT Num.seqs=5
Similarity=0.606349 0
TTAGCGATTTNANACNGCCTA

Consensus:

TTAGCGATTTNANACNGCCTA

>Bacillus_Fam_1834_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001636315.1_ASM163631v1_genomic.fna_1:5159452-5159597 Satlength=146
Nr of Repeats=6 RepeatLength=21 seed=GACGGGTAAA Num.seqs=5
Similarity=0.568182 0
GACGGGTAAAATCNAAAANTT

Consensus:

GACGGGTAAAATCNAAAANTT

>Bacillus_Fam_1835_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001636335.1_ASM163633v1_genomic.fna_1:60506-60879 Satlength=374 Nr of
Repeats=18 RepeatLength=21 seed=GGCGAATAAA Num.seqs=15
Similarity=0.855480
0 GGCGAATAAAACAGTGAGCAT

Consensus:

GGCGAATAAAACAGTGAGCAT

>Bacillus_Fam_1836_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:402480-402564 Satlength=85 Nr
of Repeats=4 RepeatLength=21 seed=TCCTATCAA Num.seqs=4
Similarity=0.474638
0 TCCTATCAAAANAAGCGGAC

Consensus:

TCCTATCAAAANAAGCGGAC

>Bacillus_Fam_1837_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:537147-537252 Satlength=106 Nr
of Repeats=4 RepeatLength=21 seed=AATGATCGAA Num.seqs=3
Similarity=0.536232
0 AATGATCGAAANATCTCNAN

Consensus:

AATGATCGAAANATCTCNAN

>Bacillus_Fam_1838_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:4338946-4339051 Satlength=106
Nr of Repeats=5 RepeatLength=21 seed=AAATGTTGCA Num.seqs=3
Similarity=0.703704
AAATGTTGCACAAAAACGAAA

0

Consensus:

AAATGTTGCACAAAAACGAAA

>Bacillus_Fam_1839_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:4195211-4195333 Satlength=123
Nr of Repeats=5 RepeatLength=21 seed=GGACGAATTA Num.seqs=4
Similarity=0.765152
GGACGAATTATCTCCTGATTG

0

Consensus:

GGACGAATTATCTCCTGATTG

>Bacillus_Fam_1840_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001645705.1_ASM164570v1_genomic.fna_58:251245-252259 Satlength=1015
Nr of Repeats=41 RepeatLength=21 seed=ATTGCGCAAC Num.seqs=25

Similarity=0.654747 0
ATTGCGCGACTTTCATNTGGN

Consensus:

ATTGCGCGACTTTCATNTGGN

>Bacillus_Fam_1841_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001645705.1_ASM164570v1_genomic.fna_61:116393-116850 Satlength=458 Nr
of Repeats=22 RepeatLength=21 seed=AGTCGCGCAA Num.seqs=18
Similarity=0.733908 0
AGTCGCGCAATGCAGGTATAA

Consensus:

AGTCGCGCAATGCAGGTATAA

>Bacillus_Fam_1842_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_55:22587-22754 Satlength=168 Nr
of Repeats=6 RepeatLength=21 seed=TGACGGGATT Num.seqs=5
Similarity=0.506061
0 TGACGGGATTNCCNNTTCTTA

Consensus:

TGACGGGATTNCCNNTTCTTA

>Bacillus_Fam_1843_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_61:58107-58295 Satlength=189 Nr
of Repeats=6 RepeatLength=21 seed=TGAAGGGATT Num.seqs=4
Similarity=0.502645
0 TGAAGGGATTTTNCACACTTG

Consensus:

TGAAGGGATTTTNCACACTTG

>Bacillus_Fam_1844_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_64:41402-41486 Satlength=85 Nr of
Repeats=4 RepeatLength=21 seed=GCACGAACTC Num.seqs=4 Similarity=0.968254
0 GCACGAACTCCGAGCGTTTCC

Consensus:

GCACGAACTCCGAGCGTTTCC

>Bacillus_Fam_1845_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_2:319626-319913 Satlength=288 Nr
of Repeats=11 RepeatLength=21 seed=TGCAAATAAA Num.seqs=7
Similarity=0.477460 0
TGCAAATAAAANTNNTCAAGN

Consensus:

TGCAAATAAAANTNNTCAAGN

>Bacillus_Fam_1846_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_36:229235-229442 Satlength=208 Nr
of Repeats=10 RepeatLength=21 seed=TTATTTGCAG Num.seqs=9
Similarity=0.379630 0
TTATTTGCAGNNTTNAATNTN

Consensus:

TTATTTGCAGNNTTNAATNTN

>Bacillus_Fam_1847_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001889165.1_ASM188916v1_genomic.fna_1:3543299-3543404 Satlength=106
Nr of Repeats=5 RepeatLength=21 seed=TTTATTTTCG Num.seqs=5
Similarity=0.520833 0
TTTATTTTCGNNTTTCCTNGT

Consensus:

TTTATTTTCGNNTTTCCTNGT

>Bacillus_Fam_1848_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_001889165.1_ASM188916v1_genomic.fna_1:3636446-3636551 Satlength=106
Nr of Repeats=4 RepeatLength=21 seed=TTTATTTTCG Num.seqs=3
Similarity=0.512077 0
TTTATTTTCGNNTTCTACGCA

Consensus:

TTTATTTTCGNNTTCTACGCA

>Bacillus_Fam_1849_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_002009555.1_ASM200955v1_genomic.fna_561:6003-6229 Satlength=227 Nr of
Repeats=8 RepeatLength=21 seed=TCGTGCGAAT Num.seqs=5 Similarity=0.654545
0 TCGTGCGAATCATNTCGGAAT

Consensus:

TCGTGCGAATCATNTCGGAAT

>Bacillus_Fam_1850_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_002019645.1_ASM201964v1_genomic.fna_1:2245902-2246234 Satlength=333
Nr of Repeats=9 RepeatLength=21 seed=AATCCGGCGG Num.seqs=6
Similarity=0.548000 0
AATCCGGCGGATNTGAAGCAG

Consensus:

AATCCGGCGGATNTGAAGCAG

>Bacillus_Fam_1851_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:767787-767892 Satlength=106 Nr
of Repeats=4 RepeatLength=21 seed=ATTCGTCCAA Num.seqs=3
Similarity=0.564815
0 ATTCGTCCAAAATCCNGTAAC

Consensus:

ATTCGTCCAAAATCCNGTAAC

>Bacillus_Fam_1852_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_002019665.1_ASM201966v1_genomic.fna_1:1184140-1184299 Satlength=160
Nr of Repeats=6 RepeatLength=21 seed=TTGGACGAAT Num.seqs=5
Similarity=0.528986 0
TTGGACGAATNAGNGCGNGAA

Consensus:

TTGGACGAATNAGNGCGNGAA

>Bacillus_Fam_1853_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_9:8023-8157 Satlength=135
Nr of Repeats=4 RepeatLength=21 seed=TATTATCGAA Num.seqs=3
Similarity=0.550725 0
TATTATCGAAATCNANAAATT

Consensus:

TATTATCGAAATCNANAAATT

>Bacillus_Fam_1854_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_900094975.1_IMG-
taxon_2617270721_annotated_assembly_genomic.fna_13:445117-445197
Satlength=81 Nr of Repeats=4 RepeatLength=20 seed=GGCGCAATTA Num.seqs=4
Similarity=0.576720 0 GGCGCAATTAATTAGANAGTN

Consensus:

GGCGCAATTAATTAGANAGTN

>Bacillus_Fam_1855_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_900103955.1_IMG-
taxon_2617270767_annotated_assembly_genomic.fna_27:91618-91930
Satlength=313 Nr of Repeats=5 RepeatLength=21 seed=TTAGATGTTA Num.seqs=4
Similarity=0.798942 0 TTAGATGTTAGTATAGCGTGT

Consensus:

TTAGATGTTAGTATAGCGTGT

>Bacillus_Fam_1856_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_11:61167-61272
Satlength=106 Nr of Repeats=5 RepeatLength=21 seed=TCGTCTTCTT Num.seqs=5
Similarity=0.898413 0 TCGTCTTCTTCATGCGCGTGA

Consensus:

TCGTCTTCTTCATGCGCGTGA

>Bacillus_Fam_1857_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_900107275.1_IMG-
taxon_2675903024_annotated_assembly_genomic.fna_35:83306-83474
Satlength=169 Nr of Repeats=8 RepeatLength=21 seed=CGGCTTGGA Num.seqs=8
Similarity=0.768707 0 CGGCTTGGAACAAAGTCGA

Consensus:

CGGCTTGGAACAAAGTCGA

>Bacillus_Fam_1858_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_900156865.1_PRJEB18960_genomic.fna_3:2979413-2979928 Satlength=516 Nr
of Repeats=15 RepeatLength=21 seed=TTATGGGACA Num.seqs=11

Similarity=0.639669 0
TTATGGGACACTGGTTTCATN

Consensus:

TTATGGGACACTGGTTTCATN

>Bacillus_Fam_1859_21_1 Nr. of seq. 1 Alignment length(with gaps) = 21
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:3145660-3145883 Satlength=224
Nr of Repeats=5 RepeatLength=21 seed=TTCATTTCTT Num.seqs=4
Similarity=0.756614 0
TTCATTTCTTGTAGATCCCGC

Consensus:

TTCATTTCTTGTAGATCCCGC

>Bacillus_Fam_1860_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000175075.1_ASM17507v1_genomic.fna_29:81534-81653 Satlength=120 Nr of
Repeats=6 RepeatLength=20 seed=TTTCTTGATA Num.seqs=5 Similarity=0.561905
0 TTTCTTGATATANTGTNAAT

Consensus:

TTTCTTGATATANTGTNAAT

>Bacillus_Fam_1861_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000285535.1_ASM28553v1_genomic.fna_2:955930-956292 Satlength=363 Nr
of Repeats=14 RepeatLength=20 seed=TTTGCGTCAA Num.seqs=9
Similarity=0.588183
0 TTTGCGTCAACANCCACAGA

Consensus:

TTTGCGTCAACANCCACAGA

>Bacillus_Fam_1862_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000285535.1_ASM28553v1_genomic.fna_60:15-376 Satlength=362 Nr of
Repeats=18 RepeatLength=20 seed=ATTGCGTCT Num.seqs=17
Similarity=0.590463
0 ATTGCGTCNNTTCCNNCNG

Consensus:

ATTGCGTCNNTTCCNNCNG

>Bacillus_Fam_1863_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1625853-1626033 Satlength=181 Nr
of Repeats=9 RepeatLength=20 seed=TAATGAGGGT Num.seqs=9
Similarity=0.974074 0
TAATGAGGGTATTAACTTT

Consensus:

TAATGAGGGTATTAACTTT

>Bacillus_Fam_1864_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000429705.1_ASM42970v1_genomic.fna_2:323368-323473 Satlength=106 Nr
of Repeats=5 RepeatLength=21 seed=TTATCCATCA Num.seqs=3
Similarity=0.666667
0 TTATCCATCACTTCGGCCGG

Consensus:

TTATCCATCACTTCGGCCGG

>Bacillus_Fam_1865_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000612665.1_FF4_genomic.fna_66:43632-44026 Satlength=395 Nr of
Repeats=8 RepeatLength=21 seed=TTTACCGGCA Num.seqs=5 Similarity=0.461728
0 TTTACCGGCACTTTCACNAT

Consensus:

TTTACCGGCACTTTCACNAT

>Bacillus_Fam_1866_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_13:80293-80396
Satlength=104 Nr of Repeats=5 RepeatLength=20 seed=GTTACTTGCG Num.seqs=3
Similarity=0.592593 0
TTACTTGCGGTTGGGGNGCG

Consensus:

TTACTTGCGGTTGGGGNGCG

>Bacillus_Fam_1867_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000752395.1_Bacillus_andreraoultii_genomic.fna_12:210479-210580
Satlength=102 Nr of Repeats=5 RepeatLength=20 seed=TTTCCGAAGT Num.seqs=4
Similarity=0.562169 0
TTTCCGAAGTTGGCGTGT

Consensus:

TTTCCGAAGTTGGCGTGTTT

>Bacillus_Fam_1868_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_13:139600-139845 Satlength=246 Nr
of Repeats=5 RepeatLength=20 seed=TTTACGTGCC Num.seqs=4
Similarity=0.593915
0 TTTACGTGCCAAATTATAGA

Consensus:

TTTACGTGCCAAATTATAGA

>Bacillus_Fam_1869_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_001420595.1_ASM142059v1_genomic.fna_11:1231069-1231171 Satlength=103
Nr of Repeats=5 RepeatLength=20 seed=TATTTGCAAA Num.seqs=3
Similarity=0.644444 0
TAATTGCAAAAATCCTTGAA

Consensus:

TAATTGCAAAAATCCTTGAA

>Bacillus_Fam_1870_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_22:116628-116728 Satlength=101 Nr
of Repeats=5 RepeatLength=20 seed=TACATTAAAG Num.seqs=5
Similarity=0.933333 0
TACATTAAAGTTCACACTT

Consensus:

TACATTAAAGTTCACACTT

>Bacillus_Fam_1871_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_2:476021-476159 Satlength=139 Nr
of Repeats=6 RepeatLength=20 seed=GGCGCAAAAA Num.seqs=5
Similarity=0.590909
0 GGCGCAAAAATCGAATGAGA

Consensus:

GGCGCAAAAATCGAATGAGA

>Bacillus_Fam_1872_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:867035-867350 Satlength=316 Nr
of Repeats=4 RepeatLength=20 seed=GCGAATATAT Num.seqs=3
Similarity=0.600000
0 GCGAATATATTCNTATNACG

Consensus:

GCGAATATATTCNTATNACG

>Bacillus_Fam_1873_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:349315-349619 Satlength=305 Nr
of Repeats=14 RepeatLength=20 seed=CGAATAAATC Num.seqs=9
Similarity=0.758377 0
CGAATAAATCAGAGTAAGGT

Consensus:

CGAATAAATCAGAGTAAGGT

>Bacillus_Fam_1874_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_64:202939-203079 Satlength=141 Nr
of Repeats=6 RepeatLength=20 seed=TTATCCTGAA Num.seqs=5
Similarity=0.760000 0
TTATCCTGAAATCTATGGGT

Consensus:

TTATCCTGAAATCTATGGGT

>Bacillus_Fam_1875_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_66:119260-119427 Satlength=168 Nr
of Repeats=6 RepeatLength=21 seed=TGACGGGATT Num.seqs=5
Similarity=0.461538 0
TGACGGGATTTTAGTNGTTA

Consensus:

TGACGGGATTTTAGTNGTTA

>Bacillus_Fam_1876_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_67:289399-289588 Satlength=190 Nr
of Repeats=8 RepeatLength=21 seed=ATTGTGACTT Num.seqs=7
Similarity=0.590608 0
ATTGTGACTTTTCCATNGTT

Consensus:

ATTGTGACTTTTCCATNGTT

>Bacillus_Fam_1877_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20

Alignment score = 0.000000

GCF_001887185.1_ASM188718v1_genomic.fna_259:169310-169414 Satlength=105

Nr of Repeats=4 RepeatLength=20 seed=CGAGTTTTTT Num.seqs=3

Similarity=0.671958

0

CGAGTTTTTTTAGGTCAGGAG

Consensus:

CGAGTTTTTTTAGGTCAGGAG

>Bacillus_Fam_1878_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20

Alignment score = 0.000000

GCF_002019665.1_ASM201966v1_genomic.fna_1:4193194-4193625 Satlength=432

Nr of Repeats=21 RepeatLength=21 seed=TTTATGAGCC Num.seqs=16

Similarity=0.603684

0

TTTATGAGCCANTACCTCTN

Consensus:

TTTATGAGCCANTACCTCTN

>Bacillus_Fam_1879_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20

Alignment score = 0.000000

GCF_002019705.1_ASM201970v1_genomic.fna_1:2674002-2674287 Satlength=286

Nr of Repeats=14 RepeatLength=20 seed=CCTGAGCTCC Num.seqs=9

Similarity=0.874074

0

CCTGAGCTCCTCTCTCTAAT

Consensus:

CCTGAGCTCCTCTCTCTAAT

>Bacillus_Fam_1880_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20

Alignment score = 0.000000

GCF_900103955.1_IMG-

taxon_2617270767_annotated_assembly_genomic.fna_7:15309-15864

Satlength=556 Nr of Repeats=5 RepeatLength=20 seed=AGTAAAATAG Num.seqs=3

Similarity=0.955556

0 AGTAAAATAGCGGGCGCGAC

Consensus:

AGTAAAATAGCGGGCGCGAC

>Bacillus_Fam_1881_20_1 Nr. of seq. 1 Alignment length(with gaps) = 20
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:3436401-3436481 Satlength=81 Nr
of Repeats=4 RepeatLength=20 seed=TTTATCCGTA Num.seqs=4
Similarity=0.547980 0
TTTATCCGTAAGAATTTTCAN

Consensus:

TTTATCCGTAAGAATTTTCAN

>Bacillus_Fam_1882_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1363446-1363522 Satlength=77 Nr
of Repeats=4 RepeatLength=19 seed=TATATTCTCT Num.seqs=4
Similarity=0.918129
0 TATATTCTCTACGTTATTA

Consensus:

TATATTCTCTACGTTATTA

>Bacillus_Fam_1883_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1618267-1618343 Satlength=77 Nr
of Repeats=4 RepeatLength=19 seed=CTTGATTGAG Num.seqs=4
Similarity=0.929825
0 CTTGATTGAGAATCCTCAG

Consensus:

CTTGATTGAGAATCCTCAG

>Bacillus_Fam_1884_19_1 Nr. of seq. 1 Alignment length(with gaps) = 19
Alignment score = 0.000000
GCF_001889165.1_ASM188916v1_genomic.fna_1:874722-874938 Satlength=217 Nr
of Repeats=9 RepeatLength=18 seed=TCATCCTCAG Num.seqs=6
Similarity=0.696491
0 TCATCCTCAGAATGAGTGC

Consensus:

TCATCCTCAGAATGAGTGC

>Bacillus_Fam_1885_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000005825.2_ASM582v2_genomic.fna_1:3039924-3040044 Satlength=121 Nr
of Repeats=6 RepeatLength=18 seed=GGCAATGGAA Num.seqs=5
Similarity=1.000000
0 GGCAATGGAAACGGGAAT

Consensus:

GGCAATGGAAACGGGAAT

>Bacillus_Fam_1886_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000008505.1_ASM850v1_genomic.fna_1:4344849-4345011 Satlength=163 Nr
of Repeats=9 RepeatLength=18 seed=CGTCTGGTTG Num.seqs=9
Similarity=0.909465
0 CGTCTGGTTGTTTGTCTC

Consensus:

CGTCTGGTTGTTTGTCTC

>Bacillus_Fam_1887_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000025805.1_ASM2580v1_genomic.fna_1:1137271-1137343 Satlength=73 Nr
of Repeats=4 RepeatLength=18 seed=TCAAAACCGT Num.seqs=4
Similarity=1.000000
0 TCAAAACCGTAGTTAAGG

Consensus:

TCAAAACCGTAGTTAAGG

>Bacillus_Fam_1888_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000025805.1_ASM2580v1_genomic.fna_1:2256750-2257164 Satlength=415 Nr
of Repeats=23 RepeatLength=18 seed=CCTGGTATGG Num.seqs=23
Similarity=0.839054 0
CCTGGTATGGGCGGATCA

Consensus:

CCTGGTATGGGCGGATCA

>Bacillus_Fam_1889_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:1820901-1821153 Satlength=253 Nr
of Repeats=13 RepeatLength=18 seed=TGTGTTTACG Num.seqs=12
Similarity=0.852974 0
TGTGTTTACGGCATGTTG

Consensus:

TGTGTTTACGGCATGTTG

>Bacillus_Fam_1890_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:4034040-4034130 Satlength=91 Nr
of Repeats=5 RepeatLength=18 seed=TGACCGTGAT Num.seqs=5
Similarity=0.822222
0 TGACCGTGATGGACGTGA

Consensus:

TGACCGTGATGGACGTGA

>Bacillus_Fam_1891_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000242895.2_ASM24289v3_genomic.fna_1:1111316-1112777 Satlength=1462
Nr of Repeats=65 RepeatLength=18 seed=GTTGTCGTCG Num.seqs=47
Similarity=0.825813 0
GTTGTCGTCGGTGCGGCN

Consensus:

GTTGTCGTCGGTGCGGCN

>Bacillus_Fam_1892_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_57:3327-3507 Satlength=181 Nr of
Repeats=10 RepeatLength=18 seed=GTAACTGAG Num.seqs=10
Similarity=0.965432
0 GTAACTGAGGAAGAAGG

Consensus:

GTAACTGAGGAAGAAGG

>Bacillus_Fam_1893_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000307875.1_BABA1.0_genomic.fna_120:4680-4752 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=AAAGAACAAC Num.seqs=4 Similarity=0.851852
0 AAAGAACAACCAATCATC

Consensus:

AAAGAACAACCAATCATC

>Bacillus_Fam_1894_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000321185.1_ASM32118v1_genomic.fna_87:138564-139038 Satlength=475 Nr
of Repeats=26 RepeatLength=18 seed=GATGCCTGGT Num.seqs=25
Similarity=0.892839 0
GATGCCTGGTGGTGAAT

Consensus:

GATGCCTGGTGGTGAAT

>Bacillus_Fam_1895_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:14090-14162 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=TAATTAGTTA Num.seqs=4 Similarity=0.802469
0 TAATTAGTTACCAAGCAA

Consensus:

TAATTAGTTACCAAGCAA

>Bacillus_Fam_1896_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000429725.1_ASM42972v1_genomic.fna_19:52932-53076 Satlength=145 Nr of
Repeats=8 RepeatLength=18 seed=TGCTGCTGAA Num.seqs=8 Similarity=0.928571
0 TGCTGCTGAAGAGCAGGC

Consensus:

TGCTGCTGAAGAGCAGGC

>Bacillus_Fam_1897_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_12:155300-155504 Satlength=205 Nr
of Repeats=10 RepeatLength=18 seed=GGAAAGAGAA Num.seqs=9
Similarity=0.843621
GGAAAGAGAACGCGAGCG 0

Consensus:

GGAAAGAGAACGCGAGCG

>Bacillus_Fam_1898_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000430785.1_ASM43078v1_genomic.fna_4:98178-98286 Satlength=109 Nr of
Repeats=6 RepeatLength=18 seed=CATCTAAACC Num.seqs=6 Similarity=0.876543
0 CATCTAAACCAACTACAG

Consensus:

CATCTAAACCAACTACAG

>Bacillus_Fam_1899_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_000430785.1_ASM43078v1_genomic.fna_13:56715-57603 Satlength=889 Nr of
Repeats=13 RepeatLength=18 seed=AGAGCGTTTA Num.seqs=9
Similarity=0.905350
0 AGAGCGTTTAGACTGCTT

Consensus:

AGAGCGTTTAGACTGCTT

>Bacillus_Fam_1900_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_000496285.1_ASM49628v1_genomic.fna_1:3550735-3550825 Satlength=91 Nr of
Repeats=5 RepeatLength=18 seed=TATTATGAAT Num.seqs=5
Similarity=0.911111
0 TATTATGAATAAAGAATC

Consensus:

TATTATGAATAAAGAATC

>Bacillus_Fam_1901_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_000706725.1_ASM70672v1_genomic.fna_1:3385744-3385960 Satlength=217 Nr of
Repeats=10 RepeatLength=18 seed=AGCTCTTGAA Num.seqs=9
Similarity=0.827160
AGCTCTTGAAGACGACAC 0

Consensus:

AGCTCTTGAAGACGACAC

>Bacillus_Fam_1902_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_000712595.1_ASM71259v1_genomic.fna_17:58333-58441 Satlength=109 Nr of
Repeats=6 RepeatLength=18 seed=CACGGACATC Num.seqs=6 Similarity=0.846914
0 CACGGACATCACCATGGC

Consensus:

CACGGACATCACCATGGC

>Bacillus_Fam_1903_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_000712615.1_ASM71261v1_genomic.fna_14:133-205 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=CCTAAGGACC Num.seqs=4 Similarity=0.888889
0 CCTAAGGACCCTATAGAC

Consensus:

CCTAAGGACCCCTATAGAC

>Bacillus_Fam_1904_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000724485.1_ASM72448v1_genomic.fna_1:375647-375902 Satlength=256 Nr
of Repeats=14 RepeatLength=18 seed=CCAGGACAGC Num.seqs=13
Similarity=0.856600
CCAGGACAGCCAGGCANC

0

Consensus:

CCAGGACAGCCAGGCANC

>Bacillus_Fam_1905_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000751775.1_A1A_genomic.fna_98:19034-19286 Satlength=253 Nr of
Repeats=14 RepeatLength=18 seed=TCACCTGGTT Num.seqs=14
Similarity=0.844526
0 TCACCTGGTTCTTCGTTA

Consensus:

TCACCTGGTTCTTCGTTA

>Bacillus_Fam_1906_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_158:156695-156902 Satlength=208 Nr
of Repeats=8 RepeatLength=18 seed=AGCAGAGGGT Num.seqs=7
Similarity=0.795414
AGCAGAGGGTCAAAAGGC

0

Consensus:

AGCAGAGGGTCAAAAGGC

>Bacillus_Fam_1907_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_162:138323-138431 Satlength=109 Nr
of Repeats=6 RepeatLength=18 seed=CACTAGCCGT Num.seqs=6
Similarity=0.801170
CACTAGCCGTCGTCGCTT

0

Consensus:

CACTAGCCGTCGTCGCTT

>Bacillus_Fam_1908_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_000775975.1_ASM77597v1_genomic.fna_1:4349695-4349794 Satlength=100 Nr
of Repeats=6 RepeatLength=18 seed=TCTTGTTTGT Num.seqs=4
Similarity=0.913580 0
TCTTGTTTGTCCCTGTTTA

Consensus:

TCTTGTTTGTCCCTGTTTA

>Bacillus_Fam_1909_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_001278705.1_ASM127870v1_genomic.fna_1:501198-501288 Satlength=91 Nr
of Repeats=5 RepeatLength=18 seed=AGCCAGGCC Num.seqs=5
Similarity=0.925926
0 AGCCAGGCCCGGATCCGC

Consensus:

AGCCAGGCCCGGATCCGC

>Bacillus_Fam_1910_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_001315085.1_ASM131508v1_genomic.fna_3:122565-122745 Satlength=181 Nr
of Repeats=10 RepeatLength=18 seed=AAGCTCTTGG Num.seqs=10
Similarity=0.965432 0
AAGCTCTTGGTCTACATC

Consensus:

AAGCTCTTGGTCTACATC

>Bacillus_Fam_1911_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_83:56856-56928 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=TGGCGTTTGA Num.seqs=4 Similarity=0.888889
0 TGGCGTTTGATTATTACC

Consensus:

TGGCGTTTGATTATTACC

>Bacillus_Fam_1912_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000

GCF_001439915.1_ASM143991v1_genomic.fna_105:175228-175444 Satlength=217
Nr of Repeats=10 RepeatLength=18 seed=GGATCAGGAA Num.seqs=9
Similarity=0.893004 0
GGATCAGGAAACGCGAA

Consensus:

GGATCAGGAAACGGCGAA

>Bacillus_Fam_1913_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_001584325.1_ASM158432v1_genomic.fna_11:35994-36075 Satlength=82 Nr of
Repeats=5 RepeatLength=18 seed=CGTTCGCACC Num.seqs=3 Similarity=0.802469
0 CGTTCGCACCGTTCGCGT

Consensus:

CGTTCGCACCGTTCGCGT

>Bacillus_Fam_1914_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_001590785.1_ASM159078v1_genomic.fna_7:4154-4364 Satlength=211 Nr of
Repeats=11 RepeatLength=18 seed=TCATCTCCTC Num.seqs=10
Similarity=0.957202
0 TCATCTCCTCCTGTTCCG

Consensus:

TCATCTCCTCCTGTTCCG

>Bacillus_Fam_1915_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_001591665.1_ASM159166v1_genomic.fna_33:162141-162213 Satlength=73 Nr
of Repeats=4 RepeatLength=18 seed=ATCACTGACA Num.seqs=4
Similarity=0.888889
0 ATCACTGACACCATTGAT

Consensus:

ATCACTGACACCATTGAT

>Bacillus_Fam_1916_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_001636425.1_ASM163642v1_genomic.fna_1:588164-588470 Satlength=307 Nr
of Repeats=12 RepeatLength=18 seed=TGCCTTGACC Num.seqs=11
Similarity=0.846465
TGCCTTGACCGCTGCCAT 0

Consensus:

TGCCTTGACCGCTGCCAT

>Bacillus_Fam_1917_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_001645555.1_ASM164555v1_genomic.fna_1:264316-264442 Satlength=127 Nr
of Repeats=5 RepeatLength=18 seed=GTTGTTCTCA Num.seqs=3

Similarity=0.802469
0 GTTGTTCCTCAGTTTTTGC

Consensus:

GTTGTTCCTCAGTTTTTGC

>Bacillus_Fam_1918_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_001645685.2_ASM164568v2_genomic.fna_1:2895676-2895748 Satlength=73 Nr
of Repeats=4 RepeatLength=18 seed=GCTGCATTTG Num.seqs=4
Similarity=0.851852 0
GCTGCATTTGCGGTGTCG

Consensus:

GCTGCATTTGCGGTGTCG

>Bacillus_Fam_1919_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_001648575.1_ASM164857v1_genomic.fna_66:20878-20950 Satlength=73 Nr of
Repeats=4 RepeatLength=18 seed=TCTTCCATGT Num.seqs=4 Similarity=0.802469
0 TCTTCCATGTTTGTATCA

Consensus:

TCTTCCATGTTTGTATCA

>Bacillus_Fam_1920_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_001712755.1_ASM171275v1_genomic.fna_1:278428-278518 Satlength=91 Nr
of Repeats=4 RepeatLength=18 seed=GTCCATGGGG Num.seqs=3
Similarity=0.802469
0 GTCCATGGGGCTGGGGCC

Consensus:

GTCCATGGGGCTGGGGCC

>Bacillus_Fam_1921_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_002019595.1_ASM201959v1_genomic.fna_1:4176749-4176929 Satlength=181
Nr of Repeats=8 RepeatLength=18 seed=CCTTGCATCA Num.seqs=7
Similarity=0.978836 0
CCTTGCATCATCGGCTGG

Consensus:

CCTTGCATCATCGGCTGG

>Bacillus_Fam_1922_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_900093775.1_EVONIK_BGLY_genomic.fna_1:1113432-1113558 Satlength=127
Nr of Repeats=5 RepeatLength=18 seed=CAGCTCCAGC Num.seqs=3
Similarity=0.950617 0
CAGCTCCAGCAGCTTGAA

Consensus:

CAGCTCCAGCAGCTTGAA

>Bacillus_Fam_1923_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_900093775.1_EVONIK_BGLY_genomic.fna_1:1232676-1232982 Satlength=307
Nr of Repeats=16 RepeatLength=18 seed=GAGAAAAGCA Num.seqs=15
Similarity=0.950617 0
GAGAAAAGCAAGGAGCAC

Consensus:

GAGAAAAGCAAGGAGCAC

>Bacillus_Fam_1924_18_1 Nr. of seq. 1 Alignment length(with gaps) = 18
Alignment score = 0.000000
GCF_900109925.1_IMG-
taxon_2651870116_annotated_assembly_genomic.fna_16:169169-169439
Satlength=271 Nr of Repeats=9 RepeatLength=18 seed=CCTGGTTGCG Num.seqs=7
Similarity=0.802840 0 CCTGGTTGCGGNGCAAAG

Consensus:

CCTGGTTGCGGNGCAAAG

>Bacillus_Fam_1925_17_1 Nr. of seq. 1 Alignment length(with gaps) = 17
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_3:53390-53458 Satlength=69 Nr of
Repeats=4 RepeatLength=17 seed=ATGATGCAAAA Num.seqs=4 Similarity=0.960784
0 ATGATGCAAAAAAGACG

Consensus:

ATGATGCAAAAAAGACG

>Bacillus_Fam_1926_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:5573108-5573288 Satlength=181 Nr
of Repeats=12 RepeatLength=15 seed=GTAACAATGA Num.seqs=12
Similarity=0.894949 0
GTAACAATGAACCAA

Consensus:

GTAACAATGAACCAA

>Bacillus_Fam_1927_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000242895.2_ASM24289v3_genomic.fna_1:2772134-2772299 Satlength=166 Nr of
Repeats=10 RepeatLength=15 seed=GCAGCAGTTC Num.seqs=9
Similarity=0.829630 0
GCAGCAGTTCNCGGC

Consensus:

GCAGCAGTTCNCGGC

>Bacillus_Fam_1928_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000292245.2_ASM29224v2_genomic.fna_7:15608-15698 Satlength=91 Nr of
Repeats=6 RepeatLength=15 seed=GGATCTTCTT Num.seqs=6 Similarity=0.638562
0 GGATCTTCTTTNACC

Consensus:

GGATCTTCTTTNACC

>Bacillus_Fam_1929_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000307875.1_BABA1.0_genomic.fna_55:97122-97182 Satlength=61 Nr of
Repeats=4 RepeatLength=15 seed=AATAATGGCA Num.seqs=4 Similarity=0.896296
0 AATAATGGCAACGGC

Consensus:

AATAATGGCAACGGC

>Bacillus_Fam_1930_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1522649-1522889 Satlength=241 Nr
of Repeats=16 RepeatLength=15 seed=TATTCGCTCC Num.seqs=16
Similarity=0.870370 0
TATTCGCTCCAGTGC

Consensus:

TATTCGCTCCAGTGC

>Bacillus_Fam_1931_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000

GCF_000331575.1_ASM33157v1_genomic.fna_2:602668-602743 Satlength=76 Nr of Repeats=4 RepeatLength=15 seed=ATCACGAATT Num.seqs=3 Similarity=1.000000
13 CACGAATTCTATAAT

Consensus:

ATCACGAATTCTATA

>Bacillus_Fam_1932_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000

GCF_000331575.1_ASM33157v1_genomic.fna_4:168656-168731 Satlength=76 Nr of Repeats=5 RepeatLength=15 seed=ATTTCTCCGC Num.seqs=5 Similarity=0.813333
0 ATTTCTCCGCTTGGC

Consensus:

ATTTCTCCGCTTGGC

>Bacillus_Fam_1933_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000

GCF_000331575.1_ASM33157v1_genomic.fna_6:23405-23463 Satlength=59 Nr of Repeats=4 RepeatLength=15 seed=ATTGTAAAAA Num.seqs=3 Similarity=1.000000
0 ATTGTAAAAATAAAT

Consensus:

ATTGTAAAAATAAAT

>Bacillus_Fam_1934_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000

GCF_000374345.1_ASM37434v1_genomic.fna_6:64384-64486 Satlength=103 Nr of Repeats=4 RepeatLength=15 seed=TTCAAGTTCA Num.seqs=3 Similarity=1.000000
0 TTCAAGTTCAAGCAA

Consensus:

TTCAAGTTCAAGCAA

>Bacillus_Fam_1935_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000

GCF_000474275.1_Bmar1.0_genomic.fna_8:95892-95952 Satlength=61 Nr of Repeats=4 RepeatLength=15 seed=AGATTGAGTA Num.seqs=4 Similarity=1.000000
0 AGATTGAGTAAACAG

Consensus:

AGATTGAGTAAACAG

>Bacillus_Fam_1936_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000612625.1_JCE_genomic.fna_2:32740-32845 Satlength=106 Nr of
Repeats=7 RepeatLength=15 seed=GCTGGTGCCT Num.seqs=7 Similarity=0.898413
0 GCTGGTGCCTTCGCT

Consensus:

GCTGGTGCCTTCGCT

>Bacillus_Fam_1937_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_19:633-873 Satlength=241 Nr of
Repeats=16 RepeatLength=15 seed=TTAATTGGTG Num.seqs=16
Similarity=0.873333
0 TTAATTGGTGCTNCT

Consensus:

TTAATTGGTGCTNCT

>Bacillus_Fam_1938_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000759675.1_ASM75967v1_genomic.fna_19:225767-226489 Satlength=723 Nr
of Repeats=13 RepeatLength=15 seed=TGAACTTCTT Num.seqs=10
Similarity=0.952593
TGAACTTCTTATTTT 0

Consensus:

TGAACTTCTTATTTT

>Bacillus_Fam_1939_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000787375.1_ASM78737v1_genomic.fna_1:295361-295436 Satlength=76 Nr of
Repeats=4 RepeatLength=15 seed=TTCATCGGTT Num.seqs=3 Similarity=0.881481
5 GCTGGTTCATCGGTT

Consensus:

TTCATCGGTTGCTGG

>Bacillus_Fam_1940_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_000812025.2_ASM81202v2_genomic.fna_59:10143-10233 Satlength=91 Nr of
Repeats=5 RepeatLength=15 seed=ATGCATGAGA Num.seqs=4 Similarity=0.911111
0 ATGCATGAGAACACC

Consensus:

ATGCATGAGAACACC

>Bacillus_Fam_1941_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_001420715.1_ASM142071v1_genomic.fna_24:95921-96146 Satlength=226 Nr
of Repeats=14 RepeatLength=15 seed=AGACGTTCTA Num.seqs=13
Similarity=0.831339
AGACGTTCTAGTAGA

0

Consensus:

AGACGTTCTAGTAGA

>Bacillus_Fam_1942_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_001590785.1_ASM159078v1_genomic.fna_7:40479-40902 Satlength=424 Nr of
Repeats=8 RepeatLength=15 seed=TCTCCGTGCT Num.seqs=6 Similarity=0.875556
0 TCTCCGTGCTCATGG

Consensus:

TCTCCGTGCTCATGG

>Bacillus_Fam_1943_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_001591665.1_ASM159166v1_genomic.fna_29:1963-2053 Satlength=91 Nr of
Repeats=4 RepeatLength=15 seed=GAAGTGTTCC Num.seqs=3 Similarity=1.000000
0 GAAGTGTTCCGTCTC

Consensus:

GAAGTGTTCCGTCTC

>Bacillus_Fam_1944_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_001591805.1_ASM159180v1_genomic.fna_17:30976-31126 Satlength=151 Nr
of Repeats=10 RepeatLength=15 seed=CAACCGATCC Num.seqs=10
Similarity=0.899259
CAACCGATCCAGGAC

0

Consensus:

CAACCGATCCAGGAC

>Bacillus_Fam_1945_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_001636325.1_ASM163632v1_genomic.fna_1:2446901-2447021 Satlength=121
Nr of Repeats=7 RepeatLength=15 seed=AATCCTGGAC Num.seqs=6


```
Similarity=0.946667 0
AATCCTGGACCTCCA

*****
Consensus:

AATCCTGGACCTCCA

>Bacillus_Fam_1946_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_002019595.1_ASM201959v1_genomic.fna_1:1565861-1565951 Satlength=91 Nr
of Repeats=6 RepeatLength=15 seed=CCGGGGAAAC Num.seqs=6
Similarity=0.946667 0
CCGGGGAAACCGCCA

*****
Consensus:

CCGGGGAAACCGCCA

>Bacillus_Fam_1947_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_002019635.1_ASM201963v1_genomic.fna_1:1407148-1407343 Satlength=196
Nr of Repeats=12 RepeatLength=15 seed=CACTGATGAT Num.seqs=11
Similarity=0.938586 0
CACTGATGATCCGGG

*****
Consensus:

CACTGATGATCCGGG

>Bacillus_Fam_1948_15_1 Nr. of seq. 1 Alignment length(with gaps) = 15
Alignment score = 0.000000
GCF_900156875.1_PRJEB18969_genomic.fna_11:2364715-2365012 Satlength=298
Nr of Repeats=8 RepeatLength=15 seed=TGCATCAT TG Num.seqs=7
Similarity=0.718254 0
TGCATCAT TGGTGAT

*****
Consensus:

TGCATCAT TGGTGAT

>Bacillus_Fam_1949_14_1 Nr. of seq. 1 Alignment length(with gaps) = 14
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1707310-1707394 Satlength=85 Nr
of Repeats=6 RepeatLength=14 seed=ATTTTG TAGT Num.seqs=6
Similarity=0.917460
0 ATTTTG TAGTCGTG

*****
Consensus:
```

ATTTTGTAGTCGTG

>Bacillus_Fam_1950_13_1 Nr. of seq. 1 Alignment length(with gaps) = 13
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_3:37579-37631 Satlength=53 Nr of
Repeats=4 RepeatLength=13 seed=TACTAGGAGA Num.seqs=4 Similarity=0.948718
0 TACTAGGAGACAG

Consensus:

TACTAGGAGACAG

>Bacillus_Fam_1951_13_1 Nr. of seq. 1 Alignment length(with gaps) = 13
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_6:130918-130983 Satlength=66 Nr of
Repeats=5 RepeatLength=13 seed=AGTGTTTCAGG Num.seqs=5 Similarity=1.000000
0 AGTGTTTCAGGATA

Consensus:

AGTGTTTCAGGATA

>Bacillus_Fam_1952_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000161455.1_ASM16145v1_genomic.fna_1:175339-175456 Satlength=118 Nr
of Repeats=5 RepeatLength=12 seed=CGTGATGGTA Num.seqs=3
Similarity=0.851852
0 CGTGATGGTAAT

Consensus:

CGTGATGGTAAT

>Bacillus_Fam_1953_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000242895.2_ASM24289v3_genomic.fna_1:2189079-2189571 Satlength=493 Nr
of Repeats=39 RepeatLength=12 seed=CGTTCAAGCC Num.seqs=37
Similarity=0.830831 0
CGTTCAAGCCGT

Consensus:

CGTTCAAGCCGT

>Bacillus_Fam_1954_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000307875.1_BABA1.0_genomic.fna_97:105197-105245 Satlength=49 Nr of
Repeats=4 RepeatLength=12 seed=CAAATATGAT Num.seqs=4 Similarity=1.000000
0 CAAATATGATGC

Consensus:

CAAATATGATGC

>Bacillus_Fam_1955_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1702114-1702162 Satlength=49 Nr
of Repeats=4 RepeatLength=12 seed=CGTTGTATTA Num.seqs=4
Similarity=1.000000
0 CGTTGTATTATT

Consensus:

CGTTGTATTATT

>Bacillus_Fam_1956_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_4:145562-145634 Satlength=73 Nr of
Repeats=6 RepeatLength=12 seed=ATGCAAACCTC Num.seqs=6 Similarity=0.731624
0 ATGCAAACCTCTA

Consensus:

ATGCAAACCTCTA

>Bacillus_Fam_1957_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000380245.2_ASM38024v2_genomic.fna_12:2893696-2893756 Satlength=61 Nr
of Repeats=5 RepeatLength=12 seed=CTTTTTTACA Num.seqs=5
Similarity=1.000000 0
CTTTTTTACAAC

Consensus:

CTTTTTTACAAC

>Bacillus_Fam_1958_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000429725.1_ASM42972v1_genomic.fna_2:378953-379145 Satlength=193 Nr
of Repeats=12 RepeatLength=12 seed=ACGACATGGA Num.seqs=8
Similarity=0.773810
0 ACGACATGGACA

Consensus:

ACGACATGGACA

>Bacillus_Fam_1959_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000430765.1_ASM43076v1_genomic.fna_4:178616-178796 Satlength=181 Nr
of Repeats=9 RepeatLength=12 seed=TGGTTCCATT Num.seqs=7
Similarity=0.883598
0 TGGTTCCATTGC

Consensus:

TGGTTCCATTGC

>Bacillus_Fam_1960_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000751775.1_A1A_genomic.fna_68:68366-68414 Satlength=49 Nr of
Repeats=4 RepeatLength=12 seed=TCTTTGATTC Num.seqs=4 Similarity=0.944444
0 TCTTTGATTCCT

Consensus:

TCTTTGATTCCT

>Bacillus_Fam_1961_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_000752035.1_Bacillus_rubiinfantis_genomic.fna_13:49986-50062
Satlength=77 Nr of Repeats=5 RepeatLength=12 seed=ATTGGTGCCT Num.seqs=3
Similarity=1.000000 0
ATTGGTGCCTTT

Consensus:

ATTGGTGCCTTT

>Bacillus_Fam_1962_12_1 Nr. of seq. 1 Alignment length(with gaps) = 12
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:3481278-3481350 Satlength=73 Nr
of Repeats=6 RepeatLength=12 seed=GGGCGTTCTT Num.seqs=6
Similarity=1.000000 0
GGGCGTTCTTCG

Consensus:

GGGCGTTCTTCG

>Bacillus_Fam_1963_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_1:1378343-1378409 Satlength=67 Nr
of Repeats=6 RepeatLength=11 seed=GCACTATTTT Num.seqs=6
Similarity=0.935354
0 GCACTATTTTC

Consensus:

GCACTATTTTC

>Bacillus_Fam_1964_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
GCF_000831065.1_ASM83106v1_genomic.fna_1:2961625-2961669 Satlength=45 Nr
of Repeats=4 RepeatLength=11 seed=AGGGGCTTAG Num.seqs=4
Similarity=1.000000
0 AGGGGCTTAGA

Consensus:

AGGGGCTTAGA

>Bacillus_Fam_1965_11_1 Nr. of seq. 1 Alignment length(with gaps) = 11
Alignment score = 0.000000
GCF_001636345.1_ASM163634v1_genomic.fna_1:595400-595488 Satlength=89 Nr
of Repeats=8 RepeatLength=11 seed=CCAAAAACCG Num.seqs=8
Similarity=1.000000
0 CCAAAAACCGC

Consensus:

CCAAAAACCGC

>Bacillus_Fam_1966_10_1 Nr. of seq. 1 Alignment length(with gaps) = 10
Alignment score = 0.000000
GCF_000331575.1_ASM33157v1_genomic.fna_2:525802-525852 Satlength=51 Nr of
Repeats=4 RepeatLength=10 seed=TTGTCGCGGA Num.seqs=3 Similarity=1.000000
0 TTGTCGCGGA

Consensus:

TTGTCGCGGA