Table S6a. Archaea satellite families

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>Fam_1_126_16  Nr. of seq. 16 Alignment length(with gaps) = 136 Alignment score = 0.626532
GTAATTGACACtGCaACaAAcAatGTTACAGCcACnGTganTGTAGGAaantaTCCTTgnGGAGTTGCAGTcAacCCGGaTGGAACAAAgGTATATGTGgCgAAntgnaGn
nAgcAacAcTGTcTCT
>Fam_2_12_13  Nr. of seq. 13 Alignment length(with gaps) = 13 Alignment score = 0.648258
 AtTATTATTAgt
>Fam_3_12_10  Nr. of seq. 10 Alignment length(with gaps) = 14 Alignment score = 0.625132
 TAAAAntAAAAa
>Fam_4_12_10  Nr. of seq. 10 Alignment length(with gaps) = 12 Alignment score = 0.642593
 TgTTaTTgTTaT
>Fam_5_16_8  Nr. of seq. 8 Alignment length(with gaps) = 16 Alignment score = 0.667411
 aTTanttTaTTatTtt
>Fam_6_10_8  Nr. of seq. 8 Alignment length(with gaps) = 12 Alignment score = 0.679067
 ATAAAATAAt
>Fam_7_12_8  Nr. of seq. 8 Alignment length(with gaps) = 12 Alignment score = 0.777282
 tTTTCaCCcAAC
>Fam_8_16_7  Nr. of seq. 7 Alignment length(with gaps) = 17 Alignment score = 0.700280
 TgAtnAAAAACTAAAC
>Fam_9_14_7  Nr. of seq. 7 Alignment length(with gaps) = 16 Alignment score = 0.602183
 TntgAAAGGAAAAn
>Fam_10_13_7  Nr. of seq. 7 Alignment length(with gaps) = 15 Alignment score = 0.661376
 TTATTATtTTAtt
>Fam_11_14_7  Nr. of seq. 7 Alignment length(with gaps) = 15 Alignment score = 0.634392
 tTCtTTaaTCnTTA
>Fam_12_12_7  Nr. of seq. 7 Alignment length(with gaps) = 13 Alignment score = 0.636142
 aTTgATAAAtAA
>Fam_13_10_7  Nr. of seq. 7 Alignment length(with gaps) = 12 Alignment score = 0.666667
 TTAtTTTTTA
>Fam_14_10_7  Nr. of seq. 7 Alignment length(with gaps) = 12 Alignment score = 0.619048
 TatTTTttTC
>Fam_15_246_6  Nr. of seq. 6 Alignment length(with gaps) = 260 Alignment score = 0.646752

CCAAAatcCCATTTCCATTTaGTnGGtgtTCCTGTgCTtgTGTCAGTAAATTTAACgtTTAAtGGtacTtTTCCTGAgGTnGGAGAtGCaGAgAAtgCAGCAacgGGTTTT
GtTatnACtgTTATATAnTcTGtTTTTGTTaCtGTgTTACTGCCTGCaGCATTngTTACTGTAAGTnTAACaGTATAtnTTCCTGCTTTtGAATACTTATGagTTGGATTC
TGgagGaaTGActTTGtTCCaTCT
>Fam_16_141_6  Nr. of seq. 6 Alignment length(with gaps) = 141 Alignment score = 0.668558
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AAAcTTCTGAATGCGATtATTncCtGtATCGGCAACATAAACATTgCCcGAAGAATCtACAGCAAtACCanatGGataattAAATTgtCCgTcgcCGcTGCCataaGAACC
CCATTgagTaAggaAttTaCCacTGCTaTC
>Fam_17_78_6  Nr. of seq. 6 Alignment length(with gaps) = 82 Alignment score = 0.664228
 aGCACCACCATAcTcatTaGCATGgTTATTgacAAAAGAACAAtCacTTAAAatACCATTAgCACCATcCCAATaAAc
>Fam_18_12_6  Nr. of seq. 6 Alignment length(with gaps) = 14 Alignment score = 0.651587
 AAGaAGAAAAAG
>Fam_19_13_6  Nr. of seq. 6 Alignment length(with gaps) = 14 Alignment score = 0.647619
 TcTTCTATTTTaA
>Fam_20_12_6  Nr. of seq. 6 Alignment length(with gaps) = 13 Alignment score = 0.671795
 CTCTTCnTtCTT
>Fam_21_12_6  Nr. of seq. 6 Alignment length(with gaps) = 12 Alignment score = 0.733333
 gTCGTGtTCGtG
>Fam_22_11_6  Nr. of seq. 6 Alignment length(with gaps) = 11 Alignment score = 0.751515
 aaAtAtaAaaA
>Fam_23_156_5  Nr. of seq. 5 Alignment length(with gaps) = 158 Alignment score = 0.831646

TCAGTCCAGCAGACCctCGATGGcGGgTATATCATTAcGGGctatACAtagTCCTTCGGGGcAGGCnAnannGATCTgTGGCTGATcAAGACCGATGAcCAGGGAAACAaG
CTATGGGAgAGGACgTTTGGCGGaGcAGAAtntGATgaGGGCnAt
>Fam_24_141_5  Nr. of seq. 5 Alignment length(with gaps) = 142 Alignment score = 0.677700

CCAGAAGTTCAcnTCGACCGGcgnaTTCaTCAcgaaaTGGgcaGTnnnGgctCnGgAgaCGGGCaGTTCaactnnCCcnatGGtaTCGCnGTgGACAgCGCcGGcAAcGT
CTACGTcancGAcncgnnnAACaaCCgGnT
>Fam_25_120_5  Nr. of seq. 5 Alignment length(with gaps) = 128 Alignment score = 0.693750

tTGTTgTtTAtcGtGTTAATtACAGtgACaGTaTTGCTGttAacaTTaGTCACATAtgCnTttgnTCCtgCnAcTGCaATTCCaGcAGGAtacTctCCAACATtAAttGTG
cCTatAACa
>Fam_26_108_5  Nr. of seq. 5 Alignment length(with gaps) = 109 Alignment score = 0.735474
 TCCATGCCTgTTGtTTATCtGGtAcTTGAgAAAAtGCAGAAcCAAGAGCnntgGcaGCactAgacCTcACATcatgaTctTcATCatTggTcAGTcTAagTAAaTCaT
>Fam_27_37_5  Nr. of seq. 5 Alignment length(with gaps) = 37 Alignment score = 0.756757
 CACAgAGGaCACagAGAggAtaTTcACCACgGAGGTt
>Fam_28_17_5  Nr. of seq. 5 Alignment length(with gaps) = 19 Alignment score = 0.673684
 AATAAcAAAaTAAAaaG
>Fam_29_16_5  Nr. of seq. 5 Alignment length(with gaps) = 17 Alignment score = 0.603922
 TAaCAGatTTAtTcnn
>Fam_30_15_5  Nr. of seq. 5 Alignment length(with gaps) = 16 Alignment score = 0.652083
 aGaaGAgAAGaAAgA
>Fam_31_15_5  Nr. of seq. 5 Alignment length(with gaps) = 16 Alignment score = 0.716667
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 CTAAtCTTnaAGgAG
>Fam_32_12_5  Nr. of seq. 5 Alignment length(with gaps) = 15 Alignment score = 0.702222
 GTTGAATCaTCt
>Fam_33_14_5  Nr. of seq. 5 Alignment length(with gaps) = 15 Alignment score = 0.666667
 gAAaaAGAgAaAAt
>Fam_34_14_5  Nr. of seq. 5 Alignment length(with gaps) = 15 Alignment score = 0.624444
 CTTAatnAAGtTaC
>Fam_35_15_5  Nr. of seq. 5 Alignment length(with gaps) = 15 Alignment score = 0.773333
 tTAAAAaACGATAna
>Fam_36_13_5  Nr. of seq. 5 Alignment length(with gaps) = 14 Alignment score = 0.633333
 AtTctTCtTnCTA
>Fam_37_14_5  Nr. of seq. 5 Alignment length(with gaps) = 14 Alignment score = 0.885714
 ACTcGGGTGAcGGa
>Fam_38_14_5  Nr. of seq. 5 Alignment length(with gaps) = 14 Alignment score = 0.885714
 CAACGGTTTcGggT
>Fam_39_13_5  Nr. of seq. 5 Alignment length(with gaps) = 13 Alignment score = 0.610256
 TTcTaACttcTan
>Fam_40_12_5  Nr. of seq. 5 Alignment length(with gaps) = 13 Alignment score = 0.648718
 tTCAgtTAATAn
>Fam_41_11_5  Nr. of seq. 5 Alignment length(with gaps) = 12 Alignment score = 0.644444
 TTctTttnTaa
>Fam_42_12_5  Nr. of seq. 5 Alignment length(with gaps) = 12 Alignment score = 0.672222
 nAgtTTcAGATt
>Fam_43_10_5  Nr. of seq. 5 Alignment length(with gaps) = 11 Alignment score = 0.630303
 tTaanTatTt
>Fam_44_255_4  Nr. of seq. 4 Alignment length(with gaps) = 260 Alignment score = 0.755769

CCTGTgCTCTGGtCAgTAAAACtAACaGTAAGAGGcGctTTTCCTGAAGtngGaGAtGCAGAgAAncTGGnaACAGGagcATcTAaAaCGTTTGAgACAGcAATATAgCcG
GaTTTTGTcAAtGcatTACTgCCgTTTgCATtaCTTgCtGTCAATGTAACAGAaTAtagTCCTGatTTatTGTAtgTgTGtACaGGATTctTtTCTGTTGAAnTAcTtCCa
tCTCCaAAAgtCCATtTCcaTGaagTTGGngAt
>Fam_45_123_4  Nr. of seq. 4 Alignment length(with gaps) = 124 Alignment score = 0.768817

AAtAcaTtGCaACgGCGAGtgaTGACAAtACAgCACGtTTATGGaAtgcAtCTACAGGTAAAcAAATttttTGTTCTGAACCAtgatggTtcGgTaAAtAaTgtTgTaTTCA
GtCCTGATGGAA
>Fam_46_102_4  Nr. of seq. 4 Alignment length(with gaps) = 103 Alignment score = 0.779935
 ttTTTCATAGCATTCcAaTGCCTCaTCATATcTCccAAgTtCtTcaAGGAcTAcTCCTTTgTTGTTCCATGcTTCtaCaagTTtTGGaTtTATTTgTAgTGC
>Fam_47_69_4  Nr. of seq. 4 Alignment length(with gaps) = 70 Alignment score = 0.722619
 tAAGATTTTTcAacTCtGagATTTCaGGaGGcAgcGAAgTCAaTtGATTncaAGAtAtgTtaAGTggAG
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>Fam_48_45_4  Nr. of seq. 4 Alignment length(with gaps) = 47 Alignment score = 0.725768
 gGCGACGGgCCGaAGGaCCGGAGtTtGAGCaCCGcAGGTGcGant
>Fam_49_27_4  Nr. of seq. 4 Alignment length(with gaps) = 30 Alignment score = 0.642593
 AAGCatTTtTtgAAAAGGgTTGCGGgc
>Fam_50_18_4  Nr. of seq. 4 Alignment length(with gaps) = 20 Alignment score = 0.627778
 cTAAaAAAcAAAAAAcaG
>Fam_51_20_4  Nr. of seq. 4 Alignment length(with gaps) = 20 Alignment score = 0.613889
 atACaaAAnAAGaaaaAAAT
>Fam_52_16_4  Nr. of seq. 4 Alignment length(with gaps) = 18 Alignment score = 0.643519
 tTTAatAAATATAanT
>Fam_53_16_4  Nr. of seq. 4 Alignment length(with gaps) = 18 Alignment score = 0.646605
 aTaATTgCTtTTTAAc
>Fam_54_18_4  Nr. of seq. 4 Alignment length(with gaps) = 18 Alignment score = 0.654321
 CGgcGTcTCcGTggcCgT
>Fam_55_16_4  Nr. of seq. 4 Alignment length(with gaps) = 17 Alignment score = 0.699346
 aAAAATAAAAATnCTa
>Fam_56_16_4  Nr. of seq. 4 Alignment length(with gaps) = 17 Alignment score = 0.655229
 tGAtAAATGAAtgaTg
>Fam_57_15_4  Nr. of seq. 4 Alignment length(with gaps) = 17 Alignment score = 0.684641
 ctAGAAtTAAAGAAA
>Fam_58_16_4  Nr. of seq. 4 Alignment length(with gaps) = 17 Alignment score = 0.673203
 gATTCAATTtCaTAan
>Fam_59_15_4  Nr. of seq. 4 Alignment length(with gaps) = 17 Alignment score = 0.660131
 AAAAtAAcTGGgACA
>Fam_60_17_4  Nr. of seq. 4 Alignment length(with gaps) = 17 Alignment score = 0.653595
 cCTtTctcTTCtATcTt
>Fam_61_14_4  Nr. of seq. 4 Alignment length(with gaps) = 16 Alignment score = 0.630208
 TGAaatTTaAtTTA
>Fam_62_14_4  Nr. of seq. 4 Alignment length(with gaps) = 16 Alignment score = 0.671875
 GTtgTTAAAAAaCa
>Fam_63_14_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.622222
 cATATaATcTCAac
>Fam_64_14_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.609259
 AaAtACTAAaTAat
>Fam_65_14_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.659259
 ATCTcATtTTAAat
>Fam_66_14_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.640741
 GAAACaGatAAgAG
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>Fam_67_14_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.707407
 AGCtAAAAaCagAT
>Fam_68_14_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.751852
 CTTTTTcCTTTctT
>Fam_69_14_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.751852
 TACaATTTTTaCAt
>Fam_70_15_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.603704
 ATCaGttAAtaaAGg
>Fam_71_15_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.681481
 CCTGAATCtattaAa
>Fam_72_15_4  Nr. of seq. 4 Alignment length(with gaps) = 15 Alignment score = 0.777778
 AGAAGaACCaGTaGa
>Fam_73_13_4  Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.656746
 gAaATAgAAAnTG
>Fam_74_14_4  Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.650794
 tGaAgGTAAaTAta
>Fam_75_13_4  Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.648810
 GaAGaAaCTAAAn
>Fam_76_14_4  Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.654762
 CAGAaatCcTTAtT
>Fam_77_13_4  Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.619048
 TTTTgAgTtTcgA
>Fam_78_11_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.653846
 TTACTTtTTnT
>Fam_79_13_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.670940
 tATCtGttCATTc
>Fam_80_12_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.685897
 AAAtCAaTCAaa
>Fam_81_11_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.666667
 aATcAAAATCA
>Fam_82_13_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.779915
 gAATTcAGGTtAa
>Fam_83_13_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.858974
 TATCaATCAGTtt
>Fam_84_13_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.698718
 AgCAAGtTActCa
>Fam_85_12_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.711538
 AAaTAATatcTA
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>Fam_86_13_4  Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.698718
 AAACTAAaagCTc
>Fam_87_11_4  Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.671296
 aTTATAtTaTA
>Fam_88_12_4  Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.648148
 TTaaTaGTTtAG
>Fam_89_12_4  Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.692130
 TTTctttaTTcA
>Fam_90_12_4  Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.685185
 GGtTCagGcTCT
>Fam_91_12_4  Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.685185
 TTgCtattTGAA
>Fam_92_10_4  Nr. of seq. 4 Alignment length(with gaps) = 11 Alignment score = 0.638889
 TAAAaAgGat
>Fam_93_11_4  Nr. of seq. 4 Alignment length(with gaps) = 11 Alignment score = 0.717172
 ATTGaAAAttA
>Fam_94_11_4  Nr. of seq. 4 Alignment length(with gaps) = 11 Alignment score = 0.858586
 AtATTATGAGa
>Fam_95_258_3  Nr. of seq. 3 Alignment length(with gaps) = 264 Alignment score = 0.640152

TAcACngTaAaaCTnACAGCAACcAATGCnGCAGGcAGtAAtACgntAACAAAATcaAAtTAcATaAcAgTnACAGgaACanctgCACAAacnCCgGTTGCagnaTTTTcG
GcaTctCCnACtTCaGGAAAtgCaCCAttgAntGTnAcnTTTACTGAcAgcAGTACaGGntCtCCAACagCnTGGAacTGGaaTTTcGGAGAcGGnACanctTCAaCAgtc
CAGAatCCaAnaCACACATATTCaaCaGCAGGAAct
>Fam_96_137_3  Nr. of seq. 3 Alignment length(with gaps) = 142 Alignment score = 0.667449

AATCTTGAAACtGCtaTCngTcTTTAcgGnGAtGCCAGgAAATaTTCCCaAAAacAAGcgtAgaTTACGCTcgTGCgTTGAtgAAcGAGGGTaaTGCAAGAcAAacACTTG
CaGaaATGGGtgTTGAnAGtAgggaA
>Fam_97_126_3  Nr. of seq. 3 Alignment length(with gaps) = 132 Alignment score = 0.647306

TCTGTAATTGAcACAgCTACAAACActGTTACAGcCACtGTnaaTGTAGGAgActnaTCCTantGaaGTTGCAgTCAgtCCtgAcGGAAAAAAaGTnTATGTgACaAAnnc
AatAGcaAcaATaTt
>Fam_98_120_3  Nr. of seq. 3 Alignment length(with gaps) = 121 Alignment score = 0.666667

AAGAAGCagTgaAAAagTATAACCAgtCaCTggAAATtaaaGAAGAncTtGGagAcAAaagcGGAATTgCAnnAaCAcTgCACCAgcTTGGAAngATTtATtAtcaTCAGG
GcAAtTAcG
>Fam_99_120_3  Nr. of seq. 3 Alignment length(with gaps) = 120 Alignment score = 0.679630
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TAagtCCATTTgAGgGTTCCGTCAGggTTcAgtGCaTAtAGtTTnTTgTCanngCTTCCgATgTAGATGGTtCCGTCngctCCnATTGCtGgtGAACtGtagATctnattT
CCgGTGGTg
>Fam_100_102_3  Nr. of seq. 3 Alignment length(with gaps) = 102 Alignment score = 0.738562
 TTATACTGTTCTTCTGCtTCtTCnaGnCGcCCCATtTcTtnaAGGAGAtTtCCGTAAtTgnAGTGtGtattnACATgTTTtGGgTCtGcTTCCAGaGCAAGc
>Fam_101_93_3  Nr. of seq. 3 Alignment length(with gaps) = 93 Alignment score = 0.930705
 TTTCCAAGTGCCTCTGCCGCACTnCtCCGCACATATGAATCTTcATCTTTGAGTGCGTTGATTAaCGGCTGCACtGCTgTATCCGAtTTaATA
>Fam_102_51_3  Nr. of seq. 3 Alignment length(with gaps) = 54 Alignment score = 0.602881
 TTCGcGtttTCTCctGCTCCgGCCCTTCGgcCcgtCGCcAgTCgAAaAcgC
>Fam_103_42_3  Nr. of seq. 3 Alignment length(with gaps) = 48 Alignment score = 0.800926
 CCTCTTCGGTAGGTTCAGGAGTCATCGTAGgCTCtGGAGTGA
>Fam_104_23_3  Nr. of seq. 3 Alignment length(with gaps) = 25 Alignment score = 0.622222
 GAAAAgTaAAGAAgAnAcAAaaA
>Fam_105_21_3  Nr. of seq. 3 Alignment length(with gaps) = 24 Alignment score = 0.625000
 TnTtTTTTAAtTaTAAGTTAa
>Fam_106_19_3  Nr. of seq. 3 Alignment length(with gaps) = 22 Alignment score = 0.601010
 atTattTATTTtatnTtTt
>Fam_107_18_3  Nr. of seq. 3 Alignment length(with gaps) = 21 Alignment score = 0.629630
 aAAGAaTAACTTcAAAAt
>Fam_108_19_3  Nr. of seq. 3 Alignment length(with gaps) = 21 Alignment score = 0.613757
 TTnGtTtTCTTAtTTTCTn
>Fam_109_17_3  Nr. of seq. 3 Alignment length(with gaps) = 20 Alignment score = 0.627778
 ttTTTaAGAATTTATcA
>Fam_110_20_3  Nr. of seq. 3 Alignment length(with gaps) = 20 Alignment score = 0.644444
 aaGAGATaGaGTaaATAAAa
>Fam_111_19_3  Nr. of seq. 3 Alignment length(with gaps) = 20 Alignment score = 0.755556
 gAaTCTAAAAAAAcGAAtG
>Fam_112_16_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.631579
 AACTTacTTTTTTCcC
>Fam_113_17_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.654971
 AAATTAAAAgAgAGAtn
>Fam_114_17_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.649123
 AAAgaAACtAAAAACaC
>Fam_115_18_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.684211
 TaATATTtGGaCTTAtCt
>Fam_116_19_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.602339
 AgcaagtAATACcTGtTAA
>Fam_117_19_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.789474
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 TCAATTTtACAnTTTcaTA
>Fam_118_18_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.725146
 AGgAtAAAAAAGGaAgAA
>Fam_119_18_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.678363
 TAATCTcATTGATttCtt
>Fam_120_18_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.631579
 TTTTcTTTTaActATtaT
>Fam_121_18_3  Nr. of seq. 3 Alignment length(with gaps) = 19 Alignment score = 0.608187
 AAaATaAATTaGntaTTT
>Fam_122_15_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.617284
 CAtCGCtaCCGtCAC
>Fam_123_17_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.629630
 cTCAGTATTcTgTaTtc
>Fam_124_16_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.691358
 AAAAATGaAGAAaAcG
>Fam_125_18_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.641975
 TCCaGTAtttTCTTTTnn
>Fam_126_17_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.611111
 AaAtTTTaAttTACAaC
>Fam_127_17_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.611111
 TATanTTTCAAgAAtAn
>Fam_128_17_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.635802
 ATTtTTGtTCTnaTCtT
>Fam_129_18_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.802469
 CTgCAACcGAAGagATGA
>Fam_130_15_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.627451
 AaATTAtTTTtATCt
>Fam_131_16_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.624183
 AACTTTAAGTaanGag
>Fam_132_17_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.647059
 AAnaTGATCTTgAaAtn
>Fam_133_15_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.679739
 TtACTTaGTTTcAGA
>Fam_134_16_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.653595
 ttTtTAAGAAAnTGAG
>Fam_135_15_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.738562
 AAAATCAATtACAnT
>Fam_136_15_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.627451
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 nCaTTTTCATCAGTg
>Fam_137_15_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.607843
 TTAAACAaAAttgCa
>Fam_138_15_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.660131
 AnTGAAAAtAAcACA
>Fam_139_16_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.653595
 TtAtAnGTTTAtTTTt
>Fam_140_16_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.725490
 TTcgTTTTTCCTGATa
>Fam_141_17_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.614379
 TTnTaCTgaGTnTTTAa
>Fam_142_16_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.699346
 AGnTATTCAGcTatTC
>Fam_143_17_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.607843
 GnAttATgATTGAAAct
>Fam_144_17_3  Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.692810
 tgCTTTAaTCtGTTtTc
>Fam_145_13_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.645833
 tCgAAGAAAAAGA
>Fam_146_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.604167
 tAAnATCCTTtcTCt
>Fam_147_14_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.625000
 ATCTGGTAAtnGTt
>Fam_148_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.618056
 CTGAcATAcAAgGAn
>Fam_149_14_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.625000
 AGTGTTaaTTTGAt
>Fam_150_14_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.659722
 AaATTAcTTTCTgT
>Fam_151_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.618056
 CAAaGAntAAGAGaC
>Fam_152_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.673611
 cTATTTTTnTtACTT
>Fam_153_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.638889
 ATTcAtAGaTTGatA
>Fam_154_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.618056
 TTTTaTTtTAtaCTa
>Fam_155_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.673611
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 ACCAgTatTGAAAAa
>Fam_156_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.659722
 TTttAAAAcAAncCTt
>Fam_157_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.645833
 TaTTnCtAAcCAGAT
>Fam_158_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.729167
 TTTatTTCAGgTTTct
>Fam_159_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.673611
 ATGTtgAaCTaAATT
>Fam_160_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.638889
 CTTAActangTAAtAA
>Fam_161_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.666667
 TTTAGTtaATTCCnnt
>Fam_162_12_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.614815
 TTTCTTCATtGg
>Fam_163_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.762963
 CCGCCGCaTCGTcaT
>Fam_164_13_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.800000
 TTTTAGAATCCGt
>Fam_165_12_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.622222
 TTTTTCTtTCCc
>Fam_166_13_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.644444
 tttTATTTATTCA
>Fam_167_14_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.629630
 AGCTTTAAGatTtn
>Fam_168_14_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.718518
 AATAAAtcAACAAt
>Fam_169_13_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.659259
 GGAATcAgTTACT
>Fam_170_14_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.629630
 TTTTcTGtTTGtAn
>Fam_171_14_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.711111
 TGAaTTTTTgTTCc
>Fam_172_14_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.666667
 TGgaCtCTTAAATn
>Fam_173_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.651852
 tcnAgntaTTttcat
>Fam_174_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.711111
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 tTTTCgaCtTTTCTt
>Fam_175_14_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.711111
 TTAGcAaGAATAgG
>Fam_176_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.829630
 tTTGAGAaTTATcTC
>Fam_177_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.792593
 GAagTTTGATtGTGT
>Fam_178_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.703704
 TGAAAAaAAnTtAGa
>Fam_179_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.674074
 CCTaaAgTnGaAGAA
>Fam_180_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.659259
 GAaGAAGaaGtAgcT
>Fam_181_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.733333
 CnGAtGGaAAcCAGA
>Fam_182_15_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.762963
 aAATAAaaAAaTCAG
>Fam_183_11_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.626984
 GTTTACnGAAT
>Fam_184_13_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.730159
 TAAGtCTGAAAAn
>Fam_185_12_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.650794
 TActTaTTTACT
>Fam_186_12_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.738095
 TTGaACTCTATT
>Fam_187_14_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.682540
 TTTAtTnAAATTtt
>Fam_188_14_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.714286
 AAtAAAAtnGAACT
>Fam_189_13_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.690476
 atTTTTAcCTGAT
>Fam_190_13_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.730159
 tATAATTgCaCAG
>Fam_191_14_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.698413
 ATactTTatAAGTT
>Fam_192_14_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.650794
 TTTcacCAnTaTCT
>Fam_193_14_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.746032
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 AACTggcTATTcTA
>Fam_194_14_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.650794
 AATCannAATCAAn
>Fam_195_14_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.746032
 agaTCAGTAAATtA
>Fam_196_14_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.809524
 TCAAAGtAgAGAAg
>Fam_197_12_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.632479
 ATTTTTCaatAG
>Fam_198_11_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.641026
 AaCaTTTTTTG
>Fam_199_12_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.649573
 TTctcTTACTGa
>Fam_200_11_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.675214
 GtTTATCTTTT
>Fam_201_13_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.709402
 TTTTGAATAgnga
>Fam_202_12_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.632479
 TCCaAnTaCAAG
>Fam_203_13_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.632479
 aTtnACATaTACt
>Fam_204_12_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.641026
 ACTTCcGtGgTa
>Fam_205_12_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.709402
 tGAAGATtGGTa
>Fam_206_12_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.666667
 cACCTTtTTcTC
>Fam_207_13_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.623932
 GGAgTggaAAGcA
>Fam_208_12_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.675214
 TATTTTCCngAa
>Fam_209_13_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.794872
 tATTcACAAtTGA
>Fam_210_13_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.692308
 TTAtTgAAAAgnG
>Fam_211_13_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.658120
 TTTtTATnTgnAC
>Fam_212_10_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.657407
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 ATTTaGGAAT
>Fam_213_11_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.638889
 AAtTTtGAACt
>Fam_214_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.675926
 GTTTnCatTCAg
>Fam_215_11_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.611111
 tTGGCTTTcAn
>Fam_216_11_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.685185
 AtTCAgTATCt
>Fam_217_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.712963
 nAAGGGAtAaTT
>Fam_218_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.712963
 AaGaTAGATAAn
>Fam_219_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.703704
 TgTAAAAgAAnA
>Fam_220_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.722222
 AgAgGaAGgGGA
>Fam_221_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.703704
 GTGtCtGtGTCg
>Fam_222_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.703704
 TGGtTtTGgtTT
>Fam_223_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.703704
 ctTTaAGtTATT
>Fam_224_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.851852
 ATTTgATTCTTc
>Fam_225_10_3  Nr. of seq. 3 Alignment length(with gaps) = 11 Alignment score = 0.606061
 TtgtTTGAAA
>Fam_226_10_3  Nr. of seq. 3 Alignment length(with gaps) = 11 Alignment score = 0.737374
 AAGGAAAGat
>Fam_227_11_3  Nr. of seq. 3 Alignment length(with gaps) = 11 Alignment score = 0.676768
 acAATcAaACT
>Fam_228_10_3  Nr. of seq. 3 Alignment length(with gaps) = 10 Alignment score = 0.644444
 TCTTCcctTg
>Fam_229_261_2  Nr. of seq. 2 Alignment length(with gaps) = 261 Alignment score = 0.833972

GTTTCGGTATCCGTGCCGTTTGCATTGCTaACcGTCAGTTTgGCTTCATAAGTCCCTCTGGAAgTGTAaaTaTAAGCAAAGCTTGccgCATTAGAGTCcTCGACcCCGTCA
CCATTAACATCCCAGCTcaaTCtCGaaGTTGCATTCTcCGAAagGTCGGTaAAGAGaACaGTAAGaGGGTAaTAaCCGCTGGTTTTATTCAaTGTGAAGTTTGCTACGGGA
AGAAcAGGAAgTTCTTCTTCCAgCACGGTAATCACAGCA
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>Fam_230_159_2  Nr. of seq. 2 Alignment length(with gaps) = 159 Alignment score = 0.781971

TATGACCTTATGATCGGTGaAtcTgaaGGAGTtACATATGGTTATGAGAATACCGGGTCTTCGGacAGCCCGGaGTGGaCTGCGAAaTCTTCcTGGAATAccCCTgaTaTA
GGTacTgcTgCAtCACCAGCTTTgGCCGAcCTTGACgGTGATGGcGAC
>Fam_231_158_2  Nr. of seq. 2 Alignment length(with gaps) = 158 Alignment score = 0.618143

TACGGaGGaAaaGGaGAgGaATatGcCttacGCgGTTGCaATaGCTCaAAAcGGgGAcATaATaGTgaCaGGcgaCACTaACAGcTTCGGCGCTGGTaAtGATGAcGTTTG
GGTTCTcAGaCTTGATnGcaAaTGGaAAcaTcAAGTGGCAaAAaACT
>Fam_232_145_2  Nr. of seq. 2 Alignment length(with gaps) = 145 Alignment score = 0.786207

AAAAAGCACTCaAAATcgAcGcAAAAACTACTCaAAAAaGACCCCGAAAAcGTAgCaTACCAATCaTACGTAGGAAtGACaCTAAACAATTTAGGAAACTTGCTTaaaaAT
ATGGGGagaATTGAAGAcGCGAAAaAaAGGTACG
>Fam_233_141_2  Nr. of seq. 2 Alignment length(with gaps) = 141 Alignment score = 0.806147

TATATGTTGCCaGcacCATCAACcGCAATACCagAcGgtcGaTCGAATTGTCCTGGcTCGtcGCCATgGCTgCCCATTGTTGTCCAGGTGTTTGTGGcTTTGTTCCATACC
TGAATCCTgTgATTAAagGTGTCGGcTACG
>Fam_234_131_2  Nr. of seq. 2 Alignment length(with gaps) = 131 Alignment score = 0.753181

CCATTTTGCCACAGGAAAGCAtGTGAttCAcCAgTATCCGTCTTGACTGAcaCCcACTACCTGCCCATTgTCATTGATTCCaCTGGCAcaGCTATatgCTaCatcCgagcG
TTCCAAgATCAGTCATCaca
>Fam_235_126_2  Nr. of seq. 2 Alignment length(with gaps) = 126 Alignment score = 0.788360

ACCTTGAGGGTCTGATCACCGGAaGCaGATACaGCTcTcaGACCGTCcGGGGTCACcGCCACCGCgCTGACCcAAgcgGAATGaCCTTTCAGcGTCCgcAgCTCcTCGCCC
CTcTCCAGGTCCCAt
>Fam_236_126_2  Nr. of seq. 2 Alignment length(with gaps) = 126 Alignment score = 0.817460

AGTGCTTTTTCGTAaTCTCCCATACTTTCATAGAGTCCTGCGAGATTaTTTAGgGTTGTTGCAACATCTGGaTGTTGcGGcCCcAGaACCTTTTCActtATtTCaAGTGcc
CgTTGAgAAAGTggG
>Fam_237_123_2  Nr. of seq. 2 Alignment length(with gaps) = 123 Alignment score = 0.691057

TCAATTGCTTTTcTcagcTCgCCTAGaTGAaTATATgCTaacCCCAAATcTCCAAGATgATTTCCTTCTCtgCaTacTTATCaTTCnATTTcTCTtGAAATTTTCAAcGCC
TGcTcaTAAaAT
>Fam_238_110_2  Nr. of seq. 2 Alignment length(with gaps) = 110 Alignment score = 0.721212
 TTCTTCTTTTCTTTGcCCATCCAAATaAGGaACAAgAGCaGAAAGgGCaTaTaaTCTgTGnATAaTCATCTTcAATCcTgGAGGcTGacaTCAAGGGCTTTTTCcATCAC
>Fam_239_104_2  Nr. of seq. 2 Alignment length(with gaps) = 104 Alignment score = 0.637821
 AGGGccagCCCCCGGTTGTaCCAGGCcagGGCGaAGccCGGaTCGAtCTcCAGGGCCccgTCGTAgcAcTCGAcCGCCTCCTCgTaCCggCCGAGaaGgCgnCG
>Fam_240_103_2  Nr. of seq. 2 Alignment length(with gaps) = 103 Alignment score = 0.621359
 GTTaTGATAAGGCTTTAGAaATaGATcCtAAtaATgagTaATgCaTGGaaTAAcAAAGGATATgCtTTagCaGAaCTTGaAAaATAcgaAGAAGCaaTAGAAt
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>Fam_241_102_2  Nr. of seq. 2 Alignment length(with gaps) = 102 Alignment score = 0.686275
 ATAAcAAAGGTaaTGCCCTTaaTAAtTTaGGcAaATATaAaGAGgCAATaaaAGCTTATGAtAAAGCCaTAGAGATAaACCCaAAaTATgcCtaTGCaTGGA
>Fam_242_79_2  Nr. of seq. 2 Alignment length(with gaps) = 79 Alignment score = 0.738397
 GTTGCATATGAATTgTTcAaTGtTgCCTCgATTatatCCAACCAGTCCACCGACAtAaCaANaaCCNTCAACATTTCCA
>Fam_243_57_2  Nr. of seq. 2 Alignment length(with gaps) = 57 Alignment score = 0.827485
 cGCGGTTCTCACTCACTTCGTTCGCTCGCGGGTCACacTcGTTCCCCGCTCGcaGcC
>Fam_244_54_2  Nr. of seq. 2 Alignment length(with gaps) = 54 Alignment score = 0.632716
 gAAAAAGAAATACAAGAACAAATAAaAGGAAtgttAAAtcCAgAacCGaAAcTC
>Fam_245_45_2  Nr. of seq. 2 Alignment length(with gaps) = 45 Alignment score = 0.614815
 TCgTCGTCCTcgCTGCtTTCCTCcTCcTCAGCcTCcTCaTCacTc
>Fam_246_39_2  Nr. of seq. 2 Alignment length(with gaps) = 39 Alignment score = 0.722222
 CCCGAATTGCGcCTCGGGAGTACGCgGTCCTTtcgctg
>Fam_247_36_2  Nr. of seq. 2 Alignment length(with gaps) = 36 Alignment score = 1.000000
 AGCGGAAGTTCTGATACAGGAGATTCAGTCTCAGAT
>Fam_248_35_2  Nr. of seq. 2 Alignment length(with gaps) = 35 Alignment score = 0.809524
 gTaACCACAGAGGCACAGAGGgaCACAGAGAACgG
>Fam_249_33_2  Nr. of seq. 2 Alignment length(with gaps) = 33 Alignment score = 0.676768
 cCCaaCGCGCCTGcTCGGgCCGCGcCGcCgTCG
>Fam_250_33_2  Nr. of seq. 2 Alignment length(with gaps) = 33 Alignment score = 0.969697
 CCCCAGTCGGTGACNGTATCGACGGTGTCGCCG
>Fam_251_33_2  Nr. of seq. 2 Alignment length(with gaps) = 33 Alignment score = 0.686869
 AaAGTaTATgcCTAAATAggcGaGGAAATAAAG
>Fam_252_33_2  Nr. of seq. 2 Alignment length(with gaps) = 33 Alignment score = 0.737374
 GTcGAAGgTCGCCCCaTcAAAACcGGCAtaTCC
>Fam_253_31_2  Nr. of seq. 2 Alignment length(with gaps) = 31 Alignment score = 0.612903
 GTTaGAGTTGGGGTgGGTGTagcTgTCtGGa
>Fam_254_31_2  Nr. of seq. 2 Alignment length(with gaps) = 31 Alignment score = 0.913979
 CACCTGAaGGcGCTCACGCTCCGGTTCTTCG
>Fam_255_29_2  Nr. of seq. 2 Alignment length(with gaps) = 29 Alignment score = 0.637931
 TaTCtTTCTaTAttTTCTaTTTCTTTTTg
>Fam_256_29_2  Nr. of seq. 2 Alignment length(with gaps) = 29 Alignment score = 0.770115
 AATAATACCGTTTTTcaCAAATTAaGaaG
>Fam_257_28_2  Nr. of seq. 2 Alignment length(with gaps) = 28 Alignment score = 0.607143
 TTgCTTTCTCTacTCgGCTTCTcTcCtt
>Fam_258_28_2  Nr. of seq. 2 Alignment length(with gaps) = 28 Alignment score = 0.648810
 GacGAAcACGACGGccACAgCCACCACt
>Fam_259_28_2  Nr. of seq. 2 Alignment length(with gaps) = 28 Alignment score = 0.642857
 TTCTTaTTTTTAcTccTTATTaaTTgAC
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>Fam_260_27_2  Nr. of seq. 2 Alignment length(with gaps) = 27 Alignment score = 0.709877
 TTTcCaGaTTTTAaTTTTAGCGTTTct
>Fam_261_27_2  Nr. of seq. 2 Alignment length(with gaps) = 27 Alignment score = 0.802469
 GCCGCCCATGCCGCCgGGaCCGCCacc
>Fam_262_26_2  Nr. of seq. 2 Alignment length(with gaps) = 26 Alignment score = 0.615385
 CTTCAAtaCaCaTCcTGAGTaTATaT
>Fam_263_26_2  Nr. of seq. 2 Alignment length(with gaps) = 26 Alignment score = 0.621795
 TTCacTTTTAaTCTTCtTgCTTTaAt
>Fam_264_26_2  Nr. of seq. 2 Alignment length(with gaps) = 26 Alignment score = 0.615385
 AGTaAATaAATAAACaTgAaCaAaTA
>Fam_265_26_2  Nr. of seq. 2 Alignment length(with gaps) = 26 Alignment score = 0.602564
 TTagAATTTaaAAAtTAATgAaaAAA
>Fam_266_25_2  Nr. of seq. 2 Alignment length(with gaps) = 25 Alignment score = 0.686667
 TATTTAAAAAaTaAAAAActTAGAa
>Fam_267_25_2  Nr. of seq. 2 Alignment length(with gaps) = 25 Alignment score = 0.606667
 cAccAAAAcaTGAAATagTatAAAa
>Fam_268_25_2  Nr. of seq. 2 Alignment length(with gaps) = 25 Alignment score = 0.620000
 AcACaCCGACGGAaACtGAaAcCGn
>Fam_269_25_2  Nr. of seq. 2 Alignment length(with gaps) = 25 Alignment score = 0.660000
 TaGATTTTGaAaTTGACTTAAcAcg
>Fam_270_25_2  Nr. of seq. 2 Alignment length(with gaps) = 25 Alignment score = 0.633333
 AGaGAAgAaaTTAGAAAAAaaACTt
>Fam_271_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 0.666667
 cTCaGTCGGCGTcgGcTCCGGCTC
>Fam_272_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 0.694444
 CAATaTCAAACATTACtgAACtAA
>Fam_273_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 0.618056
 tTTTAAgGTcaATTATaTTAAcCA
>Fam_274_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 0.638889
 AGaAATAAGaTAAgaAAATAtTaC
>Fam_275_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 0.611111
 gCggACAACgACcCCGAaCCCaCG
>Fam_276_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 1.000000
 GAGGACGAGGAAGAGGACAATGAG
>Fam_277_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 0.611111
 TACaGATAcagcAaCTGAAGAcAC
>Fam_278_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.623188
 TaCAaTTTGAAGAGGATacctTA
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>Fam_279_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.637681
 TaaGTTAGTACATTGaAtTATat
>Fam_280_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.695652
 TGAGAaTGAtTAGAAaATAAAcc
>Fam_281_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.652174
 GaTTTAGATTagCTcTAAgTTCA
>Fam_282_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.601449
 aTTCgTgTTTTAGAAGtTTGTca
>Fam_283_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.608696
 aTAAAATCAacaAaAGAAaCAAc
>Fam_284_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.601449
 TAcTCTTACCTaaCtTACCTcTc
>Fam_285_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.630435
 GTAAGATTagTAaaAgTTATTGa
>Fam_286_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.659420
 TTTaAcTTTATATTAaAgcAAGc
>Fam_287_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.739130
 CCAGATCAgCGCTTCTGcAcaCG
>Fam_288_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.797101
 AAAAGAAGaAAAAcGAAGAGGGa
>Fam_289_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.659420
 cAgTAAaCAAACAGaGTTGAGat
>Fam_290_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.681159
 cTTACaATTTTcCcAaTTTTTAC
>Fam_291_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.739130
 GAAAAAcAAAAcAGAAgAaAGGT
>Fam_292_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.710145
 ATTAAAAAATaACcTAATaTcaA
>Fam_293_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.652174
 TAaGATAaaAATAaaATCAGAaT
>Fam_294_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.613636
 tCaTTAaAAAAGGAAAtcCAAc
>Fam_295_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.606061
 GaAATcGaaaTAAAATCaAAAA
>Fam_296_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.696970
 CTTTAATTgTTcACtTcTTATT
>Fam_297_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.674242
 TaATAgaTAATTTACAGaTAAt
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>Fam_298_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.666667
 gTCGtGGaGTGTCTGTGCcGTg
>Fam_299_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.666667
 aCTTTTcCTTcTAtTTTcTTCC
>Fam_300_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.666667
 aGAATATTGAaAGAGTAtTaaA
>Fam_301_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.613636
 TAaGTCTCATgTTaaATcTTAa
>Fam_302_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.643939
 AATTCaAAAAGATcTgAaAaGa
>Fam_303_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.606061
 TccTTCCAgAAGATTAcTTcgT
>Fam_304_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.606061
 aaTaCTgaAAAcTTTCTATAAT
>Fam_305_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.606061
 AAaTCtAAGGaAaaTTTAAGaG
>Fam_306_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.643939
 TCTTTaAGAaAacTcATTCTAc
>Fam_307_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.636364
 TcGTGATGTGGcgGTGagGGgG
>Fam_308_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.636364
 AAATaaAgaGTaGAATTATaAA
>Fam_309_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.696970
 TAAAAAcaTATTagATTAATcT
>Fam_310_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.603175
 GAAcCTGAAGtAACCgAGacA
>Fam_311_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.658730
 AAcCtaAGAAACCCgAAATTa
>Fam_312_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.658730
 TCATTTTCTAcAaTTccTGTt
>Fam_313_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.611111
 ATAAcCTGAAtAGaTTTGcat
>Fam_314_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.626984
 GGATAAcCTcAAcACTTTaAa
>Fam_315_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.626984
 taTAATTaAGTTTaAACTaAG
>Fam_316_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.603175
 ggTaCTGAccTGAGAAAATCc
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>Fam_317_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.698413
 CaTTTCTTTCTaCTTTcTTct
>Fam_318_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.722222
 aTTTTTACtTATTTTTATTat
>Fam_319_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.650794
 CTTaaTTATTTCtTCAGaTaC
>Fam_320_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.626984
 aTACTTaCTGcCTTCTagCCt
>Fam_321_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.650794
 AAaAACAGAcaGGAAGcTaAG
>Fam_322_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.619048
 CGacGACGaCGGCGAACaaaC
>Fam_323_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.682540
 CGcCcGTCGcGgTCGTCGaGT
>Fam_324_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.682540
 AACGAcACcGaGaCcGCTGAC
>Fam_325_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.873016
 TGCTgGAgAAACAGGATCAGA
>Fam_326_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.682540
 TTTaAATaAaaAATgGTATAC
>Fam_327_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.634921
 cTCTTCAaCTaCaTCcAAgTC
>Fam_328_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.682540
 CcGTTAcaTTcTCCTCaGGTA
>Fam_329_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.641667
 TAaTCTTTTTAAATCcagcg
>Fam_330_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.750000
 AATAAATaTAATcAAAaTAT
>Fam_331_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.716667
 CCaTGCAATATcAATAATca
>Fam_332_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.641667
 AcTTaCTGgTTaATTCTTCa
>Fam_333_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.683333
 aAAAATAAcCaGAATTAGnt
>Fam_334_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.700000
 ATCaAATTTAATaCCAgGAG
>Fam_335_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.608333
 AAAAACtGAACaTgATaCGa
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>Fam_336_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.633333
 aaAgTcAAAAAAAGaATATG
>Fam_337_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.608333
 aaAAATTCATaTATAaAcAg
>Fam_338_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.666667
 TAAAtATATaaTTTAAtAGT
>Fam_339_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.633333
 aAAAAaGAgcTAAGAaGCAA
>Fam_340_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.666667
 TTaTaTGGAAGTTTaGTGaT
>Fam_341_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.666667
 TAAAAATcATGcAACgTATg
>Fam_342_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.700000
 TaAAAgTCAGcTaGAATAAA
>Fam_343_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.766667
 aTAAAAaAAGGaTAAAAGAA
>Fam_344_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.675000
 TACaAaATTcAAGTCAATat
>Fam_345_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.666667
 TTTTTAagTTTaTTAacTAA
>Fam_346_20_2  Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.666667
 TTgaTaCTTaTTaTGTATAT
>Fam_347_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.657895
 AATAAtgCAAATAATCtGa
>Fam_348_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.649123
 GGATAAaAGaATAtaTTCA
>Fam_349_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.640351
 aTCATTTTAcCTTaAtTCt
>Fam_350_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.631579
 TTGAAAGaAAgCtCATTgc
>Fam_351_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.622807
 TTTcAGATTACAcGaTaAc
>Fam_352_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.692982
 aTCtCATTTTTGcAATTCt
>Fam_353_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.692982
 TAATTAAAATaAAcCTAaa
>Fam_354_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.692982
 TTcAAaAATTAAcTTAAAa
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>Fam_355_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.649123
 AAAgGTaATAATcTaTTTA
>Fam_356_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.666667
 TCTcTTTCTTaaGCTTAtt
>Fam_357_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.614035
 ATTCAGGagTTAATTacTc
>Fam_358_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.622807
 gCCCGaCTCGcCTGcTCCc
>Fam_359_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.614035
 CCcCTCCaaCTaCTCCaCC
>Fam_360_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.684211
 aTATCAgTaAATTcAAATT
>Fam_361_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.622807
 gCTGtTGGaGTTaCTTCTa
>Fam_362_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.692982
 aAGgAaTAGAAATaATAAG
>Fam_363_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.614035
 TAAgTGCAGcAACcTGaAc
>Fam_364_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.649123
 CGAgaTTTCaCAcACTTAA
>Fam_365_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.719298
 TaAGTTaAATAAtATTAAG
>Fam_366_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.649123
 aTTCaAATaACTCCAgATG
>Fam_367_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.614035
 acTGAgAaACATTGAaAAT
>Fam_368_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.684211
 AAAAATGGGaAAtCAaGAc
>Fam_369_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.684211
 TcaGAAAAcAgGAAAATAG
>Fam_370_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.684211
 GATTAagTAAAtcTTGATT
>Fam_371_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.614035
 TATTGgcACATTATaTcaT
>Fam_372_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.684211
 ATTTCaCAaAcTATTaTAT
>Fam_373_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.614035
 AGaAAACaCAGaGAaAcGG
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>Fam_374_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.614035
 TgCTcATAtaTTATCCAaG
>Fam_375_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.789474
 TTTAAAACTTTCTaAaGaG
>Fam_376_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.929825
 AGTAATTTAGCTATCAGTa
>Fam_377_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.649123
 TTTGCcTTgAcTTTaCaTA
>Fam_378_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.649123
 TTGacgAAaATCTcTAAAT
>Fam_379_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.638889
 AACGAGAgCgCCAGcGCc
>Fam_380_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.638889
 AATTGTaaATTgTGATTc
>Fam_381_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.731481
 ATTATCCaCTGAAATatc
>Fam_382_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.685185
 TTCTgTAaTTTAGGGAtg
>Fam_383_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.638889
 GAACTGTTaaAGCAtAAc
>Fam_384_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.611111
 aATCCAcAATaGAAACta
>Fam_385_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.694444
 ATTAAaAGATCAtgAAAt
>Fam_386_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.675926
 TTTCtTCAGaTGTTTaCg
>Fam_387_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.648148
 AAAACaaTAGAcAATGtc
>Fam_388_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.611111
 TATGAAAAaTaGGAcTtg
>Fam_389_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 aAGTTAGAgGaTgAGGAT
>Fam_390_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 AtTATaATGaACTCAcTA
>Fam_391_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.601852
 AAcTAtcGGAAcTACGGa
>Fam_392_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.638889
 cAgaTTTCTGGAAAaATa
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>Fam_393_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.666667
 TTTcAcaTTACTCTGtCC
>Fam_394_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.675926
 TAGAgAaAATACTaAATt
>Fam_395_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.666667
 TTCaAAcaTAaCAGATCC
>Fam_396_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.601852
 ACACTgACtATcaTTTAg
>Fam_397_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.703704
 TAGAAACtTGAgTaTAAT
>Fam_398_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.638889
 AaTAAcATTaCAcTATTc
>Fam_399_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.666667
 gACTgATTTaTaGTTCTA
>Fam_400_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.638889
 GAATAaaGAaTGGATTct
>Fam_401_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.666667
 AAgTAACATATTcCcTgA
>Fam_402_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.638889
 GTTCTATaaaATCTaCCt
>Fam_403_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.638889
 aGATGAGaTTTGTcATac
>Fam_404_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.759259
 tTTTTAtTTTTTCACTaC
>Fam_405_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.666667
 TTcTCAGAAgATAcTaAG
>Fam_406_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.703704
 TaCcTCCTCTTCAGcCgG
>Fam_407_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.703704
 ACACCAgAAAACaAaaAA
>Fam_408_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.703704
 TATaTTcGTgaTCTTGAT
>Fam_409_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 AaTCTAAAaAacAGTcTG
>Fam_410_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.703704
 GATACAGaAGAcACgGaT
>Fam_411_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 ATcCGGgAGaTGgAAaGT
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>Fam_412_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.703704
 aTaCCGAcGCGGACaACG
>Fam_413_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 1.000000
 TCTACTCCAGTTAATACA
>Fam_414_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.851852
 TAATCTTaGAATTCCTTc
>Fam_415_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 TgGTTAATCcaTacTATC
>Fam_416_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 ATTTATCcTAAccTTcTa
>Fam_417_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.648148
 AaAGgAAaCagAGAAAAC
>Fam_418_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 ATCTCACTaACaacTAAc
>Fam_419_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 ACTCCAGcTacGGaAGaA
>Fam_420_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.777778
 TCcTcAATCTCAGcTTTT
>Fam_421_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.777778
 AaTAGAaCcGATAATGAG
>Fam_422_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.666667
 ACTGGAAATcaCTTTtt
>Fam_423_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.627451
 TCaGAGCCaCTgTCCta
>Fam_424_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.607843
 CCaTcGTGTTTCtaATC
>Fam_425_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.735294
 gAAAAAATAGtTGAGAt
>Fam_426_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.705882
 AgTTTAAGGAAGaAGta
>Fam_427_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.735294
 tTTCTTTTaATTCCTTc
>Fam_428_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.735294
 ATAGaCTAAAAtTCCAg
>Fam_429_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.627451
 CcTTTAgTTTATCTgTa
>Fam_430_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.705882
 GAAAAATAGAGAggAca
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>Fam_431_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.666667
 cCAAAtGAGGAGAATta
>Fam_432_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.696078
 aATTTCTTcAGAGcTAT
>Fam_433_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.725490
 TTAACAGCtaCTTATaG
>Fam_434_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.656863
 ATTTGAgTTAGTgTaAt
>Fam_435_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.735294
 AAAaTAAGATTGtGGTc
>Fam_436_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.647059
 caAAGaTAAAGcTCCTA
>Fam_437_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.686275
 TAcAAGAGAAGtATCaT
>Fam_438_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.656863
 TTTTTAAtTCAAgaGTa
>Fam_439_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.725490
 TTACTTacTaTTACTGT
>Fam_440_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.725490
 AGaTAAGAGAGTTAagA
>Fam_441_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.686275
 GAcTATGTGaATTCgTA
>Fam_442_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.725490
 TGTAAAaTCATTacTCT
>Fam_443_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.656863
 cCTAAcTaATTGaCTTT
>Fam_444_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.647059
 TAAAAccTAAAgAaGAG
>Fam_445_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.774510
 AAGGAAGTAaAATcAAt
>Fam_446_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.696078
 AcTCTCAAAaTCTCAat
>Fam_447_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.725490
 TATTTaGTTCAAAtTaA
>Fam_448_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.647059
 TTCAgCTTTAAcaaTCT
>Fam_449_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.696078
 ATGAAaTTaAGAGTgAa
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>Fam_450_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.686275
 TGGATGaAATCTGaTAc
>Fam_451_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.647059
 CTGtTCTTCAaAATaAc
>Fam_452_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.725490
 TCTTCaAATTcATAGgC
>Fam_453_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.647059
 ACTTAGAACTAcgTAaa
>Fam_454_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.725490
 TAACATATcAAaCGAaT
>Fam_455_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.647059
 AAGTAaGGAGaAACAca
>Fam_456_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.725490
 aGTTTCAATcATAAtTC
>Fam_457_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.764706
 aAcTTaCTTTTTATCTT
>Fam_458_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.686275
 TAcCTTTTTgaTTTCaC
>Fam_459_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.607843
 ATCaATTATAaAaaGaC
>Fam_460_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.921569
 TTAAACAAACCTTAaAC
>Fam_461_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.686275
 AGcTACAaAAATgaATT
>Fam_462_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.607843
 AcAcAGccAaAACTTCT
>Fam_463_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.686275
 TGTcATTAACTgAATac
>Fam_464_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.686275
 TTTTCTAaaTaGAaATC
>Fam_465_17_2  Nr. of seq. 2 Alignment length(with gaps) = 17 Alignment score = 0.607843
 aaATCAgATTaATGAcG
>Fam_466_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.625000
 aTaacaTAccacctcc
>Fam_467_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.635417
 CATAAcCTTGACatCa
>Fam_468_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.729167
 ATTaTAGAATGTAAga
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>Fam_469_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.677083
 cGGTTTAcATTaAATC
>Fam_470_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.718750
 TTCAAATGAgtAATAa
>Fam_471_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.645833
 TTGcGaGAATTTCTag
>Fam_472_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.687500
 taGACAAgAATTcATG
>Fam_473_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.718750
 GcTTTTTAtATTTTGa
>Fam_474_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.687500
 AAAACCaTTTaCTCaa
>Fam_475_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.718750
 AAGACGTTTTCaTcAa
>Fam_476_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.718750
 TTAGACTgTTaCAAGc
>Fam_477_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.687500
 AAAACCTGaAaAAGgt
>Fam_478_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.708333
 TGaTTCGGTGGtTcGG
>Fam_479_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 GAAcTAAcACaAACTA
>Fam_480_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.625000
 cTCTGaaTGGTAGTAc
>Fam_481_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.677083
 TATTgTGcAGTAAcAt
>Fam_482_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.677083
 TccTTGTATTcCAGAt
>Fam_483_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.625000
 CTTAaCtCaAATcAAG
>Fam_484_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.708333
 cGATGTTATcTTTTAa
>Fam_485_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.791667
 ATTGATTTGTaTTgAG
>Fam_486_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.708333
 TGTAaTTCTCTaTTCa
>Fam_487_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.718750
 taTTCATAGAtCTTGA
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>Fam_488_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.677083
 tCTGAaTTTCAaAAaA
>Fam_489_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.708333
 TTaAAAAAACATaTTa
>Fam_490_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.677083
 AAcCTATTGAaATTga
>Fam_491_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.760417
 ATTTgcTTCCTGCTTa
>Fam_492_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.760417
 ACAATaAAAGGAAaAc
>Fam_493_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 AATAAgAAAGcAgAAT
>Fam_494_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.708333
 ATaAATCAAAgTAAAa
>Fam_495_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.708333
 AAAAGAGTAgAgAAaG
>Fam_496_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.760417
 AAAaTGAAATGAAgTc
>Fam_497_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.708333
 AATATAAAaTGacACA
>Fam_498_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.635417
 ATTTCAaTATaaCCGg
>Fam_499_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.760417
 AcAaTTACCTGAAATt
>Fam_500_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.677083
 TGAGGaAaTcAATCCc
>Fam_501_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 cTACcAAAaAAaCTAG
>Fam_502_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 GGaTTaGaTAGTTaAT
>Fam_503_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 aTTTaCcgGTTAACGG
>Fam_504_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 ATaTaTaaGATCTGAA
>Fam_505_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.750000
 GAAGaAgTCTATaCAG
>Fam_506_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.750000
 CAaTAATCTAGaaCTC
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>Fam_507_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.833333
 TGACTTCaTACCTTAc
>Fam_508_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 cTTTTATTGAaACaAg
>Fam_509_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.833333
 ATTaGCTAAaTTATGG
>Fam_510_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.750000
 AcTTATaTCGAAcTTT
>Fam_511_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.750000
 TTAaCcAGCTCTAAAa
>Fam_512_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 TTAaTCAgAACTTcaG
>Fam_513_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 TTCaTTAgaTaTATTC
>Fam_514_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.854167
 CTCTAATCAAaAGTcA
>Fam_515_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.916667
 TCCcAACCGCGCTCGC
>Fam_516_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.677778
 TaTCGTTCTCGCcgt
>Fam_517_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.677778
 tctTCGGATTCgGAG
>Fam_518_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.611111
 cTAATTTCTAGtagG
>Fam_519_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.700000
 CGTGGTCGTCGtgat
>Fam_520_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.677778
 aCGACGACGTTGagg
>Fam_521_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.677778
 GATAGAcATAGAgat
>Fam_522_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.700000
 AGCTaAACaAAGGAt
>Fam_523_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.700000
 aTTTAATAAcTGCTa
>Fam_524_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 TCTATgAAAGATgAA
>Fam_525_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.666667
 TaATATCGATTGagg
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>Fam_526_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.666667
 ACAcaTTGTCATCag
>Fam_527_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
 TgAAAaATGCTAaAt
>Fam_528_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.744444
 aAGTGTTTCTcAAAc
>Fam_529_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.688889
 TTATGGAcCcAtTTA
>Fam_530_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.777778
 TTATTTTCTTCaGtG
>Fam_531_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.688889
 TTgGGAATAtGTAAa
>Fam_532_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.744444
 aATgACATATTGAGg
>Fam_533_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.611111
 aACTTAcAaATCTGg
>Fam_534_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.700000
 tTCAAAgAGAACaTA
>Fam_535_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
 AcATAGcAATTaTAa
>Fam_536_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.666667
 taTCTAATAAaTTCa
>Fam_537_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.688889
 cTACTAAGAAaAGtG
>Fam_538_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.611111
 tTTaCAGgGTAGtCA
>Fam_539_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.744444
 TCCCTTaAATcCAGt
>Fam_540_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.744444
 AAaTgAAAACTTGGa
>Fam_541_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.688889
 TGTcAAGcTgTGTAT
>Fam_542_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 TCAAGcCTTAAgTTA
>Fam_543_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
 AACcAAGaAGAcCCa
>Fam_544_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 TTgATGCTGcTTaAC
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>Fam_545_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
 AcAAacAAGTTCAGa
>Fam_546_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
 GAAaAcTAAGAATac
>Fam_547_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.688889
 TaAGAGTTTcATCAa
>Fam_548_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
 aCAgcTTAAAGTCTg
>Fam_549_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
 GAGAaTAGgTATCct
>Fam_550_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.688889
 TTTTTaAGtATCcCT
>Fam_551_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.744444
 ATaTTTTCTTcTTAc
>Fam_552_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 CGAaGACGACaCcGA
>Fam_553_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.822222
 CGCCGTTCTCcTCgT
>Fam_554_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 CaCCAGAaTCATCAg
>Fam_555_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 TTTAAGTaATcTAaT
>Fam_556_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 TTGaTTCTaTaCCTa
>Fam_557_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.755556
 AGAGAAAGAAaGacT
>Fam_558_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 cCTTACTTaCCaaAC
>Fam_559_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.911111
 GGAACCAGTGACAAc
>Fam_560_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 AGATTCATcCAaTTa
>Fam_561_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 TTaTGAAaCgATGTa
>Fam_562_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 aTAcTCTCaaCTAAA
>Fam_563_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 CaTTTTTTCATAacT
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>Fam_564_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 aaAGGTcATTTCGgT
>Fam_565_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 TaaTTACgGATCAAA
>Fam_566_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 TCaATCCcTCTATga
>Fam_567_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 aTacTTTCATTTCCa
>Fam_568_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 1.000000
 AGCTACAATTTGCTA
>Fam_569_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 CTcTTCTaCTaCATC
>Fam_570_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 TTCATCAaCaTaGAT
>Fam_571_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 TaacTGAGAGAAaGT
>Fam_572_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.733333
 CAATTTCCGAacCTg
>Fam_573_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 CaTCTaCTCTTAaaG
>Fam_574_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.750000
 catAACTCTAAATG
>Fam_575_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.654762
 aAATGaAAGTGAac
>Fam_576_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.773810
 GAACgGGGAACGGg
>Fam_577_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.678571
 CTACcGaCCACCAa
>Fam_578_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.678571
 ATTGAcCATcCTTa
>Fam_579_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.773810
 TGAGtTTATTCAGa
>Fam_580_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.642857
 tgAGAcTCTAACTg
>Fam_581_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.678571
 ATaGTGGAATcAGg
>Fam_582_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.678571
 TTTGtCGCTTAcTt
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>Fam_583_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.726190
 cgAaTTTATCTATC
>Fam_584_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.761905
 TCATTTaTCgCTTC
>Fam_585_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.761905
 TgAGGtTATTAGAG
>Fam_586_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.678571
 aAAACgTAAATGGc
>Fam_587_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.726190
 GTTCATaAaATTCa
>Fam_588_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.666667
 AaAcTCTGATAcTT
>Fam_589_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.726190
 aATAACCAGAATaa
>Fam_590_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.726190
 TCTcACTTTTGaGa
>Fam_591_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.726190
 TTTCAGAAaCaACc
>Fam_592_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.666667
 aTTTCgCAAGcAAT
>Fam_593_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.666667
 cTGAATaAATAgTC
>Fam_594_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.726190
 gCAGACaTTAAaAC
>Fam_595_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.666667
 AgAAACaTTAGgAG
>Fam_596_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.726190
 TGAAaaATAAAACt
>Fam_597_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.726190
 AaGAAATGTTcAGg
>Fam_598_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.738095
 TagAATAATAAcTT
>Fam_599_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.714286
 GGATTATTCgcaAC
>Fam_600_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.714286
 TcAcTAAACTgAAT
>Fam_601_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.619048
 TcAAcGAAaGCAAa
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>Fam_602_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.809524
 GTAAaCTGTAAaCT
>Fam_603_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.809524
 AAGaaATCAATTGA
>Fam_604_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.619048
 aAaaAaTgaaTGTc
>Fam_605_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.714286
 TTTGaAGAAAcCAg
>Fam_606_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.714286
 GAAGGaATTTaAcA
>Fam_607_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.809524
 ATaAAaTACCAAGA
>Fam_608_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.904762
 CAACTCTGCTGGCa
>Fam_609_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.619048
 AAaAGgTTGaAaTG
>Fam_610_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.714286
 aAAAaTgGTTAGTT
>Fam_611_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.714286
 TGATgaACTCAaAC
>Fam_612_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.717949
 AAaAACAAAGGcg
>Fam_613_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.653846
 cTCGgCATCATcA
>Fam_614_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.756410
 tGTTCaTGATTCA
>Fam_615_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.743590
 AaAAGAAGtGAAT
>Fam_616_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 AaGACcCAAGTCt
>Fam_617_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 TCCCTaGTTaCTa
>Fam_618_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.743590
 CATTTCAtTTgCT
>Fam_619_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.653846
 aTATCTTcTaCAA
>Fam_620_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.641026
 CAtTCTaAcCATC
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>Fam_621_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 aATATTTGTgTCg
>Fam_622_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 AGGTAaTTTgATc
>Fam_623_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 GTCAGGaAAaCTg
>Fam_624_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 CAaTGAAAAaATc
>Fam_625_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 AaATcTTATCAAg
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>Fam_673_11_2  Nr. of seq. 2 Alignment length(with gaps) = 11 Alignment score = 0.757576
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GGCTCCTCCAGTCATAACCAGCATTGCGGTATAGCCCTGCCAGCCCCAACCATTGATATAGGAGACACGCAAGCAGTTTACCGCCACCTGCTACGATCAGTATGACAATGA
GATGCCCGANGTGACNNNTGTTTCCTGGTCAAGTGAGAATACAACAGTA
>Fam_675_264_1  Nr. of seq. 1 Alignment length(with gaps) = 264 Alignment score = 0.000000

TGGGACTTTGATAACGATGGAACTGTAGACAGTACTAAGCAGAATCCAGTCTACACTTATGCTGCATCTGGTAACTACACTGTCAATCTTACTGTTTCCAATGCAGGTGGA
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AGTGATTCTGAAGTCAAGACTGATTACATTGTCGTAAGTGAACCACTACCTGGAGTACCAGTTGCAAACTTTACTGCAACGCCTACTTCTGGCGATGCACCACTTAGTGTG
AACTTCACTGATGCTTCAACCGGCACTGTCTCCTCATATGCA
>Fam_676_258_1  Nr. of seq. 1 Alignment length(with gaps) = 258 Alignment score = 0.000000

ATGTATTATCGTGACGGAACAAACTACACTATCACATTGAAAAACACGAAAGGAACACCACTAACTAATGCCGATGTAACATTCACAATCAATAATGAAAACTACACAAGA
ACAACTAATAAAAATGGTATCGCATCCATTACAATCAACCTGCCGGAAGGAACATACACAATAAAAGCAACATATAAAAACGCATCAACAACCAATAAAATTATTGTTAAA
GACTACGAACCAGTAATCACTGGAAAAGATGTGGAA
>Fam_677_258_1  Nr. of seq. 1 Alignment length(with gaps) = 258 Alignment score = 0.000000

TGCAGATTTCGTTGGTTCTCCAGTCTCAGGAAGTTCCCCATTAAAAGTGCAGTTTACTGACAAGAGTACAGGGTCCCCGACTTATTGGAAATGGAACTTCGGAGATGGATC
GGATCTGGTAACTGAATATAATCCAACACATACATACTCAAAACCCGGAACGTATACTGTGAAAGAGACCGTGAGTAATGCAGCAGGTAAGGATACGGAAATAAAAACGGA
TTATATAACCGTGACAGAAGCTTCACAAACTCCTGA
>Fam_678_255_1  Nr. of seq. 1 Alignment length(with gaps) = 255 Alignment score = 0.000000

TATGCCAGGGNGCNGCNGCAACATTCNCTGTTCAAGCANANAGCAGTGAGCCATTGAGCTATCAGTGGCTCAAAGATGGAATGAAGATNCCNGGTGCTACGTCTGATACGT
ACACCATCCCTGCCGCTAACCTNANCGATACGGGAAGCTACTCNGTNCAGGTGACAAATAANTGCAGCCAGATCGAATCGGAGGCTGCTGNTCTGGATATCATCGCNATGC
CTGANATCCTGNCCCAACCGACCAGCCAGAAGG
>Fam_679_254_1  Nr. of seq. 1 Alignment length(with gaps) = 254 Alignment score = 0.000000

GATGAAAACGGTACTGCNAGATTAAACATTTGGTTACATCCNGGCAGCTATATTATAACTGCTTANAATCCAANTAATAATGAAGCAANNNCAAACAATGTAACTGTTTTA
TCNACAATTAATGCAAAAGATGTTACANTATANTACAAAATGGTACTCANTATTATGCAGTTGTTTTAGACGGTCAAGGTAATGCTTTAGCTAATCAGACTGTTAAATTNA
ATATTAATGGTGTATTCTATACTAAAACTACT
>Fam_680_254_1  Nr. of seq. 1 Alignment length(with gaps) = 254 Alignment score = 0.000000

AATTCTTCCTGTAGCGAATTTCACTGCAAATCCGACAGAGGGTTTTGCTCCTCTCACTGTCCAGTTTAACGACAGTTCTAAAAATGCAACTTCTGTAAGCTGGGACTTTGA
CAATAATGGAGTTAGTGACTCCACAGAACGAATGATCCAATTTATGAGTTCACAGTTGCAGGACTCTATACCGTTAATCTGACTGCAATCAATGTAAACGGTACGAATTCA
ACGTCAGCTATAATCAACGTTACTGAGAAACC
>Fam_681_252_1  Nr. of seq. 1 Alignment length(with gaps) = 252 Alignment score = 0.000000

CCATGCTGTCGGGTTGTTTTCACTTTTGTCCTTGAATTGAACGGTAAGAGGAACCGGTCCTGTAGTTGTATTTGCTTCAAAATCTGCTGTNGGTTCAACTATTGNATATGC
CCGGATGTAAGAAAGAGCTTCCGAGGTATCGGANCCGTACNCATTTTTTACTGTCAGCTCCACGGTATANTTTCCTGCTGAGGAATATGTATGGGAAGGATTTTGTTTTGT
TGAAGTAGTTCCGTCTCCGAAGTTCCAGTT
>Fam_682_249_1  Nr. of seq. 1 Alignment length(with gaps) = 249 Alignment score = 0.000000

TTCTGGTTTCTCTTTCTTGTCCTTATCTGGCAGTAAAACCTGAGCACCAGGCTTGGTACCGGTTGTACCGTCATAATTCGGAGTGGCAAGAGTTGTACCTTCATCAGTGAT
CTCCTGAGAACCGGAAGGAGTAGTAACCTGGGCACCTTTCTTCTCCTTATCTTCCTCAGTCTCCTGAACAGGGATTATAGTCGACGTGGCCTCAGGACTAACAGTTACAAC
TGGCTCGACATCCGAAGTCTTTTCAGA
>Fam_683_211_1  Nr. of seq. 1 Alignment length(with gaps) = 211 Alignment score = 0.000000
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GACCTCCAGAACGGTTTCATCGCAGGAGGGGCGGAGGCCGCTGGCGTGGGAGTCCTGGCTGAAGGCNGNAGAAACNGGATCGCNAGCGAGTACCCTGGCGGCCGGAACCGG
ATGGTATGGAACCGGCGCCTACGGCGGAGGCATNGAGGCNTCCAACAGGGAGGGTGCNGTTGNNGCNGCCGCNGCCGCCGGNGGCCTGGGCGCAANCNTC
>Fam_684_195_1  Nr. of seq. 1 Alignment length(with gaps) = 195 Alignment score = 0.000000

ATGTTATCTGAAACATTTATCGTCTTGTCACCGCTTGCATTGTAATTACCTGCATCGTCATAGAAGGTAGCGTTGAAGACAATGTCCTCCACTGAATCCATTGGGACATTC
AGGGTATAGTTGTACCAGTTATCGTTCTTTGTGAGTTCAGCAGTATCGTTAGTTGAAATGTTGAACTCTGTACTAGTAATTCCA
>Fam_685_192_1  Nr. of seq. 1 Alignment length(with gaps) = 192 Alignment score = 0.000000

TTGATCTTGGCGACAAAAGCGTCAAACGAACCGGCATTCGATGCCTGCAATGGATTTTTTGTCGGGAAGTTGGCGGAGNCTGTATACCCGGTGACATAGGCGTTGCCGCTC
CCATCTACAGCGATGCCTTCGCCATAGTCATAGCCGCTTCCTCCCAGGTAGGTGGAATAAGACAGTGCCGACCCGGCGGAA
>Fam_686_176_1  Nr. of seq. 1 Alignment length(with gaps) = 176 Alignment score = 0.000000

CTGTCGCCATCATCAGGGGTGAGTTTGGCCTGCTGACTCCAGGATCCGTCNTCGGCCTCGAACACGTACGCCGAGCCCGCCTCCTCGCCGTTGGAGGTCTTCGTCGACTGT
GGGCNCCGATAATNGCAGTGGTCCCGTCACTCGACATTGCCACTGACNNGCCAAACCAGTCTTCA
>Fam_687_159_1  Nr. of seq. 1 Alignment length(with gaps) = 159 Alignment score = 0.000000

GTGTTCTCATAACCATATGCNNNACCACTNGAANCNCCTATTAGTAGGTCATAGTCTCCATCGCCGTCNAGGTCAGCTAAACATGGTGCTGCNNTACTTCCTATGTCAGGA
GCATCCCATTCAATTTTTCTTGTCCACACTGGACTGCTTGGAGTCCCT
>Fam_688_156_1  Nr. of seq. 1 Alignment length(with gaps) = 156 Alignment score = 0.000000

ATAGTAGACACGCGGATCTCCAACGTAAGTTATTGATGAAAGCNGACTTANAGNCAATGCTGGCTGTCCACCAGAATCTACAGTCACATCTCTGTTATGCCAGGTACTGTC
AGAGCTATGCCATGCATATTCGTAGACATGATAATTATTGCCAAN
>Fam_689_156_1  Nr. of seq. 1 Alignment length(with gaps) = 156 Alignment score = 0.000000

GATGCCTGGCTAATAAAGACNGANTCNAATGGCAANGAGCNNTGGAACAGAACCTTTGGAGGGNCNAANGACGATTGTGGCTANTCGGTACANGAGATNAANGATGGCGGC
TATATCATTGCNGGTGNGACGAGNTCCTATGGNGCAGGNGGAANN
>Fam_690_154_1  Nr. of seq. 1 Alignment length(with gaps) = 154 Alignment score = 0.000000

CCGTACGTCTCGTCGAGGTACTCGACGATGTCAGACCCACCTTTTCCTCCTCGGGTTCGGTCACTCCGTTCCCGAACCACTCGTCGCAAAACGTGGGCGAAAAGACCGCCC
ACTCGCTTCGCTCGTGGACGAAGAGAACCCTTACGCTACGGTT
>Fam_691_154_1  Nr. of seq. 1 Alignment length(with gaps) = 154 Alignment score = 0.000000

TCCAGACCTCCCGNCCCTTCGAGTCGGCCTTGAGGAGCCAGAGGTCCTTNCCNCCGGCGCCGAAGGANTCGGTNCTGCCCGACGATGACGAAGCCNTCGGCCGTCTCCTGG
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>Fam_692_154_1  Nr. of seq. 1 Alignment length(with gaps) = 154 Alignment score = 0.000000
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AGAAGGAGATGTNTGGGTTCTCAGGCTCGACGAGTATGGAAAT
>Fam_693_153_1  Nr. of seq. 1 Alignment length(with gaps) = 153 Alignment score = 0.000000

TATGATGTAGCCNCCGTCGNCTGTCTGCTGGACCGAATNTCCCTCCTCTTGNCCNGCTCCTCCGAAGGTTCTGTCCCATACCCTGTATCCGGANGAGTCCGTCTTGATCAG
CCAGAGGTCTTTNCCGCCNAAGTCGTCGAGGGTATAGCCTGT
>Fam_694_150_1  Nr. of seq. 1 Alignment length(with gaps) = 150 Alignment score = 0.000000

TCGTAGAATAGGAGGTCGGTGAATCCGTCNCCGTTGAANTCTCCGGGGACGATCGTCGACCATGTCCTCCTCCATCCGCTGTGAGATTTCAGGAGCCTGATGTTCCCGCTC
CCGTCGGTGGCGTAGAACTCGCCCTGGCCTGCGGCGGGG
>Fam_695_149_1  Nr. of seq. 1 Alignment length(with gaps) = 149 Alignment score = 0.000000

TCGACCGCCACACATCGTTCTGANAGGTGTTNCCGTCTAACCGCCCATGAGTACGATGCTNCCGTCCNGCATCGCGACACNGCTCTGTTCGGNTCGTCCCGACCACCCGGA
ACTCGGGTTCTGCTCTGTCCACGTTNTGCCGTTATCGG
>Fam_696_147_1  Nr. of seq. 1 Alignment length(with gaps) = 147 Alignment score = 0.000000

CACAGCAGTGTTGTTCTTCCCGACGGCAGTATCGTGCTCATGGGCGGTNATGNTAGCAACGTTAAGAATGACACGTGGCGGTCAACTGATAACGGTGCAACCTGGACCGAG
GTCAACTCAAGCGCCGGCTGGTCTGCAAGGTATTCT
>Fam_697_145_1  Nr. of seq. 1 Alignment length(with gaps) = 145 Alignment score = 0.000000

TGGAGGGAACTGATATGATCTTCGAGATGTTCTATAAAAATGTCAAAATCGCCTACGAATCAACTGTATTCAGCATGTTTTACTGCTTCTAATTAAGCTGTAAGACAGGTG
CATAACGGGAAACGACCAAAATCCAGGAAAATAT
>Fam_698_142_1  Nr. of seq. 1 Alignment length(with gaps) = 142 Alignment score = 0.000000

CAAAAAGCTCTAGAAATATATACAGTTAGATAAATATCCACTTGACTATGCCATGGTTCAAAATAATCTTGGAAATGCATATAGATGTTTAGCTGAGGTTAGAGATAAGGA
AAAAAATGCTCAAAATGCTATTAATGCATAC
>Fam_699_141_1  Nr. of seq. 1 Alignment length(with gaps) = 141 Alignment score = 0.000000

CCCAGTGGGGATCAGCAGGATCAGGAAACGGGCAGTTTAACCAGCCCTAGGGGATCGCCATCAACACGACCGGGTATGTCTACGTGACAGACTAGGACAACAACCGGATCC
AGGTATTTGATCCGAGCGGAAACTATGTTA
>Fam_700_141_1  Nr. of seq. 1 Alignment length(with gaps) = 141 Alignment score = 0.000000

TTCCAGGCAATGTATAGACTATTGTTATGTACACAAAGAGCCGGGGATTCAGGACTTGTCTCAGAAGAAGTGTATTTGTTCCCAAAGGTCATTCCGTTGTCCGCCGAGTAC
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>Fam_702_141_1  Nr. of seq. 1 Alignment length(with gaps) = 141 Alignment score = 0.000000

TAACTGATCCGGGGGTTGCCGGCGCTGTCCAGCGCCAGGGANGTGTACCACCCGACANACCCCTCTGAATCCACCGTTTCATTGTGCCAGCCCGAGTCATCGTGCCACGCA
TACTTCAGGTCGTTATTCGTNTNATCGAAG
>Fam_703_138_1  Nr. of seq. 1 Alignment length(with gaps) = 138 Alignment score = 0.000000

GCATCGTTGTTGTAATCCAGATACCAACCCCGATTAGAAGGCCTGAAAACACCTATTGTGTCCTTACCATCACCATTCCAATCGCCTGCAACTGCCAGGTCACCATTCAAG
CCGTACACAATGATAAAGTCAGGAACA
>Fam_704_137_1  Nr. of seq. 1 Alignment length(with gaps) = 137 Alignment score = 0.000000

TTTTCCAATTTCTGATGGTAACTGTNTTAGATTATTATGACAAAGNAAAGTTTTATAAGNTTTNTAAGTTCCCCAATTTCTGGAGGTAGTAGAGTCAATTGATTNCTAGAT
AAGTCAAGTTCTCTAAGGTTCTTAAG
>Fam_705_133_1  Nr. of seq. 1 Alignment length(with gaps) = 133 Alignment score = 0.000000

CGGTGTCCTTTTCGCTCGCTTTGCTCTCTCAAGAGGACTAATTGACATATTTATGAATCAGCCGTGAATCAAACGTGGAAGGCATCGAGTACAAACCCACATGCTCTCCAT
CCCGAGTTCCTTCTCGGGAGGA
>Fam_706_129_1  Nr. of seq. 1 Alignment length(with gaps) = 129 Alignment score = 0.000000

TGCTGATCCACTGGTTGTAATTTGAGTTTCTACGGAGGTGGACAAATTGTACATGTAGANCTCAGATTGATTCCATCCGTTGCGATTATCCTTCCACACGATTTTATCCCC
GTAAATTGCAGGATAATC
>Fam_707_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

AATCTTGCAGGACTTTACNCNAAAATAGGAAGATATGAAGAAGCTNTACNTCTTTATAATCGTGCTTTAGAGATCNATAAAAAATTNTTTGGAGAGGAACATCCCTATATT
GCNATNACTCTAAAC
>Fam_708_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

CCAGGGCAAATATTCTGATGCCGAACCACTTTACACTCGTGCCCTGGAAATCCACGAGAAGGTTTTGGGGTCAGAACACCCTTACGTAGCAACTTCTCTTAATAATTTAGC
AGGACTCTACGTACA
>Fam_709_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

AATAATCTAGCGGAACTATATAGAAATTCAGGCAGATATTCTGAAGCTGAACCTCTGTATACCCGTGCCTTGGAAATTACAGAAAGAGCACTGGGACCGGAACATCCAGAT
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>Fam_710_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000
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>Fam_711_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

ACGTATATGTATCCATTACTAGGATCATANAANATACTCNATGGATCTTGTCTNATNGATATATTAGCTATNACANTGTTNGTAGTAGAATTAATTACAGAAACTGTATTA
GACCTAGAATCTGCA
>Fam_712_122_1  Nr. of seq. 1 Alignment length(with gaps) = 122 Alignment score = 0.000000

AATTGCTTTTTTAGATTCNCCCTTTGTAAATGAATGCTAGACCTATATTNCCGATNCGAATTCCTTCACTTNACCATATTGTTTATNTCCTTTGAAATTTTCAAAGCTTGT
TCATAATATTC
>Fam_713_121_1  Nr. of seq. 1 Alignment length(with gaps) = 121 Alignment score = 0.000000

CCTTCCAATGGTTACGTGTATGTAACGAACTTACATTCAAATNACAGTCTCTGTTATCTCAGGTACTAATGTTGTAGCTAACGTCCCTGTTGGTGTTGGCCCGANCTATGC
TCTTTACGAC
>Fam_714_120_1  Nr. of seq. 1 Alignment length(with gaps) = 120 Alignment score = 0.000000

TATGATCCTGAGAATGGGTATATGTATGTTACAAACTTTGGTTCTAATACAGTTTCTGTAATCTCTAATACATCAGTAATTGAAAATATTAATGTTGGGAATGGACCTATA
GGTATTGCT
>Fam_715_120_1  Nr. of seq. 1 Alignment length(with gaps) = 120 Alignment score = 0.000000

TAAATCCTGACGGAACAGAAAAATGGAGATTTAATACGGGAAAGTCGATTGATTCAACTCCNGCNATTGNAAAAGATGGTACAATCTATTTTGGTTCANATGATGGTAATT
TATATGCCA
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TGTATGCGATCGATGCCGNNACNGGAAAAGAGAAGTGGCGGTTCGCTACGGNAGATNGNGTGGTTTCATCTCCNGCNGTAGCGAACGGNATTGTCTATGTCGGGAGTGAGG
ATAANAACC
>Fam_717_120_1  Nr. of seq. 1 Alignment length(with gaps) = 120 Alignment score = 0.000000

AATATTATGAGCAGGCTCTTTTAATTTCTCGAGAAATTGGTGATCGACGCGGAGAAGGAANNCATCTTGGCAACCTTGGTAGTTCCTACNTCCATCTTGGTGAAGTTACTA
AAGCTATCG
>Fam_718_120_1  Nr. of seq. 1 Alignment length(with gaps) = 120 Alignment score = 0.000000

CTCGATGATTCNAAATTTCAGTCAATTATCCTGAACAGTTTGGGAAGCATTCTTCAGAAACAGGGTAGATTGAGGGAAGCAGAAACTACTTTTCAAGAGAGCTTGCATATA
GCGAAAAAA
>Fam_719_120_1  Nr. of seq. 1 Alignment length(with gaps) = 120 Alignment score = 0.000000
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TCCATTTGAGGGTGCCGTTGGCGTTGAGCGCATAGAGACTGTTATCNTAACTCCCNGCGTACACGGTCCCGTCCGAAGCGATCGCAGGGGAGCTATAAATGCGTCCACCGG
TAGCGTACG
>Fam_720_120_1  Nr. of seq. 1 Alignment length(with gaps) = 120 Alignment score = 0.000000

CACCGTCTTCGTCGGGAGCAACGACGCCAATCTGTACGCCGTAGACGCCGAAACGGGTACCGAACAGTGGCGTTTCGAAACCGACGACCGGGTCCANTCGTCGCCGACAGT
GGCCGACGG
>Fam_721_117_1  Nr. of seq. 1 Alignment length(with gaps) = 117 Alignment score = 0.000000

CTAAATCCTATGTTTCTAATGGTAAGGTTGCTTTCAAAGTTAATGATAAAACTGTTGGTTATGGTAGTGTTTCTAATGGTAAGGCTTATTATACTTATGATTCTAGTAAGT
TATCTG
>Fam_722_117_1  Nr. of seq. 1 Alignment length(with gaps) = 117 Alignment score = 0.000000

AATTCCCAAATCTCCCTACCAGTTTTTAAATCCAAGGCGTAGGTGTATCCTNCANNACATCCCAATACAACAATATCGTCTTTTATGGATATTNCCNATACACTCTCAGCA
GCCTTA
>Fam_723_113_1  Nr. of seq. 1 Alignment length(with gaps) = 113 Alignment score = 0.000000

GCGTGACAAAAACGACACGGTAAAGCGAATACGGTTGTACTGGTCCTACATATTATTCAGTAGTCCTCTTGAGCGCAGCGAAAAGGACCTCGTGCTCCCGAAGCGAAACTC
GG
>Fam_724_109_1  Nr. of seq. 1 Alignment length(with gaps) = 109 Alignment score = 0.000000
 TTATCTGGCACGTCAGAAAATACAGCCATAAGAACTTTAGCGGCCCACGTTCTCACTTCATCGNTCTTGATCAGTGAGAAGTCTAATTAAGTCATTGTATGCCTGTTGC
>Fam_725_108_1  Nr. of seq. 1 Alignment length(with gaps) = 108 Alignment score = 0.000000
 GCTTTATCGTATTCTTCTTTTAANNGATAACAGAAACCCANATTGTTATTTATCTGCCATTTTTCTTTATCGGGGCTGATTTCCAGTGCTTTCTTATAATATTTAATG
>Fam_726_108_1  Nr. of seq. 1 Alignment length(with gaps) = 108 Alignment score = 0.000000
 TTTTCAATATGTACCGGANAAAAATCAGGCATGGGAAGANTTAGTTAGATTGACNTCAGATAAAGANAGTGATNTACGTTGGANAGTAGCAGAGGCNNTTGGAANTGT
>Fam_727_105_1  Nr. of seq. 1 Alignment length(with gaps) = 105 Alignment score = 0.000000
 AAGCAGAAGAATTTTACAGAAAAGCTCTGGAAATTGANCCAGANNACGCTAATAACCTTGGAAATTATGCAAATTTCCTNNANNATATTCGNAAAGATTACAATA
>Fam_728_103_1  Nr. of seq. 1 Alignment length(with gaps) = 103 Alignment score = 0.000000
 CAAGCTTATAATGTTTTTCAGCTTCTTCCATACGTCCCATTCCGCTNCAGGAAAAGTCCGTAATTTAANTGTATGGATACAATTTTTGGATCGATTTTCAAAG
>Fam_729_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
 CTTTTTCATATCTCTCTAATTTATATAACGAATCTGCTTTATAATACCAAGCGGCTGGATTATTTGGATCGAGTTTTATTGCTTTATCAAAACATTCTATCG
>Fam_730_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
 TCTATCGCTTCATTGTACCTTTCAAGATTACAAAGTGCATCGCCCTTGTTATTNCAATATGAACTAAAATCTGGATCTATCTCAATTGCTTTATCATAGCAC
>Fam_731_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
 ATTGCTTCTTCGTATCTTCCCAAGCTACTAAGTGCCAAACCCTTGCTATCCCATGNACTATCAGACNTTGGGTTTATTTCTATGGCTTTATCATATGCCTGT
>Fam_732_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
 GACCGCCTCCGAGAGCCGCCCCAGGTCCCNGAGGGCGACCCCCTTGTTGTTCCAGGCGTGGGGGTANNCGGGGTCGAGGCTCAANGCCATATCGTANGCCTC
>Fam_733_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
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 TCAGGATTCAGCCTCATAACCTCATCAAAAGCCTGGATGGCCTCGTCGTACCTGCCCAGTGAATCGAGAGCNGCACCTTTGCTGTTCCAAGCATCGACATAC
>Fam_734_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
 AAAGCGCAAACTCATCGTCAGGATTTAGTTCCAAAACCTTATTAAAAATCTCAACAGCTTCCTCATATCTATCTAATAAAACTAAAGAAGATCCTTTGTTAG
>Fam_735_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
 TCAATTGCTTTATCAAAGGCTTTTACTGCTTCCTCGTAATTGCCTAAACACTCAAGAGAATATCCTTTATTGTACCATGCATCTGAATTTTGAGAGTTAATT
>Fam_736_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
 ATGGCCTCATCGTATTTGCCTAGGGCCNNGAGCGCANTGCCTTTGTTGGACCAGGCNTAGGCATACTGNGGATCNATGCTGATAGCCTGATCGNAAGCCTTG
>Fam_737_99_1  Nr. of seq. 1 Alignment length(with gaps) = 99 Alignment score = 0.000000
 GTTTAGTTGGTTATAATCACGGTTATTATGGTGGTNATTTGACAATCACAAACAGCTATGCTACAGGAAATGTAACAAGTTATGGCGACCGTGCAGGTG
>Fam_738_99_1  Nr. of seq. 1 Alignment length(with gaps) = 99 Alignment score = 0.000000
 TTAATATTCAGGATGAAAACGGCGANACNGCTTTGATTTCTGCGGCAAANGGNGGAAANAGGAACATTGTTGAGTTGCTTATTAAAAGTGGTGCCGANC
>Fam_739_98_1  Nr. of seq. 1 Alignment length(with gaps) = 98 Alignment score = 0.000000
 AAAAATAGCGAGGAGAAGTTCCAAACGAAAGGGCTACGCCCCTTTCAACCCTAGCGGGATAACAAGTTATCCCACTGGTAAAGTTTTAAGTTTTACAA
>Fam_740_87_1  Nr. of seq. 1 Alignment length(with gaps) = 87 Alignment score = 0.000000
 GACAACCACAATCCGGATCAGAACAAGAATCCTCATCCTCATGCCCATGATGATGCTCATGCTCGTGCCCATGGCCATGCTCATCAT
>Fam_741_86_1  Nr. of seq. 1 Alignment length(with gaps) = 86 Alignment score = 0.000000
 AGATGATTCCCGGAACCGCCGTTACTCGAAAACGCTTCGCGTTTTCTCGAACTCCTGCCGGTCGCTCCGCTCCCGCCAGTCGTGGA
>Fam_742_84_1  Nr. of seq. 1 Alignment length(with gaps) = 84 Alignment score = 0.000000
 CTACAACAGGAGGAACTTCAGAAGGTTCATCTGATGCATCATCAACAGAAGATGTGATTTCAACAGATTCCTCTGACACATCAT
>Fam_743_84_1  Nr. of seq. 1 Alignment length(with gaps) = 84 Alignment score = 0.000000
 ACCAACAAGGCCACCTACATAATCTCCAGTTCCGGTCACATCACCTGTGGAATATGAATCTGTAATAGTACCNCNATAATTTAT
>Fam_744_84_1  Nr. of seq. 1 Alignment length(with gaps) = 84 Alignment score = 0.000000
 ACTTGATCGGTTAAACAAGGCGATAGAACTCGTNAATACCGAACTGGACCGGTTTAATAAGACACCGCAATTGATAGATACGGA
>Fam_745_84_1  Nr. of seq. 1 Alignment length(with gaps) = 84 Alignment score = 0.000000
 TGATGAGAGAATAACTAAATTGGAGGAGTCTACGAAGAAGTTGGAGCAAGCTGTACAAGAGCTTATTGAGGCTCAGAAAAAACA
>Fam_746_79_1  Nr. of seq. 1 Alignment length(with gaps) = 79 Alignment score = 0.000000
 TTGTTTATTATCTCTCCACTNCTCTACTNTTATGNTGATGGCNCCTCCTCNGTAGGATGCGNTGTTGTTTTTGAATGTG
>Fam_747_78_1  Nr. of seq. 1 Alignment length(with gaps) = 78 Alignment score = 0.000000
 TTACAGCTTCAAGACGAACANTCNAATCAGNATCATTTTTAGCAANATNNNCTAAAACAGANTNATCATTTATCTTCC
>Fam_748_78_1  Nr. of seq. 1 Alignment length(with gaps) = 78 Alignment score = 0.000000
 AAGAAAATGACTCAACGAGTTCAAAAACTAATGTATCTAACGGGTATAAACTAATAACAGTAAATAAAACAGTCGCTC
>Fam_749_75_1  Nr. of seq. 1 Alignment length(with gaps) = 75 Alignment score = 0.000000
 CCACAGTCAAACTACCACCATTGCAGATAGCACCACCACTAACATCGGCTTTATTACCCGTGAATGTACTATTAC
>Fam_750_75_1  Nr. of seq. 1 Alignment length(with gaps) = 75 Alignment score = 0.000000
 GGTGAACGTACACGAACGCTGCGCTGTACCGGCTATCACATTACTATGATACTCTCAAACTGTTATCTCTGTGGA
>Fam_751_75_1  Nr. of seq. 1 Alignment length(with gaps) = 75 Alignment score = 0.000000
 CCGCTCGTGCCGCAACCCGTTCGACTCGCTCAGGCCGCCGCCTTCGCTTCGTCGAAGTCACAGCGTCACGTCACT
>Fam_752_73_1  Nr. of seq. 1 Alignment length(with gaps) = 73 Alignment score = 0.000000
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 CCCCGCGAGTCCACTCCTCTCACTTCGTTCGAGTTGTTTCCTCGCTTGCCCCCGCTCGCTTCGCTCGCGGGGA
>Fam_753_73_1  Nr. of seq. 1 Alignment length(with gaps) = 73 Alignment score = 0.000000
 ATAGCTCCACCNACTGTTGCGGTGTTGTTGTNGAATGTACTGTTAGTTACAATTAAAGTTCCATNATTCGCTN
>Fam_754_73_1  Nr. of seq. 1 Alignment length(with gaps) = 73 Alignment score = 0.000000
 ATTCGAGAGCAAGATCCACTAAAACAAGGATTGAAACCNGTAATCATGACTNNTGANATTTAANCNTAACATT
>Fam_755_72_1  Nr. of seq. 1 Alignment length(with gaps) = 72 Alignment score = 0.000000
 TGAAATTGTTGAAAATCCGGAAAATAACACTTCCAATCAAACAGCTGCTGAAAACCTGACAGTTCCGGAAAC
>Fam_756_71_1  Nr. of seq. 1 Alignment length(with gaps) = 71 Alignment score = 0.000000
 CCCGCTCGCCCTTTCGCGGCCCGCTGCTCGCTTCGCTCCCAGCGCGCCGCGCTACTCACGGATCGTTCCTC
>Fam_757_71_1  Nr. of seq. 1 Alignment length(with gaps) = 71 Alignment score = 0.000000
 GCGGGCGACGCCATGTCGCTCGCTCGGAGACTATGCCGTGGCTGTGTGTAGCCGAACGTGGCACACGACCA
>Fam_758_71_1  Nr. of seq. 1 Alignment length(with gaps) = 71 Alignment score = 0.000000
 TTTTAGTAGATTAGCTTTTGCAATACANTAGANTAAACATNNNAAATGAGNGNANAATGTCGCAATCCTTG
>Fam_759_71_1  Nr. of seq. 1 Alignment length(with gaps) = 71 Alignment score = 0.000000
 TTCAATCCTTGTTTTCGTGGAGTCTACTTCTCGACATTANAAATGACTTANATGGTANGAGANATACGNGT
>Fam_760_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 CTCGACGACGGTTCCGAAGTCGACGAGCTCGGGACGGATCCAGTGGTCGCCGACACGGACGATGACGGT
>Fam_761_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 TTTGCGAATATGAAGTTGTNTTCGATTTCGGTGAAGTCAGATCCGTATACGCTTATTCCGTCATCTTCG
>Fam_762_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 CAGCAGAAAATAAATTTGAANANGCAACAAAATATGCAGTGATGGCATTGGGTCAAATTGGGGAAAAAG
>Fam_763_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 GGTCACGGATGCGAGCGATGAACAATCGTNGAACGCANNNTCCCCGATGGATGTTACCGAGTCGGGGAT
>Fam_764_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 GAACTTAAAAACCTTACAACACTTGACTTATCTAGGAACCAGCTGACACAATTGCCACCNGAAATTGCA
>Fam_765_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 CGATGCTGGTGACNCTGTTCGGNATGGTCACCGAGGTCAGGGCGGTGCAGCCGTAGAACGCACNGNNGC
>Fam_766_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 ATGACGGCAATCCTTGCACTGCCGACTCCTGTGTGAATGGAGAATGCTACCATAGGCGAAAGAACTGCA
>Fam_767_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 ATCTTAGTCTGATTTTAACGGCGNGCANCGAGNTCAAGATCGTCAAGGNAGGAGANGCTTTCAATCCT
>Fam_768_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 CCCTCGCTTCGCTCGGCATGCCCTTCGCTGCTCGCGTGTCGCTACGCTCCCGCTCGCAAAAACGAGAC
>Fam_769_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 AAAATAACGCCCCTAAGGGGATGGAAACATNATCTCNCNTCTTCACAACATNCAANNTGTTGTATTNC
>Fam_770_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 TTATTCCAGAATCNGTTAAGTAGTATCGGAGAATNATGCTTTTAAAAATAATAAATTAACAGGCATAA
>Fam_771_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
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 AGGATGCGACTGCCGGAACGGCAGGAGCTCGAGAAGATGCGAAGCATCTTCGAATGGCGACTGTCCGT
>Fam_772_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 ATGGAGCAAATTAAGGACGGCTTGAAAACCGATCCAGAAATCTACTTCNTTGACGCGTAAGCTGCAAG
>Fam_773_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 GTCTTATTGCAACATNTCGTCANACAGCAGAACCTNCAACTAGACCGTNCGGTTTCAATTCTCCTCGA
>Fam_774_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 AGAAGAATTGAAATAATTGACCTTTTAGAGGACTATGGCATAAGTAAGGTTAGTTTCAATAAGACTTT
>Fam_775_67_1  Nr. of seq. 1 Alignment length(with gaps) = 67 Alignment score = 0.000000
 GTTCATTTCAAACCTTGTTATAGTGGATGTTGCCAAGCAACTGATAGATATTTTGTTAAATGAAATA
>Fam_776_67_1  Nr. of seq. 1 Alignment length(with gaps) = 67 Alignment score = 0.000000
 CTTTCAATTCTATTTTAGTCTTATTGGAACNNTNANNGATNCACNTGCTCNNAANNAGCNNNTNANN
>Fam_777_67_1  Nr. of seq. 1 Alignment length(with gaps) = 67 Alignment score = 0.000000
 CTCTTAGAGTCTTATTGAAACCANTACTCTGTNNANATGANCTNNTGAANCTTCANTNCTTTCAATT
>Fam_778_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 ACCACATGGTACTTCTTCTACTGATNTGAAAANGANATANGNTAAAGTGANAGAAATNGTTTCCAC
>Fam_779_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 CGTCAGTGTCNGCGNCTGTCGGGTTCGTGCCNATGGACAGCTCNCGCCCGTCGGNNACCCCGTCGN
>Fam_780_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 GTTAAAATAAGACCGTCTCGGTATCTAATACAAAAANTNCTCATAGCTTNGATTNCGTCTTTAATT
>Fam_781_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 GGAATAACCAAACTCTTCAACTGGTTATNTGAAAAAGCACCTCTNCCAATACTAGTTACNGAATCT
>Fam_782_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 AACCAGATCAGCGATCTGAGCCCCCTCGCCGGACTGACCAACCTGGNGTATTTTCTAGATATATCC
>Fam_783_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 GAGAATGCTGACGTTATTGATTCTGACGCTACTAATGATGATTTAAACGGAAATTCTGATTTAAAT
>Fam_784_65_1  Nr. of seq. 1 Alignment length(with gaps) = 65 Alignment score = 0.000000
 TCTACTATAGAATTGAAAGAAAGTTNNNAGAAGANTTTAATTACCATTCCGCNTGATGACGATAA
>Fam_785_65_1  Nr. of seq. 1 Alignment length(with gaps) = 65 Alignment score = 0.000000
 CCACAAGGGTTCGTCTGTAACTACGGTGAGGACGTGNACCGATNNCGTNCGACGNTGCTTCAACC
>Fam_786_65_1  Nr. of seq. 1 Alignment length(with gaps) = 65 Alignment score = 0.000000
 TCTGATTCTAACNNTTAANNTNNNTNANNANNTNNANNTNTAANNNAATTTCAATCCTAAAATAG
>Fam_787_65_1  Nr. of seq. 1 Alignment length(with gaps) = 65 Alignment score = 0.000000
 CTTTCAATCCTATTTAGGTTATTATTTAACNNNATNGGATTTCNNNNCCNTATCGAGATACTATA
>Fam_788_64_1  Nr. of seq. 1 Alignment length(with gaps) = 64 Alignment score = 0.000000
 GTTGCATCCCAAAAGGGATTGAAAGNAGATTNAGANNAGTAGTANCTGNNCTTNATGTCGGTTN
>Fam_789_64_1  Nr. of seq. 1 Alignment length(with gaps) = 64 Alignment score = 0.000000
 TTAAAATCAGACCTTAGAGGGATTGAAACNNANANNTNAANNTTNNAGNNNNTGNACATNATNG
>Fam_790_64_1  Nr. of seq. 1 Alignment length(with gaps) = 64 Alignment score = 0.000000
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 TCCGGAATCTTCAGCTCGTGACACACTCTTTAAAAAAAATCCTCAGCAGCTGAGTGACCGATTT
>Fam_791_64_1  Nr. of seq. 1 Alignment length(with gaps) = 64 Alignment score = 0.000000
 CAATAAGACTCTAGGAGAATTGAAAATNATCANTGACGTNCTCAANGCNAGCTNANGCNNGTTG
>Fam_792_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 GAGGCACAGAAGAGAAGCGAGGAGAGACTAACTAGACTCGAGTCCGCGGTTGAGAAACTAGCC
>Fam_793_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 ACTAAAATCAGACCATTTTGGGATTGAAACTNANTNANANNATNTNNAGNNNNTNNATTNANN
>Fam_794_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 TTTTCGACCGGCGACTGGTGTTTCCGACAAGCGCCCAGCAGGAGCTGGAGAAAATGCGCAGCA
>Fam_795_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 TCTTATTGCAACGNACAGCACACTCAGGGGGNATCAGGCCCCTCTCTTTCAATTCTCTTAGAG
>Fam_796_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 GTTTGAGAGTGTTGTCAAATACGAGGTAACTCAATCANTATNGGCCGGGNNTANNCAGNCTTC
>Fam_797_62_1  Nr. of seq. 1 Alignment length(with gaps) = 62 Alignment score = 0.000000
 CTAACAAAAGTAGCACAAACTTCTTTGATCAACCTTTCTGTCTAAGAAAGGTTGGCTTACAG
>Fam_798_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 TAAAAAGAAATAGTGTTTTTTAGTTAAATAAGGTGAAAATTGTTATTTTTAATTAAAAAGT
>Fam_799_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 GTTCACCCCCACGCCTGTGGGGACTTTNTCNNNNNNGNNANNGNNTNNNCTGNNNCNTNCG
>Fam_800_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 GAAGCCCCCCTTCAGTCACTAGATTTAGAAGATGTGGTGTTTAACCATCCATTATCTCAAA
>Fam_801_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 TTCATCCCCACGTGTGTGGGGAACTCNANTANNNTCANANNTNTCNNNANNNNTNAANCGG
>Fam_802_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 AACTCTGAAATATATTTCGCTCACGCTTTTTGATCAAACTTTTTTGGAAAAAGTTTGTTGA
>Fam_803_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 TTTTTAATGTTTGATTTGTTTTTGTAATTTATTTATTTTTTTTCTTCTTTTCTTTTTCAT
>Fam_804_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 CCTCCAGGCCTACTCGATCGGTTCCGGGAGCCCGTATCAGTACACATCGGAGTCCAGCGG
>Fam_805_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 TGTGGGGAACTCNNANTTCNCNTANCANTTTGACNNNNANNANCGGTTCATCCCCACGCC
>Fam_806_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 CAGGGCGACAGGCCCTACAAGCCCCGCGAAGGAGCAGCACCCACATCCGGCGACCGCCCC
>Fam_807_59_1  Nr. of seq. 1 Alignment length(with gaps) = 59 Alignment score = 0.000000
 AAATTGACCAAATAGACGTTAATTTGATCAATAGATGTAAATCGATCAAATAAATTGTT
>Fam_808_59_1  Nr. of seq. 1 Alignment length(with gaps) = 59 Alignment score = 0.000000
 TCACCTCGTGACGGTTCGTGTGCCCGGGACGCCCTCGGCGGCCAGACGTTCACGAAGCG
>Fam_809_58_1  Nr. of seq. 1 Alignment length(with gaps) = 58 Alignment score = 0.000000
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 GAGTTCCCCATGCATGTGGGGATAAACCGNNNATNNCATNNNANCNNNCNNANNNNTN
>Fam_810_58_1  Nr. of seq. 1 Alignment length(with gaps) = 58 Alignment score = 0.000000
 TGGGGATGAACCGNNGANNNGACATGACATCCGNGNCNCANNGAGTTCCCCACGCATG
>Fam_811_58_1  Nr. of seq. 1 Alignment length(with gaps) = 58 Alignment score = 0.000000
 TGTGGGGAACTCNCNNNTNNGNTCNGNNNANNNNNNGANNNCGGTTCATCCCCACGCT
>Fam_812_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 GAGTCGTCACCACTATCCTGGTTCGAGGAGTTATCACCGTCGTCGTTTTGACTCGAA
>Fam_813_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 ACTTCTGAAAGGTACTTTTGTGAATCTTCAATTGCCTTGAACATTGAAGGGGAATAA
>Fam_814_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 AATAAGTCAAAAACCGGAACCGGAACAAGTACCGAAACCCCGGAAACAGTAATAGAT
>Fam_815_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 GGTTCATCCCCATACACACGGGGAACTCNNTNNATNNNCNNNTNNGNNTNNTNTTNC
>Fam_816_56_1  Nr. of seq. 1 Alignment length(with gaps) = 56 Alignment score = 0.000000
 ATCAGTGAAGTTGTTTTGAACGTCTGCATCATTGCTGAACTCACAGCTCTATTCAC
>Fam_817_54_1  Nr. of seq. 1 Alignment length(with gaps) = 54 Alignment score = 0.000000
 TAGGGATGATATCTGTGATTCTAATGTGGAGTTAACGTTTGATAGTGAAGTGCT
>Fam_818_54_1  Nr. of seq. 1 Alignment length(with gaps) = 54 Alignment score = 0.000000
 TCGCCGTCCTTGGTTCGAACATCGGCGTCNCCTGTCGTCTTGCGGGCGGTGGCG
>Fam_819_54_1  Nr. of seq. 1 Alignment length(with gaps) = 54 Alignment score = 0.000000
 CCGCGAGGTCGACCAGCGGGAGACCTCGGAACGAGCGAGCGGTGAAACCGTGAG
>Fam_820_54_1  Nr. of seq. 1 Alignment length(with gaps) = 54 Alignment score = 0.000000
 CCAAAGCCCCAGCCGCTCGGTAGTACGTGATCGACGACTCCGCGGTGAACACCG
>Fam_821_54_1  Nr. of seq. 1 Alignment length(with gaps) = 54 Alignment score = 0.000000
 GATTCTCCTTTAATGTCTGATTCTGTCATTTCTCCTTCCTTACCTGATCCATTG
>Fam_822_53_1  Nr. of seq. 1 Alignment length(with gaps) = 53 Alignment score = 0.000000
 AAATAAAAAATTAGATTAAATTCCTAAGGTAAAAAATACCAATATAGGAATTA
>Fam_823_52_1  Nr. of seq. 1 Alignment length(with gaps) = 52 Alignment score = 0.000000
 CATATGAAATTATGTTTAGAAGCAGATCTTAGGAACCTAATTTTCTAAGTTA
>Fam_824_52_1  Nr. of seq. 1 Alignment length(with gaps) = 52 Alignment score = 0.000000
 TTGTTTTGTAATGAGTTTTGGTATGGTTTTTTTTAGTTGTTTGGGGATTTGT
>Fam_825_51_1  Nr. of seq. 1 Alignment length(with gaps) = 51 Alignment score = 0.000000
 ATAAAGATTTAGAAAAATAGTTTAAAAAAAATAACTAAAATAACTTAAATT
>Fam_826_50_1  Nr. of seq. 1 Alignment length(with gaps) = 50 Alignment score = 0.000000
 TTTGAACCTTATCTGGAATACTTTTGACCCTGGTCTGCTGACAGAATGCG
>Fam_827_50_1  Nr. of seq. 1 Alignment length(with gaps) = 50 Alignment score = 0.000000
 CTAGAACATCTCCCTCTCATGCTCCAGATGGTGTTCCGAAGTAACCTCTG
>Fam_828_49_1  Nr. of seq. 1 Alignment length(with gaps) = 49 Alignment score = 0.000000
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 GTATTTCGAAACCCTTTGGGTTTCTCAAACTCCGTTCTGTCGGAACGTC
>Fam_829_49_1  Nr. of seq. 1 Alignment length(with gaps) = 49 Alignment score = 0.000000
 GAGGAGAAGCTTGAATTTAAGAGGAAGTGGGGTATTGAGTAGTTTTTT
>Fam_830_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 GGTTCCACGAGCCCCCGCTCGCAGGCTCGCGGGGACGCCGTAGAACAC
>Fam_831_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 AAAAAATAGGCGAATTTTATTTTTGTTTATTTAAACTTTAAGAAAAGG
>Fam_832_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 TAAAATAAGTAAAATGTCTACTTTATTAATTAATGAAGTATAAAGCCT
>Fam_833_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 ATAAAAATAAAACCTAAAATAGAACAAAAAAAAAGATTCAAAAACTGA
>Fam_834_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 CAATTAATGAAGATGAATTTACAGCAACTGAGGAACCTGTGTTCCCAT
>Fam_835_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 GAGAAGACGAAGTCTTCGAGATTCGAGAGGTTATCAAACCTCGAGACG
>Fam_836_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 CATCGGCTCGCCGATAGATCCGCTGAAGGACTCGTTCATCGATCCATT
>Fam_837_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 GTTTCATTATCAGATTCTATTTTTGTATTTTCCGAGGAATTTGTTTCG
>Fam_838_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 GGAACAGGACTCGGAACAGCGGTAGCATCTACAACCGGAACAGCAGTG
>Fam_839_47_1  Nr. of seq. 1 Alignment length(with gaps) = 47 Alignment score = 0.000000
 GTTTTTTAATAATTTGAAATAATATTAATTTTTATTTTTAATTAGGT
>Fam_840_47_1  Nr. of seq. 1 Alignment length(with gaps) = 47 Alignment score = 0.000000
 TCGCGGCTCGAAGCCTACGGCTTCTCACGCTCCCGTCCTGTGGACAG
>Fam_841_47_1  Nr. of seq. 1 Alignment length(with gaps) = 47 Alignment score = 0.000000
 TTTGTATTCCTTATTTCAGATCTTCAGTGTTTCTCATTTCTAGACAA
>Fam_842_46_1  Nr. of seq. 1 Alignment length(with gaps) = 46 Alignment score = 0.000000
 AAAAATTAATGAAATTATGATTGAAGGAATAAAAAAATTTTATCTA
>Fam_843_46_1  Nr. of seq. 1 Alignment length(with gaps) = 46 Alignment score = 0.000000
 GTAATAATTCTATGTCTCTTTATCAATATAGAAAGTAATGATAAAA
>Fam_844_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 TGGACGTCTCCGGGACGACGGTCCCGATCCAGGAAGACACCGCTC
>Fam_845_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 ACGTCGAACACGAGGTGTTCCATCGACTCGAGAACTACGGGCACG
>Fam_846_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 CAACAACTACTGTAGAACCGACTACCACTCAAACAACCGAAACCA
>Fam_847_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
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 GCTCTCTTCGGTCGCCCACATCGCTCGCGGCGTCCCTCGCGCGGC
>Fam_848_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 ATTAGTTTTTAAAATGAAAAAATTAAGATAGCTATTTTTATATT
>Fam_849_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 TGATTCTTTTTTTTTAAAATTGTTTTTAATATTTAATCACTATTC
>Fam_850_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 CCTAATTTAGTTTTTAAAAATATTATAAAATTTAATTTTAATTAG
>Fam_851_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 AAGATAATCTTAAAATAATTTAAAATCTTATAAATTAAGAATTAA
>Fam_852_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 CCGCACCTACGGTGCCTCAACTCCGCTCTTTCAGAGCATCGCACT
>Fam_853_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 ATGGTTCTGTTTCCGTTTCAGTGGGCTCTTCTAATGGCTCTTCCA
>Fam_854_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 ACTTCAAGTGTCAACCTTAATGGAGAAGATAATNCAGGAATAAAT
>Fam_855_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 ATGATAGGATAGCCCAGTCCCAGTCAGCAATCTCAGATCAAGTCA
>Fam_856_44_1  Nr. of seq. 1 Alignment length(with gaps) = 44 Alignment score = 0.000000
 TTTTTAAAGTTAATTAGATTTAAAAAGGATTAATTAAGTTTTCT
>Fam_857_44_1  Nr. of seq. 1 Alignment length(with gaps) = 44 Alignment score = 0.000000
 GTTTTGTTATGACTTACCTATTACTTTATAGTTGCTTAATGGTA
>Fam_858_44_1  Nr. of seq. 1 Alignment length(with gaps) = 44 Alignment score = 0.000000
 TCTCCTCTGTCATTGCTTCCTAAATTCAACAATAGCCTTTGTGT
>Fam_859_43_1  Nr. of seq. 1 Alignment length(with gaps) = 43 Alignment score = 0.000000
 TTTATAATATTTTACTAAAACAAACTAACATTATGTAAACATA
>Fam_860_43_1  Nr. of seq. 1 Alignment length(with gaps) = 43 Alignment score = 0.000000
 AACCAAATTAAATTAAGTAAATTGTATCAGATCAATTAAATTA
>Fam_861_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 GACGACACCTTCGAGGAGACGGCAACGGAAACGGTCACCGAG
>Fam_862_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 GGGTCCAGGGAGTAGACAACTCTCCTCAGAGGGTAGACAACA
>Fam_863_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 AACCAAGAAAAAACAAACAAATTCATAGAAAAATACGAACAC
>Fam_864_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TTGTCTTTTTGTAGGGTTTCTATTTGATTATTGAGCTTATTT
>Fam_865_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 CTAATTCATATAATGATTTAAGTGTTGGCTTTGAATCTGATG
>Fam_866_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
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 AGAAATTAAGTGATGCCTTAGAGAATAGTGAAAAGGAACGGC
>Fam_867_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 GTCTTTTCAGTGTTGACTTTNGCTGAACTGTTTGTAGTGTTA
>Fam_868_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TTCTAGATTCCGAAGCTGAAGCTGATTTTGGTAACGACATAA
>Fam_869_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 CTTTCTGAATTTAGCTCAATCATTCCAACCTTAATTCCTATA
>Fam_870_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TTAAAAACTAAAATTAGTAACCTACATACACGACTATCTTTA
>Fam_871_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TCTTCCTTTTCAGTTGCAGTTTCTGCTTCAGTCTCTACTTTT
>Fam_872_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 ACTGGAAATTAAACAAACTTTAATTATATAAACTGTAATTAT
>Fam_873_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TTTTCTCTTTTTTCAGTTATATTCTCACTTAAATTTGATAAA
>Fam_874_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 AAAAGTTCAACTCNTCTGAAATTGGAACNATGCAGAACTCTN
>Fam_875_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TTTCCGCTGTTCTTTGTTCCGCAGTGGGTGTGAGAGAGTACG
>Fam_876_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 CCGATTGCTCCGTAGCTACTGACTCTACCGTCTCCGACAACT
>Fam_877_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TCACTCCAAGAAGAGGTGAAGAGACAAGGTGAAGCCATTGTA
>Fam_878_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TCCTGCCATAGCCTCTCNATGTTTTCGTTAATNCTCCTATTC
>Fam_879_41_1  Nr. of seq. 1 Alignment length(with gaps) = 41 Alignment score = 0.000000
 CGATCCGGCTCGCTTGACTCACGCCGGATCGGTGGAGATGT
>Fam_880_41_1  Nr. of seq. 1 Alignment length(with gaps) = 41 Alignment score = 0.000000
 ATTATTCCAATCATTTTTAAGAGTATTTCAGAGGCATTTTT
>Fam_881_41_1  Nr. of seq. 1 Alignment length(with gaps) = 41 Alignment score = 0.000000
 TGAAATTACTCATTTACCTTACGTTTCCTTAATGATCTAAA
>Fam_882_41_1  Nr. of seq. 1 Alignment length(with gaps) = 41 Alignment score = 0.000000
 TCTTCGAAGAATCTTCTGGATTCTTCTCACGTCTTTGAGAC
>Fam_883_40_1  Nr. of seq. 1 Alignment length(with gaps) = 40 Alignment score = 0.000000
 AAGTTATATAAACAAGTATCTTTACTAATTGTTTATAAGA
>Fam_884_40_1  Nr. of seq. 1 Alignment length(with gaps) = 40 Alignment score = 0.000000
 AGTTTATTTTACTTTAATTACTCTCTATTTTTCTAAAATC
>Fam_885_40_1  Nr. of seq. 1 Alignment length(with gaps) = 40 Alignment score = 0.000000
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 TTTCTAAAATTAGTTAATATTTTTTTTATTTAGATTATTT
>Fam_886_40_1  Nr. of seq. 1 Alignment length(with gaps) = 40 Alignment score = 0.000000
 TAATAATTTCGAAAACAAGAGTCCTGGTATATCTTGGAAC
>Fam_887_40_1  Nr. of seq. 1 Alignment length(with gaps) = 40 Alignment score = 0.000000
 AGACTACTTCATGGACATTGATATTGAAATTCGTTCAAGC
>Fam_888_40_1  Nr. of seq. 1 Alignment length(with gaps) = 40 Alignment score = 0.000000
 CGGCCTCGCCCCGGTAAGTCGATCCGCGTCGGCCCGACAT
>Fam_889_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 GGGGTGTGTCGGGGCGGGGCCGAGCGGCGTGGGCTCGAT
>Fam_890_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 CACGAGACGATAATGCGGCGGAGACGAACGCGAGTACGC
>Fam_891_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 CCGTCACCGTCNGTGTCAGATNCTGCAGTATCAACGTAG
>Fam_892_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TTAAATAAATGAGATATTCCTTTTTTATATGGAAAATCT
>Fam_893_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TCTGTCCAGTTGANTGTTAGGCTGTCTCCNCCTAATAGG
>Fam_894_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 CGCCGCTGCTTCCACCACTGCTACGGTCGCTGCTTCTTC
>Fam_895_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 GTCGAGGTTCCGGTCGTCGCTGATACCGAGGCCGAGGAT
>Fam_896_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 CAGAGGATCTTGCGCCTGAGGGATCTGAGGAGCCGGTTG
>Fam_897_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TCTCCACCATTATTGGTCTCCGTGACGGTGGCCGTATCC
>Fam_898_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TTTTGTTTTTGAGCATCTGCTACGGTACTAGTATCTGTG
>Fam_899_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TCACAGCAGTCGCCTTCACAGTCTGCCTCGGTACAGTCG
>Fam_900_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 CAGCATTGTCACATGTTTTTTCTTCTGTTGAGGTATCTG
>Fam_901_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 GGTTTTTTATTTGGTTTCACATTTTCGCTATTGATATCT
>Fam_902_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 AATACAGTCATACACAATAATTCATGCAGTTGTCATCAC
>Fam_903_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TCCTGAATCATCATCCCAAGAACTGCCTCCATCATCACT
>Fam_904_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
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>Fam_905_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
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>Fam_906_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
 AAAATTAAAAAATTAAAAATAATATACTATAAAAATAG
>Fam_907_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
 TAATAAATAGTAAACCAAGCTTCCACTTAAAAAATTTC
>Fam_908_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
 TTAAACTTTTAAAACTGATTAAATTCTTGAATAATTAT
>Fam_909_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
 CAAGGTTTATTGGTTAGATCAAGATTTACTGATTAGAC
>Fam_910_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
 TTAAACTTTATACGGTTTTAACAGTACTGAAATTTCTC
>Fam_911_37_1  Nr. of seq. 1 Alignment length(with gaps) = 37 Alignment score = 0.000000
 CGGGGCGTATTCTTCCACCACCCCGGCTGTCCGGTGC
>Fam_912_37_1  Nr. of seq. 1 Alignment length(with gaps) = 37 Alignment score = 0.000000
 ATTTTCTTATTTTAACAAATCATATTTATTTTATTTA
>Fam_913_37_1  Nr. of seq. 1 Alignment length(with gaps) = 37 Alignment score = 0.000000
 AAAGAATAAAAAATATTCTCTAAAAATGTTTAAAACT
>Fam_914_37_1  Nr. of seq. 1 Alignment length(with gaps) = 37 Alignment score = 0.000000
 AAAAACATGAAACACCAGAAAAAATCACAATGCCCCA
>Fam_915_37_1  Nr. of seq. 1 Alignment length(with gaps) = 37 Alignment score = 0.000000
 ATTTATTAAATATCTTTATAATATTTTTTAGAACTAG
>Fam_916_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 GGTCAGCCGGCGATGTCGGGAGTAGAAGCCGACAAC
>Fam_917_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 ATCTTTAGACCTGTCTTTCCTAGATTTATTAAAATT
>Fam_918_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 AATTTAAAATATTTATACTTAATAAGTTTTTTAAAG
>Fam_919_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 TTCTTTATTGGAGGTTATGGTTGTGTTCTTGTTTTC
>Fam_920_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 AATTAAAACTAGAATTAAGTGAAATTTGAATAATTC
>Fam_921_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CTGCTGATTCCGATGACATTGTTGAATCTGTTGATG
>Fam_922_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
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>Fam_923_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
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>Fam_924_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
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>Fam_925_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CTGTAAGCTGACCTATAAGCTAACTTATAAGTTGAC
>Fam_926_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CCAACCACTGTGTCGACTCCAATACCGACTGCAATC
>Fam_927_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CGTCTTCGTACGGTTCGATGTCGGTCGGCTGATCCT
>Fam_928_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 TCGCTTTCGTCTCCGTCCTCTCTCTCACCGTCTTCC
>Fam_929_35_1  Nr. of seq. 1 Alignment length(with gaps) = 35 Alignment score = 0.000000
 GGCGGCGTCGACAGACGGGACGCCGGCACCTCTCA
>Fam_930_35_1  Nr. of seq. 1 Alignment length(with gaps) = 35 Alignment score = 0.000000
 AAATATAATAAAACTAAATAGCCCATTAAGTATTC
>Fam_931_35_1  Nr. of seq. 1 Alignment length(with gaps) = 35 Alignment score = 0.000000
 AAAAATATCATACTCATTCGAGTTAATATAATATT
>Fam_932_35_1  Nr. of seq. 1 Alignment length(with gaps) = 35 Alignment score = 0.000000
 CAGTTTTGAATATTATATCAGTGTGTAAGTTTCTT
>Fam_933_35_1  Nr. of seq. 1 Alignment length(with gaps) = 35 Alignment score = 0.000000
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>Fam_934_35_1  Nr. of seq. 1 Alignment length(with gaps) = 35 Alignment score = 0.000000
 GTTTTATTCTTAGATTCATATTTTGTTGTCTTCAG
>Fam_935_34_1  Nr. of seq. 1 Alignment length(with gaps) = 34 Alignment score = 0.000000
 CGTTCAGCCGAGTCGTCTGTTCGATGCGACTCGA
>Fam_936_34_1  Nr. of seq. 1 Alignment length(with gaps) = 34 Alignment score = 0.000000
 CATTGGAGTGTAATAAAAAAGGTGATTTTTATTA
>Fam_937_34_1  Nr. of seq. 1 Alignment length(with gaps) = 34 Alignment score = 0.000000
 TTATTTTTTTATCCAATCTTTTATATACTATTGG
>Fam_938_34_1  Nr. of seq. 1 Alignment length(with gaps) = 34 Alignment score = 0.000000
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>Fam_939_34_1  Nr. of seq. 1 Alignment length(with gaps) = 34 Alignment score = 0.000000
 CTTGATCGAAACTCACTTTTCCAATAATAGTCTG
>Fam_940_34_1  Nr. of seq. 1 Alignment length(with gaps) = 34 Alignment score = 0.000000
 TCCTTTCTATTCTTCTCTTCTTTTCTAAGACAAA
>Fam_941_34_1  Nr. of seq. 1 Alignment length(with gaps) = 34 Alignment score = 0.000000
 AAAGTAAGTAACCAAAGGAGTTCTTTAAAGAAAT
>Fam_942_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
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 CGTCGAAGGTCGCATCCCCGAAGANCGCCGTAT
>Fam_943_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
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>Fam_944_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 AAATCTAAAGCCGAAGATATNTCTGAAGATGTN
>Fam_945_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 AACGGAACCAGTATAGACATATCNAGTCTATTN
>Fam_946_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 CAGCTACAGAACCCCGAACATCCTCCAAATCAC
>Fam_947_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 ACAAAAGAAAAACTAGACCACAGAATAGACAAC
>Fam_948_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
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>Fam_949_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 AATCTTCAGCTNGCTGAGCCACACATTTTCTGA
>Fam_950_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 ACTGAGCTAAAGGAAGACTGAGACGGAAGGAAA
>Fam_951_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 GCAGAATCGCCAAAAGTAGAATACCGAAAANAG
>Fam_952_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 TTTGTATATCAGATTGCGCTTATTAGGTCAGTA
>Fam_953_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 TAATAGCCTGTTAGAACAGCTTACTTAAAACAA
>Fam_954_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 AAATTCTGCTCTTAAACTCTTAGTAAGTTCACT
>Fam_955_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 ATAACCAGTCCCCCAGAGGTCACNAGTCCCGGC
>Fam_956_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 TTCAACATTTAAAGGAGGAGTTTATTTTATTTT
>Fam_957_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 GACCCGTCCGAATCATCCGATCCATCATCGTCC
>Fam_958_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 GACGACGAAGATGACGAGATGAACGACGAGGTT
>Fam_959_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 GTCGAATCGCGTTACTCGGCGTGAAAAGCGGCG
>Fam_960_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 CGTCGGCGTCTTCCGCGTCGGCACCGTGTTCGT
>Fam_961_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
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>Fam_962_32_1  Nr. of seq. 1 Alignment length(with gaps) = 32 Alignment score = 0.000000
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>Fam_963_32_1  Nr. of seq. 1 Alignment length(with gaps) = 32 Alignment score = 0.000000
 AATCCATTATTTCATAATTTAACCACTAAAAG
>Fam_964_32_1  Nr. of seq. 1 Alignment length(with gaps) = 32 Alignment score = 0.000000
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>Fam_965_32_1  Nr. of seq. 1 Alignment length(with gaps) = 32 Alignment score = 0.000000
 TTCTGAGAATCCAATTTAATCTTTTTAAATAA
>Fam_966_32_1  Nr. of seq. 1 Alignment length(with gaps) = 32 Alignment score = 0.000000
 TGAAAACTTAGTCTCCTTAAACCTTAAACTCC
>Fam_967_32_1  Nr. of seq. 1 Alignment length(with gaps) = 32 Alignment score = 0.000000
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>Fam_968_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_969_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_970_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_971_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_972_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_973_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_974_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_975_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_976_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
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>Fam_977_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
 ATGTTAAGTCCATAAACTAAGTCCATGTACT
>Fam_978_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_979_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_980_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_981_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_982_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GGCTGATCTGGCGTGTCAGTTGGCGTGTCG
>Fam_983_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 CATCGTCTCGTTCTCCATCGACCCATCGTC
>Fam_984_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_985_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_986_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_987_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 AAAGATAAAAAGAATTAAAATAATTAAAAG
>Fam_988_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 AACACCAACGGAAACGGCCACGACAACCCC
>Fam_989_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 AAATCGGCTCCATAAAGAGATGCACAAGAG
>Fam_990_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_991_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GATTCAGGTTTTTTTTCAGTTTTGGTTTCT
>Fam_992_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 AGACTTACGGAGATGAACCGACTAGGGATC
>Fam_993_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 AGTCTAAGTAATAACAGTTAGAGCATTAAC
>Fam_994_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 TTTTTTAATAAATTATTACTCATCTAGTTC
>Fam_995_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 CTCTAAACAAAGTNTNTCTGAACAAAATAA
>Fam_996_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 TTAACACGTGATATAGAGATAATTAGGTAG
>Fam_997_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 AGCAGTGTCGTCAGCTGCAACATCTTCTGC
>Fam_998_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 TACACTTTCCTGACTCCACTCCAGGGTTGT
>Fam_999_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_1000_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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>Fam_1001_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 ATCTTGAAGGAGCTAACCTTNATGAAGCTC
>Fam_1002_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 CCTCAGATAAAGGCAAACACAGATGCCATA
>Fam_1003_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GCCCTCGAGCGAGACATCGCCAAACTGGTC
>Fam_1004_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 CCCGGCGACTCGCCGTCGTCACCACTCTGG
>Fam_1005_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GTGTCGTGGAAGTGGTGGTGTGGCGAGTGC
>Fam_1006_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 TCTTCGTATTCGTCATCCTCGTGCTCCTCA
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>Fam_1008_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1009_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1010_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1011_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1012_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1013_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1014_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
 AGATTTTTTTAGGCAATTGTAATTAAACT
>Fam_1015_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
 TTCAGGAGTTCTAAACTCTAAACCAGCCC
>Fam_1016_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1017_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
 CATGTTATTTTTCAGGAACTATGATTTTA
>Fam_1018_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1019_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1021_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1022_29_1  Nr. of seq. 1 Alignment length(with gaps) = 29 Alignment score = 0.000000
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>Fam_1023_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 CCAACCGCTAGTCTCACAACTGCTCTGA
>Fam_1024_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 ACGACCGAGGTGCGTCGGTTAAGGACAT
>Fam_1025_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1026_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1027_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1028_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1029_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1031_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 ATCAGTTAATCATAATTGGTTAATTGTT
>Fam_1032_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1033_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1034_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 TTTATTGCCATATTACATTTTGCCACTT
>Fam_1035_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 TTTCCTTAACCTATATTTACAGGCTTAT
>Fam_1036_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1037_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1039_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1040_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 ATTATCAGTAACATGCTTAATATGCTTA
>Fam_1041_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 AATTTACTAATTTTAATTCAATAGTTTT
>Fam_1042_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 GCTGTTTATCTGGACAGCTCTTCCTCTG
>Fam_1043_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1044_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
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>Fam_1046_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1047_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1052_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1053_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1054_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1055_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1056_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1059_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1060_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1061_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1062_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1072_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1073_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1078_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1085_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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>Fam_1087_26_1  Nr. of seq. 1 Alignment length(with gaps) = 26 Alignment score = 0.000000
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>Fam_1088_26_1  Nr. of seq. 1 Alignment length(with gaps) = 26 Alignment score = 0.000000
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>Fam_1089_26_1  Nr. of seq. 1 Alignment length(with gaps) = 26 Alignment score = 0.000000
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>Fam_1090_26_1  Nr. of seq. 1 Alignment length(with gaps) = 26 Alignment score = 0.000000
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>Fam_1092_26_1  Nr. of seq. 1 Alignment length(with gaps) = 26 Alignment score = 0.000000
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>Fam_1111_25_1  Nr. of seq. 1 Alignment length(with gaps) = 25 Alignment score = 0.000000
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>Fam_1112_25_1  Nr. of seq. 1 Alignment length(with gaps) = 25 Alignment score = 0.000000
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>Fam_1116_25_1  Nr. of seq. 1 Alignment length(with gaps) = 25 Alignment score = 0.000000
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>Fam_1117_25_1  Nr. of seq. 1 Alignment length(with gaps) = 25 Alignment score = 0.000000
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>Fam_1146_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
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>Fam_1148_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
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>Fam_1158_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 ATTGGAAAGTTAAGTGATTACTTG
>Fam_1159_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 AATGCAATTAGTAGTACAATCAGC
>Fam_1160_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
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 GGATTAGAAACAGGATAAGTAAAA
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 TTTCATTTCTTGGCTCAGCAAGAN
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 CGTCGTGGTGGCCCTCGTGATGAT
>Fam_1166_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 GGCGAGACGGCTGCGGACGACAGC
>Fam_1167_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
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>Fam_1168_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CGTCTGTGTGTGCGTGGTGGTCGT
>Fam_1169_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
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>Fam_1170_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
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 AGCCAGATGTTTATAGCTAACCC
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>Fam_1188_23_1  Nr. of seq. 1 Alignment length(with gaps) = 23 Alignment score = 0.000000
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>Fam_1189_23_1  Nr. of seq. 1 Alignment length(with gaps) = 23 Alignment score = 0.000000
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>Fam_1194_23_1  Nr. of seq. 1 Alignment length(with gaps) = 23 Alignment score = 0.000000
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>Fam_1195_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
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>Fam_1196_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
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>Fam_1197_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
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>Fam_1212_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
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>Fam_1214_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
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>Fam_1215_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
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>Fam_1250_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
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>Fam_1305_20_1  Nr. of seq. 1 Alignment length(with gaps) = 20 Alignment score = 0.000000
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 ATGTCAAACTGAGATAAGG
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 ATTCTTAAGATCCTAATCA
>Fam_1320_19_1  Nr. of seq. 1 Alignment length(with gaps) = 19 Alignment score = 0.000000
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 CACTACTCAATGTTAAAAT
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 GTTACCTTAATACAGATGA
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>Fam_1326_19_1  Nr. of seq. 1 Alignment length(with gaps) = 19 Alignment score = 0.000000
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 TCCTTCTTTTATCACTTCG
>Fam_1331_19_1  Nr. of seq. 1 Alignment length(with gaps) = 19 Alignment score = 0.000000
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>Fam_1374_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
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>Fam_1377_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
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>Fam_1379_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
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>Fam_1382_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
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>Fam_1384_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
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>Fam_1385_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
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>Fam_1420_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 AGAAGAGTTTTGAGTTA
>Fam_1421_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 TATGTCTATTATCCGAT
>Fam_1422_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
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>Fam_1423_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
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>Fam_1424_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 AACGAAGTTATTCCATG
>Fam_1425_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
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>Fam_1426_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
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>Fam_1427_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
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>Fam_1446_16_1  Nr. of seq. 1 Alignment length(with gaps) = 16 Alignment score = 0.000000
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 AATTGATAATTGGACT
>Fam_1449_16_1  Nr. of seq. 1 Alignment length(with gaps) = 16 Alignment score = 0.000000
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>Fam_1473_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
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 TAACAGCAAAACTCG
>Fam_1482_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 TGTAGGACTTGCACT
>Fam_1483_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CCTGAAGAGAAGCCT
>Fam_1484_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 ATCTTCAGGTACCGT
>Fam_1485_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CTCTTTTTCAGAGAC
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>Fam_1487_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
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 TACGGAAATAACACC
>Fam_1493_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
```

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 CACAGATCCACAGAC
>Fam_1494_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 GTGGGATGTGAGAGT
>Fam_1495_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 TTCGGCGTCTTCGAT
>Fam_1496_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 GCGTCCCGCGTCCT
>Fam_1497_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 GGCAGGTCGTAAGC
>Fam_1498_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 CTGAGGGAGAGAGC
>Fam_1499_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 AAGAAAGATCTGCC
>Fam_1500_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 TTCGTGAGCACTTA
>Fam_1501_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 ATAGAGTCACCATC
>Fam_1502_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 TTTTGTTGCACTGC
>Fam_1503_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 GTATGAAAATGACC
>Fam_1504_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 ACCAGTTGGATTTT
>Fam_1505_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 AACTCGGGAAGCGA
>Fam_1506_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 TCACATTACGTTTC
>Fam_1507_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 CTTATTATTCCACT
>Fam_1508_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 TGGTATTTATGAGT
>Fam_1509_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 AGATTACTGAGCAG
>Fam_1510_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 AATCAAAAACTGCG
>Fam_1511_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 TCACATAGAATCTG
>Fam_1512_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
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 TAGCTGTAGCTCGG
>Fam_1513_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 CCAGTCAGCTTTC
>Fam_1514_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 AGTTTAGCAGGCA
>Fam_1515_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 ATCACTATTTCTA
>Fam_1516_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 TGTCAGCTATTGA
>Fam_1517_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 TTATAGTGAATTT
>Fam_1518_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 TTGCACTCACACC
>Fam_1519_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 TCTTTTATAAGTG
>Fam_1520_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 AAAACGAAATCCG
>Fam_1521_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 AACAGATCACTAA
>Fam_1522_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
 TTAGGTTTTATGC
>Fam_1523_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 TCGACGGTCTGT
>Fam_1524_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 GTGTCAGTCGGN
>Fam_1525_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 TGTACTTCCATG
>Fam_1526_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 AACTCGGGCCGT
>Fam_1527_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 GGTTTAAAATNG
>Fam_1528_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 GAGAGGGTGTGT
>Fam_1529_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 TTCCTCTCCGAA
>Fam_1530_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 TGTGCCCGACTT
>Fam_1531_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
```

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 TTGCTCCCTCAA
>Fam_1532_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 ACTTGCTAATCG
>Fam_1533_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 ACAGGTGCAGGG
>Fam_1534_11_1  Nr. of seq. 1 Alignment length(with gaps) = 11 Alignment score = 0.000000
 TTATCAAAGTG
>Fam_1535_11_1  Nr. of seq. 1 Alignment length(with gaps) = 11 Alignment score = 0.000000
 AGGAATGAGAC
>Fam_1536_11_1  Nr. of seq. 1 Alignment length(with gaps) = 11 Alignment score = 0.000000
 AAATTCACAGC
>Fam_1537_10_1  Nr. of seq. 1 Alignment length(with gaps) = 10 Alignment score = 0.000000
 ACCTTACCTC
>Fam_1538_10_1  Nr. of seq. 1 Alignment length(with gaps) = 10 Alignment score = 0.000000
 GCACCACAAC
>Fam_1539_10_1  Nr. of seq. 1 Alignment length(with gaps) = 10 Alignment score = 0.000000
 AGATCCCAGG
>Fam_1540_10_1  Nr. of seq. 1 Alignment length(with gaps) = 10 Alignment score = 0.000000
 TAATTTACTC
>Fam_1541_10_1  Nr. of seq. 1 Alignment length(with gaps) = 10 Alignment score = 0.000000
 GCGGGCAGTC
```

Table S6b. Bacteria satellite families

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>Fam_1_14_23  Nr. of seq. 23 Alignment length(with gaps) = 16 Alignment score = 0.673254
 GATAGaAgATAGGA
>Fam_2_14_12  Nr. of seq. 12 Alignment length(with gaps) = 16 Alignment score = 0.641256
 CGGCAagCGGCAaG
>Fam_3_12_12  Nr. of seq. 12 Alignment length(with gaps) = 13 Alignment score = 0.636364
 CAAcaGCAAnaG
>Fam_4_14_11  Nr. of seq. 11 Alignment length(with gaps) = 16 Alignment score = 0.636364
 GaGgCGCGaGgCGC
>Fam_5_12_10  Nr. of seq. 10 Alignment length(with gaps) = 14 Alignment score = 0.652910
 GCtgGTGCtgGT
>Fam_6_14_10  Nr. of seq. 10 Alignment length(with gaps) = 14 Alignment score = 0.860317
 tCGGGAAtcGGGAA
>Fam_7_20_9  Nr. of seq. 9 Alignment length(with gaps) = 22 Alignment score = 0.613216
 GATATAttTnGAganTCGCt
>Fam_8_18_9  Nr. of seq. 9 Alignment length(with gaps) = 18 Alignment score = 0.754630
 GAcAGcGAcTCnGAcTCa
>Fam_9_15_9  Nr. of seq. 9 Alignment length(with gaps) = 16 Alignment score = 0.837963
 CGCGCcGGCCAGGTT
>Fam_10_16_9  Nr. of seq. 9 Alignment length(with gaps) = 16 Alignment score = 0.814815
 GCcGAaCCGCcGAaCC
>Fam_11_14_9  Nr. of seq. 9 Alignment length(with gaps) = 14 Alignment score = 0.809524
 AGCtAcAAGCtAcA
>Fam_12_12_9  Nr. of seq. 9 Alignment length(with gaps) = 13 Alignment score = 0.638177
 CcgACGCcgACg
>Fam_13_96_8  Nr. of seq. 8 Alignment length(with gaps) = 111 Alignment score = 0.661197
 CGCGcAAAGCcGCcGTcGAAGCcGCTATtGCCCGcGCCAAAGCaCGcAAGCtGGAaCAGcaaCAGGCtaAtGCgGAACCaGaaGAACaGGTCGAtC
>Fam_14_39_8  Nr. of seq. 8 Alignment length(with gaps) = 39 Alignment score = 0.941392
 GGCTGCTGATAcTGCgGCTGCGGCGCaACCGGtTGTTGC
>Fam_15_14_8  Nr. of seq. 8 Alignment length(with gaps) = 14 Alignment score = 0.746599
 gCcGAACGCcGAac
>Fam_16_14_8  Nr. of seq. 8 Alignment length(with gaps) = 14 Alignment score = 0.720663
 cTAGAAcCTAGAAC
>Fam_17_100_7  Nr. of seq. 7 Alignment length(with gaps) = 108 Alignment score = 0.661817
 GGATGCGGCGTgAACGCCTTATCCGGCCTACGgatGGCgCnaGAaTnTGTAGGCcTGATAAgacGCGntAGCgtcGCATCAGGCATntGgCaCnAtTGCC
>Fam_18_14_7  Nr. of seq. 7 Alignment length(with gaps) = 16 Alignment score = 0.646825
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 cATCGCAcATCGCA
>Fam_19_16_7  Nr. of seq. 7 Alignment length(with gaps) = 16 Alignment score = 0.904762
 gTAGGGGAgTAGGGGA
>Fam_20_12_7  Nr. of seq. 7 Alignment length(with gaps) = 14 Alignment score = 0.688209
 GCTTCGtCtTCg
>Fam_21_12_7  Nr. of seq. 7 Alignment length(with gaps) = 14 Alignment score = 0.664399
 TGGCTCTGGCtC
>Fam_22_14_7  Nr. of seq. 7 Alignment length(with gaps) = 14 Alignment score = 0.746032
 GAGcCGtGAGcCGt
>Fam_23_69_6  Nr. of seq. 6 Alignment length(with gaps) = 70 Alignment score = 0.773651
 ACAGAATTAGGAATtGTAACtGATGTTAAACCAGAACAAnCTgcAAAAGCaCCaTcTCCAATAGtAGTC
>Fam_24_46_6  Nr. of seq. 6 Alignment length(with gaps) = 51 Alignment score = 0.627233
 TGTGGGAACTCTTACAAATTGaGATTTTACggttaAACTTTAAAaT
>Fam_25_46_6  Nr. of seq. 6 Alignment length(with gaps) = 49 Alignment score = 0.650340
 ACAtTTTagAAgTttnaCTGTAAAaTCacGaTTTGTGGTAGTTCCC
>Fam_26_37_6  Nr. of seq. 6 Alignment length(with gaps) = 38 Alignment score = 0.693567
 cAaAACGCTtTccTATGGgTCGCGTTgGaaAACTCAg
>Fam_27_14_6  Nr. of seq. 6 Alignment length(with gaps) = 16 Alignment score = 0.728472
 CCgGTCGCCgGTCG
>Fam_28_15_6  Nr. of seq. 6 Alignment length(with gaps) = 15 Alignment score = 0.717037
 GCCGatGTTGnCGNt
>Fam_29_14_6  Nr. of seq. 6 Alignment length(with gaps) = 14 Alignment score = 0.692064
 CCAcCGACCAcCGA
>Fam_30_12_6  Nr. of seq. 6 Alignment length(with gaps) = 12 Alignment score = 0.644444
 gntGCCGCCGCC
>Fam_31_69_5  Nr. of seq. 5 Alignment length(with gaps) = 70 Alignment score = 0.729048
 tgtAAATTcTgtAgTTGTCCnATTTCtTTnGGAAGnGttGTGAGTtGGTTATnatnCAAATncAAcnnT
>Fam_32_45_5  Nr. of seq. 5 Alignment length(with gaps) = 45 Alignment score = 0.911111
 CTgACTTCGTCAGTTctATCtgCAACCTCAAAACaGTGTTTTGAg
>Fam_33_30_5  Nr. of seq. 5 Alignment length(with gaps) = 30 Alignment score = 0.698889
 CCGCTGCCcacaTTGgnGnTaCCGntgTTt
>Fam_34_15_5  Nr. of seq. 5 Alignment length(with gaps) = 17 Alignment score = 0.698039
 gtAGGGGCGGGTTtg
>Fam_35_14_5  Nr. of seq. 5 Alignment length(with gaps) = 16 Alignment score = 0.725000
 cGTTTGGcGTTTGG
>Fam_36_16_5  Nr. of seq. 5 Alignment length(with gaps) = 16 Alignment score = 0.716667
 GCaCgaCnGCAcGAcc
>Fam_37_14_5  Nr. of seq. 5 Alignment length(with gaps) = 15 Alignment score = 0.728889
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 cggGCGTcgGGCGT
>Fam_38_13_5  Nr. of seq. 5 Alignment length(with gaps) = 14 Alignment score = 0.711905
 CCCGCAcCCGcAn
>Fam_39_14_5  Nr. of seq. 5 Alignment length(with gaps) = 14 Alignment score = 0.723810
 nCCaAGCnCCaAGC
>Fam_40_12_5  Nr. of seq. 5 Alignment length(with gaps) = 12 Alignment score = 0.822222
 CAGCGtCCCaGg
>Fam_41_12_5  Nr. of seq. 5 Alignment length(with gaps) = 12 Alignment score = 0.711111
 nGGCGAgGGcgA
>Fam_42_93_4  Nr. of seq. 4 Alignment length(with gaps) = 103 Alignment score = 0.703344
 GCCGCATCCGgCAaTCAaTGCCTGATGCGACGCTGaCGCGTCTTATCAgGCCTACAactattGCCnGAaCcGTAGGcCGGATAAGGCacTcgc
>Fam_43_39_4  Nr. of seq. 4 Alignment length(with gaps) = 39 Alignment score = 0.965812
 TTTTCTTTCTTcACTTGCGGtGATACTATATTTCCTACA
>Fam_44_36_4  Nr. of seq. 4 Alignment length(with gaps) = 36 Alignment score = 0.845679
 GGtGGTTGaTTgTTATCCATgATcGGCATaATgTTt
>Fam_45_36_4  Nr. of seq. 4 Alignment length(with gaps) = 36 Alignment score = 0.870370
 TTGtTCTTCTACGACcGGtGcTTCcTCTgCAACTgG
>Fam_46_36_4  Nr. of seq. 4 Alignment length(with gaps) = 36 Alignment score = 0.882716
 CTTctGtTTCtGCAATTACTTCcACTTCTTCTgACT
>Fam_47_33_4  Nr. of seq. 4 Alignment length(with gaps) = 34 Alignment score = 0.602941
 CCCCAGCgGggGaATaCaCcctaCaaTTCCTCC
>Fam_48_18_4  Nr. of seq. 4 Alignment length(with gaps) = 18 Alignment score = 1.000000
 GAGCTTTAGCTGCTTCTT
>Fam_49_15_4  Nr. of seq. 4 Alignment length(with gaps) = 16 Alignment score = 0.661458
 CCgGCCAAGaAGgca
>Fam_50_14_4  Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.650794
 GaCtCAGGnCtCAg
>Fam_51_14_4  Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.746032
 GATgcGCGATgcGC
>Fam_52_14_4  Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.682540
 GCGgggAGCGgggA
>Fam_53_12_4  Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.627315
 GcCGGgGcCGgg
>Fam_54_12_4  Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.703704
 CcGCgACcGCgA
>Fam_55_12_4  Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.888889
 CCGAgCTAAGcG
>Fam_56_150_3  Nr. of seq. 3 Alignment length(with gaps) = 170 Alignment score = 0.649673
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GACGCgGAGCGTCCAGAAcgGCATacCcACGCGGAGCaTggGtACGATGGTGTccTTnaGnnCACCTATCGTTCCTCACGCTCCAGCGTgGGAATGCtnTgcGTGACGCTC
tGCGTCAcAgaTCTGCGCCgCGCtgCaCAtTCAgGaccG
>Fam_57_156_3  Nr. of seq. 3 Alignment length(with gaps) = 156 Alignment score = 0.933048

TTTATTATGTAAAAATCAgCAtATCCTGCACCAAAAGAATaTGTcnaTCCTGCAACTATATATCCTCCATCAcTTGTCTGCTGTATGGAAnAAGCCCaATCATAAtTGCTT
CCTCCATAGGTTTTCTCCCAAACCTTATcCCCATTACTaTCAAGC
>Fam_58_114_3  Nr. of seq. 3 Alignment length(with gaps) = 126 Alignment score = 0.760141

GACGCAGAGCGTCGaGAaCTGCATTCCCACGCtGGAGCGTagGGAACGAtaAtCtCAACTATCGTGCGgCGCTCCGCGTCGCATGCCtTTCnGGAcGCTCtGCGTCCTCtT
TGC
>Fam_59_108_3  Nr. of seq. 3 Alignment length(with gaps) = 108 Alignment score = 0.720165
 cCTTCGCGAaCAAGtTCGCtCCTACgGGaGttcgCgGgnccTTGTaGGAGCGAaCTTGctCGCGAAgAGGncGtTaCAgTCgATGgAtTTtCTGCGTCaGgaATATaG
>Fam_60_60_3  Nr. of seq. 3 Alignment length(with gaps) = 65 Alignment score = 0.675214
 ATGGTACTACCTcAACGCtAAtGGTGCtATGGCnACAGGtTGGCTcaAAgacaAtGGTTc
>Fam_61_56_3  Nr. of seq. 3 Alignment length(with gaps) = 60 Alignment score = 0.688889
 ccGTGnCGATCGCaAGCgCGGCGCaGCCGgGCGcaGCGGGTCGgCACCATCggaCc
>Fam_62_46_3  Nr. of seq. 3 Alignment length(with gaps) = 49 Alignment score = 0.643991
 TTTtAAaTtgAtCtGTAAAAnCtTtaAcTTGTgAGAGTTCCCACAt
>Fam_63_48_3  Nr. of seq. 3 Alignment length(with gaps) = 48 Alignment score = 0.791667
 TACGGCAGCACcCAGACcGCnGGnnNNGACAGCnCgCTGACCGCcGGc
>Fam_64_45_3  Nr. of seq. 3 Alignment length(with gaps) = 45 Alignment score = 0.881481
 TCTTCTTGTTGtTTACGAGCTTGtTCATCAGCctGgCGTTTTTGt
>Fam_65_42_3  Nr. of seq. 3 Alignment length(with gaps) = 42 Alignment score = 0.830688
 TCTTCCACTTGTGGTTCcACTACtACtTGtTGCAtTGGtttT
>Fam_66_39_3  Nr. of seq. 3 Alignment length(with gaps) = 39 Alignment score = 0.954416
 TCAgGGGCAACAGAAACACTCTAAGCAAGACGACTCCgA
>Fam_67_39_3  Nr. of seq. 3 Alignment length(with gaps) = 39 Alignment score = 0.931624
 GGTCAAGGAAATACaACcCCTCCAGCAAATAAcGGAGGA
>Fam_68_36_3  Nr. of seq. 3 Alignment length(with gaps) = 36 Alignment score = 0.824074
 TCTTCCTTAGgTTTNGCTAcTTCTTGgaCTTTcaCT
>Fam_69_27_3  Nr. of seq. 3 Alignment length(with gaps) = 27 Alignment score = 0.806584
 TGTCGTTGCCGncgCCGCCaTACAGct
>Fam_70_27_3  Nr. of seq. 3 Alignment length(with gaps) = 27 Alignment score = 0.802469
 GGAATAACGGGAGtgACaGGTcCaACa
>Fam_71_24_3  Nr. of seq. 3 Alignment length(with gaps) = 24 Alignment score = 0.740741
 CAGgtAAGgATCcAggAACAGAtA
>Fam_72_21_3  Nr. of seq. 3 Alignment length(with gaps) = 22 Alignment score = 0.727273
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 tCtCCTATtTCCTaTCTtCTC
>Fam_73_21_3  Nr. of seq. 3 Alignment length(with gaps) = 21 Alignment score = 0.788360
 CGCGTgcCTGGAcGGaCGaCT
>Fam_74_21_3  Nr. of seq. 3 Alignment length(with gaps) = 21 Alignment score = 0.873016
 AAGaAACAGaAAAgCCAGGTG
>Fam_75_16_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.722222
 GCTTCGgCGCTTCGnC
>Fam_76_18_3  Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.641975
 CanAAgaAAgcaGAAGAA
>Fam_77_12_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.680556
 GACTCGGACTCG
>Fam_78_13_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.652778
 tTGGTGTTGGTGg
>Fam_79_14_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.791667
 CCTGAAACCTGAAA
>Fam_80_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.736111
 GCCAaGAAGGcCGtA
>Fam_81_15_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.791667
 ggCGGTGCTTCCGGT
>Fam_82_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.777778
 TGATTgCtTGATTgCt
>Fam_83_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.777778
 GCaaGGCTGCaaGGCT
>Fam_84_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.777778
 GgtCTTCGGgtCTTCG
>Fam_85_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.833333
 CGcCACGcCGcCACGC
>Fam_86_16_3  Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.833333
 TTTAAagCTTTATTTa
>Fam_87_12_3  Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.718518
 GGTGGaGACGGC
>Fam_88_12_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.674603
 AAAcAGAAAcAG
>Fam_89_12_3  Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.761905
 TGGCTGTGGCTG
>Fam_90_12_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.777778
 AAgGTaTAGAAC
>Fam_91_13_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.692308
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 CGAaGCGaCtGaT
>Fam_92_13_3  Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.794872
 GActCGAACCgCC
>Fam_93_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.703704
 GtCGnTGTCGaT
>Fam_94_12_3  Nr. of seq. 3 Alignment length(with gaps) = 12 Alignment score = 0.777778
 ATCTTnATCTTn
>Fam_95_220_2  Nr. of seq. 2 Alignment length(with gaps) = 220 Alignment score = 0.769697

GACGTCAACGGCGACGGaCTcGAcGAccTcATcaTCGGGGCTCCcGGTGCCGACCCGGACaGaCGGTaCgaAtGCcGGcCGCAGCTACGTGGTcTTCGGCAAGCGcaaCGG
CCAACCGGTCGAaTTGGCcaCaaTCGAAAGCGGCACcaGcCGcaACGGCTTTGcCATCAACGGCAGCAATGACTACGATacCgCCGGCgTTgCTGTCAGCGGAGCGGGG
>Fam_96_155_2  Nr. of seq. 2 Alignment length(with gaps) = 155 Alignment score = 0.638710

CTCCAGCGTaGGaAcGCcGTTCcGGACGCTCTGCGTCCGaTCTTGAAcaTGTGcaacGCGACgCaGAAtTTGTGACGCAGAGCGTCACGaAACgGCATGaCaACGCGGAGC
agTcGCACGATAGtcatcTcGaGGcacaaGTcATCGTTCCcaCG
>Fam_97_153_2  Nr. of seq. 2 Alignment length(with gaps) = 153 Alignment score = 0.612200

TTGCGCCAGAGaATGTCcGGcTTGCCGTCGaaagCGanAAaTCGcCcGCCCCGaCGATCTGCCAGcccaGATCGCCCACaGaaCgGtAGaGaaACcGaCGaacAGaAGaCc
GtGCCGTTCATcAaCCAGACGcaaTTGGCACCGcTgGcCtTG
>Fam_98_141_2  Nr. of seq. 2 Alignment length(with gaps) = 141 Alignment score = 0.971631

AATGCCATGCTCTGCAAGATGCTGCATCAGACGCTGAGCCACATCAGGCAaAGGTCTTGATTGTTCATTTTGTACTGGCGGcGgTGGCGCAGGCCAGTTAGGTGCCGGAGG
AATATGTTCAGCCATATTCCGGGCTGGTTG
>Fam_99_138_2  Nr. of seq. 2 Alignment length(with gaps) = 138 Alignment score = 0.978261

CCAACCCTGGAGGGCAACACCTGCCAGGGGAACAAGgaGAGCGGCATCGCCTACGTTGGCAGTGCAGGGGGCATCGCTCGCCAGAACACCTGCAGCGGCAATGAGTACCAT
GGCATCTATGTGGGCgAGCAGGCGCAA
>Fam_100_130_2  Nr. of seq. 2 Alignment length(with gaps) = 130 Alignment score = 0.621795

gCCGGaTGGCGGCTaaCGCCTTAcCCGGCCTACaGaGcCCtgtaTaTCAaAcGGttaCTCAtACacCGcAGGCCCGCGCAAGCGCAGCGCCGCCGGGCAAGctaTAcCAGa
CaCcGTaCCcGTaATTgTc
>Fam_101_130_2  Nr. of seq. 2 Alignment length(with gaps) = 130 Alignment score = 0.989744

CCTTCGCGGACAAGTCCGCTCCTACGCCCGTTGGGCAGAATCAAAAACGGCCTCCTGCCCGAGGGGTAGGAGCGAACTTGTTCGCGAAGACGGTCGCTCAGGCGATGCATG
TcCGGAAAGCTTGGCGGCC
>Fam_102_118_2  Nr. of seq. 2 Alignment length(with gaps) = 118 Alignment score = 0.830508
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CTTGTTCGCGAAGaCATTGTTTcaAACGaCaAATCTTccGCGACTGTACGGGCCCTTTCGCGAACAAGTTCGCTCCTACGTTcGaGCaTGGGAgaCGGatGGCTTTTGTAG
GAGCGAA
>Fam_103_114_2  Nr. of seq. 2 Alignment length(with gaps) = 114 Alignment score = 0.859649

GcCTGATGCGAcGCtTaACGcGTCTTATCAGGCCTACGcCAGACAGCGCAATAGCCTGATTTaGCGTGAtTTTTGTAGGTCGGATAAGGCGTTTAcGCCGCATCCGaCATC
AAc
>Fam_104_112_2  Nr. of seq. 2 Alignment length(with gaps) = 112 Alignment score = 0.625000

GAGCGCGCCGGAGGCGcGCGCTCCCAGGgGATactGacaCGCCcCCGCcGGGcGCGGGaAccaCCGaTGCCGGATGGcTcCCGCTGtcGCGaGttGaGCTGGggcAcGTGG
g
>Fam_105_111_2  Nr. of seq. 2 Alignment length(with gaps) = 111 Alignment score = 1.000000

CGTGGCGATCGCAAACCCCGCGCCTGGCGACAATGCGGCCCGCAAAACGGGCCGAGGAGGAGCCAGGCAATCACCCCAGAGCCGGGTGCAGCGGGTCGCCACCATCAGCCC
>Fam_106_88_2  Nr. of seq. 2 Alignment length(with gaps) = 88 Alignment score = 0.765152
 GCCCGGATAAGGCGcaAGCCGCcATCCGGGaAcCtCTCCCCGGTGGCGCTGaCGCTTACCGGGGCTACaAACCGaAtGCcaAaCcGTA
>Fam_107_66_2  Nr. of seq. 2 Alignment length(with gaps) = 66 Alignment score = 0.797980
 ATAGTTAATCTAAAACACTTTATgTATTNATNTCATCCAtTTAnGNNacTANaATTTACATTCCAT
>Fam_108_63_2  Nr. of seq. 2 Alignment length(with gaps) = 63 Alignment score = 1.000000
 TGGTATCTCTTTGATCGCTCTTCTGGAATCATGAGAAAAGGACAGGTCAATGATGCTGGGAAT
>Fam_109_60_2  Nr. of seq. 2 Alignment length(with gaps) = 60 Alignment score = 0.933333
 CCGATGTTGTAGCTGCCGGNGTTGGCAAAGCCCAGGTTGTCGNTGCCGANGTTNGCGAAG
>Fam_110_60_2  Nr. of seq. 2 Alignment length(with gaps) = 60 Alignment score = 0.966667
 CGGCAGGCTGGTCAGCTGGTTACCAGAGACCNACAGCTCCTNTAGTCCTGACGGCAGCGC
>Fam_111_57_2  Nr. of seq. 2 Alignment length(with gaps) = 57 Alignment score = 1.000000
 CTAGCGTGGCGACGATGCGGGCTGGGATGGGCCGCTGAGGAGCCGCGCGGTCGAGCT
>Fam_112_54_2  Nr. of seq. 2 Alignment length(with gaps) = 54 Alignment score = 0.759259
 TGAccTCgCGCCGGcGACGATGCAGAGCGaAGCGATGAGcAGGAGCGGCGCaga
>Fam_113_54_2  Nr. of seq. 2 Alignment length(with gaps) = 54 Alignment score = 0.833333
 CCTTTTTCACCTTTaGCaCCTTGcGCTCCAGTcAGACCaCGTTCaCCTcGGTCT
>Fam_114_50_2  Nr. of seq. 2 Alignment length(with gaps) = 50 Alignment score = 0.613333
 AGGCTCGGGAAAaAAcaaTccACaaaACtcAGCCTCGCTaTcTcATTTTC
>Fam_115_45_2  Nr. of seq. 2 Alignment length(with gaps) = 45 Alignment score = 0.940741
 ACTGGACCTCAAGGTGTTCAAGGACCAGCAGGTGCTACcGGTGCc
>Fam_116_45_2  Nr. of seq. 2 Alignment length(with gaps) = 45 Alignment score = 1.000000
 GAACGATTAGAGGCAGAGAGAAAAGAGCAAGAAAGATTGGAAGCA
>Fam_117_45_2  Nr. of seq. 2 Alignment length(with gaps) = 45 Alignment score = 0.911111
 AAGAAGAAAGCGGAgGCCGAGGCGGCGAAAGCaGCGGCGGAcGCG
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>Fam_118_44_2  Nr. of seq. 2 Alignment length(with gaps) = 44 Alignment score = 0.772727
 GCGGGGACAGGCACCgcaAGGAaTcGGCGGGTGCCAGTccCCCT
>Fam_119_42_2  Nr. of seq. 2 Alignment length(with gaps) = 42 Alignment score = 0.809524
 GGaATaACTGGTCCTACTGGaGTTACAGGacCTACCGGAATc
>Fam_120_41_2  Nr. of seq. 2 Alignment length(with gaps) = 41 Alignment score = 0.837398
 CCaGCcGACTcCCGGGGTGCCTGTCCCcACGaGGACAGGCA
>Fam_121_39_2  Nr. of seq. 2 Alignment length(with gaps) = 39 Alignment score = 0.662393
 GGATCTTCCGGTTTCACTTCTGGcTCcTTCggctcttc
>Fam_122_39_2  Nr. of seq. 2 Alignment length(with gaps) = 39 Alignment score = 0.606838
 GTGGccGTcCGgCGCgGCCGcgTCCaCGcTCGTCGGcGC
>Fam_123_39_2  Nr. of seq. 2 Alignment length(with gaps) = 39 Alignment score = 0.606838
 TgcAAAATGTaGGAACTCaCaCaAAGaTcTAAGTTcaaC
>Fam_124_39_2  Nr. of seq. 2 Alignment length(with gaps) = 39 Alignment score = 1.000000
 AATCCGGAACAAAATCCAGCAACTAAACCTGCTACTGAC
>Fam_125_31_2  Nr. of seq. 2 Alignment length(with gaps) = 31 Alignment score = 0.967742
 CCCGAGTTGAAGNCAGCCCGTATTCAAGGCG
>Fam_126_30_2  Nr. of seq. 2 Alignment length(with gaps) = 30 Alignment score = 1.000000
 TTGTTGTTGCCGAGATTCGCAATGCCCAGG
>Fam_127_30_2  Nr. of seq. 2 Alignment length(with gaps) = 30 Alignment score = 0.966667
 CCGAGTTGAACNAGCCGGTGTTGATGTTGC
>Fam_128_30_2  Nr. of seq. 2 Alignment length(with gaps) = 30 Alignment score = 0.933333
 AAACCGGTGTTCGAGTCACCCGCATTNNCG
>Fam_129_26_2  Nr. of seq. 2 Alignment length(with gaps) = 26 Alignment score = 0.602564
 GGaCaAgGCGGCTaCGGCGGcGGTca
>Fam_130_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 1.000000
 AGCTTCTTCTTCAGCTTTTTTTGT
>Fam_131_24_2  Nr. of seq. 2 Alignment length(with gaps) = 24 Alignment score = 1.000000
 CATCTTCTTTCACATTCTCTTCTA
>Fam_132_23_2  Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.739130
 TTTTCGGGGATaaCCtATCCCCc
>Fam_133_22_2  Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.863636
 AGAAGNTGAAAGANCCAAAGAN
>Fam_134_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.809524
 GCCGAGCAaGAaCGcCAACGC
>Fam_135_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.809524
 TGTcTTcTGTcTTTCTTGTTC
>Fam_136_21_2  Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.952381
 GGTACCGGTGCGCCcGGGATC
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>Fam_137_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.614035
 GGCgcGCAGGGCAGAgccg
>Fam_138_19_2  Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.622807
 CGaACGaCGcGaACGGCCg
>Fam_139_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.731481
 gtACGACCCGGGcCGGCa
>Fam_140_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.666667
 TcGcCGGGTaaCGCTGGG
>Fam_141_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
 GCTAaAcAAcATAGAtTA
>Fam_142_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.851852
 CCTTGGTTGTcGTTTCCa
>Fam_143_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.722222
 AGTTAAATAATtcaCAGa
>Fam_144_18_2  Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.703704
 AACgGCAGaGaAAAGGTc
>Fam_145_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.718750
 TgACTTATTgACTTAt
>Fam_146_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.635417
 cCACCATgcCACCATg
>Fam_147_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.635417
 GCCGaGAAGAcAGGct
>Fam_148_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 1.000000
 GAGGCGGTGAGGCAGT
>Fam_149_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 cGCTTcTCcGCTTcTC
>Fam_150_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 1.000000
 CCGCAGCACCGCAACG
>Fam_151_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 GAACTGacGAACTGac
>Fam_152_16_2  Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
 CaGCTaAACaGCTaAA
>Fam_153_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 GAgCcGGCGGCTcaG
>Fam_154_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.822222
 CCAGAACCGTTaCCa
>Fam_155_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.644444
 TAAACaaGAaAATAa
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>Fam_156_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 1.000000
 TTTAAATGAAGAAAA
>Fam_157_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 1.000000
 TGGACGGGCGCTTGC
>Fam_158_15_2  Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.822222
 TGCCCGTACTGGgcC
>Fam_159_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.773810
 ATAGAGtATAGAGt
>Fam_160_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.619048
 CGTTaaCCGTTaaC
>Fam_161_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.809524
 CaTTCGACaTTCGA
>Fam_162_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.619048
 aAAGAaGaAAGAaG
>Fam_163_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.619048
 cGATTAacGATTAa
>Fam_164_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.714286
 CATTgCTCATTgcT
>Fam_165_14_2  Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.809524
 AGTcCCTAGTcCCT
>Fam_166_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.653846
 gGAGGAgGTaGTT
>Fam_167_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 CgCTGCTaCGGGg
>Fam_168_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.602564
 TGAGcaAGGaCGc
>Fam_169_13_2  Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.705128
 CGaTGTGACGcCt
>Fam_170_12_2  Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.722222
 CacCGGTCGGGT
>Fam_171_12_2  Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.666667
 GCAGTCGgcGaT
>Fam_172_12_2  Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.777778
 GTCTCcGTCTCc
>Fam_173_12_2  Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 1.000000
 GAAAAGCCTAAC
>Fam_174_12_2  Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 1.000000
 GACCACGCCGGT
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>Fam_175_12_2  Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.777778
 GAACaCAAGcCG
>Fam_176_12_2  Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.777778
 CCATaACCATaA
>Fam_177_12_2  Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.777778
 TTTACcTTTACc
>Fam_178_11_2  Nr. of seq. 2 Alignment length(with gaps) = 11 Alignment score = 0.696970
 AGCGCaGGGgA
>Fam_179_10_2  Nr. of seq. 2 Alignment length(with gaps) = 10 Alignment score = 1.000000
 GCGAGCAAAG
>Fam_180_10_2  Nr. of seq. 2 Alignment length(with gaps) = 10 Alignment score = 1.000000
 CGACGCAGGC
>Fam_181_10_2  Nr. of seq. 2 Alignment length(with gaps) = 10 Alignment score = 1.000000
 CGCGTGTCGT
>Fam_182_297_1  Nr. of seq. 1 Alignment length(with gaps) = 297 Alignment score = 0.000000

GGTTACTGGATAAACACCTGGTATGGTACCTACTGCTACGTTGATAGCACCTGTTGTTGGATTTAAAGTTACTCCTACTGGCCATACGCCTGAGGTTGCTATTGTCGCATT
ACCGCTTACTCCTAAAGTCGCTGGTAATCCATTTACAACATCGTTTAATGCTACATTTGGTATGGCTTCCCCTCCTGTTGATGGTGCTGTACCGCTATCTGCTACTGGATT
TAATACCGCTGTTACAGTGACTGTATTTACTACTGTAGCACATGTTTGTGGCGTTAGTTTATCACACAATTGGTA
>Fam_183_291_1  Nr. of seq. 1 Alignment length(with gaps) = 291 Alignment score = 0.000000

TTTTCTTCTTTTCCTTCTACTATTGCTGGTTCATCTGCTCGATAGTAGATGTCTACCACTGCGTCCAAACTTTCTGAAGTTACTTCTACTTCATCTACTGTGCCTGGAATT
GCTGTGTAGCCTTCTTGCTCTGGGGCTGTAAAGCTTTCCCAACGACCTACGGTCCATGGTCCATATTTCTTCTCGTCGCTGCCTGCTACACTCGTGTACTTCCTTTCCAAG
GTTACTGGCTGTCTTGTTGTTTGAACTTCACCATTTGGCAAGTGTACATTAATTGTTCGCGTGATTGTC
>Fam_184_276_1  Nr. of seq. 1 Alignment length(with gaps) = 276 Alignment score = 0.000000

GGTGACCTCGTCGGCGAAGGCGGAGAGCTGGTCGACCATGGTGTTGATGGTCGTCTTCAGCTCCAGGATCTCGCCGCGGGCGTCCACGGTGATCTTCTGGGACAGGTCGCC
CCGGGCCACGGCGGTGGCCACCTGGGCGATGTTGCGGACCTGGTTGGTCAGGTTGNNCGCCATCAAGTTGACGTTGTCGGTGAGGTCCTTCCAGGTCCCCGNGACGCCCGG
CACGTNGGCCTGGCCGCCGAGCCGCCCGTCGGTGCCGACCTCGCGGGCGACGCG
>Fam_185_261_1  Nr. of seq. 1 Alignment length(with gaps) = 261 Alignment score = 0.000000

TTTATCTGAACCTTTTCCTGTTATTTCAACACTTGTTGTTGCTTCATCATCAGTACGAGCAACTGTAAAGTCTACATAATCAGTTCCATTTACTAATCCAGCTGCAGTTAA
CACAGTTTCAATTTGTGTTTTAACAGTTGAAACATCATTTCCTTTAGCAGCTGAAATTTTTAAATCATCAGCTTTAATAATATCTGCTAAATCTTTTGAAAAGTCTGTTGA
TCAAGTTACAACAAAAGTTACTTTAGAACCATCAACAAC
>Fam_186_258_1  Nr. of seq. 1 Alignment length(with gaps) = 258 Alignment score = 0.000000

GCTGTAAAGTTTTGACCATTGANATCTAATATAATATTTTCAATCGGATTTGGNGCAATATCATCAATCAANGCATTCTGCTTGACCTCTGTACTGCGGTTACCCGCTCGG
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TCAACGACAACAAAAGTAAGCTCTTCGCCATGTAAATGCACTTGATANAAATAACCTGAAACATTACCNGCGCTATCNGCTGAACCAGAACCTACGACNTCACCANTAGCA
TTTTTGACTTCAATTTGAGTATTTGCTTCTGCCTGA
>Fam_187_255_1  Nr. of seq. 1 Alignment length(with gaps) = 255 Alignment score = 0.000000

TCACCCAAGACACTGGCAGCTCCAGCAGTGACTTTATCACCAACGACAACACCCTGATTTTCAAAGGTACCGTCGATTTAGGTGACAACAGCACCTTAGCCGTCACCATCA
ACGGCGTGGTCTACACCACCGCCAACGGCTTAGTGATTGATGCACAAGGCAACTGGAGTGTTGACCTGACNGGCACCGTGCTGCCTGACGGCATTTACCCTGTCAGCGCCA
CCGTCACCGACGTGGCCGGCAACAGCAAAACCG
>Fam_188_255_1  Nr. of seq. 1 Alignment length(with gaps) = 255 Alignment score = 0.000000

CTTCGCTTGGCGTTACTGTGAATGAACCATCATTCGTTAANAAATCACCATTACTAATACCNGAATCAGTATCCAATGTGATTGTCGGNGCATTCGGAGCCTGAGTATCTA
AAACAAAATCTAGTGTACTCGAGCCAGACACATTACCCGCAGCATCAGTTTCTCGAACCGTAATTGAGTTGTCGCCTTCAACCACAGCAGGAGGGGTTGTTGACCAACTGC
CATCCGCAGCCTGATATTCAACTGTATTGCCAA
>Fam_189_252_1  Nr. of seq. 1 Alignment length(with gaps) = 252 Alignment score = 0.000000

CTGATTTGGCAGACGGCACGAAAGCCACTCCAACGCAGCCAGCTAAGACAGAAGTGAAGACCGCTGATGGCACTTGGACCTTCAAGTCTTACGACAAGGCTGAAGAGACCA
TCAATGGAGCAGACGCTCACTTTGTTGGTACATGGGACTTTACACCAGCGCCAACCTATAAGGCGACTCACGAGTTCGTTAGTGGTACAGCAGGTAAGGAATTGCCACAAG
AAGTGAAAGCCTTGCTTCCAACCGACAAAC
>Fam_190_243_1  Nr. of seq. 1 Alignment length(with gaps) = 243 Alignment score = 0.000000

TAGTAACCGTAGATAAAACCGCACCTACTGCTACTGCTGGTACAGCACAAACCCTTACTTGTACTATTCCTACTGTAACTTTAGGTGGAACAACTACTTCTACAGGAACTA
ATTTACACACAGCTGGAGCAATGGTACTACAACGGTAGGAACTACGCCTACAATAACGGTAAGCACAGCAGGTACTTATACCTTAACGGTAACCAACACCTCTAACGGAT
GTACAAGCACCAATAGCGTAA
>Fam_191_243_1  Nr. of seq. 1 Alignment length(with gaps) = 243 Alignment score = 0.000000

ACCTGGTAGGTCAGGCTCGGATCGGCATCGCCGTAGACCTTGGTCTTGGCGTCGGCGATCACATTCAGCAGTGCCTTGGTGATGGTCAGGTTGTTGCCCTGGTAAGCCAGG
TCATAGTTACCGCTGACCAGACCCAGGCCACCCTGCTGAATCCCATACACGCCGACGTTCTCGCCAGACACACGAACCAGGCCGCCGCCATTGAGCACCGCGCCAGCGGTA
TCGCCATTCTTCAGGCCGCTG
>Fam_192_237_1  Nr. of seq. 1 Alignment length(with gaps) = 237 Alignment score = 0.000000

CAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTCAATGTAGGTGAGACACCGAAGGCAGAAGATTCTATTGGTAACTTACCAGATCTTCCGAAAGGTACAA
CAGTAGCCTTTGAAACTCCAGTTGATACGGCAACACCGGGAGACAAACCAGCAAAAGTTGTTGTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAGG
TTGTCGATCCACGTA
>Fam_193_228_1  Nr. of seq. 1 Alignment length(with gaps) = 228 Alignment score = 0.000000

GCCTCGCCACCTGGTTGCGCACTTGCCACATCCGATGCACCATGACCTGGGTCTACCGGTGTCCCAGCTTTCGCTAACGATGCCGGTTCACCTTGTGGGTTATGGCCTTGT
GCCACCTGTGGGCGACCGTCGTCTTCCCCCCCTTGTGTGCCTTGTGCTCCGCCAGTTTGAGTCGCGGTCGAGATTGGCTCGCCCTGAGTGTGCAGACTCGGTGTCTGAGCA
CCTTTA
>Fam_194_227_1  Nr. of seq. 1 Alignment length(with gaps) = 227 Alignment score = 0.000000
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CTCGTCACAGGGATGAGAGCAGCGCCGCGTCTGCGGCGCGGAAGAGTCTTTTCAGCCCAAGGACTTGGTCTGGCTGGATTCCTGTGACGAGCACAGGAATGAGGGAGGCGG
GGATGCACGGGCGCTNCCGCAACCTCGTTTGGGGACTGCGCGCCATCTCCTCGATATCCGCGCACCTATGAGAACTATTCCGAGGGACCGGGACCCTCTCTCCCCTCATCC
CTGTG
>Fam_195_219_1  Nr. of seq. 1 Alignment length(with gaps) = 219 Alignment score = 0.000000

TGCTGATGTTTGAGTTATATAATCAATTGAAATATCAGAAGCTAATAAATTTGAGTTTTTTGCTAAAATACTTGCTTGAATTGTTGAAGCATTATTATCTTGTAGATTACC
TAAATTAGTATTAATTAAAACTGAACTTAAATTTTGTTTAACAACTTGAATAGTAAATGTTACATTTACAGAACCTGTATATCTTCCAGAAGCTGATGAATTAACTCT
>Fam_196_219_1  Nr. of seq. 1 Alignment length(with gaps) = 219 Alignment score = 0.000000

TATCTGTTCAGCTTTACCGACACGACGTTTTCGGGTGGCACGCTCGAGGCGGTGATCGGCAAGGGCTATACGGGCGGCAAGAATGTCGATGTCGCCGCGCTCGNTGNANAT
GATGNGTTCGGTGNTTCNGTCTCGCTGAACGCGGCGGGGGACCGTCTGGCGGTCGGGGCGNATCTGGACGACGGGTCCGGCAACNGCGTGANAGATTCGGGCGCGGTG
>Fam_197_207_1  Nr. of seq. 1 Alignment length(with gaps) = 207 Alignment score = 0.000000

CTCGCGTTGCTCGGTACGGCCTACTTGGCATGCTCAGCAACGTTTGACATGTGACCCATCCGTAGGCCGGACCGCAGCGTCAGCGGAGTTCCGGCAATCAGTCGGCACGAT
TTGATTCCGACCGAGTGTTTGATCGCGGGTTTTGTTCTTTGGTGGGTGGTTCACGTTGGGGACCAACGTGCGACAGGTTAGGTGTGGATGCCGTAA
>Fam_198_204_1  Nr. of seq. 1 Alignment length(with gaps) = 204 Alignment score = 0.000000

GTGAAAAAAGGTGCTTCAGGTAACACTGGTGGCTCAAGCAACGGTGGTTCTAACAATAATCAATCAGGAACGAATACGTACTACACNATTAAATCAGGCGATACCTTGAAC
AAAATTGCCGCCCAATATGGCGTGAGTGTTGCTAATTTACGCTCATGGAATGGCATCTCTGGCGATTTAATTTTCGCTGGTCAAAAAATTATC
>Fam_199_198_1  Nr. of seq. 1 Alignment length(with gaps) = 198 Alignment score = 0.000000

TGTCTATGTGGCGGGGGAGACCTNTTCCACCGACTTCCCCACCACGGCGGGAGCGTATGATAGGACGTACAATGGTGGTGGCAGCGATGCGTTCGTGAGCCGCTTGAGCGG
CGACCTGGGCAGCCTGCTCGCCAGTACCTTCCTCGGCGGGAGTGATTGGGACTCNGCCACCGCCCTCGCGCTGGACGGGCAGGGGAN
>Fam_200_193_1  Nr. of seq. 1 Alignment length(with gaps) = 193 Alignment score = 0.000000

GACACAGAGGACACAGCGAGGATAAATACCGAGGTCTCCCACAGCGGCAAGAATACCCTTCCCGCCAGGATTGCCCGTGTTTGGAGTGCGCCAGCCATGCTGCCGCGCCCA
CCACACTCACCGTGGCGGGCGTGTTCCAGCGCTAACTCCGCTGGCAATGGGAAGTCTTGACACGTCTGTATTGCACCACCGA
>Fam_201_189_1  Nr. of seq. 1 Alignment length(with gaps) = 189 Alignment score = 0.000000

ACTTTATCATAATTAAATTTNAAATTATGAATTTTATTTGCCTCTTCAATGAATTCTTGCCTAGTTATTTTCTTTTTTCCATTACACTCAACACAGCCATTACCTCTTAAA
TGGTCTTGAGGTACTTGTTCAAAATCNCCATGTTTTTTACAAGTAATAATTACTTTTGAGTTGCTATTTACATAAACG
>Fam_202_189_1  Nr. of seq. 1 Alignment length(with gaps) = 189 Alignment score = 0.000000

TCAGCGTACCGCCGATAATGGTGGTGCCGCCGGAGTAACTGTTGTCGCCGCTTAACGTCAGCTCGCCNGTACCGGTTTTGACCAGCGAACCGCTGCCGGAAAGCGTATTTT
CCAGCTCGCCCTCGCCGACCTGAAGCACGCCGCTGTTGGCAACAGCTCCGGTACCCAGCGAATCCGCATGGTCAGCCG
>Fam_203_186_1  Nr. of seq. 1 Alignment length(with gaps) = 186 Alignment score = 0.000000
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GATTCGCCTGTTTGGCAGAGGTGTCGTATGCGTGACTGTGACCGCCATCCGTGACGGCGGCACACANCACGTAGGAGCGCGCTTGCGCGCGATGAAGCTGTCNCGGTGACG
CCCCATCGCGCGCAAGCGCGCTCCTACGACCGCCGATGCGTGCGGGAGTGTCGTGACATCAGACCAGNCACAGCA
>Fam_204_185_1  Nr. of seq. 1 Alignment length(with gaps) = 185 Alignment score = 0.000000

ATGGCGGTGAGGGGGGGATTGACTCGCTGCGCTCGCCCTTCGGGCAGCCCGTTCGCTGCGCGCCCGGTCTGTCCAACTGGCTGCGCCAGTTGTCGAACCCCGGTCGGTGGT
TCTCATCCCCCCTTGGTTTGGGGGATACATATAAGCAAAAAGCCTGTACTTCTGTACAGGCTCTCAACTTGAAG
>Fam_205_182_1  Nr. of seq. 1 Alignment length(with gaps) = 182 Alignment score = 0.000000

GCTGACGCGTCGGGTTGGGACAGAAATGTAGGCCAGGTTGTACCTGGCGGGGTGAATGGACGGACATCGCTGAGTCTTGCGTGACCGGCTGGACGGCTCGCTTTGTTCCAA
AGCATCGGCTGGGTGCCAGGTAATGACCTGGCCTACGTTGGTGGCTTCGCCAGAATTCAGACGTGTCTCTC
>Fam_206_178_1  Nr. of seq. 1 Alignment length(with gaps) = 178 Alignment score = 0.000000

ATGGTGGTGGGGGAAGGATTACTCAGCGCTGCGCGCTTCGCCCTTCGGGTCGTTGCCTGCGGCAACGCTCTCTCGCTGGCGCTCGAGTCGAACCTTGGTCGAAGCTTCTCA
TCCTTCCCCGCATGGGCAGAATATTTGATTGCGGATTCGNTTGAGAGTTCAGGGACTTTTGAAAGTG
>Fam_207_178_1  Nr. of seq. 1 Alignment length(with gaps) = 178 Alignment score = 0.000000

ATTTTATTTCTGCCGAAGAAGGGACTCGCCCCTTCACAGTCTCGCGTCGTGCTCGACTGGGTTCCGGGGCGTCTCGAACTTGCCTCAGCACATCGTGTGCTTCGGTCGCGT
TTCTCGCTTTTTAGGAAAGCTCAAAACGCTTTTCAAGTTCTCGCTTCGAGTCCCCGTTATGTTGTTA
>Fam_208_178_1  Nr. of seq. 1 Alignment length(with gaps) = 178 Alignment score = 0.000000

TCGCGCCCGAGGGCGCTCCTACGGGAGATCCGTTGCGAGGTGAGAGCTTGCCGATCACGTGGCTCGTGCATCGATTTGCAGCGGAGTGGATCACGACTAAACCAGCGACGG
CTGTGAGATGGCGTTGGCCGTGTAGGAGCGCCCTTGGGCGCGATGGGGCGTTACCGGGAAGGCCTCA
>Fam_209_177_1  Nr. of seq. 1 Alignment length(with gaps) = 177 Alignment score = 0.000000

TGTAGCTGGTGACTTTAATGGTGATGGTAAANCTGATATTGCTGCTATGTACGATTATGGCGGNGGTGAAACTAGAATCCATGTATTNACTTCAACTGGAGATTCNTTTAC
CTACACTGGNGCAAATGGTTGGTGGAACACTACTGGTTATGATGCTAACAGAGTTACTGGAAGGGT
>Fam_210_177_1  Nr. of seq. 1 Alignment length(with gaps) = 177 Alignment score = 0.000000

AAAAGTCTTGTCCATTGTTTGTTTCCACCACTATCATACTTTGTCACAAATAGATCTTGGGTTCCACTTAAGGCTTGACCGTCTAAATTTCCGGAAGTCANTCCGGTTATA
TATACATTTCCAAAACTATCAGATGTAATTCCATTNGCCTAAGTAGTTTGAACTCCCGCCACTCCT
>Fam_211_174_1  Nr. of seq. 1 Alignment length(with gaps) = 174 Alignment score = 0.000000

TTAAGTTAGGTAAATGTAAGATTTCATAGAAAGCATTTTGTTGTTCTTTGTTGAATTTGTTATCAGCTTTCGGTGCTTGAGATTCATTTAACTTTTTAGCTTCTGCTAAAA
GGTTAGCGCTTTGGCTTGGGTCATCTTTTAGGCTTTGGATGAAACCATTGCGTTGTTCTTCGT
>Fam_212_174_1  Nr. of seq. 1 Alignment length(with gaps) = 174 Alignment score = 0.000000
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AATCCTTCCCCCACCACCATCTATTAATTATTCACCATCTCCTCAGTAAATAACTAAATCAAAAAATAGCACCCATCAGGGGAAGGTAAGAACCTTCGACCAAGGTTCGCG
CCGAGCATAGCGAGACAACGACGCGCAGCGGCGGCCCGAAGGGCGAGGAACAACGTGACGAGT
>Fam_213_173_1  Nr. of seq. 1 Alignment length(with gaps) = 173 Alignment score = 0.000000

TGGTTGCGGGGGCCGGATTTGAACCGACGACCTTCGGGTTATGAGCCCGACGAGCTACCGAGCTGCTCCACCCCGCGTCCGAATTGTACTGCCACCACAAGAGACAGAGCA
GTTGCCCCTTGCTGTCTTCGTTTCCACCGCAGGCGCTAGCGCTTGCCATGGACACAAATAGT
>Fam_214_173_1  Nr. of seq. 1 Alignment length(with gaps) = 173 Alignment score = 0.000000

CCGTCGGCCGAGATCGACGGNAGNCGCTGGCGNNCCGTGCCCTCCGCGCCGTTCGCGTCGACGCTGACCCGGTCGGTCGCGGTGNCNGCTGGTCGTACACGAACACGTCNC
GGNCGCGGTTCGTGTCGACCGGCACGAGGNTCCNGGCGAAGGAGTCGAACGCGATGTAACGG
>Fam_215_173_1  Nr. of seq. 1 Alignment length(with gaps) = 173 Alignment score = 0.000000

CGCCCGGCAGCGCATGCCACGCTATAAACGAGTCAACTCGCACTCGGTGTGAAACCCGGTTTCTGTAGGAGCGGACTTGTCCGCGAAAGGGCCTGTACATTCACAACATTT
CTGCTGCCCAAACGCCCTCTTCGCGAACAAGTTCGCGCCTGCACAAGCGTCCGATTTCGTAG
>Fam_216_169_1  Nr. of seq. 1 Alignment length(with gaps) = 169 Alignment score = 0.000000

CGTAGGCCAGGTTCCACCTGGCGATGGTTGCTTGCCGGTGAACGTCCCCTTGCGATGGCTTATAAATCACGCCTCGCTTTGTTCCAAAGCATCGGCGCGGATGCCATGTGT
AACATGGCCTACGAGTGGCGATTGCAAACTGCGAAATGCACTTTGCAATGGTTTCCAA
>Fam_217_168_1  Nr. of seq. 1 Alignment length(with gaps) = 168 Alignment score = 0.000000

CAACTGAGCAGTGCCACCAACAACACGTCTGAAACGCTGGCCGCCACACCGAAAGCGGTCAAGGCTGCATACGACCTGGCAGCCGGCAAGGCGCCTGCCAGCCACACTCAC
CCGTGGAGTCAGATAACGGGAGTGCCTGCGGCTTCACTGACGGCAAAAGGCACCGTA
>Fam_218_162_1  Nr. of seq. 1 Alignment length(with gaps) = 162 Alignment score = 0.000000

AAAACACAAAATCACGCCAACAAGCCATTAAGGATCTAAACGAATTCTTAAAAAACAATCCCAATGACGCCCAGGCCTCTAAAACTTTAGCTCAAGCTAATAAAATACAAC
ACCTGGAGGACCTTAAATCTAAGGTTCATTCAATAAAACCCATTGATCTTG
>Fam_219_159_1  Nr. of seq. 1 Alignment length(with gaps) = 159 Alignment score = 0.000000

TTTAGCTTCTTGAACCTCTTGTGCCTCTTGTGATGTATCACTTAAATTATTTGCACTTGCTTCTTCTTTTATCGCTGCTTGTTGTGCTTTCAATGCCACTGCTTTTGGTTC
TTCATTTGATACAGCTGCACTTTTATCTGTTTCTGCTTGTGCTTCTTT
>Fam_220_156_1  Nr. of seq. 1 Alignment length(with gaps) = 156 Alignment score = 0.000000

CAGACCGACGTGTTCGCCGTCGACNACAACGGCGCGTTGAACGTNGCNTGGGTNGTCAGCGCCGANCGCTGGAACGGNCCGATTCCGATCAGCCCNGCGGGGCTCTTCCCG
NCCGGCGCGGCGGTCGCGGCATCGAACCAGTTCGGCATCCCGAAT
>Fam_221_156_1  Nr. of seq. 1 Alignment length(with gaps) = 156 Alignment score = 0.000000
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AATTTAGTGGTTGATGGAACGACTAACTTAAACAATTCTTTATCAGTAAATAATCAGTCTCCAGCCAATTTAACGGGAACATTAAATGTAGATGGTGCTACAACTTTAAAT
AATACATTTACCGTAGCAAATCAATCGCTATCACGTTTAACTGGC
>Fam_222_154_1  Nr. of seq. 1 Alignment length(with gaps) = 154 Alignment score = 0.000000

ACCGGCTGATGCCTGTACTATGTGAATGATTGAACGAGTCAGTACTCGCGTTTGCCCCGCTCCTGCGGCCGCCGGATGAAAAGCCTGCCATTCGTCGGAGAGAGAGGGCTG
GCGCGTCAAACACGCTGAGGTTACACTGGTACGGGAATGGAGC
>Fam_223_150_1  Nr. of seq. 1 Alignment length(with gaps) = 150 Alignment score = 0.000000

TGGGGCGGCATCNCCGACNCGCATGCNCCANCNCGACNACNCCGTCGCGGGTGGCGNCNACGNCACCNACGGCGACGACGCCGTCGTCGGCGGCANCGTCGTCGACGCGCC
GGTGGCGNNGCCGGCCAGGTCANCNGCANCGCCGGCGCG
>Fam_224_148_1  Nr. of seq. 1 Alignment length(with gaps) = 148 Alignment score = 0.000000

CATGTTCCACATGGCATCCACGCCGATGCTTTGGAACAAAGCGAGTCGTGTTATTTGAGTGCTCACGCAAGGTCGATGATGGTCGTCCAGTCACCCCGCCAGGTAGAACCT
GGCCTACGTGGTTGGCTGCGTTGATTGGGTCGTAGGC
>Fam_225_145_1  Nr. of seq. 1 Alignment length(with gaps) = 145 Alignment score = 0.000000

CGCTGGTCTTCTGACGGAAATGGCAGCAGCGGATCACATCCTGGCGGCCAGGGTCGGCCTGACTGCTTACAGCACGCACGGTCATTGCGAGAGCGTTGTAACCGGGGACAC
CTGGCTAGCCTGCCGGGTCGTGAGCCATTCGCGG
>Fam_226_143_1  Nr. of seq. 1 Alignment length(with gaps) = 143 Alignment score = 0.000000

ATAGGCTATTTTACTTGCCATTTTGGGCTTGAGCAGTGCGCGGCGCCGTCACGTACTGGGTGTACGCTCCGTTGCCTGTGCGCTGGTCGCACCCAAACTGTCTGCGACAAT
AACGCCTATTGGATAAGTTGGATTTTTACACA
>Fam_227_141_1  Nr. of seq. 1 Alignment length(with gaps) = 141 Alignment score = 0.000000

TGCCGTTGTCGGCGNACTGGACGACNNGCGCGCTGTCNGCNGTGGACATCCGGTCGACGCCGAGCACCTTGCCCGAGTGGNGGTTGCGGATGCGGNACCAGCCGTCGCCGT
TGTCGATCAGCTGCCAGAGGTGGTCGTCGG
>Fam_228_141_1  Nr. of seq. 1 Alignment length(with gaps) = 141 Alignment score = 0.000000

GCAGAAAGCAGCCAACCAGAAGTTCATGTCTCACCAACAGAAGAAGAAAATCCAGATGAAAGTGAAACACTAGGCACGATTGAACCAATCATACCTGAAAAACCAAGTGTG
ACAACTGAAGAGAATGGCACAACAGAAACT
>Fam_229_141_1  Nr. of seq. 1 Alignment length(with gaps) = 141 Alignment score = 0.000000

GGATTCGAACCTCCGACCGCTCGGTTCGTAGCCGAGTACTCTATCCAGCTGAGCTACGGATGCATCGGGAAACTTACTTTACTGCAGATTTTTTGATACCGCTACTAAAGC
CGTATCAAGTAAGAGATGGTGCATCCGGGA
>Fam_230_139_1  Nr. of seq. 1 Alignment length(with gaps) = 139 Alignment score = 0.000000
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ACAACTTAAAAGTNTNAAGAATCTGNNTTTGAATCACAATNAANTNACTACTCTTCCGAAAGAAGTTANGACANTTGNAAAATTTACAAAAGTTGGATTTANGANNCAATA
AACTTACGACNCTTCCNAAAGAGATAAN
>Fam_231_138_1  Nr. of seq. 1 Alignment length(with gaps) = 138 Alignment score = 0.000000

GAGCGCGCCGGAGGCGCACGCTCCCAGTGCTGCCGGTGAGTGAGTCGGCGGCGTGCTCGCAGGGTATGCAGACCCGCCCCTACCCTGCCCTGCACCCGCTGGGGGCAGGAA
CCGGCGGCGCCGAATGGCGCAGGTGGG
>Fam_232_138_1  Nr. of seq. 1 Alignment length(with gaps) = 138 Alignment score = 0.000000

AGGAGCGAACTTGTTCGCGAAGGCAGTGTTTTGAACGCCAAATCTTCTGCGGCTGTACGGGCCCTTTCGCGAACAAGCGAAGCGTCGCCCGGTTCGCTCCTACATTTTTGC
CGTACGCTCAAGCATGGGGGCTTTTGT
>Fam_233_138_1  Nr. of seq. 1 Alignment length(with gaps) = 138 Alignment score = 0.000000

CAGTTAGAGCCTGCCGCAGAATCGGAAGTTGAGCCAGAGCTTGAGCTGGCAAGTGAGCCAGNNGAGGAAGAAGCCTTTACCGAGCTTGATGAGCTCGATTTGCCTGAGTAC
ACCGAAGAAGACGCCTTGGCGGATGCG
>Fam_234_134_1  Nr. of seq. 1 Alignment length(with gaps) = 134 Alignment score = 0.000000

GGATTCGAACCTCCGACCGCCTGGTTCGTAGCCAGGTACTCTATCCAGCTGAGCTAAGGACGCGCAGTTTTCGATATCAGTATTACCAATATCAGGAGTTCACAAGGAAAC
CCTAAAGAGTGGCGCGTCCTGGA
>Fam_235_133_1  Nr. of seq. 1 Alignment length(with gaps) = 133 Alignment score = 0.000000

AAGAACTTCTAGCTTTTCTCTTTCGTTCAAAGAGAAGCAGCTGTTCGCAGTTTAATCAAAACCACATAAAGCTTTTAACTTTACTCTTTGATTTAAAGAGTGATAAATGTT
TACAGTTTAATTAAAACTGCAT
>Fam_236_132_1  Nr. of seq. 1 Alignment length(with gaps) = 132 Alignment score = 0.000000

GCGCCCGCGAGGCGCAGACCACGCTGGTCACCGCCTCCTCCGATGCCGCCAACCAGATCAAGGCGCTCGCCGCCGACGTGCAGCGCTCGCTCTCGCTGGCCGGCNCCACGA
CCGCCGAGACCATCACGACCG
>Fam_237_132_1  Nr. of seq. 1 Alignment length(with gaps) = 132 Alignment score = 0.000000

TTGGGCGGATACTCGTGGATAGCTCCACTCCGCACCCCCCTCCGCGCCGATCCGCGTCATTCGCGTGTATCCGCGTTCCGCATCACCCGTGCCTACTCCTGGATGCGCCGG
ATGCACCCGGAACAACGCGGC
>Fam_238_132_1  Nr. of seq. 1 Alignment length(with gaps) = 132 Alignment score = 0.000000

AATCTTGGTTTTATCTCAAATTTGATGGGAAAATAGCTGAAAAAGAATGGGTCTACGATTCTCATAGTCAAGCTTGGTACTACTTCAAATCCGGTGGTTACATGACAGCCA
ATGAATGGATTTGGGATAAGG
>Fam_239_132_1  Nr. of seq. 1 Alignment length(with gaps) = 132 Alignment score = 0.000000
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TCTTCTTCAAGAGCTTCNGTANTTTCAACGTCAGATGCNACTGCTTCTTCAACAGTATNTTCTGCTATTCCTTCAGATTCTGTTGGCTCTTCAAGTTCAGAAACTTTTGTC
TCTTCTACTTCTGACTCAAGC
>Fam_240_129_1  Nr. of seq. 1 Alignment length(with gaps) = 129 Alignment score = 0.000000

TTCAGCCCCGACGGCAAGCATCNTGGCCACCGGCAGCTCCGATCAGACCGTGCGGCTGTGGGAGACCACCACCGGCCAATGCCTGAGAATCCTGCAGGGCNACATGCCAAC
GGCATCTAGTCGGTGGCC
>Fam_241_129_1  Nr. of seq. 1 Alignment length(with gaps) = 129 Alignment score = 0.000000

GCATCTTCTTCGTCGAACTCTGGCAGTTCCAGTTCGTCGAAGTTGAATTCTTCTTCCGCGTCAGCGCTNGGCGCTGCNGCTTGNACTTCAGCTTCTGGTAGCTCAGGCTCA
TCGGCCATNGATGCCAAT
>Fam_242_127_1  Nr. of seq. 1 Alignment length(with gaps) = 127 Alignment score = 0.000000

TTGAATAAATAGTTTTCACCCCAGAGCTTAACTGACCNGCGACTGCGCTGCTGTCACCGCCAGAGATCGCNATCCCCCCAAGTAACCACCGAGCCATCATCTTTTACGGCC
GCAAAGGCANTAATAG
>Fam_243_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

GTCGGCGGGACGCCTGAACGAAGCAATCGCCCTGTACGAGCAGACCCTCGCCGATCGCGAGCGGCTGTTGGGAGACGAACACCCGAGCACCCTGACCTCGCGAAACAACCT
CGCCNGCGCCTACAN
>Fam_244_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

CGATGGCGGCGGCCCAGCACGGCCTCCTTAATCGCCAGCGCTTCTTCGTAGTAGCGGCGGGCGGTGGGGTAGTCGCCTGCGGCTTGCGCGACCTTCCCCAGTGCGTGCAGG
GTGACGGCGGTCTCA
>Fam_245_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

AAAGAACTAGACAATTCCTTGCTGAAAGCCATCGCTCAAAATGCCAATCGGTTTAATCCTCAAGATATCGCCAATACCCTCTGGGCATTAGCTACCATGGGGATCAACTGG
CGTGATATTCAAGAA
>Fam_246_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

TAAAGCCCATAATGCGTTAGCAATACCTTGGGGGTTGAATCGCTCAGCGTTGCGGCGAACAGCNCCAAGCAAGCGATCACTTAATCNTTGGTCTTCCAACTCTCGCCACCT
CATACCCATCGTGGC
>Fam_247_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

AGCGGCTCGGCCTCGGCGTACTCGCCCCGCTCGGAGTACAGGAGGGCCAAGTTGTCGAGGCTCTTCGCCATCTCCGGGTGCTCCGGCCCGAAGGCTTTCTCCCGGATAGCC
AAAGCGCGCCTGAAA
>Fam_248_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000
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GCCTCCCGGTAGCGGCCCTGATCGACGTACAGAAAAGCCAGGTTGTTGAGGGTTTTGGCCACCTCGGGGTGATCAGGACCGAGGACTTTTTGGTGAATGGCCAGGGCCCGC
TCGTACAGCGGCTCC
>Fam_249_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

CCGTCCGGGGCAAACGCCACCGAGCGGATCCAGCCGGTGTGCCCNNGGAGCGTGGCGAGGCACCTTCCCGTGGCCGCATCCCAGAGTTTGACGGTGCNGTCCTGNCCGGCG
CTTGCGAGGAGGCTC
>Fam_250_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

CCACCGCCGACAGCCGTGCTCCCGCCAACAGAACCCGAACCACCCAACGACTCACTAATGCCACCACCAACATGAGAACCAACACCCACACCAGTGCTCACACCCCCACCA
ACACCGGTATGAGCA
>Fam_251_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

AGGACCATCCCGACACGCTCACTTCCGCCNGCAACCTCGCCACTANCCTGAACTCCTTGGGGGAGCATGCGGAGGCNCGTCGCATGCAGGAGGATGTTCTTGCGCGTCGTG
GTCTTGTCCTGGGTC
>Fam_252_126_1  Nr. of seq. 1 Alignment length(with gaps) = 126 Alignment score = 0.000000

GGTGGTCGTCGCCGAGGGTGCGGCGTNGGCGGGTGAGGGTGTCNTCGANGATGCGGNGGGCTTCGGTGTGCTCGCCGAGGTTGTGCAGGGNGNCGGCGAGGTTGTGGGCGG
ACTGGAGGGTGTGGG
>Fam_253_123_1  Nr. of seq. 1 Alignment length(with gaps) = 123 Alignment score = 0.000000

TAAAAGTAACTGATTTAGTACCAGGCAGTTACCAATTTGTCGAAACAAGTGCTCCAACAGGCTACAAGTTAGACAACAGTCCAGTAAGTTTTGAAGTTGTCGCTGGTGAGA
CAGACCAAGTAG
>Fam_254_123_1  Nr. of seq. 1 Alignment length(with gaps) = 123 Alignment score = 0.000000

GTGAACCACAGGGCGCCGTCCGGCCCCGCGGTGATCCCGANCGGCCCGGCCNCNGGGGTCGGCAGCGGGTACGCGGTGATGGCCGTCGGGGGTGATCCGGCCGATNGCGNT
GCCCCGGTCTCG
>Fam_255_123_1  Nr. of seq. 1 Alignment length(with gaps) = 123 Alignment score = 0.000000

TCTTTCAAATTGCAGGGGTGTTGTCGGCTCTCGCTTACCCGAATCACTTACCAGTGTAAGCTCATCGGGATGCACTCTTTTGCCGCCTACCTGTAATCCGAAATCTATAGG
GGATACTTATTT
>Fam_256_121_1  Nr. of seq. 1 Alignment length(with gaps) = 121 Alignment score = 0.000000

AAGTAGGCCGTATCAAGGACCAAAGGGACGCAGCTACGGCATCACCCTGAACCCCACAACACTCTCGCCATCCTTCCGGAACTCCACTTCGTTCCGGTCCGGCCTACAAAG
CTTTCCAACC
>Fam_257_116_1  Nr. of seq. 1 Alignment length(with gaps) = 116 Alignment score = 0.000000
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CTCTCGCGGGTGGACGGGCGGGTTGAGGACGGGCCTGGCTAGCGCGCCGGGGGTGGCGGGACTGGAGGCGGTGTTATCCATACCATCAGCAAACCGTGCTGCAAGCGCGGC
AAGCG
>Fam_258_116_1  Nr. of seq. 1 Alignment length(with gaps) = 116 Alignment score = 0.000000

CCGCTTTCTTTCGGGTATAGCGTCGTGGACAGTCATTCATCCTGCCGCCCTGTAAAAGCAAAAACCCGCCAGCTTACACTGACGGGTTTTATGAAGAGATGAAACTGACCG
ATAAG
>Fam_259_115_1  Nr. of seq. 1 Alignment length(with gaps) = 115 Alignment score = 0.000000

AGTTCCCACAGATCATTAAGTCATTTTTTCGATTCTAAAATATTCGTTTTTTATAATTTAGTTTGTAATAGTTCCTAGAATTTCAAAACTAATTTATAAAATCTAAATTTG
TGAG
>Fam_260_115_1  Nr. of seq. 1 Alignment length(with gaps) = 115 Alignment score = 0.000000

AGGGCGAATAACCGCTCGCGGTCATCCGCCGCTCATCCGCGACATCGGCGGATAACGCCCATGGCGTTATTCGCCCTACACACCCCGAAAAAGCCGGACTGCGCCCCAGCT
CCGT
>Fam_261_114_1  Nr. of seq. 1 Alignment length(with gaps) = 114 Alignment score = 0.000000

ACCAAGGTGGGCGACGGCANGGCGCTGGCCGCCATGNTGGGCAAGGCCAACNTNTTCACCCANGTCGGCNACGGCGANNCCTGGCGCTGNNNGCCGGGCNAGGCCAACNTG
NTC
>Fam_262_114_1  Nr. of seq. 1 Alignment length(with gaps) = 114 Alignment score = 0.000000

TGCTTGCCGTCCACGTCGAGCCGTCCCGTTGCCGACAGCTGGTCGGCCCGGAGCGCGGCGCCCGCGCTCACGGACAACGCGTCGCCGCTGGCGGCCGAACCCAGCGTGACG
GCC
>Fam_263_114_1  Nr. of seq. 1 Alignment length(with gaps) = 114 Alignment score = 0.000000

AAGAAAGCCGCGGTCGCTGCTGCTATTGCTCGTGCAAAAGCGCGTAAAGCGCAACAAGAGACTGAATCTCAACCTGTTGAAGAAACAGCTTCTCAAGAGCCAGCCGAAGAT
CCG
>Fam_264_113_1  Nr. of seq. 1 Alignment length(with gaps) = 113 Alignment score = 0.000000

CACCCCGTAGGTCGGATAAGGCGGTTACGCCGCATCCGACATCCAACGCCCGAGCCGGTTGCCTGATGCGACGCTGGCGCGTCTTATCAGGCCTACACCGCTGTGAAGTGC
TC
>Fam_265_113_1  Nr. of seq. 1 Alignment length(with gaps) = 113 Alignment score = 0.000000

CAAAAACCCGCCGAAGCGGGATTTTGTGGAATGAGTGGCGTTGACCGGTAAGCCGCTTTCTTTTATAAAAAGTGTCGTGGACAGTCATTCCCCTCACGCCCTATCCTCCAA
AG
>Fam_266_112_1  Nr. of seq. 1 Alignment length(with gaps) = 112 Alignment score = 0.000000
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GCGGGGACACGGATAGACGCAGATTAGGCGGATGACCGCGGATAGGTTGTCTGTAGAGCAGGTTGAAGGATGGGCCATTGGCATATCCACCAGCGGCCGTGGGCAGCATTT
G
>Fam_267_111_1  Nr. of seq. 1 Alignment length(with gaps) = 111 Alignment score = 0.000000

TGGAGCAGGGCGGTGATTACCGGCTCTCTCAGCTCTCCAGCATCAGCCAGCACTGATCCCGCCTGCACCCGCACGTACGGGTCGATGTCGGGGTTGGAGTCGGTGGCGAGC
>Fam_268_111_1  Nr. of seq. 1 Alignment length(with gaps) = 111 Alignment score = 0.000000

GTGGACCTGGCCACGGATGGTGCACTGCTCAGGCTTCGGCCGGATCGGGCGGCAGGCATTGCCNTTCCGCACCTCGGTNCCCCGCGGGCAGACACAATCGCCATCCGCATC
>Fam_269_108_1  Nr. of seq. 1 Alignment length(with gaps) = 108 Alignment score = 0.000000
 CGCGACGATGCTCACTTTGCGCCGGCGCATCCTGCCAGGGCTCGTTCAGACACCTACGCTGGTCTTGAGCCATTTGTTGATCTGAATGCGCCGACGCCGTCCGAGTTG
>Fam_270_108_1  Nr. of seq. 1 Alignment length(with gaps) = 108 Alignment score = 0.000000
 AAAAAACAAGCTTTTTATTGGTACACAAAAGCTGCCGAACAGGGATATGCAGNAGCACAGTTTAATCTTGGTCTTATGTATTATAATGGAGATGGAATACTGGCTGAC
>Fam_271_105_1  Nr. of seq. 1 Alignment length(with gaps) = 105 Alignment score = 0.000000
 GGTAACAATGCCGATCCTGACGATGACAATGACAGCGTCAATGATGCACAAGATGCCTTCCCACTCGACCCAAATGAAACTGTCGACACCGACAAAGACGGTATC
>Fam_272_105_1  Nr. of seq. 1 Alignment length(with gaps) = 105 Alignment score = 0.000000
 CATTAACGGCGGCCAGCTTCACAGCTTAAGCAGCAACATCGCCAACTACTTTGGGGGNGATGCTTCTGTGGGTGATGACGGTACGTTTACCGGCCCGACCTATAA
>Fam_273_103_1  Nr. of seq. 1 Alignment length(with gaps) = 103 Alignment score = 0.000000
 GTAGGAATTCTTACGAAGCTAAATTAGAATATATGAGTATTTAAAATTCGTAATGTGACTAAAACTGTGGGAACTACCGCAAATTTGGGTTTATTGTTAAGTT
>Fam_274_102_1  Nr. of seq. 1 Alignment length(with gaps) = 102 Alignment score = 0.000000
 CGCGGATGTCGGGTCCCGTGCGGGGAGACATACCGTCTTGGCCGGCCAGCGTCCATGGCGTACGGCGGCGTGCCTGTCCCGGCGGGGACAGGCACACTCTGC
>Fam_275_101_1  Nr. of seq. 1 Alignment length(with gaps) = 101 Alignment score = 0.000000
 AATTTTGGTATGTACTCAATTTAGGCTTCACTTTAGTTTCTCCTTAGTGAAAACTGCTCTACTATAACCCTATGTATGTACCATAATTCTTTGATGATTAG
>Fam_276_99_1  Nr. of seq. 1 Alignment length(with gaps) = 99 Alignment score = 0.000000
 CTCGAAGAACTGGGCCTGTCACCAGAAGAGATTGCCCAACTTGAAGGCCAGGCGCCCGCTGCTGCGGCCAGCGCCGAACCGAACCTGAAACCCTTCTCC
>Fam_277_99_1  Nr. of seq. 1 Alignment length(with gaps) = 99 Alignment score = 0.000000
 GCTTCCCAAGCAATCGGTGAGGGTTCTTATCGGACAATCGCTTTTGTGAGCGAGCTTTACTAGCAATACGTGCGGGTATAGTTGAATGGTACAACTATT
>Fam_278_98_1  Nr. of seq. 1 Alignment length(with gaps) = 98 Alignment score = 0.000000
 GTGATTTGTGGGAGTTCCCACATTTTAGGAATCGAGATTACAACTTTTTTTAGAAAAATGAACCATGGATTTCCTTACGTCGAACTCACGTTAAAATC
>Fam_279_97_1  Nr. of seq. 1 Alignment length(with gaps) = 97 Alignment score = 0.000000
 GAAGCCGGTCACACAGTTCGGCGCGCAGGCGTAACGCGCAGATCGTTCGCCACGCAGCACTGACGCATGGCCACGCACGCGAAGCGCTCCATGCGAT
>Fam_280_96_1  Nr. of seq. 1 Alignment length(with gaps) = 96 Alignment score = 0.000000
 CAGGTGGGGGGCGAGGGCGGCCAGCGCGTTGCTGCGCCACACCCCATCGGCAATCTCACGGGCGGCGGCGAGGGCCTCGGGCAGCAGCGCCGGCGG
>Fam_281_95_1  Nr. of seq. 1 Alignment length(with gaps) = 95 Alignment score = 0.000000
 TTATGGTGCGGGCTATATATTTTAGTTTCAATAGGTTTATTAACTTTTTCAAAGTAAGAATAAGACCAAAAGAAAAAATCACAATCAACAAGTGA
>Fam_282_93_1  Nr. of seq. 1 Alignment length(with gaps) = 93 Alignment score = 0.000000
 GAAACAACGTGGGAGTTCCCACAATTTCAAGGTCTAACCCTAAAATCAAAACGGCAGAAGCCACTACAATTTTTTAACAACAAGCTTCAATTA
>Fam_283_93_1  Nr. of seq. 1 Alignment length(with gaps) = 93 Alignment score = 0.000000
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 CAGTCAAACCACTGCCCAGGTCAGCAGAAGATTCGGAGCCAGTTCTATCGGCTGGTTTATCCGAAACGAAACTGCTTAAGCTGTCCGGATTAG
>Fam_284_92_1  Nr. of seq. 1 Alignment length(with gaps) = 92 Alignment score = 0.000000
 AAAAAACACGTCATTCAAAAAAGAAAATAAACTAATTAAGGATGTCGTTAATAAAGAGGTTTGGGCGGAGCCCATTATATTCATGAACTTAG
>Fam_285_90_1  Nr. of seq. 1 Alignment length(with gaps) = 90 Alignment score = 0.000000
 GCCTTGCTGGCGGCAGTGGAGCTGGCAAACAGTGAATCATGGTTTTTGAGGAAAGNGTTCACAACGGAGTTGCGTGTCATTGCCTCGAAT
>Fam_286_90_1  Nr. of seq. 1 Alignment length(with gaps) = 90 Alignment score = 0.000000
 GCCATCAGCAATGATGGCCTTTTTGTTTACAGAATTTGAACCTNGGGTTCCTTATTCTAAGCGCAGCTCCTGCGCCATGTTTCATGGAAA
>Fam_287_90_1  Nr. of seq. 1 Alignment length(with gaps) = 90 Alignment score = 0.000000
 TTCTCTTTATTAGCCATTTGTTCTTGAGGTGTTACGACCATGTCGTTCACAATGCTTGGCATCTGTTTTTCAGAGATTACAACCTTATCG
>Fam_288_89_1  Nr. of seq. 1 Alignment length(with gaps) = 89 Alignment score = 0.000000
 TCCGTGCCGCTGTGGTGCACCTACCACCCTGCCACCGGAAACACGCCGGAGGAGGAAAGCATGCCGCAGCGCTACATCCCTCTATGCCA
>Fam_289_88_1  Nr. of seq. 1 Alignment length(with gaps) = 88 Alignment score = 0.000000
 GGTGCGAATGCAGGTGCATTCTGGCAAACCCGACAGACGCAAAGTGCGCCGGAGGCGCGCGCTCCCAGTGCTGCGCNGGGTGGTGATC
>Fam_290_88_1  Nr. of seq. 1 Alignment length(with gaps) = 88 Alignment score = 0.000000
 CAACGCGCCGCCATCCGGGGGTATTCCCTGCTCGCGCTGCGCTTAGCAGGGCTGCGGTTCCGTGCCGTTAGGTAGCCCGGATAAGGCG
>Fam_291_88_1  Nr. of seq. 1 Alignment length(with gaps) = 88 Alignment score = 0.000000
 CGGTCAGGTGTACACCGAACTTGTGNGAGCTTGCTCGCGAAGAGGCCCGTGCAGTCGCTGGATGTCTGCTGGGTAGCTGCTCACCTGT
>Fam_292_86_1  Nr. of seq. 1 Alignment length(with gaps) = 86 Alignment score = 0.000000
 TTCTCCATTTGCAGAAGTGTAGAAGTAACAATCCGTCAAAGGAGACAGTGAAGGAAAGCCATAAGGCATATACGGTTCACTGCCCA
>Fam_293_84_1  Nr. of seq. 1 Alignment length(with gaps) = 84 Alignment score = 0.000000
 ATTATAAGATTCTATCTTTGTAGTGCTATGTGCAACTACAGCTTTTAAAATATCTAAATTGCCTTTATCTATAGCCCTATCAAT
>Fam_294_82_1  Nr. of seq. 1 Alignment length(with gaps) = 82 Alignment score = 0.000000
 TGGGACACGGATGCACGCGGATTGGGCGGATGTGCGCGGATATGGCAGAAGTACCGGTCATCCGCAGGGTGGGTATTACCGG
>Fam_295_81_1  Nr. of seq. 1 Alignment length(with gaps) = 81 Alignment score = 0.000000
 TGTTCGGCCGGCGCCTGCTCGGTCTGCTGCTGCTGGTCACGCTTCTTCCTGCGCGGCTGCTGTTCCTCTGCGGGTGCTGCC
>Fam_296_81_1  Nr. of seq. 1 Alignment length(with gaps) = 81 Alignment score = 0.000000
 GTAACAACACATGCAAACGGCCAAGTATCATACGGAGCTCGCCCGACACAAAACAAGCCAAGCAAAACAAATGCATACAAC
>Fam_297_79_1  Nr. of seq. 1 Alignment length(with gaps) = 79 Alignment score = 0.000000
 TGGATGTAAGTAATTTTGATACCAGTTCAGTAACTAATATGTATNACATGTTTAAAGATTGTAGAAATCTTGAAGAAGC
>Fam_298_78_1  Nr. of seq. 1 Alignment length(with gaps) = 78 Alignment score = 0.000000
 GTTTGTAATCCNCTACAATCANCAAACATATTACTCATATNTGTCACTTGACTCGTATCAAAATTNGATACATCTAAT
>Fam_299_78_1  Nr. of seq. 1 Alignment length(with gaps) = 78 Alignment score = 0.000000
 ACGGTGATGTTGGCTGGTGTGGTGGCGGCCGGGATGTTCAACGACGGCAACGTCAACCCGGGCAGGCTGAAGGCGCCG
>Fam_300_77_1  Nr. of seq. 1 Alignment length(with gaps) = 77 Alignment score = 0.000000
 TACGAAAGCGATGATTTTTACAACTCCGTTGAAAGCAAAAGACTACGCTACGCTTGTCTTTTTGCAACATCGCTTTT
>Fam_301_77_1  Nr. of seq. 1 Alignment length(with gaps) = 77 Alignment score = 0.000000
 GATGACCTGCGCCGACGACGATGCAGAGCGTAGCGATGAGGTGGGGGCACCACCCGCTTGCGGGGGAGAGTGGCGCT
>Fam_302_75_1  Nr. of seq. 1 Alignment length(with gaps) = 75 Alignment score = 0.000000
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 CCCAACGGGATTGCCGGAAGTGAGTAGCCATCCGGGAACACCGTAAACGGGCCTAACCCTCCGCCCACATCAATA
>Fam_303_74_1  Nr. of seq. 1 Alignment length(with gaps) = 74 Alignment score = 0.000000
 GTTGGTAATTATAAGCTAAAATACAATTTTGAAAGCAATTCACAACNNAATATNTATNTANTTANNATNTTNNT
>Fam_304_74_1  Nr. of seq. 1 Alignment length(with gaps) = 74 Alignment score = 0.000000
 GTTTCAACCCTCGCCCGGCATGGAAGCCGGGCGCGACGANNACNTNCCNNANGTNNNCCNTNGGCNATNGNNNN
>Fam_305_73_1  Nr. of seq. 1 Alignment length(with gaps) = 73 Alignment score = 0.000000
 TGTCTGTAGTTCCGACCTAAGGTTTTACTGTTAAAATCTTGTGATTTGTGGTAGTTCCCACGTTTTTCAAATC
>Fam_306_73_1  Nr. of seq. 1 Alignment length(with gaps) = 73 Alignment score = 0.000000
 CCGCGGAGCGGTGACAGTTGTCAGCCTCGGGTTTTCAACCCGAGGTCTCGGTTGCAAAACCGCGTCCTCCAAG
>Fam_307_72_1  Nr. of seq. 1 Alignment length(with gaps) = 72 Alignment score = 0.000000
 TGCTTTAGGTGGTGNNGCTGGTNNTGCAGTTGGTAAAAGCATNGGCGGTACANAAGGTGNNNCAATTGGTGC
>Fam_308_72_1  Nr. of seq. 1 Alignment length(with gaps) = 72 Alignment score = 0.000000
 GCCAGCGCCGTATCAGCAGCCGGCTTACGATCCGCATGCCGGTCAACCTGCGCCGCAGGCCTATCAGCCTGA
>Fam_309_72_1  Nr. of seq. 1 Alignment length(with gaps) = 72 Alignment score = 0.000000
 GTCAGTAAAAAGTGACTGAATAAGGAGCATTTTATCGGCAAATAAAAGAAAGATCAGCTTGCTGAACTTTCT
>Fam_310_72_1  Nr. of seq. 1 Alignment length(with gaps) = 72 Alignment score = 0.000000
 TGCGATTGAATAGTGAGCATTTTAGTTGTAGATAAAAGAACCGTCAGCGCAGCTGACAGTTCTGTCAGTAAT
>Fam_311_72_1  Nr. of seq. 1 Alignment length(with gaps) = 72 Alignment score = 0.000000
 ATAGGCGGAACATTGATTGGCCCCACCAACGCCCCCGAACTACTCACACCCAAACCGATGGCGGGAACAGTA
>Fam_312_70_1  Nr. of seq. 1 Alignment length(with gaps) = 70 Alignment score = 0.000000
 TAAGATATTACTATCAAGTAGTGAATTATATTGAACGATATATCAATAATTGGCAGTAAATTATATTAAA
>Fam_313_70_1  Nr. of seq. 1 Alignment length(with gaps) = 70 Alignment score = 0.000000
 GTTTAAAAAAGCGAATTTTATCGACACATAGCNAGAANGTGTCGATGCCATAAGCATATTCCGGCAACAT
>Fam_314_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 CCACTGCCACCGTACAGCAGCAGGCCACCAAGGCCGTGACCGAACCGGCCAAGCAGGCGGCCAGCAGCG
>Fam_315_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 GCTCAACGGAACATCCAACCCAAACGGATTAATCGCGAAACCAGGGATCGTGACCGCGCTCGTGCCCCC
>Fam_316_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 GCTCAACGGAATACCAGGAATAGTAATATCCGGCACCACAATCGGACCGACACCACCCAGCGCGTTCAG
>Fam_317_69_1  Nr. of seq. 1 Alignment length(with gaps) = 69 Alignment score = 0.000000
 ACTTGTTAAGCCCGTACAGTCGGAAAAAGCATACTCGCCTATTTTGGTAAGATTTGCAGGCAGGCTTAT
>Fam_318_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 AGCGGTTCGAGGGAGCTGATGTCGGTGCGTNGATACCCAGNGCGTTGAGAGATGTCAGAATTTCGNGC
>Fam_319_68_1  Nr. of seq. 1 Alignment length(with gaps) = 68 Alignment score = 0.000000
 ATAATTCCTTAGAGGTATGGAAACANCTGTCGTGNATNNGGNNNATCTNTGCAANGAATNTNGTTTCA
>Fam_320_67_1  Nr. of seq. 1 Alignment length(with gaps) = 67 Alignment score = 0.000000
 ATTTATTAAATTTGTGCTAACTGTACAAAATATATTGATTAAGTTTAGATTAGTGATAAAAAGATAT
>Fam_321_67_1  Nr. of seq. 1 Alignment length(with gaps) = 67 Alignment score = 0.000000
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 AGATAATATCCTAATCAAATTCTAGTCATTTAAACATAACATCATAAGTAATTTATCTGACAAATTA
>Fam_322_67_1  Nr. of seq. 1 Alignment length(with gaps) = 67 Alignment score = 0.000000
 GTTTTAGAGCTATGCTGTTTTGAATGGTCCCAAAACTGNGCATANGGANNACTTAATTGCGCTTTNT
>Fam_323_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 AATTCCATAAGGTACAATTAATACACNAGGCNTNNGCGTNTNCATNNTTNNNNNNACNTATATTTC
>Fam_324_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 GCAACCAGATCACCGACATTGCGCCGCTCGCATCGCTCAAATCGCTCACGGAACTCTNGCTCTCCA
>Fam_325_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 TTACTGCTTCTAAACAAATTTNTTCTGTTTGNTTNTTTACATANTNTAAAGCTTTATAATTTTGTT
>Fam_326_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 TTTACATACCACATAGTTAATATAAAACNANAANTATTTNTAGGGAANATACTTNGTTATNNAACC
>Fam_327_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 TACCACTTAGTTAATATAAAACNNATTANTACTNTNANANNNNTAGNNNACNTANTNNNATTTACA
>Fam_328_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 GAGGCCAGCCAGGGGGGCGAGGTCGGTGACCGCAGTGTAGCTGAGAGTGAGGTTTTGGAGGTTTTC
>Fam_329_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 GCTCTAAAACTGACNATNATGACTNAATAGCTTTTCANNNGTTTTGGAACCATTCGAAACAACACA
>Fam_330_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 TTCCTTAGAGGTATGGAAACAGACNTNCTATCTTNTAGNNTCGAAACNNNTTCTACGTTTCAATAC
>Fam_331_66_1  Nr. of seq. 1 Alignment length(with gaps) = 66 Alignment score = 0.000000
 TTTGAGAGTTGTGTAATTTAAGATGGATCTCAAACNNNNTNNAANTNNNNNATNNGNNAATNNNNG
>Fam_332_65_1  Nr. of seq. 1 Alignment length(with gaps) = 65 Alignment score = 0.000000
 GTTTTAGAGCTGTGCTGTTTCGAATGGTTCCAAAACNNNTNCTNNTNNTTNNAATTGNANAGNNT
>Fam_333_64_1  Nr. of seq. 1 Alignment length(with gaps) = 64 Alignment score = 0.000000
 AAGATTTTGATATGAAATTAAAAAATGCAGTAGTTCCCACAGAATTACGCCTCTTAGAACGATC
>Fam_334_64_1  Nr. of seq. 1 Alignment length(with gaps) = 64 Alignment score = 0.000000
 GTGTGGGACGGGGCCATGGAACNGNAGNAGNGCGNCCNATCNCGGCANGNACTCTACCATGGCG
>Fam_335_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 GCACGCGCGGGGCTGGTCCNACGGGTGCAGCCGCATGNCCCAGGCGGCCGGCGTGTTGTCCCC
>Fam_336_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 AAACATGGGAGCGCTCTCATCCCATTAGAACCGCCTGTTTCCTCCCGCGAGACTTTGCCCCAC
>Fam_337_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 GAACAGGCCCGCCGCGAAGCCGAGGCGCGGGCGGCGGAAGCGGCAGCACGAGCTGTCGCCGAA
>Fam_338_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 GGTTTATCCCCGCTGGCGCGGGGAACACNACGGCTCNNGCAANAGCAGNACCCNTGTCAGCTC
>Fam_339_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 ACGAAAGTTTTGATGAATCAACAAGTGTGAGTTACAAAGAGACGTAATGTTGCGGGAACTCCC
>Fam_340_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
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 CTAACATCTAAATTTGTTAACTGATTNTTAGNACAAGCCAAATNNNCTAAAGCNGGATTTTTA
>Fam_341_63_1  Nr. of seq. 1 Alignment length(with gaps) = 63 Alignment score = 0.000000
 AGTGAGGTAAGTTNATTTTCGGAACAGTCCAGTTCCTNTAAAGCNGTTAANCCCTGTACATCG
>Fam_342_62_1  Nr. of seq. 1 Alignment length(with gaps) = 62 Alignment score = 0.000000
 GGGCTGGTCCCACGANNGCCAGCGCCCGNCGNGCNNCNNGNTNNGTCGTCCCCGCGTACGCG
>Fam_343_62_1  Nr. of seq. 1 Alignment length(with gaps) = 62 Alignment score = 0.000000
 GGGATAAACCGNACTGNCAGNNNGTGNCNNCNNNAACNNGTNANGAGTTCCCCGCGCCAGCG
>Fam_344_62_1  Nr. of seq. 1 Alignment length(with gaps) = 62 Alignment score = 0.000000
 GTTTCAGAAGTATGTTAAATCAATAAGGTTAAGACCNNATANTANTNNAAANTNNNNATNNA
>Fam_345_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 CGGTTTATCCCCGCTGGCGCGGGGAACTCTAGNTGTCNNGCATTNCANCCGGCTNCNGCNG
>Fam_346_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 GCGCGGGGAACACNNNNNNNCAANNTNNNNNNTNCNANNANCNTNCGGTTTATCCCCGCTG
>Fam_347_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 TTTCTAAGCTGCCTGTGCGGCAGTGAACATAANGTNAANNATAGCANTCGANTTNCCACAG
>Fam_348_61_1  Nr. of seq. 1 Alignment length(with gaps) = 61 Alignment score = 0.000000
 GTTCACTGCCGCACAGGCAGCTTAGAAACCGANATNATCANTTCTANNTNNGTTCTTTNCN
>Fam_349_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 AAAAGGCGGAGAAGCCACTAGCAAAAACCATGACAAAGAATTCTATCAAGAAATCGGTGA
>Fam_350_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 ATACTGTCATTGAGGACAATCGCGGTAATAGGAAAACCATCAAGAAAGACATCTTTGGAG
>Fam_351_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 GGCGACCGTGACCGCGGCGGCTTCCGCCCCCGCGAAGACCGTGGCGAGCGCAGCTTCGGC
>Fam_352_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 GTTCACTGCCGTACAGGCAGCTTAGAAANGAANNCGGNNNNANNNGCACGNCGNNATNNN
>Fam_353_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 CCGCATACGCGGGGGTGATCCCGATCNNTANNGNNGNTNNAANGCNTNNTNANGTATTTC
>Fam_354_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 CATCCCCGCGCATGCGGGGAACAGNCGGCCAAGGCNNNCNNNGNCNGNTNNNGGGCGGTT
>Fam_355_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 CCCGCGTGTGCGGGGAACAGNGTNGCCNNNNCNGCNNGANNGNCGCNNGANCGGTTCATC
>Fam_356_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 GTTTATCCCCGCTGGCGCGGGGAACACNGAAACGCCGTNTNCGCGACCTCGTGANGANCG
>Fam_357_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 GTTTATCCCCGCTGGCGCGGGGAACACNNTNNTTNCNNATNNTANNCNGNNNANCNGNCG
>Fam_358_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
 CTTTAACTTAAGTTATTAGAGCCTCTTATGCAGTTGCTCAGTCAACTGTATACCTTTTGC
>Fam_359_60_1  Nr. of seq. 1 Alignment length(with gaps) = 60 Alignment score = 0.000000
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 CTTTAACCCAACCAGTAGCCATTGAACCTGATTCGTTTAAGTAATACCATAAGCCTTTGT
>Fam_360_59_1  Nr. of seq. 1 Alignment length(with gaps) = 59 Alignment score = 0.000000
 CCTCCGGCGCGCTCATCACCGGCAACACTTCCTCGTGAGGCGCAGACTGGGAGCGCGCG
>Fam_361_59_1  Nr. of seq. 1 Alignment length(with gaps) = 59 Alignment score = 0.000000
 CCGGCTTCCAGAGGGGTGCGCCGGAGGCGCGCGCTCCCAGCTTGCAGGCGAGCGCGTGC
>Fam_362_59_1  Nr. of seq. 1 Alignment length(with gaps) = 59 Alignment score = 0.000000
 GTTCACTGCCGTACAGGCAGCTTAGAAAANGCANCNTGNNGATNCGCGNTNNTNNCNNN
>Fam_363_59_1  Nr. of seq. 1 Alignment length(with gaps) = 59 Alignment score = 0.000000
 GGGCCCCAACACAGAAGCTGGCCAATAGTCAGCTTTCAATAATGTGCAAGTTGGGGTAA
>Fam_364_58_1  Nr. of seq. 1 Alignment length(with gaps) = 58 Alignment score = 0.000000
 GTGTTCCCCGCATGCGCGGGGATGAACCGNNNNCNGNCNNNNCNGNNCNGNCNGNNGN
>Fam_365_58_1  Nr. of seq. 1 Alignment length(with gaps) = 58 Alignment score = 0.000000
 GCCCGACGACGATGCAGAGCGCGCAGCGCGATGAGAAGGAGTTGGGCGGTTAGGTCGA
>Fam_366_58_1  Nr. of seq. 1 Alignment length(with gaps) = 58 Alignment score = 0.000000
 TCGTCGCCGAGCTCGATTTGATTGCCCGGCTCCTCCTCACCCCGTTACCCGGGGCGCA
>Fam_367_58_1  Nr. of seq. 1 Alignment length(with gaps) = 58 Alignment score = 0.000000
 CGTGGGGATAGACCCNCNCGNCNNNNTCNNGNNCANGCGNNGGCGGTTCCCCCGCACT
>Fam_368_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 GGTGCGGGGGCGGAAACCGCCGCGGCCGAAGCTTCCTCGGCCAACGCAGTGGCGCCC
>Fam_369_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 TCTACCACAAGTGATAGCACGGACACATCAGCTTCAAGCGACAGTACAGATACTACC
>Fam_370_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 GGATCACCTCCACATACGTGGAGAAAANCATTTNNTNTNACNAAAANTCNGNATNGA
>Fam_371_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 GTTTTCCCCGCACATGCGGGGGTGATCCCGNNAATNCNANTNTTNCCAGCGNCAANN
>Fam_372_57_1  Nr. of seq. 1 Alignment length(with gaps) = 57 Alignment score = 0.000000
 TTCAGTGAGATGTCTTCACCTCAGTTTATGGAGCGTCAGCTTGCCACCAGCAAGATG
>Fam_373_56_1  Nr. of seq. 1 Alignment length(with gaps) = 56 Alignment score = 0.000000
 TGATCGACGTGCTGGCGAGGGACGAGCCGGTAGGAGATCAGGCAGTCGGCACGGCC
>Fam_374_56_1  Nr. of seq. 1 Alignment length(with gaps) = 56 Alignment score = 0.000000
 GGGGCGGGTTAGGGTGGGGGCGTATCGCAACCCACACGGCAGACCCGGCTACCGTA
>Fam_375_56_1  Nr. of seq. 1 Alignment length(with gaps) = 56 Alignment score = 0.000000
 CCGGCCCGCATCGTCACACGGCCTAAGCCCATTGCCGTCCTCCTCAACGGGCCGAC
>Fam_376_56_1  Nr. of seq. 1 Alignment length(with gaps) = 56 Alignment score = 0.000000
 TGCAAGTTGGCGGGGCCCCAACATAGAGAAATTGGATCACCAATTTCAACAGACAA
>Fam_377_55_1  Nr. of seq. 1 Alignment length(with gaps) = 55 Alignment score = 0.000000
 AGATAAACTTCAATATGGGTTTAACTTGTGGTTAATAGAGTAAGAGTGTAAATAG
>Fam_378_55_1  Nr. of seq. 1 Alignment length(with gaps) = 55 Alignment score = 0.000000
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 TATGATGAAAGATGGATTTAATGTATAAGGAATCAATGAANTTACAAAAAGANCT
>Fam_379_54_1  Nr. of seq. 1 Alignment length(with gaps) = 54 Alignment score = 0.000000
 CCATATAGATAGTCCGTACCTGTATTAGAAATTAGTGTGTCATTCCCATCACCA
>Fam_380_54_1  Nr. of seq. 1 Alignment length(with gaps) = 54 Alignment score = 0.000000
 GTGCAGAGCCAGAACGGCGCCAATATCGGCTCGGGCGCCAATGGCATCAGCGTC
>Fam_381_54_1  Nr. of seq. 1 Alignment length(with gaps) = 54 Alignment score = 0.000000
 TGTCGTTGCCGGCGCCACCATCAAGGGTGTCCGCACCTGCACCACCNTAAAGCG
>Fam_382_51_1  Nr. of seq. 1 Alignment length(with gaps) = 51 Alignment score = 0.000000
 CGGCGAGCGGGGGCGGGAGTTTGAGCGAGAACCACGGGCACGGCGCGATAG
>Fam_383_51_1  Nr. of seq. 1 Alignment length(with gaps) = 51 Alignment score = 0.000000
 TACTTATTAATAGCATTTAGATATTAATTGTATTTACCTATTTGAGTGAAT
>Fam_384_51_1  Nr. of seq. 1 Alignment length(with gaps) = 51 Alignment score = 0.000000
 CTAGTAAGATATACTAATATATAAATACTTAAATTTAATTTTATTTAAACA
>Fam_385_51_1  Nr. of seq. 1 Alignment length(with gaps) = 51 Alignment score = 0.000000
 GTACAAGCAAACAAGAAGCCAACAGTACCAAAAATACTAATCAAACAACCA
>Fam_386_50_1  Nr. of seq. 1 Alignment length(with gaps) = 50 Alignment score = 0.000000
 TATTATAGATGAATATTAATATTGATATTCTAGGTAATTGCTAGAGCTAA
>Fam_387_49_1  Nr. of seq. 1 Alignment length(with gaps) = 49 Alignment score = 0.000000
 GCATGGGATCGGGGCAAGCGCCGAAGCGCTAACTCCGATCGACAGCTTT
>Fam_388_49_1  Nr. of seq. 1 Alignment length(with gaps) = 49 Alignment score = 0.000000
 CCCATGCTTCACGCTCGACCAGAGTTGGCGCTTGAGCACTTACTCTGGT
>Fam_389_49_1  Nr. of seq. 1 Alignment length(with gaps) = 49 Alignment score = 0.000000
 AATCTTAGAAAATGTAGGAACTACTACTTTCAAACAAAGAACCGCAATC
>Fam_390_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 GCAACCACGCCGGTACGTCGCTACCCGCCGCTGGAGCNGCCTCTTCCC
>Fam_391_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 GCTGCTGAACTGCCCGCACTCGATGCTGACGAACTAGCAGCACTGGAT
>Fam_392_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 AAACCTGGGACTACCGAACCCGAGAAACCCGGAGTCACCGAACCAGAA
>Fam_393_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 TGTAGGCGGTGATGAAGACTGGCTGTCGCTGCCACTGCTGCTACTGTC
>Fam_394_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 ACCATCTTGCAGACGGTGTAGTTGCAAGTCTTGGTGCGGCACTCAGGA
>Fam_395_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 GTGTAGTTGATCACTTTCGTACGAGTTTCGTACACAGGCTTCTTGACT
>Fam_396_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
 GTGCTTGCTGAGGCTGAAGCACTTGTTGAGGCTGACTCAGATGCNGAT
>Fam_397_48_1  Nr. of seq. 1 Alignment length(with gaps) = 48 Alignment score = 0.000000
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 TGAAGCACTTTGGCTTGCNCTTGTTGANGCGGACTTAGACGCGCTTGT
>Fam_398_47_1  Nr. of seq. 1 Alignment length(with gaps) = 47 Alignment score = 0.000000
 TTTTCAAAGTTAGTCCGTAAAATACAGATTTGTGGGAACTATTACAC
>Fam_399_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 CATATGGATTTTGTTGATATTGTTGTTCTTGGTTTTGTGGTGCTA
>Fam_400_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 AACGGAACCCAGTACGAAAGAAACCAGCAGGAAGAACCCAAGCAC
>Fam_401_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 AAGTAAGAAATTTAGGAAGTAGGAAGTTTAGTAATAATTTGTAGT
>Fam_402_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 AAAGAAAATAATTAATATAGAGTAAATCTATTGCAATGAATTAAC
>Fam_403_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 TTTTTATTATCTGTTGACTTATCTTCTTCTGGGGTCTGCTCTGGC
>Fam_404_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 AATTAGTTTATTATACTTCTTTAGATTAATTTTCTATACTTCCTA
>Fam_405_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 CGGGAGCTGCAGGCCCGGCAGGNCCACAGGGACCGAAAGGGGATA
>Fam_406_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 GTCGGAACTGGAGTCCACAGCGCTTGAACTTTCCGAACTAGAATC
>Fam_407_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 CAGGGATTACCNGGACCTAAAGGAGACCAAGGGGAGGCAGGACCG
>Fam_408_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 TGCTTGTCCTGATTTTGCTGATCCTGGTTCTGTTGATCTTTGTTT
>Fam_409_45_1  Nr. of seq. 1 Alignment length(with gaps) = 45 Alignment score = 0.000000
 CTGATCGAACGTTCTGGCCGCGTTGCTGAAGGTGGCTCCGATCGT
>Fam_410_44_1  Nr. of seq. 1 Alignment length(with gaps) = 44 Alignment score = 0.000000
 CGCCGTACGCGGCTCTCCCCGCCATCGCTCCGGGTACCCCTCCT
>Fam_411_43_1  Nr. of seq. 1 Alignment length(with gaps) = 43 Alignment score = 0.000000
 GAGCACTGCTCACNNGCGGCGCCGGCGNAGTGCTCNGCNTCGA
>Fam_412_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 CCCGCAAACTTCGAGGGAGTCTGGCCCGAAGGGGGACAGGCA
>Fam_413_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 AACAGCACGGCGANCGGGACGAACTCGACCGCGTCGGGCGAG
>Fam_414_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 AGCACGGCAACGGGCCAAGGNTCGCAAGCGACGGGNNGCAAC
>Fam_415_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TCGCTGTCGACGGGGCTCAGCACGACGAACAGCAGCGTCGCG
>Fam_416_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
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 ATTTCCTATCTCCTCACTCCTATCTCTTACCCTCTCACTCCT
>Fam_417_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 GAAGAGCAGGCGCGGCGCGAAGCCGAGGCGCGCGCTGCTGCC
>Fam_418_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 CTTGCATATCGCTAATAGTGCCATTCATACTACTGATACTGC
>Fam_419_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TTGCTTGTTAGTATTAGTATTTCAATTGTCAATATTAGTGTT
>Fam_420_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TAAAAAATAATTGAGTTAATTATGCATTAGATGTATATTATA
>Fam_421_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TCAGCTTTTGGATNTNATAATANAGCTANTGGANTNNATAGT
>Fam_422_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TGGCGCTCGGCNCCGGTGCGCAGGCCACCNNCGTCAACGNCG
>Fam_423_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TGCGGCCAAACCGGCTGCCAAGGCGACCGCTGCCGCCAAGCC
>Fam_424_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 GGACAAGAAGCGGGCCCCGCGCCCCGGTGTGCCGGCTCGCGG
>Fam_425_42_1  Nr. of seq. 1 Alignment length(with gaps) = 42 Alignment score = 0.000000
 TCCGCGCCCGCTCCCGGTCCCTCCGAACCCGCATCCGGGCCT
>Fam_426_41_1  Nr. of seq. 1 Alignment length(with gaps) = 41 Alignment score = 0.000000
 AATTAAAAGTGAATGGAGAGTAAGAATAAGTTCTAATGAAG
>Fam_427_40_1  Nr. of seq. 1 Alignment length(with gaps) = 40 Alignment score = 0.000000
 TTAATCTATAGTATAATAGTTTAATTTGAAGTACAACGAT
>Fam_428_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 GCTTCTGCTTGNCGTTTNGCTTCAGCNGCTTTTTTGTCT
>Fam_429_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TAAGCAACAAAGTNCTAAACAAGANGATTCCTCTCAGGA
>Fam_430_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TTATCTTTAGATTTCCACCAATCGTCATCACAATTGTGC
>Fam_431_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TGCTCTTCTTGCTTACGTTTTTCTTCTTCTACTCTTTGC
>Fam_432_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 ATTCCCCTCCTCTGGAGGGGTGCCCGTCAGGGCAGTTTT
>Fam_433_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TCCCAGGTATCTCGGTCGGTGCGCGCCGGAGGCGTGCGC
>Fam_434_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 CTTTGAATATTCTACAAGACTATAGATTAGTTTAAATCC
>Fam_435_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
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 GCAGATATAAGGGAAGTATTGAGGGAACTTGGGAAGAAG
>Fam_436_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 CCGCCGTCTAAACCATCAACACCTTCTAGCTCAGTGACA
>Fam_437_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 TATGTGAAGTTCAAGCCATTTGAAGTCGCGGGTCACCCA
>Fam_438_39_1  Nr. of seq. 1 Alignment length(with gaps) = 39 Alignment score = 0.000000
 GCGGCGACGACCGGCGGAGACAGCGCGCCACCGTCGAGA
>Fam_439_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
 GGGGAGCGACATCTGCGGCCAGGGAGCCTGTCCCTGCC
>Fam_440_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
 AAAATATTTAAATAATATATCATAATACAGAGTGANGA
>Fam_441_38_1  Nr. of seq. 1 Alignment length(with gaps) = 38 Alignment score = 0.000000
 GTCGCACGATAGTCGAGATTACGGCCTGCCGACGCGGC
>Fam_442_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CCGCAGAAGAGGCGCGTATTGCTGCCGAGGCCCGTG
>Fam_443_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 AAAACCTGATACGGGAGGAAATCCAGACACAGGAGG
>Fam_444_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 ACCGGAGCAACAGGCCCGACTGGAATAACGGGCCCA
>Fam_445_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CCAGTCGGTCCAGTAATACCAGTCCTTCCAGTAACA
>Fam_446_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 GCGGGTTCACCTCGGGGCTCGACCGCAGCGCCTTCT
>Fam_447_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 GCGAGACGGTCGGTGTTGCCGTTTCCGTTGGTGTCG
>Fam_448_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 TACTCATTAAAGCGACTACTATAGAGTAGATAAAAT
>Fam_449_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 TCTATATTTATATCTGGTTTTCCATCCCCATCTGTA
>Fam_450_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 GGTGGATTTANCACTGCATCATCCATTGGTGGCACT
>Fam_451_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CAAGTGGCGAACCAGACAAAGATAAAGAACCAGATG
>Fam_452_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CACAAGAAGAAAGCGGCCAAGAAACATAAGAAGTCG
>Fam_453_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 TGGTTGCTCAGGTTGACCCGGTTCTTCCGGTTGACT
>Fam_454_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
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 GGCCTTGCCCTGGGCCTGCTGGTCGGTGGTGGTGCT
>Fam_455_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 GCCATACCGGGGTGAGGCGGCAAACCAGGACGAGGA
>Fam_456_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 GCAGATAAAAAAGCAGCAGCTGAAAGGAAGGCCGCT
>Fam_457_36_1  Nr. of seq. 1 Alignment length(with gaps) = 36 Alignment score = 0.000000
 CAAGTACGTCNGCNTCNACGAGTGCATCAGTAAGNG
>Fam_458_34_1  Nr. of seq. 1 Alignment length(with gaps) = 34 Alignment score = 0.000000
 TCGAGCGCCCATAGAAGCGAGATGCTGAGTTATT
>Fam_459_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 TATTCACAAAACAGAGACAACAGAACTGGTGGA
>Fam_460_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 ATGGTTTCTCCCCATCTGGTATCTGACCATCTG
>Fam_461_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 CTACTGGGTCTCCTATAAATTTCCCTTGGAATT
>Fam_462_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 GAATTAAAAGATGANGCAGNAGNAAAAGCAGAG
>Fam_463_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 GGTTTACTTGGTTCAGTCGTCCCTGGCTCACCT
>Fam_464_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 GGTCAGCTTTTGCTCCACTGCATCAATACGCTG
>Fam_465_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 CGATGAGCCGCTTGCGCGAAGAGGTTCAGGGCC
>Fam_466_33_1  Nr. of seq. 1 Alignment length(with gaps) = 33 Alignment score = 0.000000
 ACCCCGCCCGACGATAGCGGCGATGACGATGTG
>Fam_467_32_1  Nr. of seq. 1 Alignment length(with gaps) = 32 Alignment score = 0.000000
 TTCGGACCGCGGTACTTTCGGACTCCGGTAGG
>Fam_468_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
 GGGTGCCTGTCCCTGTACGGGAGAAGTTTGC
>Fam_469_31_1  Nr. of seq. 1 Alignment length(with gaps) = 31 Alignment score = 0.000000
 CCCCCAGCGGGAAACCTCTCCCCACCTCCTC
>Fam_470_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 CGCGACATCTCCACGCGCGGGATATCCGGC
>Fam_471_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GGGCTGGGCGTCGTGCTCGCCGTGGCCGAT
>Fam_472_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 ACGGCCACCAACACACCGACCAATACACCC
>Fam_473_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
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 TTGCTATTTCCTCCATTACCTGAATCCGGT
>Fam_474_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GGCGGTGATACGCCTGTTCCGCCAGACGAC
>Fam_475_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 TTCACATCCGGCACGTTCACGCCGGGCACA
>Fam_476_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GTTTCGCCGCCTCCGGTCCCCGGGTCGACG
>Fam_477_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 CTGCTGGTTTGTTTTCTGCCGGCTTATTGT
>Fam_478_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GAATCCGAAGAATCTGAACCGAAACCGCCG
>Fam_479_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 CCCGGCGGCGGGGCCCTCAGGTCGGGACAG
>Fam_480_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 CCACACCGCCGGAGCCAGCACCACCAGGCC
>Fam_481_30_1  Nr. of seq. 1 Alignment length(with gaps) = 30 Alignment score = 0.000000
 GACCGTCCGGCGCGGGGTCGCGCTCGGGCT
>Fam_482_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 ATTGCAAAGTGCAAATTGATCAATGCAA
>Fam_483_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 TACATTTCAGAAGAAAATGCTGCGCCGT
>Fam_484_28_1  Nr. of seq. 1 Alignment length(with gaps) = 28 Alignment score = 0.000000
 TCACTTACTTGAGTAAGCTCATCGGGAT
>Fam_485_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 GTTACCTGCACCACCTGCTATTGTATC
>Fam_486_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 CCAAGAAGGCGGCAAGCAAGACCGCCN
>Fam_487_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 GGCGTCACCGACGGCGTAGGGGTGGTC
>Fam_488_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 CTGCATTTCCTGCATTAGCATCTCCTT
>Fam_489_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 GATGAACTTGAACCACCTGTACTTGAT
>Fam_490_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 CCGGTGGTGCCGCCTGGTGGGTTTCCC
>Fam_491_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 GATACTAAAGAAGTGAAGGAAGCTAAA
>Fam_492_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
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 ACGCGGAGCGTCCAGCACTGCATTCCC
>Fam_493_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 TGAGGCGTCCCGCCTCAGAAGACAGCT
>Fam_494_27_1  Nr. of seq. 1 Alignment length(with gaps) = 27 Alignment score = 0.000000
 CGCCATAGCCCGACGCGCCGGGAGCGG
>Fam_495_26_1  Nr. of seq. 1 Alignment length(with gaps) = 26 Alignment score = 0.000000
 CTGGACGCGGCACGCGTCGGTTCGGT
>Fam_496_25_1  Nr. of seq. 1 Alignment length(with gaps) = 25 Alignment score = 0.000000
 CCTCCGCCAGGACTGGAAGCACGCG
>Fam_497_25_1  Nr. of seq. 1 Alignment length(with gaps) = 25 Alignment score = 0.000000
 GGCACGCGCTAATGGTGGTCGTGCA
>Fam_498_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CCTGGAACACCAGATCCAGAAAAA
>Fam_499_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CGGTCGCCGAAGTCGCGCTGGGGN
>Fam_500_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 ACCGGGCTGGTCGTTACCGTCGGC
>Fam_501_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 GCACGCGCACCGCTACGCCAACCG
>Fam_502_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CCAACTACAGGTGGAAACACAACA
>Fam_503_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 TCTGGTTTTTCTTCTGGGTCTACC
>Fam_504_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 GGCAGGAAGGNCATCAAATTGGCT
>Fam_505_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CAAACTTGAGGAAGAGCAACGAAT
>Fam_506_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 TGAATCTCTTCTATCTCCACGACC
>Fam_507_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CTGGTGTTGCCGGACGTGCCACCA
>Fam_508_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 TGGTCCATCCCAGCCATGTTGCCG
>Fam_509_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CGCAGCAAGGTGCGGGAGCTGGCT
>Fam_510_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 GGCTTCGCCACCACCGGTTCGGCG
>Fam_511_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
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 CCAGGCTTGTTGTTGTCTTCTTTG
>Fam_512_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 TTAACGTCTGGCTTAGCTTCTGGC
>Fam_513_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CCCGCACGCGCACGTCCCCACCGC
>Fam_514_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 GCGTACGGCGGGNCCCGTTCCGAC
>Fam_515_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 TCCGGTGCCGGGTCCGGTGCTACT
>Fam_516_24_1  Nr. of seq. 1 Alignment length(with gaps) = 24 Alignment score = 0.000000
 CGCCCGGTCCGTCATCCGGCGTCA
>Fam_517_23_1  Nr. of seq. 1 Alignment length(with gaps) = 23 Alignment score = 0.000000
 GGGGTTGCGGAGAGCGGCAAGGC
>Fam_518_23_1  Nr. of seq. 1 Alignment length(with gaps) = 23 Alignment score = 0.000000
 ATCCGGACACCCATTCCACNGGC
>Fam_519_23_1  Nr. of seq. 1 Alignment length(with gaps) = 23 Alignment score = 0.000000
 GGTGGCAGCCGTCGACCCGCACG
>Fam_520_23_1  Nr. of seq. 1 Alignment length(with gaps) = 23 Alignment score = 0.000000
 AGGGGTGTCGGCCTCACGCGGTA
>Fam_521_23_1  Nr. of seq. 1 Alignment length(with gaps) = 23 Alignment score = 0.000000
 GCGGCTCCTCGCCAGGCGTCCGT
>Fam_522_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
 TTACGGTGCTGCGTAGCCAAAG
>Fam_523_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
 ACAAAGTAAAACCACAAAGTTC
>Fam_524_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
 TTCGGGGCTGTTGATATTGCAT
>Fam_525_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
 GAACCATCAGATTTTGAGCGAA
>Fam_526_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
 TCAACTATCGTGCCACGCCCTT
>Fam_527_22_1  Nr. of seq. 1 Alignment length(with gaps) = 22 Alignment score = 0.000000
 CGACGAACGAGCAGCGGACCAC
>Fam_528_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 TCAGAAGCAGCAGCAGCAGCT
>Fam_529_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 CAATCACGCGAGTTGCCTCCN
>Fam_530_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
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 TTCAAATCTTTTATCNACNTG
>Fam_531_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 GCCAACCACCGTGTCCGCCTT
>Fam_532_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 GTGTCAGAGTCNGCATTNAAA
>Fam_533_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 TATCTGCTCATTATAACCAGT
>Fam_534_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 AGCTCGCCGACGGCACCGGCG
>Fam_535_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 CCTCCTCGGCGGCGCTCTCGC
>Fam_536_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 CTGTTCTTCCCACCGCCGAGC
>Fam_537_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 TCGGGGCGGGTTGGGTACCGG
>Fam_538_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 TACACAATATATAATAGCAAT
>Fam_539_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 CCTGACGATGGCGGCAATACT
>Fam_540_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 TTGGTGAACTTTCTTGCTCTT
>Fam_541_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 AAATCTTTCTGTTCTTTAACC
>Fam_542_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 TCATAATTAACCCTCAAATCA
>Fam_543_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 GCCGGCTTCATGGCATCNGCN
>Fam_544_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 TCTATGGAAAGTCGTTTAGAC
>Fam_545_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 GGCGGCATGGGAGGCATGGGC
>Fam_546_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 GGCAAGGGCAGCCAGGACAAC
>Fam_547_21_1  Nr. of seq. 1 Alignment length(with gaps) = 21 Alignment score = 0.000000
 TCAATTCTTTTATTTGTTTCA
>Fam_548_19_1  Nr. of seq. 1 Alignment length(with gaps) = 19 Alignment score = 0.000000
 TAGATATTTAATTAAGTGG
>Fam_549_19_1  Nr. of seq. 1 Alignment length(with gaps) = 19 Alignment score = 0.000000
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 TATATAAAATTTANTAATT
>Fam_550_19_1  Nr. of seq. 1 Alignment length(with gaps) = 19 Alignment score = 0.000000
 AACTGGTTTAATCGTGACT
>Fam_551_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GCGCGGTTGTGGACGACG
>Fam_552_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 CCTGTTACTCCAGTTGGA
>Fam_553_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 ACGGGGAACACCGGACCC
>Fam_554_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 CCTGATACAGGAGAAAAA
>Fam_555_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GTGATGCCTGTAGGACCA
>Fam_556_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 CGTCTGGTTGTTTGTCTC
>Fam_557_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 CTGGACAAGCAAGACAAT
>Fam_558_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GACGGCAAGCCNGGCGCN
>Fam_559_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 CCCGAGCCGGTGNTCGAG
>Fam_560_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GGCGGGTTTAGCACCCAC
>Fam_561_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GTGCGGGTTGGTGTCGGC
>Fam_562_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 TGACCCTGGTTTTTCTGT
>Fam_563_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GTGATCGGGGTTCCCGGC
>Fam_564_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 CGCCTGGCCAGTACGGCC
>Fam_565_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 TGCTCGGGGTAACCGCGT
>Fam_566_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 AAGCTGCCCAAGAACTTA
>Fam_567_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GAACCAGGTAAACCAGCG
>Fam_568_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
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 CCGTCCCGGGCGCCGTAN
>Fam_569_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GCCGCGGCGGGCTCCGGG
>Fam_570_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 TACGGCCAGCAGCCCCCN
>Fam_571_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GGGTGGCCGGGCGGCCGT
>Fam_572_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GAAGCGGCACTGGCTTCC
>Fam_573_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 AGGAGCCTTTGGAGCCTC
>Fam_574_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 TTCAAACGGCTTGCAGCG
>Fam_575_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 GTCGGCTCTGGCGTTACC
>Fam_576_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 ATCGGTAGCCCTGTGCAA
>Fam_577_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 TTTCAAGCTGAATGTGTG
>Fam_578_18_1  Nr. of seq. 1 Alignment length(with gaps) = 18 Alignment score = 0.000000
 ACGGCACCGCCGGAAACA
>Fam_579_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 CAGGAGCAACAGGTCNA
>Fam_580_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 GGGCGGAGCGGTGCGAG
>Fam_581_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 TAGGATGTAAAAGTAAA
>Fam_582_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 TAAATATAAATAATGTA
>Fam_583_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 CAGGCCAGAAAGCACCA
>Fam_584_17_1  Nr. of seq. 1 Alignment length(with gaps) = 17 Alignment score = 0.000000
 TTACTGATATGGGCTAA
>Fam_585_16_1  Nr. of seq. 1 Alignment length(with gaps) = 16 Alignment score = 0.000000
 GCGAATGGGCGAATGA
>Fam_586_16_1  Nr. of seq. 1 Alignment length(with gaps) = 16 Alignment score = 0.000000
 CCCGAGAGCCCGAGAG
>Fam_587_16_1  Nr. of seq. 1 Alignment length(with gaps) = 16 Alignment score = 0.000000
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 TATATTGGTATATTGG
>Fam_588_16_1  Nr. of seq. 1 Alignment length(with gaps) = 16 Alignment score = 0.000000
 AAAGATATTTGTAGAA
>Fam_589_16_1  Nr. of seq. 1 Alignment length(with gaps) = 16 Alignment score = 0.000000
 GCCGGTGTTGNTAGTN
>Fam_590_16_1  Nr. of seq. 1 Alignment length(with gaps) = 16 Alignment score = 0.000000
 ATGTGATGATGTGATG
>Fam_591_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 GCCAGCGCAGTCCCC
>Fam_592_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CTGCCGGATTCTGCG
>Fam_593_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 ATGCCACTGCCCGGG
>Fam_594_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 GGCATCTGGCCGCTG
>Fam_595_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CGTTTCGACCGGAGC
>Fam_596_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CGAGCCGGTCCCAGA
>Fam_597_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CCGTCGTCACCGTTC
>Fam_598_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 GGTTGATCGACACAC
>Fam_599_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 ACCTGCGCGGNGCGG
>Fam_600_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 GCCCGATGCANGGTG
>Fam_601_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CTTAAATTTGCAAAN
>Fam_602_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CCCGACATTGCCCAA
>Fam_603_15_1  Nr. of seq. 1 Alignment length(with gaps) = 15 Alignment score = 0.000000
 CTGAATCGGACGGGA
>Fam_604_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 CGCAGGCTGCAGAA
>Fam_605_14_1  Nr. of seq. 1 Alignment length(with gaps) = 14 Alignment score = 0.000000
 TATAATCTAATAAA
>Fam_606_13_1  Nr. of seq. 1 Alignment length(with gaps) = 13 Alignment score = 0.000000
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 CGTGCGCACCCGC
>Fam_607_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 ATTGAAAAAGGC
>Fam_608_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 CCTGTTTCACAA
>Fam_609_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 GAAGCGCCGCAA
>Fam_610_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 ATGGCGGCGGTA
>Fam_611_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 AGCTTGGTTGGA
>Fam_612_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 GCCGCTGAAGTT
>Fam_613_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 TCCTCTTTAGCC
>Fam_614_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 ATAATAACAATA
>Fam_615_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 ATTAATGAAGAT
>Fam_616_12_1  Nr. of seq. 1 Alignment length(with gaps) = 12 Alignment score = 0.000000
 TAATGCTAATGC
>Fam_617_11_1  Nr. of seq. 1 Alignment length(with gaps) = 11 Alignment score = 0.000000
 TCCCGGGCCGC
>Fam_618_11_1  Nr. of seq. 1 Alignment length(with gaps) = 11 Alignment score = 0.000000
 CGATTGCCCGG
>Fam_619_10_1  Nr. of seq. 1 Alignment length(with gaps) = 10 Alignment score = 0.000000
 GCTGATATTC
>Fam_620_10_1  Nr. of seq. 1 Alignment length(with gaps) = 10 Alignment score = 0.000000
 CAACTATCAC
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