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dISFV-NC_017086.1
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MBFV-NC_040776.1
MBFV-NC_034151.1
MBFV-NC_00943.1
MBFV-NC_006551.1
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MBFV-NC_009029.2
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MBFV-NC_012534.1
MBFV-NC_012534.1
MBFV-NC_012532.1
MBFV-NC_01437.1
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MBFV-NC_012532.1
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MBFV-NC_012533.1
dISFV-NC_001477.1
MBFV-NC_001475.2
MBFV-NC_001475.1
MBFV-NC_0012735.1
MBFV-NC_012735.1
MBFV-NC_012735.1
MBFV-NC_012735.1
MBFV-NC_016997.1
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---UGAU-AGAGUUGACUAGAUAACGAAUUAU---CG----AUGGUG---ACUAAA
---UGAAUAGGUUUAUUGUGAAUCGAAA-UAC---CG----AUGGCG---AAUAAA
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CUAACAC - GCAUCACCAGC
GUGAGACGUGCGUUGCCUCGC
CUAAAACGCCUGGCUAGCGUG
CUGAAACGCCCAGCCAGCGUU
CUGAAACGCCCAGCCAGCCGCU
                                                                                CUUGGAAAGACC---GUUGCAAGACGGUCUG
                                                                                UCAGAAAGCCC---GCCGCAAAGCGGCUG
CCCAAGAAGCCC---GG--AAGACGGGCUA
CCAGGAAAGUCC---GCUGCAAAGCGGACUG
CCAGGAGACCC---GCCGGAAGGCGGGUUG
CCAGGAGGACCC---GGAAGAACACCGGGUUG
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                                                                                                                                           GGGAAGCCCCGGGUCG
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                                                                                 CCAGGAGGACCC--
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UGAAACGCGGUAUGCCCCGC
UAAAACGCGGAAUGCCCCGC
UAAAACGCGGCGUAUCCCGC
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-GGCAAGAGCCGGGCUG
-GGUAGAAACCGGGUUG
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CUAAAGCGCGGGGGCAUCCCG-
CUAAAGCGCGGGAACGUCCC--
CUAAAGCGCGGAACGUCCC--
CUGAAACGCGGGCCUACCCGC
                                                                                CCAGGAAAGUCC---GGCAAUCGUCGGACUG
CCAGGAAAACCC---GGGGCAACCCGGGUUG
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                                                                                CCAGGAAGACCC---GGCUCAGGCCGGGUUG
CCAGGAGGCCC---GGUAAAAACCGGGCUA
GAAGAAAUC--C---GGAGGA-UCCGGAUUG
AAAGAAAUC--C---GGAGGAUUCCGGAUUG
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                                                                                AAAGAAAUC--C---GGAGGAUUCCGGAUUG
GAAAAAAG--U---GGUUAGACC--ACCUU
GGAAAAAGA--C---GGGUCGACC--GUCUU
GGAAGAAGA--C---GGGAAAACC--GUCUA
GGAAAAAGG--C---GAAAAACAC--GCCUU
CCAAAAAAG--G---GCCGCAUCGCGGCCUA
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UGAAACGCGUGAGAAACCGC
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UGAAACGCGAGAGAAACCGC
UGAAGCGCUUUGGAUCUAGC
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GU-------AGCGGCUAGA
GU-------GACGGCCAAG
                                                                                AGAGUAGGAUCUCGGGUUAAAACCCGAGGUG
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                                                                                AUGAAUAAGUCUCGGGCUCGAUCCCGAGGCG
GCAAGCAAGUCUCGGGUCACGACCCGGGGCG
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AUAAAACGUAAGCUGC----
                                                                                GGUCGUAAAGCUCAGGGAAAAACCCUGGGCG
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CA-CUUGGGAAGAGAC<mark>C</mark>A
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150
                                                                                                                                                                                                                                                    CA-CUUGGG--AAGACCA
CG-CCUGGGA--AAGACC
CA-CCUGGGA--AAGACC
CA-CCUGGGA--UAGACU
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CA-CCUGGGAA-AAGACU
CA-CCUGGGAA-UAGACU
CA-CCUGGGA-UAGACU
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                                                                                                ---NNNNNNGAACACCACA-A-GAAACA<mark>G</mark>
                                                                                                                                                                                                                                                     CA-CCUGGGA-UAGACU
CA-CCUGGGAA-UAGACU
C-G-UGGGA-AAGACC
C-GCUGGGA-AAGACC
C-GCUGGGA-AAGACC
C-GCUGGGA-GAGACC
C-GCUGGGA-GAGACC
C-GCUGGGA-GAGACC
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CA-CCUGGGA--AAGACC
                                                                                                                                                                                                                                                                                                                               148
                                                                                GCUGGCCNNNNNNNAUAACCAA--CAUAAGACCAGAA--NNNNNNNCCAUUGGAAAUUUAGCU--UCGUGA--NNNNNNNCC-GAGCACACAUAGCGGACGCACA--NNNNNNNCC-GAGCAC-UAUAGCGGACGCAC--NNNNNNNCC-GAGCAC-UAUAGCGGAC
                                                                                                                                                                                                                                                    CA-CCAGGGAAAGACGGCG-CCAGGG-AAAGACGCCG-CCUGGG-AAAGACGCCG-CCAGGG-AAAGACGCCG-CCAGGG-AAAGACG
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MBFV-NC_009026.2
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MBFV-NC_032088.1
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                                                                                GAGGUACUCGCUGAUUCA-----GGGAGAU-CCUCUGCUUUCC-----
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                                                                                AGGGGAU-CUUCUGCUCUGC----- 167
                                                                                GGAGAAU-UUGCUGCCUCGC------ 167
AGGGGAU-UUGCUGCUCGG----- 167
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                                                                                AGGAGAC-CCUCUGUCCUAA----- 167
                                                                                AGGAGAC-CCUCUGUCCUAA-----
                                                                                GGGAGAUCUUCUGCUCUAUCUCAACAUCAGCUACUA 167
                                                                                AGAGACUCCAUGAGUUUCC-----AGAGACUCCAUGAGUUUCC-----AGAGACUCCAUGAGUUUCC-----AGAGAUCCUGCUGUCUG------
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                                                                                AGAGAUCCUGCUGUCUCUA----- 167
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                                                                                GAGACACUCCUUGAUUCU----- 167
                                                                                GAGUGGUUCUCUGCUU-U----- 167
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