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                      .........................(((((((((((((((((((((((.

dISFV-NC_016997.1     AAAC--AUAACGCAUUUGAAUAGGUUU----GAAAGAGUUGAAUCAAUGAGAUCAAUGGU  54
dISFV-NC_017086.1     ------AUAACACGUUUGAAUUGGUUUAUUGUGAAUCGAAAUACCGAUG--------GC   45
dISFV-NC_040610.1     --GA--ACAAUUUUAAGAAGUCAAAC-UAGAAAAUUU-AAUUUCAAUG--------GU   45
dISFV-NC_024017.1     UCGC--GCAUUUUGAUAGAGUU---GAC-UAGAUAACGAAUUAUCGAUG--------GU   45
dISFV-NC_027999.1     GGAU--UAAUUGUUGUUUUGAGAGAACAGCGAGAAGUACUA----CUAUG---GUUGAGAA  51
TBFV-NC_001809.1      GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGG------AUGGGCAGGAAGAC  54
TBFV-NC_005062.1      GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGG------AUGGCCGGGAAGGC  54
TBFV-NC_027709.1      GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGG------AUGGCCAGGAAGUC  54
TBFV-NC_001672.1      GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGG------AUGGUCAAGAAGGC  54
TBFV-NC_003690.1      GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGA------AUGGCCGGGAAGGC  54
TBFV-NC_003687.1      ------AGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGAGUGGUUAUG------AUGAC  48
                     .........10........20........30........40........50.......6


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dISFV-NC_016997.1     CUUUCGAGCUAGGAGGCCCGU---UAAACGGGCCGUCGAUAUAAUAAAACGUAAGCUGC- 110
dISFV-NC_017086.1     GAAUAAACCCAAGAAGCCCGG---AAGACGGGCUAUCGAUAUAGUGAGACGUGCGUUGCC 102
dISFV-NC_040610.1     UAGACAACUUGGAAAGACCGUUGCAAGACGGUCUGUCAAUAUGCGAAAGCGGA--UUACC 103
dISFV-NC_024017.1     GACUAAAUCAAGAAAGCCCGCCGCAAAGCGGGCUGUUAAUAUGCGUCAACACGCA--UCACC 103
dISFV-NC_027999.1     AACUAGAGUAGGAUCUCGGGUUAAAACCCGAGGUGUCAAUAUGAUUAGGCGUA------- 104
TBFV-NC_001809.1      CAUCCUGAAAGGCAAGGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGA----CCGC 108
TBFV-NC_005062.1      CAUUCUGAAAGGAAAGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGA----CCGC 108
TBFV-NC_027709.1      CAUCCUGAAAGGUAAGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGA----CCGC 108
TBFV-NC_001672.1      CAUCCUGAAAGGUAAGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGA----CCGC 108
TBFV-NC_003690.1      CGUUCUAAAAGGAAAGGGGGGCGGUCCCC--CUCGACGAGCGUCGAAAGUGG----CCCC 108
TBFV-NC_003687.1      CACUUCUAAAGGAAAGGGGGGCGGUCCCC--CUAGGCGCAAGCUUAAAGUGA----CCGC 102
                     0.......70........80........90........100......110.......1


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dISFV-NC_016997.1     --------NNNNNNN--AGGAAACCCCCCCAAAAAUGUAUAGGCUAUUAUAUCGA---CA 157
dISFV-NC_017086.1     UCGCGUCUNNNNNNNNAGAGGAGACCCCCCCAAAAAUG--AAGGGCACUAUAUCGA---CA 157
dISFV-NC_040610.1     ACCCGCU-NNNNNNN-------ACCCCUCAUUAUUUAUAUAACAGCAUAUUGA---CA 151
dISFV-NC_024017.1     AAGCGUG-NNNNNNN-------CCCCACU-GCUGAGAGCAAAAUAGCAUAUUGA---CA 150
dISFV-NC_027999.1     --CUGGAANNNNNNNNUGGCGAACCCCAUUGGAAAUU-----UAGCUUCAUAUUGA---CA 154
TBFV-NC_001809.1      GA------NNNNNNN-------UCUCUUCAGGGUUUUUCCUCCUCCUAUACCAAAUUUC 154
TBFV-NC_005062.1      UA------NNNNNNN-------CUCUCUUCAGGGAAAUUUCCUCCUCCUAUACCAAA-UUC 154
TBFV-NC_027709.1      AA------NNNNNNN-------CUCUCUUCAGGGAUUUUUCCUCCUCCUAUACCAAA-UUC 154
TBFV-NC_001672.1      AA------NNNNNNN-------CUCUCUUCAGGGAUUUUUCCUCCUCCUAUACAAAA-UUC 154
TBFV-NC_003690.1      AA------NNNNNNN-------CUCUCUUCAGGGAUAUUUCCUCCUCCUAUACCAAA-UUC 154
TBFV-NC_003687.1      AAAUAAGUNNNNNNN-------CU-UCCUCGGGAUUUUUCCGCCUCCUAUACUAAAUUUC 154
                     20.......130......140.......150.......160......170.......1


                      ............))))))))))))))))))))))))).)))))))))...(((((((((.(((....

dISFV-NC_016997.1     CCUAGGAA-AGACUGGGAGAUAC-CUUUGGUUCUUCGACACUAACUCCUA--AUGGCACAG 213
dISFV-NC_017086.1     CUUGGGAA-AGACCAGAGGUCAUCGCUGAUUCACCGCCACCAG-ACUAC--ACGGCACAG 213
dISFV-NC_040610.1     CCAGGG-AUAGACCGGAGAAAU-ACACAAUUUCUGGGCACUAAACCAACUACA-AGCACAG 208
dISFV-NC_024017.1     CUUGGGAAGAGACCAGAGAUAUGAGUUGUUUUGUCAAUGCUGACAACAGCCAUGGCACAG 210
dISFV-NC_027999.1     CCAGGGAAAAGACCGGAGAAACUUCUUGCUUACUCG-CAGCAACACCGAAA-CGGCACAG 212
TBFV-NC_001809.1      CCCCUCGACAGAGGGGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCCA-GACACAG 213
TBFV-NC_005062.1      CCCCUCAUCUGAGGGGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCCA-GACACAG 213
TBFV-NC_027709.1      CCCCUCGACAGAGGGGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCCA-GACACAG 213
TBFV-NC_001672.1      CCCCUCGGUAGAGGGGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCCA-GACACAG 213
TBFV-NC_003690.1      CCCCUCGUCAGAGGGGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCUA-GACACAG 213
TBFV-NC_003687.1      CCCCAGGAAACUGGGGGGGCGGUUCUUGUUCUCCCCUGAGCCACCACCAUCCA-GGCACAG 213
                     80.......190......200.......210.......220......230.......2


                      ...))))))......))))))))...

dISFV-NC_016997.1     AGCCCCAUA-AGAA--ACGGAGUUAGUAUGGAAAAAACAUAA-GUAUCU---         258
dISFV-NC_017086.1     CGCGCCGGA-AAAG--GUAGUUUGGAGGUUGUAAAACAACAA-GUAUCU---         258
dISFV-NC_040610.1     AGCGCUUCG-AGAAGUAGGUUGUUUCUUGACGAGAGAAUAU-GUAUAUCUUGG         258
dISFV-NC_024017.1     AGCGCCUGA-AGAGAGCUGUUGUUUAUAAUUUACAAAAAAUAACAUAUCU---         258
dISFV-NC_027999.1     UAUGCGAGA-AACAUUCGGUGGUU--GAUGUAGUAAACCAGUUUUCU---         258
TBFV-NC_001809.1      AUAGUCUGACAAGGAGGUGAUGUGUGAAAAAACAC-------CCGCU         258
TBFV-NC_005062.1      GCAGUCUAACAAGGAGGUGAUGUGUGACUCGGAACAACAC-------CCGCU         258
TBFV-NC_027709.1      AUAGUCUGACAAGGAGGUGAUGCGUGACUCGGAAAAACAC-------CCGCU         258
TBFV-NC_001672.1      GUAGUCUGACAAGGAGGUGAUGUGUGACUCGGAAAAACAC-------CCGCU         258
TBFV-NC_003690.1      AUAGUCUGAAAAGGAGGAUGGUGCGUGUCUCGGAAAAACAC-------CCGCU         258
TBFV-NC_003687.1      AUAGCCUGACAAGGAGGAUGGUGUGUGACUCGGAAAAACAC-------CCGCU         258
                     40.......250......260.......270......280.......290
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