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                    .......-------............((((((((.(((((((((((((((...........((((((.(....)))))))....((.((.((...
dISFV-NC_040610.1   -------GAACAAUUUUUAAAGAAGUCAAAACUAGAAAUUUAAUU-UCAAUGGUU------AGACAACUUGGAAAGACCGUUGCAAGACGGUCUGUCAAUAUGCGAAA 93
dISFV-NC_024017.1   UC-----GCGCAUUUUGAUAGAGAGUU---GACUAGAUAACGAAUUAUCGAUGGUG------ACUAAAUCAAGAAAGCCCGCCGCAAAGCGGGCUGUUAAUAUGCUAAC 93
dISFV-NC_027999.1   GGAUUAAUUGUUGUUUGAGAGAAC----AGCGAGAAGAGUACUACU----AUGGUUGAGAAAACUAGAGUAGGAUCUCGGGUUAAACCCGAGGUGUCAAUAUGAUUAG 99
dISFV-NC_016997.1   AAACAUAACGCAUUAGAAUAGGUUU--------GAAAGAGUUGAAUCAAUGAGAUCAAUGGUCUUUCGAGCUAGGAGGCCCGUUAAACGGGCCGUCGAUAUAAUAAA 99
dISFV-NC_017086.1   ----AUAACGUUUGAAUAGGUUU----AUUGUGAAUCGAAAUACCGAUG---------GCGAAUAAACCCAAGAAGCCCGGAAGACGGGCUAUCGAUAUAGUGAG 90
TBFV-NC_027709.1    GUGUUGAGAAAAAGACAGCUUAGG--AGAACAAGAGCUGGGG------AUGGGCAGGAAGUCCAUCCUGAAAGGUAAGGGGGGCGGUCCCCCUCGACGAGUGUCGAA 99
TBFV-NC_001672.1    GUGUUGAGAAAAAGACAGCUUAGG--AGAACAAGAGCUGGGG------AUGGUCAAGAAGGCCAUCCUGAAAGGUAAGGGGGGCGGUCCCCCUCGACGAGUGUCGAA 99
TBFV-NC_001809.1    GUGUUGAGAAAAAGACAGCUUAGG--AGAACAAGAGCUGGGG------AUGGGCAGGAAGACCAUCCUGAAAGGCAAGGGGGGCGGUCCCCCUCGACGAGUGUCGAA 99
TBFV-NC_005062.1    GUGUUGAGAAAAAGACAGCUUAGG--AGAACAAGAGCUGGGG------AUGGCCAGGAAGGCCAUUCUGAAAGGUAAGGGGGGCGGUCCCCCUCGACGAGUGUCGAA 99
TBFV-NC_003690.1    GUGUUGAGAAAAAGACAGCUUAGG--AGAACAAGAGCUGGGA------AUGGCCGGGAAGGCCGUUCUAAAAGGAAAGGGGGGCGGUCCCCCUCGACGAGCGUCGAA 99
TBFV-NC_003687.1    ------AGAAAAAGACAGCUUAGG--AGAACAAGAGCUGGGGAGUGGUUAUG------AUGACCACUUCUAAAGGAAAGGGGGGCGGUCCCCCUAGGCGCAAGCUUAA 93
                    .........10.......20........30........40.......50........60........70........80........90.......100.....

                    .)).).)))).................................(((((((((..........)))))............................))))).)))))))))))).)))))
dISFV-NC_040610.1   GCGGAUUACCACCCGCU---NNNNNNNACCC---CCUCAUUAUUUA-----UAUAACAGCAUAUUGACACCAGGG-AUAGACCGGACAAAU-ACACAAUUUCUGGGC 187
dISFV-NC_024017.1   ACGCAUCACCAAGCGUG---NNNNNNNCCCC---ACUGCUGAGAG------CAAAAUAGCAUAUUGACACUUGGGAAGAGACCAGAGAUAUGAUGUUGUUUGUCAAU 188
dISFV-NC_027999.1   GCGUACUG------GAA---NNNNNNNNUGGCGAACCCCAUUGGAAA----UUUAGCUUCAUAUUGACACCAGGGAAAAAGACCGGACAAACUUCUUGCUUACUCGCA 192
dISFV-NC_016997.1   ACGUAAGCUGC---------NNNNNNN--AGGAAACCCCCCAAAAAUGUAUAGGCUAUUAUAUCGACACUCUAGGAA-AGACUGGACAUAC-CUUUGGUUCUUCGA- 192
dISFV-NC_017086.1   ACGUGCGUUGCCUCGCGUCUNNNNNNNNAGGAGAGACCCCCCAAAAAUG--AAGGGCACUAUAUCGACACUUUGGGAA-AGACCAGAGGUACUCGCUGAUUCACCGC- 193
TBFV-NC_027709.1    AGAGACCGCAA---------NNNNNNNCUCU----CUUCAGGAUUUUUCCUCCUCCUAUACCAAA-UUCCCCCUCGACAGAGGGGGGCGGUUCUUGUUCUCCCUGA 192
TBFV-NC_001672.1    AGAGACCGCAA---------NNNNNNNCUCU----CUUCAGGAUUUUUCCUCCUCCUAUACAAAA-UUCCCCCUCGGUAGAGGGGGGCGGUUCUUGUUCUCCCUGA 192
TBFV-NC_001809.1    AGAGACCGCGA---------NNNNNNN-UCU----CUUCAGGGUUUUUCCUCCUCCUAUACCAAAUUUCCCCCUCGACAGAGGGGGGGCGGUUCUUGUUCUCCCUGA 192
TBFV-NC_005062.1    AGAGACCGCUA---------NNNNNNNCUCU----CUUCAGGAAAUUUCCUCCUCCUAUACCAAA-UUCCCCCUCGCAUCUGAGGGGGGCGGUUCUUGUUCUCCCUGA 192
TBFV-NC_003690.1    AGUGGCCCCAA---------NNNNNNNCUCU----CUUCAGGAUUUUUCCUCCUCCUAUACAAA-UUCCCCCCAGGGAAACUGGGGGGGCGGUUCUUGUUCUCCCUGA 192
TBFV-NC_003687.1    AGUGACCGCAAAUAAGU---NNNNNNNCU-U----CCUCAGGAUUUUUCCGCCUCCUAUACUAAAAUUUCCCCCAGGGAAACUGGGGGGGCGGUUCUUGUUCUCCCUGA 192
                    ..110.......120.......130......140.......150.......160.......170.......180.......190.......200.......210..

                    )).....((((((((((((((((((.......))))))......)))))))))...
dISFV-NC_040610.1   ACUAAACAACUACA-AGCACAGAGCGCUUC--GAGAAGUAGUUGUUUUCUUGACGAGAGAAUAU-GUAUAUCUUGG 258
dISFV-NC_024017.1   GCUGACAACAGCCAUGGCACAGAGCGCCUG--AAGAGAGCUGUUGUUAUAAUUUACAAAAAAUAACAUAUCU--- 258
dISFV-NC_027999.1   GC-AACCACCGAAA-GGCACAGUAUGCCUG--AAACAUUCGGUGGUUGAUGUAGUAAACAACCAGUUUCU----- 258
dISFV-NC_016997.1   -CACUAACUCCUAAUGAGGCACAGAGCGCCAU--AAGAAACGGA-GUUAGUAUGGAAAAAACAUAAGUAUCU----- 258
dISFV-NC_017086.1   -CACCAG-ACUACAUGGCACAGCGCGCGGG--AAAAGGUAGU-UUGGAGGUUGUAAAACAACAAGUAUCU----- 258
TBFV-NC_027709.1    GCCAC-CAUCACCCAGACACAGAUAGUCUGACAAGGAGGUGAUGCGUGACUCGGAAAAACACCCGCU-------- 258
TBFV-NC_001672.1    GCCAC-CAUCACCCAGACACAGGUAGUCUGACAAGGAGGUGAUGUGUGACUCGGAAAAACACCCGCU-------- 258
TBFV-NC_001809.1    GCCAC-CAUCACCCAGACACAGGCAGUCUAACAAGGAGGGUGAUGUGUGACUCGGAACAACACCCGCU-------- 258
TBFV-NC_005062.1    GCCAC-CACCACUCCAGACGCACAGAUAGUCUGACAAGGAGGUGAUGCGUGUCUCGGAAAAACACCCGCU-------- 258
TBFV-NC_003690.1    GCCAC-CACCAUCCAGAGGCACAGAUAGUCUGACAAGGAGGUGAUGUGUGACUCGGAAAAACACCCGCU-------- 258
TBFV-NC_003687.1    GCCAC-CACCAUCCAGAGCGACACAGAUAGUCUGACAAGGAGGAGGUGAUGUGUGACUCGGAAAAACACCCGCU-------- 258
                    .....220.......230......240.......250.......260.......270.......280.......
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