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dISFV-NC_040610.1
dISFV-NC_024017.1
dISFV-NC_027999.1
dISFV-NC_016997.1
dISFV-NC_017086.1
                                                             -----GAACAAUUUUAAAGAAGUCAA<mark>A</mark>ACUAGAA<mark>U</mark>UUAAUU-UCAAUGGUU----- 46
                                                             UC----GCGCAUUUUGAUAGAGUU---<mark>G</mark>ACUA<mark>G</mark>AUAACGAAUUAUCGAUGGUG----- 46
                                                            AISFV-NC_017086.
TBFV-NC_027709.1
TBFV-NC_001672.1
TBFV-NC_001809.1
TBFV-NC_005062.1
TBFV-NC_003690.1
                                                             GUGUUGAGAAAAAGACAGCUUAGG--AG<mark>A</mark>ACAA<mark>G</mark>AGC<mark>U</mark>GGGG-----AUGGUCAAGAAG
                                                            GUGUUGAGAAAAGACAGCUUAGG-AGAACAA CAGCUGGGG----AUGGGCAGGAAG
GUGUUGAGAAAAAGACAGCUUAGG-AGAACAA CAGCUGGGG----AUGGCCAGGAAG
GUGUUGAGAAAAAGACAGCUUAGG-AGAACAA CAGCUGGGG----AUGGCCGGGAAG
GUGUUGAGAAAAAGACAGCUUAGG-AGAACAA CAGCUGGGA----AUGGCCGGGAAG
----AGAAAAAGACAGCUUAGG-AGAACAA CAGCUGGGAGUGGUUAUG----AUG
                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                  52
52
 TBFV-NC 003687.1
                                                                   ......10......20.......30.......40.......50.......6
                                                              AGACAACUUGGAAAGACCGUUGCAAGACGGUUUGUCAAUAUGCGAAAGCGGAUUACCACC 106
ACUAAAUCAAGAAGCCGCCGCAAAGCGGGCUGUUAAUAUGCUAACACGCAUCACCAAG 106
ACUAGAGUAGGAUCUCGGGGUUAAAACCCGAGGUGUCAAUAUGAUUAGCGGUACUG----- 107
GUCUUUCGAGCUAGGAGGCCCGUUAAACGGGCCGUCGAUAUAAUAAAACGUAAGCUGC--- 110
GCGAAUAAACCCAAGAAGCCCGGAAGACGGGCUAUCGAUAUAAUAAAACGUAGCGCUUGCCCU
UCCAUCCUGAAAGGUAAGGGGGGGGCCCCCCUCGACGAGUGUCGAAAGAGCCGCAA-- 110
GCCAUCCUGAAAGGUAAGGGGGGCGGUCCCCCUCGACGAGUGUCGAAAGAGACCGCCAA-- 110
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ACCACUUCUAAAAGGAAAGGGGGGGGUCCCCCUCGACGAGUGUCGAAAAGUGGCCCCAA-- 110
dISFV-NC_040610.1
dISFV-NC_024017.1
dISFV-NC_027999.1
dISFV-NC_016997.1
dISFV-NC_016997.1
dISFV-NC_017086.1
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TBFV-NC_001672.1
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TBFV-NC_005062.1
TBFV-NC_003690.1
 TBFV-NC_003687.1
                                                             0.......70.......80........90........100.......110.......1
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dISFV-NC_024017.1
dISFV-NC_027999.1
dISFV-NC_016997.1
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TBFV-NC_027709.1
TBFV-NC_001672.1
TBFV-NC_001809.1
TBFV-NC_005062.1
TBFV-NC_003690.1
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CGUG--NNNNNNNCCCC---A UGCUGAGAG-----CAAAAUAGCAUAUUGACACUUG 154
-GAA--NNNNNNNUGGCGAAC CCAUUGGAAA----UUUAGCUUCAUAUUGACACCAG 158
-----NNNNNNN--AGGAAA CCCCCCAAAAAUGUAUAGGCUAUUAUUUGACACCUA 161
                                                             CGCGUCUNNNNNNAGAGGAGA CCCCCCAAAAAUG--AAGGGCACUAUAUCGACACUUG
                                                                                                                                U<mark>U</mark>CAGGAUUUUUCCUCCUCCUAUACCAAA-UUCCCCC
                                                             -----NNNNNNNCUCU----
                                                                                                                               CUUCAGGAUUUUUCCUCCUCCUAUACAAAA - UUCCCCC
UUCAGGGUUUUUCCUCCUCUAUACCAAAUUUCCCCC
UUCAGGAAAUUUCCUCCUCUAUACCAAA - UUCCCCC
                                                             -----NNNNNNNCUCU----
                                                                                                                                                                                                                                                  158
                                                             -----NNNNNNN-UCU----
                                                                                                                                                                                                                                                  158
                                                            -----NNNNNNNCUCU----UUCAGGAAAUUUCCUCCUAUACCAAA-UUCCCC
-----NNNNNNCUCU----UUCAGGAUAUUUCCUCCUAUACCAAA-UUCCCCC
AAGU--NNNNNNCU-U----CUCGGGAUUUUUCCGCCUCUAUACUAAAUUUCCCCC
                                                                                                                                                                                                                                                  158
TBFV-NC_003690.1
TBFV-NC_003687.1
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                                                             20......130......140......150......160......170......1
                                                              ......(((((((((((......)
                                                           GG-AUAGACCGGA AAAU-ACACAAUUUCUGGGCACUAAACAACUACA-AGCACAGAGC
GGAAGAGACCAGA AUAUGAUGUUGUUUUGUCAAUGCUGACAACAGCCAUGG ACAGAGC
GGAAAAGACCGGA AAACUUCUUGCUUACUCGCAGC-AACCACCGAAA-GG ACAGGAGC
GGAAAAGACCGGA AAACUUCUUGCUUACUCGCAC-AACCACCGAAA-GG ACAGGAUAU
GGAA-AGACCGGA AUAC-CUUUUGGUUCUUCGA--CACUAACUCCUAAUGG ACAGAGC
GGAA-AGACCAGA GUACUCCCUGAUUCACCGC--CACCAG-ACUACACCGG ACAGCGC
UCGACAGAGGGGG GCGGUUCUUGUUCUCCCUGAGCCAC-CAUCACCCAGACACAGAUA
UCGGUAGAGGGGG GCGGUUCUUGUUCUCCCUGAGCCAC-CAUCACCCAGACACAGGUA
UCGACAGAGGGGG GCGGUUCUUGUUCUCCCUGAGCCAC-CAUCACCCAGACACAGGUA
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dISFV-NC_040610.1
dISFV-NC_024017.1
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dISFV-NC_016997.1
dISFV-NC_017086.1
TBFV-NC_027709.1
TBFV-NC_001672.1
TBFV-NC_001809.1
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TBFV-NC_005062.1
TBFV-NC_003690.1
TBFV-NC_003687.1
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217
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                                                             80......290......210......220.......230.......2
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dISFV-NC_024017.1
dISFV-NC_027999.1
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dISFV-NC_017086.1
TBFV-NC_027709.1
TBFV-NC_001672.1
TBFV-NC_001809.1
TBFV-NC_005062.1
TBFV-NC_003690.1
TBFV-NC_003687.1
                                                            CUUC--GAGAAGUAGUUGUUUCUUGACGAGAAAAUAU-GUAUAUCUUGG 258
CCUG--AAGAGAGCUGUUGUUAUAAUUUACAAAAAUAACAUAUCU--- 258
CCAU--AAGAAACGGA-GUUGGUUGAUGUAGUAAACAACCAGUUUCU---- 258
CCAU--AAGAAACGGA-GUUAGUAUGGAAAAAACAUAAGUAUCU---- 258
CCGG--AAAAGGUAGU---- 258
UCUGACAAGGAGGUGAUGUGACUCGGAAAAACACCCGCU----- 258
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UCUGACAAGGAGGUGAUGCGGACAAAACACCCGCU----- 258
                                                             CCUGACAAGGA<mark>GAUGG</mark>UGUGACUCGGAAAAACACCCGCU-----
                                                             40......250.......260.......270.......280......
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