```
                    ..........((((((((((((((((((((((((((..................................(
dISFV-NC_040610.1   --GA--ACAAUUUUAAAGAAG-UCAAAACUAGAAAUUUAAUU-UCAAUG---------GU   45
dISFV-NC_024017.1   UCGC--GCAUUUUGAUAGAGU-U---GACUAGAUAACGAAUUAUCGAUG---------GU   45
dISFV-NC_016997.1   AAAC--AUAACGCAUUAGAAUAGGUUU----GAAAGAGUUGAAUCAAUGAGAUCAAUGGU   54
dISFV-NC_017086.1   ------AUAACACGUUUGAAUAGGUUUUAAUGUGAAUCGAAAUACCGAUG---------GC   45
dISFV-NC_027999.1   GGAU--UAAUUGUUGUUUUGAGAGAACAGCGAGAAGUACUA----CUAUG---GUUGAGAU   51
TBFV-NC_003690.1    GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGA------AUGGCCGGGAAGGC   54
TBFV-NC_005062.1    GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGG------AUGGCCGGGAAGGC   54
TBFV-NC_027709.1    GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGG------AUGGCAGGGAAGUC   54
TBFV-NC_001672.1    GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGG------AUGGUCAAGAAGGC   54
TBFV-NC_001809.1    GUGUUGAGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGG------AUGGGCAGGAAGAC   54
TBFV-NC_003687.1    ------AGAAAAAGACAGCUUAGGGAGAACAAGAGCUGGGAGUGGUUAUG------AUGAC   48
                    .........10........20........30........40........50.......6

                    (.((((.........((((((............................................
dISFV-NC_040610.1   UAGACAACUUGGAAAGACCCUUGCAAGACGGUCUGUCAAUAUGCGAAAGCGGA--UUACC   103
dISFV-NC_024017.1   GACUAAAUCAAGAAAGCCCGCCGCAAAGCGGGCUGUUAAUAUGCUAACACGCA--UCACC   103
dISFV-NC_016997.1   CUUUCGAGCUAGGAGGCCCGU---UAAACGGGCCGUCGAUAUAAUAAAACGUAAGCUGC-   110
dISFV-NC_017086.1   GAAUAAACCCAGAAGCCCGCG---AAGACGGGCUAUCGAUAUAGUGAGACGUGCGUUGCC   102
dISFV-NC_027999.1   AACUAGAGUAGGAUCUCGGUUAAAACCCGAGGUGUCAAUAUGAUUAGGCGUA-------   104
TBFV-NC_003690.1    CGUUCUAAAAGGAAAGGGGGGGGGUCCCC--CUCGACGAGCGUCGAAAGUGG----CCCC   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_001809.1    CAUCCUGAAAGGCAAGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGA----CCGC   108
TBFV-NC_003687.1    CACUUCUAAAGGAAAGGGGGGCGGUCCCC--CUAGGCGCAAGCUUAAAGUGA----CCGC   102
                    0........70........80........90........100......110.......1

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dISFV-NC_040610.1   ACCCG-CUNNNNNNNN--------ACCCCCUCAUUAUUUAUAUAACAGCAUAUUGA---CA   151
dISFV-NC_024017.1   AAGCG-UGNNNNNNNN--------CCCCACUGCUGAGAG-CAAAAUAGCAUAUUGA---CA   150
dISFV-NC_016997.1   -------NNNNNNN--AGGAAACCCCCCCAAAAAUGUAUAGGCUAUUAUAUCGA---CA   157
dISFV-NC_017086.1   UCGCGUCUNNNNNNNAGAGGAGACCCCCCCAAAAAUG--AAGGGCACUAUAUCGA---CA   157
dISFV-NC_027999.1   --CUGGAANNNNNNNNUGGCGA-ACCCCAUUGGAAAUUU----AGCUUCAUAUUGA---CA   154
TBFV-NC_003690.1    AA------NNNNNNNC-------UCUCUUCAGGAUAUUUCCUCCUCCUAUACCAAA-UUC   154
TBFV-NC_005062.1    UA------NNNNNNNC-------UCUCUUCAGGAUAUUUCCUCCUCCUAUACCAAA-UUC   154
TBFV-NC_027709.1    AA------NNNNNNNC-------UCUCUUCAGGAUAUUUCCUCCUCCUAUACCAAA-UUC   154
TBFV-NC_001672.1    AA------NNNNNNNC-------UCUCUUCAGGAUAUUUUCCUCCUCCUAUACAAAA-UUC   154
TBFV-NC_001809.1    GA------NNNNNNN--------UCUCUUCAGGGUUUUUUCCUCCUCCUAUACCAAAUUUC   154
TBFV-NC_003687.1    AAAUAAGUNNNNNNNC------U-UCCUCGGGAUUUUUCCGCCUCCUAUACUAAAUUUC   154
                    20.......130......140.......150......160......170.......1

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dISFV-NC_040610.1   CCAGGG-AUAGACCGGAGAAAUACACAAUUUCUGGGCACUAAACAACUACAA--GCACAG   208
dISFV-NC_024017.1   CUUGGGAAGAGACCAGAGAUAUGAUGUUGUUUUGUCAAUGCUGACAACAGCCAUGGCACAG   210
dISFV-NC_016997.1   CCUAGGA-AGACUGGAGAGAUAC-CUUUGGUUCCUUCACGACAACUCCU--AAUGGCACAG   213
dISFV-NC_017086.1   CUUGGGAA-AGACCAGAGAGGUACUCGCUGAUUCACCUGCCACCAG-ACUA--CACGGCACAG   213
dISFV-NC_027999.1   CCAGGGAAAAGACCGGAGAAACUUCUUGCUUACUCGCAGCAACCACCG--AAAGGCACAG   212
TBFV-NC_003690.1    CCCUCGUCAGAGGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCUA-GACACAG   213
TBFV-NC_005062.1    CCCUCAUCUGAGGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCCA-GACACAG   213
TBFV-NC_027709.1    CCCUCGACAGAGGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCCA-GACACAG   213
TBFV-NC_001672.1    CCCUCGUAGAGGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCCA-GACACAG   213
TBFV-NC_001809.1    CCCUCGACAGAGGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCCA-GACACAG   213
TBFV-NC_003687.1    CCCCAGGAAACUGGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCACCAUCCA-GGCACAG   213
                    80.......190......200.......210......220.......230.......2

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dISFV-NC_040610.1   AGCGCUUC--GAG-AAGUAGUUGUUUCUUGACGAGAGAAUAUGUAUAUCUUGG   258
dISFV-NC_024017.1   AGCGCCUG--AAG-A--GAGCUGUUGUUAUAAUUUACAAAAAAUAACAUAUCU   258
dISFV-NC_016997.1   AGCGCCAU--AAG-AAACGGAGUUAGUAUGGAAAAAACAUAAGUA-----UCU   258
dISFV-NC_017086.1   CGCGCCGG--AAA-AGGUAGUUUGGAGGUUGUAAAACAACAAGUA-----UCU   258
dISFV-NC_027999.1   UAUGCCUG--AAACAUUCUGGUGUUGAUGUAGUAACAACCAGU-----UUCU   258
TBFV-NC_003690.1    AUAGUCUGAAAAGGAGGUGAUGCGUGUCGUGUGAAAAACACCCG-------CU   258
TBFV-NC_005062.1    GCAGUCUAACAAGGAGGUGAUGUGUGACUCGGAACAACACCCG-------CU   258
TBFV-NC_027709.1    AUAGUCUGACAAGGAGGUGAUGCGUGACUCGGAAAAACACCCG-------CU   258
TBFV-NC_001672.1    GUAGUCUGACAAGGAGGUGAUGUGUGACUCGGAAAAACACCCG-------CU   258
TBFV-NC_001809.1    AUAGUCUGACAAGGAGGUGAUGUGUGACUCGGAAAAACACCCG-------CU   258
TBFV-NC_003687.1    AUAGCCUGACAAGGAGGAUGUGUGUGACUCGGAAAAACACCCG-------CU   258
                    40.......250......260.......270......280.......290.
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