```
              ...........................(((((((((((((((((((((((((..................(
dISFV-NC_027999.1  GGAU--UAAUUGUUGUUUGAGAGAACAGCGAGAGUACUA----CUAUGGUUGAGAAAAC 54
dISFV-NC_016997.1  AAAC--AUAACGCAUUAGAAUAGGGUUU----GAAAGAGUUGAAUCAAUGAGAUCAAUGGU 54
dISFV-NC_017086.1  ------AUAACACGUUUGAAUAGGUUUAUUUGUGAAUCGAAAUACCGAUG--------GC 45
dISFV-NC_040610.1  --GA--ACAAUUUUAAAGAAGUCAA-AACUAGAAAUUUAAUU-UCAAUGGU------UAG 48
dISFV-NC_024017.1  UCGC--GCAUUUUGAUAGAGUU----GACUAGAUAACGAAUUAUCGAUGGU------GAC 48
TBFV-NC_027709.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGG------AUGGGCAGGAAGUC 54
TBFV-NC_001672.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGG------AUGGUCAAGAAGGC 54
TBFV-NC_001809.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGG------AUGGGCAGGAAGGC 54
TBFV-NC_005062.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGG------AUGGCCGGGAAGGC 54
TBFV-NC_003690.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGA------AUGGCCGGGAAGGC 54
TBFV-NC_003687.1   ------AGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGAGUGGUUAUG------AUGAC 48
              .........10........20........30........40........50.......6
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              (.((((.........((((((.(((........((.(((((.((..(((((((..........
dISFV-NC_027999.1  UAGAGUAGGAUCUCGGGUUAAAACCCGAGGUGUCAAUAUGAUUAGGCGUAC--------- 105
dISFV-NC_016997.1  CUUUCGAGCUAGGAGGCCCGUUAAACGGGCCGUCGAUAUAAUAAAACGUAAGCUGC---- 110
dISFV-NC_017086.1  GAAUAAACCCAAGAAGCCCGGAAGACGGGCUAUCGAUAUAGUGAGACGUGCGUUGCCUCG 105
dISFV-NC_040610.1  ACAACUUUGGAAAGACCGUUGCAAGACGGUCUGUAAAUAUGCGAAAGCGGCAUUACCACCG 108
dISFV-NC_024017.1  UAAAUCAAGAAAAGCCCGCCGCAAAGCGGGCUGUUAAUAUGCUAACACGCAUCACCAAGCG 108
TBFV-NC_027709.1   CAUCCUGAAAGGUAAGGGGGGCGGUCCCCCUCGACGAGUGUCGAAAGAGACCGCAA---- 110
TBFV-NC_001672.1   CAUCCUGAAAGGUAAGGGGGGCGGUCCCCCUCGACGAGUGUCGAAAGAGACCGCAA---- 110
TBFV-NC_001809.1   CAUCCUGAAAGGCAAGGGGGGCGGUCCCCCUCGACGAGUGUCGAAAGAGACCGCGA---- 110
TBFV-NC_005062.1   CAUUCUGAAAGGAAGGGGGGGCGGUCCCCCUCGACGAGUGUCGAAAGAGACCGCUA---- 110
TBFV-NC_003690.1   CGUUCUAAAAGGAAAGGGGGGGCGGUCCCCCUCGACGACGUCGAAAGUGGCCCCAA---- 110
TBFV-NC_003687.1   CACUUCUAAAGGAAAGGGGGGCGGUCCCCCUAGGCGCAAGCUUAAAGUGACCGCAAAUAA 108
              0.......70........80........90.......100......110.......1
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              ...................))))))))..)).)))))...))))))).....)))).....)))))
dISFV-NC_027999.1  UGGAANNNNNNNUGGCGA-ACCCCAUUGGAAAUUUA----GCUUCAUAUUGA---CACCA 157
dISFV-NC_016997.1  -----NNNNNNN--AGGAAACCCCCCCAAAAAUGUAUAGGCUAUUAUAUCGA---CACCU 160
dISFV-NC_017086.1  CGUCUNNNNNNNAGAGGGAGACCCCCCCAAAAAUG--AAGGGCACUAUAUCGA---CACUU 160
dISFV-NC_040610.1  CU---NNNNNNN--------ACCCCCUCAUUAUUUAUAUAACAGCAUAUUGA---CACCA 154
dISFV-NC_024017.1  UG---NNNNNNN--------CCCCACUGCUGAGAG-CAAAAUAGCAUAUUGA---CACUU 153
TBFV-NC_027709.1   -----NNNNNNNC-------UCUCUUCAGGAUUUUUCCUCCUCCUAUACCAAA-UUCCCC 157
TBFV-NC_001672.1   -----NNNNNNNC-------UCUCUUCAGGGUUUUUCCUCCUCCUAUACCAAAAUUUCCCC 157
TBFV-NC_001809.1   -----NNNNNNN--------UCUCUUCAGGGUUUUUCCUCCUCCUAUACCAAAAUUUCCCC 157
TBFV-NC_005062.1   -----NNNNNNNC-------UCUCUUCAGGAAAAUUUCCUCCUCCUAUACCAAA-UUCCCC 157
TBFV-NC_003690.1   -----NNNNNNNC-------UCUCUUCAGGAUAUUUUCCUCCUCCUAUACCAAA-UUCCCC 157
TBFV-NC_003687.1   GU---NNNNNNNC-------U-UCCUCGGGAUUUUUCCGCCUCCUAUACUAAAUUUCCCC 157
              20.......130......140.......150.......160.......170.......1
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              )).......)))))).)))))))))))))))))))).)))))))).....................
dISFV-NC_027999.1  GGGAAAAGACCGGAGAAACUUCUUGCUUACUCGCAGCAACCACCG--AAAGGCACAGUAU 215
dISFV-NC_016997.1  AGG-AAAGACUGGAGAUAC-CUUUGGUUCUUCGACACUAACUCCU--AAUGGCACAGAGC 216
dISFV-NC_017086.1  GGG-AAAGACCAGAGGUACUCGCCGCCACCGCCACCCAG-ACUA--CACGGCACAGCGC 216
dISFV-NC_040610.1  GGG-AUAGACGGAGAAAUACACAAUUUCUGGGCACUAACCUACAA--GCACGGAGC 211
dISFV-NC_024017.1  GGGAAGAGACCAGAGAUAUGAUGUUGUUUGUCAAUGCUGACAACAGCCAUGGCACAGAGC 213
TBFV-NC_027709.1   CUCGACAGAGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCCA-GACACAGAUA 216
TBFV-NC_001672.1   CUCGGUAGAGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCCA-GACACAGGUA 216
TBFV-NC_001809.1   CUCGACAGAGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCCA-GACACAGAUA 216
TBFV-NC_005062.1   CUCAUCUGAGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCCA-GACACAGGCA 216
TBFV-NC_003690.1   CUCGUCAGAGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCAUCACCUA-GACACAGAUA 216
TBFV-NC_003687.1   CAGGAAACUGGGGGGGGCGGUUCUUGUUCUCCCUGAGCCACCACCAUCCA-GGCACAGAUA 216
              80.......190......200.......210.......220.......230.......2
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              ..............................................
dISFV-NC_027999.1  GCCUGAAACAUUCGGUGGUUG----AUGUAGUAAACAACCAGUUUCU 258
dISFV-NC_016997.1  GCCAUAAGAAACGGAGUUAGU----AUGGAA-AAAACAUAAGUAUCU 258
dISFV-NC_017086.1  GCCGGAAAAGGUAGUUUGGAG----GUUGUA-AAACAACAAGUAUCU 258
dISFV-NC_040610.1  GCUUCGAGAAGUAGUUGUUUCUUGACGAGAGAAUAUGUAUAUCUUGG 258
dISFV-NC_024017.1  GCCGGAAGA--GAGCUGUUGUUAUUAAUUUUACAAAAAAUAACAUAUCU 258
TBFV-NC_027709.1   GUCUG-ACAAGGAGGUGAUGCGUGUGACUCGGAAAAACACCC----GCU 258
TBFV-NC_001672.1   GUCUG-ACAAGGAGGUGAUGUGUGACUCGGAAAAACACCC----GCU 258
TBFV-NC_001809.1   GUCUG-ACAAGGAGGUGAUGUGUGACUCGGAAAAACACCC----GCU 258
TBFV-NC_005062.1   GUCUA-ACAAGGAGGUGAUGUGUGACUCGGAACAACACCC----GCU 258
TBFV-NC_003690.1   GUCUG-AAAAGGAGGUGAUGUGUGUGUCUCGGAAAAACACCC----GCU 258
TBFV-NC_003687.1   GCCUG-ACAAGGAGAUGGUGUGUGACUCGGAAAAACACCC----GCU 258
              40.......250......260.......270.......280.....
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