Multiple sequence alignment of viral genome terminal regions.

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                   ........10........20........30........40........50......6
MBFV-NC_012533.1   AAC-----AGUUUU------CGUGUUGAGAAAGAAAACAGAUUCUUCGG--AAAUG--A  44
MBFV-NC_012532.1   AAC-----AGGUUU-----AAUUUGGAUUUGGAAACGAGAGUGUUCUGG--UCAUG--A  44
MBFV-NC_035889.1   ACA-----GGUUUU-----AUUUUGGAUUUGGAAACGAGAGUGUUCUGG--UCAUG--A  44
MBFV-NC_002640.1   -------UCUAACAGUUGUUUGAUAUAGAGAGCAG-AUCUCUGGAAAAUG----      43
MBFV-NC_001477.1   ACG-----UAGUGCUUAACAGUUUU-AUUAGAGAGCAG-AUCUCUG----AUG--A   44
MBFV-NC_001475.2   ACG-----UAGUGCUGAACAGUUU-UUU-AUUAGAGAGCAG-AUCUCUG----AUG--A  44
MBFV-NC_001474.2   CG----UAGUGCUUAACAGUUUU-AUUAGAGAGCAG-AUCUCUG----AUG--A     44
MBFV-NC_001563.2   A--U---UAACACAGUGCGAGCUGUUUCUUGGCACGAAGA-UCUC-G---AUG---U   44
MBFV-NC_009942.1   A--U---UAACACAGUGCGAGCUGUUUCUUGGCACGAAGA-UCUC-G---AUG---A   44
MBFV-NC_009028.2   U--U---UAACACAGUCUGAAUAGUUUUUUAGCA-AGGGA-UUUCCC---AUG---A   44
MBFV-NC_040776.1   U--U---UAACACAGUGAAUAGUUUUUUAGA-GAGGU-ACUACC---AUG---A     44
MBFV-NC_034151.1   -------UAACACAGUGAAUAGUUUUUUGAACAGAGGUGAAAACC---AUG---A    44
MBFV-NC_007580.2   ---U---AACUUGACUGCGAACAGUUUUUUGGA-GGGAAAUUACCCA-----U     44
MBFV-NC_012534.1   CCGU----AAACACAGUUGAACGUUUUUUGGAGA----GAGAUUAUU----AU     44
MBFV-NC_015843.2   ACGU----AAACACAGUUUGAACGUUUUUUGGAUA----GAGACAACU----AU    44
MBFV-NC_000943.1   -------UAACGCGGUUUGAACAGUUUUUUGGAGCUUUUGAUUUCAA-----AU    44
MBFV-NC_006551.1   ---U---UAACACAGUGCCGGCAGUUUCUUUGAGC-GUUGAUUUUUCA-----AU   44
MBFV-NC_001437.1   ---U---UAGUGCAGUUUAAACAGUUUUUUGAACGGAAGAUAACC------AUG---A 44
MBFV-NC_009026.2   -------AGAAAAGUUUUCUGGGAAAGACGAGAAGCGUAA-UUCUCUG---AAUG---G 44
MBFV-NC_009029.2   UGAUUACAUAACACAGUGUGACAAGUUUUUUGUGAACAG----CA-------AUG---A 44
MBFV-NC_032088.1   UC----UAUUAACACAGUGUAAAUUUUUUGUGAGGAAUU---------AUG---A    44
dISFV-NC_040610.1  --GA----ACAAUUUUAAAGAAGUCAAAACUAGAAAUUUAAUU--UC----AUG---G 44
dISFV-NC_024017.1  UCGC----GCAUUUUGAUAGAGUU---GACUAGAUAACAGAAUC------GAUG---G  44
dISFV-NC_016997.1  AAAC----AUAACGCAUUAGAAUAGGUUU---GAAAGAGUUGAAUC---AAUGAGAU   47
dISFV-NC_017086.1  -------AUAACGCAUUAGAAUAGGUUUUAUUGUGAACUGAAACAG----GAUG----  43
MBFV-NC_008719.1   AUUUCUACUGAAAGGGU---AGAGA--A---A--AAGGAGUUUUGCUUCUC---AUGGCAA 47
MBFV-NC_012735.1   -UUUCUACUG-AAAGGA---GUAGA--AGAAAAGGAGAAGUAAUUCCCA---AUGGCAA 47
dISFV-NC_027999.1  GGAUUAUU---UGUUGUUUGAUAGAGAACAGCGAGAAGUACUACU-----AUGGUUG  47
MBFV-NC_002031.1   UAAUCGUUCG-------UUGAGCGAUUAGCAGAGAACUGACCAGAAC------AUGUC--A 45
MBFV-NC_018705.3   CCGU----AAACACAGUUUGAACGUUUUUUUGGAGAGAGACUACU---------AU    44
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                   .(((((.(((((((((((((
                   0........70........80........90.......100.......110......1
MBFV-NC_012533.1   AAA--CCCAAAAAAGG-------GCCGCAUCGCGGCCCUAUCAAUAUGGUGUUAACGCGUUUG 95
MBFV-NC_012532.1   AAAACCCCAAAGAAGAAAU--CCGGAGGA-UCCGGAUUGUCAAUAUGGUGUUAAACGCGGAG 101
MBFV-NC_035889.1   AAAA-CCCAAAGAAGAAAU--CCGGAGGA-UCCGGAUUGUCAAUAUGGUGUUAAACGCGGAG 101
MBFV-NC_002640.1   --AA--CCAACGAAAAAAG--GUG--GUUAGACCACCUUUCAAUAUGGUGUUAAGCGCGCGA 95
MBFV-NC_001477.1   ACAA--CCAACGGAAAAAG---ACG--GGUCGACGGUCCUUUCAAUAUGGUGUUAAGCGCGCGA 98
MBFV-NC_001475.2   ACAA--CCAACGGAAAAAG---ACG--GGUCGACGCUCUAUUCAAUAUGGUGUUAAGCGCGUGA 98
MBFV-NC_001474.2   AUAA--CCAACGAAAAAAG---GCG--AAAAACACGCCCUUUCAAUAUGGUGUUAAGCGCGAGA 98
MBFV-NC_001563.2   GU---AAGAAAACAGGAGGGCCCGGGUAAAAACCGGGCUGUCAAUAUGGUGUUAAACGCGGUA 101
MBFV-NC_009942.1   CU---AAGAAAACAGGAGGGCCGGGCUGUAAAAACGGGGCUGUCAAUAUGGUGUUAAACGCGAGA 101
MBFV-NC_009028.2   CU---AAAAAACAGGAAAGUCCGUCUGCAAAGCGCGUCAUCAAUAUGGUGUUAAACGCCUGG 101
MBFV-NC_040776.1   CU---AAAAAACAGGAGGACCCGCGGAAGAACCGGGUCGUCAAUAUGGUGUUAAACGCCCGA 101
MBFV-NC_034151.1   CU---AAAAAACAGGAGGACCCGGAAAAACCGGGUCGUUAACAUGGUGUUAAACGCGCACAU 101
MBFV-NC_007580.2   CU---AAAAAUCAGGAAAACCGGGUAGAACCGGCCAUCAAUAUGGUGUUAAACGCGGCG 101
MBFV-NC_012534.1   UUAACAAAAAACAGGAAAACCGGGGCAACUCCGGGUCGUCAAUAUGGUGUUAAACGCGGUG 104
MBFV-NC_015843.2   CUAACAAAAAACAGGAAAGACCCGUCUCAGGCCGGGUCGUCAAUAUGGUGUUAAACGCGGAA 104
MBFV-NC_000943.1   CU---AAAAAACAGGAGGACCCGGGAACCCCCGGGUCGUUAACAUGGUGUUAAACGCGGCA 101
MBFV-NC_006551.1   CU---AAGAAAACAGGAGGGCCCGGGAAGAAACCGGGCCAUCAAUAUGGUGUUAAACGCGGCA 101
MBFV-NC_001437.1   CU---AGAAAACAGGAGGACCCGGAUAAAAACGGGUCGUCAAUAUGGUGUUAAACGCGUACGG 101
MBFV-NC_009026.2   CC---AAAAAACAGGAAGGCCCGUGUAACAAAUGGGUCGUCAAUAUGGUGUUAAACGCGGUG 101
MBFV-NC_009029.2   CU---AAAAAACAGGAAAGUCCGGCCAAUCGUCGCACGUCAAUAUGGUGUUAAACGCGGAU 101
MBFV-NC_032088.1   CU---AAAAAACAGGAAAGUCCGGCAAUCGUCGACGUCAAUAUGGUGUUAAACGCGGAG 101
dISFV-NC_040610.1  UU---AGACAACUUGGAAAGACCGUUGCAAGACGUCUGUUCAAUAUGGAGAGCGAAAUAC 101
dISFV-NC_024017.1  UG---ACUAAAUCAAGAAAGCCGCCGCAAAGCGCGGUCUAAUAUGGUGUUAACACGCAUCA 101
dISFV-NC_016997.1  CAAUGGUCUUUCGAGCUUAGGAGGCCCGUUAAACGGGUCUGUCGAUAUAUGAAAACGAAAAC 107
dISFV-NC_017086.1  -----GCGAAUAAACCCAAGAAGUCCGGAGAACGCGGUCUACAAUAUAGUGAGACGUGCGU 98
MBFV-NC_008719.1   CAAGAGGAGCAAGCGAACGGUCUCGGGCUUCACGACCCGAGGGCUGUCAAUAUGGUGCGCCAAGG 107
MBFV-NC_012735.1   CAAAGGGGAUGAAUAAGUCUCGGGUCACGAUCCUCGAGGCGUCAAUAUGGUGAGCGGCUAGAG 107
dISFV-NC_027999.1  AGAAAACUAGAGUAGGAUCUCGGGAUAAAAACCGGAGUGUCAAUAUGGUUUAGGCGACUUGG 107
MBFV-NC_002031.1   -------UGGUCGUAAGCUCAGGGAAAAACCUCGGGGCUGUCAAUAUGGUACGACGAGGAG 98
MBFV-NC_018705.3   CAAACAAAAAACAGGAAAGCCCGGGGCAACUCGGGUCUUCAAUAUGGUGUUAAACGCGGCG 104
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                   20.......130.......140.......150.......160.......170.......1
MBFV-NC_012533.1   GAUCUAGCGCUGGCCNNNNNNNN---------AGACCCCCCGCGCCCAUAACCAACAUAAAA 147
MBFV-NC_012532.1   UAGCCCGUG------NNNNNNNN--------GUUAGAGGAGACCCCCCGGAAAACGCAAAA 147
MBFV-NC_035889.1   UAGCCCGUG------NNNNNNNN--------UUAGAGGAGAGACCCCCCGGAAAACGCAAAA 146
MBFV-NC_002640.1   GAAACCGCGUGU-AUCAANNNNNNNNC--UAGAGGGUUAGAGGAGACCCCCCAACA--CAAAA 151
MBFV-NC_001477.1   GAAACCGCGUGU---NNNNNNNN---AGAGGGUUAGAGGAGACCCCCCGCACAACAAAAA 151
MBFV-NC_001475.2   GAAACCGUGUGU---NNNNNNNNC---UAGAGGGUUAGAGGAGACCCCCCG--CAAAUAAAAA 151
MBFV-NC_001474.2   GAAACCGCGUGU---NNNNNNNN---UAGAGGGUUAGAGGAGACCCCCC--CGAAACAAAAAA 151
MBFV-NC_001563.2   UGCCCCGCG------NNNNNNNNA---GGAGACCCCGUGCCA-AAAACACCA-A-AAGAAA 149
MBFV-NC_009942.1   UGCCCCGCG------NNNNNNNN-------GAGACCCCGUGCCACAAACACCACA-ACAAAA 149
MBFV-NC_009028.2   CUAGCGUGU------NNNNNNNNU---GAGACCCCUCAGCAC-CAAGCGCGAA--ACAAA 149
MBFV-NC_040776.1   CCAGCGUUU------NNNNNNNN----GGAGACCCCUUGGCACACAAGCGCGAA--GACAAA 150
MBFV-NC_034151.1   CCCGCGCUA------NNNNNNNN---GACCCCUUGGCAC-GCACAAGCGCAAA--UAAAAA 146
MBFV-NC_007580.2   UAUCCCGCG------NNNNNNNUAGAGGAGACCCCUUGCCGUUAACGC------AAACAA 149
MBFV-NC_012534.1   CAUCCC---------NNNNNNN------GAGACCCCUUGCGAGUUAACACCACA-A-GAAA 149
MBFV-NC_015843.2   CGUCCC---------NNNNNNNN-------GGAGACCCCUUGCGAGUGUAACACCACA-A-GAAA 149
MBFV-NC_000943.1   UACCCCGCG------NNNNNNNN----------ACCCCACUCUCAAAAGCAUC-AA-A--CAA 142
MBFV-NC_006551.1   UACCCCGCG------NNNNNNNN--------CCCCGCAUCAUAAGCAUC-AA-A---AAA 142
MBFV-NC_001437.1   UACCCCGCG------NNNNNNNN---AGAGGAGACCCCGCAUUUGCAUC-A---AA 143
MBFV-NC_009026.2   CGGCCAACG------NNNNNNNCCCUUGGCAAAACAGUUAACGCA-----CCAA-AAGAAA 150
MBFV-NC_009029.2   CUCCCCGCG------NNNNNNNGAGG--AGACCCUCCACAAAGAAGCGCAAACACAAAA 153
MBFV-NC_032088.1   CAUCCCGCG------NNNNNNNGAGGUUAGAGGAGACCCCCACAAUACGCAAAAA 154
dISFV-NC_040610.1  CCACCCGCU------NNNNNNN--------------CCCCUCAUUAUUUAUAUAA 137
dISFV-NC_024017.1  CCAAGCGUG------NNNNNNN---------CCCACUGCUGAGAG-CAAAA 136
dISFV-NC_016997.1  UGC------------NNNNNNN-------GGAAACCCCCCCAAAAAUGUAUAGGC 143
dISFV-NC_017086.1  UGCCCUCGCGUCU--NNNNNNN----------GAGGAGACCCCCCCAAAAAUG--AAGGG 143
MBFV-NC_008719.1   ---------CCA--NNNNNNN----------AGGAGACCCUCCCGAGCAC-UAUAGC-G 143
MBFV-NC_012735.1   ---------UGA--NNNNNNN----------CCAUUCCCUCGAGCACCACAUAGC-G 143
dISFV-NC_027999.1  ---------GAA--NNNNNNN-----------GGCGAACCCAUUGGAAAUUUA----G 140
MBFV-NC_002031.1   UUCGCUCCUUGU--NNNNNNN----------------AGACCCUCCAGGGAACAAAUAGUGG 142
MBFV-NC_018705.3   CAUCCC---------NNNNNNNCCCGCGGAAAUCAAAGCAAGGCCCAACCUG--GCAAAG 153
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                   .)))))))))))))))))))
                   80.......190.......200.......210.......220.......230.......2
MBFV-NC_012533.1   CAGCAUAUUGACACCUGGGAA--AGACCGG--AGACUCUGUUGGCUUUCCC----CACAC 199
MBFV-NC_012532.1   CAGCAUAUUGACG--UGGGAA--AGACCAG--AGACUCCAUGAGUUUCCAC----CACGC 197
MBFV-NC_035889.1   CAGCAUAUUGACG-CUGGGAA--AGACCAG--AGACUCCAUGAGUUUCCAC----CACGC 197
MBFV-NC_002640.1   CAGCAUAUUGACG-CUGGGAG--AGACCAG--AGAUCCUGCUG-UCUCUGC----AACAU 201
MBFV-NC_001477.1   CAGCAUAUUGACG-CUGGGAG--AGACCAG--AGAUCCUGCUG-UCUCUGC----AGCAU 201
MBFV-NC_001475.2   CAGCAUAUUGACG-CUGGGAG--AGACCAG--AGAUCCUGCUG-UCUCCUC----AGCAU 201
MBFV-NC_001474.2   CAGCAUAUUGACG-CUGGGAG--AGACCAG--AGAUCCUGCUG-UCUCCUC----AGCAU 201
MBFV-NC_001563.2   CAGCAUAUUGACACCUGGGAU--AGACUAG--GGGACUUCUGCU----CUGC----ACAAC 199
MBFV-NC_009942.1   CAGCAUAUUGACACCUGGGAU--AGACUAG-GAGACUUCUGCU-U--CUGC----ACAAC 199
MBFV-NC_009028.2   CAGCAUAUUGACG-CGCCUGGAA--AGACCGG--AGACCCCUCGCU-U--UUCC----AUCAC 199
MBFV-NC_040776.1   CAGCAUAUUGACACCUGGGAA--AGACCGG--AGACCCGUCGU-U--CUGC----AACAC 200
MBFV-NC_034151.1   CAGCAUAUUGACACCUGGGAA--AGACUGG--AGACCCCUCGCUU-AUUUC----AACAC 198
MBFV-NC_007580.2   CAGCAUAUUGACACCUGGGAAA----GACAG-AGACCCCCUGCUU-U--UUUC----AACAC 198
MBFV-NC_012534.1   CAGCAUAUUGACACCUGGGAA--AGACUGG--AGACCCUCUGUCC---UAAC----AACAC 200
MBFV-NC_015843.2   CAGCAUAUUGACACCUGGGAA--AGACUAG--AGACCCCUCGUCC---UAAC----AACAC 200
MBFV-NC_000943.1   CAGCAUAUUGACACCUGGGAA--AGACAUG-GAGAUCUUCUGUCUCUAUUC----AACAU 197
MBFV-NC_006551.1   CAGCAUAUUGACACCUGGGAA--AGACAUG-GAGAUCUUCUGUCUCUAUUC----AACAU 197
MBFV-NC_001437.1   CAGCAUAUUGACACCUGGGAAU-AGACUGG--AGAUCUUGUGCUCUCUAUUCC----AACAU 200
MBFV-NC_009026.2   CAGCAUAUUGACACCUGGGAA--AGACCGG-AGAAUUUGCUGCU----CUGG----AACAC 200
MBFV-NC_009029.2   CAGCAUAUUGACACCUGGGAA--AGACCGG--AGGGAUUUGCUGCU----CUGG----ACUUC 203
MBFV-NC_032088.1   CAGCAUAUUGACACCUGGGAA--AGACCGG--AGACCCCUCGCU----CUGG----AACCC 203
dISFV-NC_040610.1  CAGCAUAUUGACACCUGGGAA-AUAGACCGGA-GAAAUACACAAUUUCUGGGCACUAAACAA 195
dISFV-NC_024017.1  UAGCAUAUUGACACCCGGGAAGAAGACAGA-GAUAUGAUGUUUGUUUGUUCGCAAUGCUGCAAA 195
dISFV-NC_016997.1  UAUUCAUAUUGCACCUCAGGAA--AGACUCGGAUAAUCGUUAUACUUUUGGUUCUACGCACUAAAC 200
dISFV-NC_017086.1  CACUUCAUAUUCGACACUUGGGAA--AGACCAGAGGUUACUCGCUGAAUCACUACCGCCACCAG-AC 204
MBFV-NC_008719.1   GACCAUAUUGACACGCGAGG--AAGACCGGAGGACACUCCUUGAUU-CUCAC----CUUUC 196
MBFV-NC_012735.1   GACCAUAUUGACACGCGAGG--AAGACCGGAGGACACUCCUUGAUU-CUCAC----CUUUC 196
dISFV-NC_027999.1  CACCAUAUUCGACACGCGGGA--AAGACCGGAGGACACUCCUUUACUCGC------AGCAA 196
MBFV-NC_002031.1   CACCAUAUUCCACGCGGGAA--AAGACCGGAGGUGGUUCUGCUGAUUCUUCC----CAGAG 196
MBFV-NC_018705.3   CUGCAUAUUCCAGGGAACAGAGGAUUAGUGGAGACCCCGUUCGGCGAGUG----AACAC 207
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                   ..............
MBFV-NC_012533.1   CAGCCCC--C--U 208
MBFV-NC_012532.1   UGGGCCGC--CAGG 208
MBFV-NC_035889.1   UGGGCCGC--CAGG 208
MBFV-NC_002640.1   CAAUCC------A 208
MBFV-NC_001477.1   CAUUCC------A 208
MBFV-NC_001475.2   CAUUCC------A 208
MBFV-NC_001474.2   CAUUCC------A 208
MBFV-NC_001563.2   CAGCCAC--AC-- 208
MBFV-NC_009942.1   CAGCCAC--AC-- 208
MBFV-NC_009028.2   CAGCCAC--UA-- 208
MBFV-NC_040776.1   CAGCCAC--U--- 208
MBFV-NC_034151.1   CAGCCAC--UC-G 208
MBFV-NC_007580.2   CAGCCAC--AA-G 208
MBFV-NC_012534.1   CAGCCAU--C--- 208
MBFV-NC_015843.2   CAGCCAC--U--- 208
MBFV-NC_000943.1   CAGUCAC--AGG 208
MBFV-NC_006551.1   CAACCAC--AAGG 208
MBFV-NC_001437.1   CAGCCAC--UAGG 208
MBFV-NC_009026.2   CUCCCAC--C--- 208
MBFV-NC_009029.2   CGGCU--------- 208
MBFV-NC_032088.1   CAG-U--------- 208
dISFV-NC_040610.1  CUACAAGCACAGA 208
dISFV-NC_024017.1  CAGCCAUGGCACA 208
dISFV-NC_016997.1  CUAAUG-----GC 208
dISFV-NC_017086.1  UACACG-----GC 208
MBFV-NC_008719.1   UCACCCUUAAGC- 208
MBFV-NC_012735.1   UCGCCCUAAAGC- 208
dISFV-NC_027999.1  CCACCGAAAGGCA 208
MBFV-NC_002031.1   GU-CUGUGAGCAC 208
MBFV-NC_018705.3   C------------ 208
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                   40.......250.
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