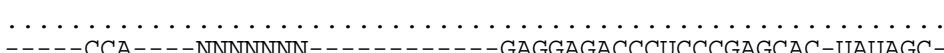


MBFV-NC_008719.1 AUUU----CUACUGAAAGG-GUAGAGAA----AAGGAGUUUGCUUCUCAUGGCAACAAG 51
MBFV-NC_012735.1 -UUU----CUACUGAAAGGAGUAGAAGA----AAGGAGUUUAGUUCUCCAAUGGGCAGACAA 51
ISFV-NC_027999.1 GGAA----UAAUUG-UUGUUUGAGAGACACGCGAGAGAACUACU----AUGGUUGAGAA 51
MBFV-NC_002031.1 UAAU----CGUUCG----UUGAGCGAUUAGCAGAGAACUGACCCAGAACAUUGC---- 45
AACAGGUUU-----AAUUUGGAUUUGGAAACGAGAGUUUCUGG--UCAUG----AAAAA 48
ACAGGUUUU-----AUUUUGGAUUUGGAAACGAGAGUUUCUGG--UCAUG----AAAAA 48
AACAGUUUU-----CGUGUUAGAAAGAAACAGAUUCUUCGG--AAAUUG----AAAA 47
-----UCUA-ACAGUUUGUUUGAAUAGAGAGCAG-AUCUCUGGAAAAAUUG----AA 45
ACGUAGUUCUA-ACAGUUU-UUUU-AUUAGAGAGCAG-AUCUCUG----AUG----AACAA 48
ACGUAGUGCUG-ACAGUUU-UUUU-AUUAGAGAGCAG-AUCUCUG----AUG----AACAA 48
-CGUAGUUCUA-ACAGUUU-UUUAAUUAGAGAGCAG-AUCUCUG----AUG----AAUAA 48
CCGU-----AAACACAGUUUGAACGUUUUUUGGAGA----GAGAUUAUUUUG----UUUAA 48
ACGU-----AAACACAGUUUGAACGUUUUUUGGAAU-----GAGACACUUAUG----UCUAA 48
A-U-----UAAACAGUGCGAGCUGUUUUUCUUGGCAC-GAAGA-UCU-CGAUG----UCUA 47
A-U-----UAAACAGUGGCGAGCUGUUUUUCUUAAGCAC-GAAGA-UCU-CGAUG----UCUA 47
U-U-----UAAACAGUCUGAUAAGUUUUUUUAGCA--AGGGA-UUUCGCCAUG----UCUA 47
U-U-----UAAACAGUCUGAUAAGUUUUUUUAGCA--GAGGU-ACUACCAUG----UCUA 47
-----UAAACAGUGUGAAUAGUUUUUUUAGAA-AGGUGUAAAAACCAUG----UCUA 47
-----UAACCGGUUUUGAACAGUUUUUUUGGAGUUUUUAGUUU-CAAAUG----UCUA 47
-U-----UAAACAGUGGCCGCGAGUUUUUCUUGAGC-GUUGAUUUU-UCAAUG----UCUA 47
-U-U-----UAGUGCAGUUUAAACAGUUUUUUUAGAACGGAAGAUAA-CC-AUG----ACUA 47
-U-----AACUUGACUGCGAACAGUUUUUUU--AGCAGGGAAUUAACCAUG----UCUA 47
UGAUUACAUAACACAGUGUGAACAAGUUUUUUUGAACAG-----CAAUG----ACCA 47
UC-----UAUAACUCAGUGUGAACAAAGUUUUUUUGACAGUGGA-----UAUG----ACUA 47
AG-----AAAAGUUUUCGAGGAAAGACGAGAGAGCGAAUUCUCUG--AAUG--GCUA 47
-----A-----UAAACAGUUUAGAAAGUUUUUAGUGA--AUCGAAAUACCGAUG---- 43
AAACA--UAACGCAUUAAGAAUAGGUUU--GAA--AGAGUUGAAUCAUAGGAGAUCAAU 51
--GAACAAUUUUAAAGAAGUCAAAACUAGAA-----UUUAAUU-UCAAUGGUUAGA-- 49
UCGCGCAUUUUUGAUGAGAU--GACUAGAUA-----ACGAAUUUACGAUGGAGACU-- 49
CGGUA-----AACACAGUUUGAACGUUUUUUGGAGAGAGACUA-----CUAUG--UCAAA 48
GUGUUGAGAAAAAGACAGCAGUUAGGAGAACAAAG--CUGGGG-----AUGGGCAGGAA 51
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GUGUUGAGAAAAAGACAGCAGUUAGGAGAACAAAG--CUGGGG-----AUGGCCGGGAA 51
-----AGAAAAGACAGCAGUUAGGAGAACAAAG--CUGGGAGUGGUUAUG----AU 45
AAUUUGUUUCUGUGCGCG--UCACGCCACUU--UUUGUGGCGGGAAUG-- 43
ACCUUGGUUUUCGGCGUG--AAACACGUCGCU--UUCGU--CAAAUGACGAAAGG 51
U-----GAAAUUAUUUCUG--AAAACAGAAAAUCAGAAUCAGACGCGAUG-- 43
-----AAAUUAUUUCCGGAAGAACACUCUGCCGGAUCAAAGACGAUG-- 43
-----UUGAAAGUUCGACUCUGGUUGUCCAGUUUGUAUUUAAAUG-- 43
-----AUUUUCUUUAGCGACAGAGGAACCCAAAAAGGGAACCCAGAUG-- 43
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-----CUUUGGUUGUUUGAAAAACUUUUGCGACGUUGUGAGAGAUG-- 43
AAG-----GCUUGAGUUGUU--AUAAUAGUCGUUUUUCUGCGAGAA--AUG----- 43
AA-----UUUCGACUCUU--AUUACCUUGGUAUAAAGUGGCACUAUG-- 43
UA-----AUUUGUACUUU--AUUACCUUGGUAUAAACGUGGCGCUAUG-- 43
UAG-----ACGUUGUUCACGG--AAUAGUGUGAGAGAAAGCUUAACUUUAG-- 43
AAU-----UUUUGCGAGAGAGACCGUGA--GGUUGAACCCGGCAAGGAAUG-- 43
ISFV-NC_005064.1 AAA-----UCAAGGAGUUGUUCGGAA--AAGUGACCUUGGUUCGUUAUG-- 43
ISFV-NC_012932.1 AAA-----AUCUAGAAGUUGUUGGAA--AAGAGAUUAUCGUUGUCGUUAUG-- 43
.....10.....20.....30.....40.....50.....6



MBFV-NC_008719.1 AGGAGCAAGCAAGUCUCGGGUACAGACCCGGGGCGUCAAAUAGGUGACGGCCAAAG-- 107
MBFV-NC_012735.1 GGGGAGUAAUAAAGUCUCGGGUCUCAGUCCCGAGCGGCUCAAUUAUGGUAGCGGCUAG-- 107
ISFV-NC_027999.1 AACUAGAGUAGGAUUCUCGGGUUUAACACCCGAGGUGCAAUAUAGUAGGCGUACUG-- 107
MBFV-NC_002031.1 ---UGGUCGUAAAGCUCAGGGUUAACCAACCCUGGGCGUCAAUUAGGUACGACGAGGAGUUCG 102
MBFV-NC_012532.1 CCCCAGAAAGAAAU--CCGAGGA-UCCGGAUUGUCAAAUAGCUAAACCGCGGAGUAGC 105
MBFV-NC_035889.1 -CCCCAAAAAGAAAU--CCGAGGAAUUCGGGAUUGUCAAAUAGCUAAACCGCGGAGUAGC 105
MBFV-NC_012533.1 -CCCCAAAAAGG-----GCCGCAUCGCGGCCUAUCAAUAGCUGAAGCGCUUUGGAUC 99
MBFV-NC_002640.1 ---CCAACGAAAAAG--GUG--GUUAGACCACCUUUAUAGCUUAAAGCCGAGGAGAAA 99
MBFV-NC_001477.1 ---CCAACGAAAAAG--ACG--GGUCGACCCUUUCAAUAGCUGAAGACCGCGCAGAAAA 102
MBFV-NC_001475.2 ---CCAACGAAAAAG--ACG--GGAAACCGUCUUAUAAUAGCUGAAGACCGGUGAAGAA 102
MBFV-NC_001474.2 ---CCAACGAAAAAG--GCG--AAAAACCGCCUUUCAAUAGCUGAAGACCGCGAGAAA 102
MBFV-NC_012534.1 CAAAAACCGAGAAACACCCGGGGCAACCCGGGUUGUCAAAUAGCUAAAGCGCGGUGCAUC 108
MBFV-NC_015843.2 CAAAAACCGAGGAAGACCCGCGCUCAGGCGCGGUUGUCAAAUAGCUAAAGCGCGGAACGUC 108
MBFV-NC_001563.2 --AGAAACCCAGGAGGGCCCGGUAAAAACCCGGGCGUGUCAAAUAGCUAAACCGCGUAUGCC 105
MBFV-NC_009942.1 --AGAAACCCAGGAGGGCCCGGCAAGAGCCGGGCGUCAAUAGCUAAACCGCGGAUAGCC 105
MBFV-NC_009028.2 --AAAAACCGAGGAAGUCCGUGCAAAGCGGACUGUCAAAUAGCUAAACCGCGUGGCUAG 105
MBFV-NC_040776.1 --AAAAACCCAGGAGACCCCGCGGAAGCGGGUUGUCAAAUAGCUAAAGCGCGGACGCCAG 105
MBFV-NC_034151.1 --AAAAACCCAGGAGGACCCCGGAAAGAACCCGGGUCGUAAUUAUAGCUGAAGCGCACAUCCCG 105
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MBFV-NC_006551.1 --AGAAACCCAGGAGGGCCCGGAAAGAACCCGGGCUCAAUUAUAGCUGAAGACCGGUAACC 105
MBFV-NC_001437.1 --AAAAACCCAGGAGGGCCCGGUAAAAACCCGGGCUUAUAAUAGCUGAAGACCGCGCUACC 105
MBFV-NC_007580.2 --AAAAACCGAGAAAAACCCGUGAAGAACCGGGUUGUCAAAUAGCUAAACCGCGGCUAUC 105
MBFV-NC_009029.2 --AAAAACCGAGGAAGCCCGGUGAAGAACCGGGCGUCAAAUAGCUAAAGCGCGGUGCUC 105
MBFV-NC_032088.1 --AAAAACCGAGGAAGUCCCGGCAUUCGUGCGGUAUUAUAGCUAAAGCGCGGAGCAUC 105
MBFV-NC_009026.2 --AGAAACCCAGGAAGACCCCGGAGAACCCGGGUCGUCAAUUAUAGCUAAAGCGUACGGCGC 105
ISFV-NC_017086.1 -GCGAAUAAACCCCAAGAACCCGGAAGACGGGCUAUCGAUUAUGAGAGACUGGCGUUGCC 102
ISFV-NC_016997.1 GGUUUUUCGAGCUGAAGGAGCCCGGUAAACCGGGCGUCGUAUUAUAAACGUAAGCUGC-- 110
ISFV-NC_040610.1 ---CAACUUGAAGAAAGACCGUUGCAAGACGGUCUGUCAAAUAGCGAAAGCGGAUUAACC 105
ISFV-NC_024017.1 ----AAAUCAAGAAAGCCCGCGCAAGCGGGGCUUUAUUAUAGCUAAACGCAUACCCAA 105
MBFV-NC_018705.3 CAAAAAACCCAGGAAGACCCCGGGCAACCCCGGUUGUCAAAUAGCUAAAGCGCGGCGCAUC 108
TBFV-NC_027709.1 GUCCAUCUGAAGAGGUAAGGGGGG---CGGUCCCCCGACGACGUGUCGAAAGAGA--- 104
TBFV-NC_001672.1 GGCCAUCUGAAGAGGUAAGGGGGG---CGGUCCCCCGACGACGUGUCGAAAGAGA--- 104
TBFV-NC_003690.1 GGCGGUUCUAAAGGAAAGGGGGG---GGGUCCCCCGACGACGUGUCGAAAGUGG--- 104
TBFV-NC_005062.1 GGCCAUCUGAAGAGGAAAGGGGGG---CGGUCCCCCGACGACGUGUCGAAAGAGA--- 104
TBFV-NC_001809.1 GACCACUUCUGAAGGAAAGGGGGG---CGGUCCCCCGACGACGUGUCGAAAGAGA--- 104
TBFV-NC_003687.1 GACCACUUCUAAAGGAAAGGGGGG---CGGUCCCCCGACGACGUGUCGAAAGAGA--- 98
NKV-NC_003635.1 -UGCGAAAAUACACGAAAAAGAA---CCUGGAAAGGUGUCAAAGAGAAAGAAAGAAUG 98
NKV-NC_004119.1 CAAAUAUGAAAAACCGAAUAAAA---GAAAGCAAAAACUCUAAG-----ACCAUUC 101
NKV-NC_008718.1 -AAUAAUCGACAGAAAGUAACACCCGGAAGGGUGUCAAAUUAUAAAUUGCAAAAUA 102
NKV-NC_005039.1 -AAAAUUCGUAGACAAAACACCCGAAUUCGGGUGUCAAAUUAUAAAAAGCAAAAUCCAAA 102
ISFV-NC_027817.1 --AGUGGAUUAAGGAGCCUUUCCCGCCGAGGAGAAAGAAAGAAAGCCUUGA--- 98
ISFV-NC_034204.1 --GACAAAA--CGGAAAGUUUUCGCCACCGGAGGUGUGCGGGCCCGCCAGAGA--GG 98
ISFV-NC_034017.1 --GAGCAUUC--GAGGAAGUUUUCCGGCCCGGAGGCGUGCGGGCGGGCCCAAGA--GG 98
ISFV-NC_024299.2 --GAGCGAAAGAAAGGAGUAAAUUAGGGGAAAGGGAAGC--UAUCCGCC--CCUCCCA 98
ISFV-NC_008604.2 --GGAAGGACGACGCGUAAGAAAGAAAGAGGGGCGGGCUCUCCGGAUGGU-UGUUACCA 100
ISFV-NC_021069.1 --AAGAAGAAGGA--GUCGGGAGUAGUGGAGAGAGGACGCGGUACCGGCC--UCCGACCA 98
ISFV-NC_012671.1 --AAGAAGAAGGA--GUCUGAGUGGUGGAGAGAGGACGUGGACGCGUCC--UCCUGCCA 98
ISFV-NC_027819.1 --UCAAGUAAGGAAGCAGUAGAAAGAGGGAUUUUCUUGGGAGGAGGAG--GAAAACCG 100
ISFV-NC_001564.2 --AAGAGGAAG--AUUUGAGGCGCGAGGAAAGCGCCAGGGAGGGAUUUUCACCG 98
ISFV-NC_005064.1 --AAUAGAGGA--GCUUGAAGAAGGGGCCUCCGGGCCCAACAUCCAACCGGUCGCGG 98
ISFV-NC_012932.1 --AAUAGGAUG--UCUUGAAGAAAGGGCCUUCGGGCCCAACAUUCUGGCGGCCAUCGA 98
0.....70.....80.....90.....100.....110.....1



MBFV-NC_008719.1 -----CCA-----NNNNNNNN-----GAGGAGACCCUCCCGAGCAC-UAUAGC-G 144
MBFV-NC_012735.1 -----UGA-----NNNNNNNN-----C-CCAUUCUCCUCCGAGCACACAUAGC-G 144
ISFV-NC_027999.1 -----GAA-----NNNNNNNN-----UGCGGAACCCCAUUGGAAAUUUA-----G 141
MBFV-NC_002031.1 CUCCUUGU-----NNNNNNNN-----G-----AGACCCUCCAGGGAACAAUAGUGG 143
MBFV-NC_012532.1 CCGUG-----NNNNNNNN-----GGUUGAGAGGAGACCCCCCGGAAACCGCAAAA-- 148
MBFV-NC_035889.1 CCGUG-----NNNNNNNN-----GUUAGGAGAGACCCCGGAAACCGCAAAA-- 147
MBFV-NC_012533.1 UAGCGCUGGC--CNNNNNNNNN-----GAGACCCCGCGGCCAUAAACAAUAUAAA-- 148
MBFV-NC_002640.1 CCGCGUAUCA--ANNNNNNNNACUAG--AGGUUAGAGGAGACCCCCCAACA--CAAAA-- 152
MBFV-NC_001477.1 CCGCGUGU-----NNNNNNNN--UAG--AGGUUAGAGGAGACCCCGCAACAACAACA-- 152
MBFV-NC_001475.2 CCGUGUGU-----NNNNNNNNACUAG--AGGUUAGAGGAGACCCCCCG--CAAAUAAAA-- 152
MBFV-NC_001474.2 CCGCGUGU-----NNNNNNNN--CUAG--AGGUUAGAGGAGACCCCCCG--CGAAACAAAA-- 152
MBFV-NC_012534.1 CC-----NNNNNNNN--GG--AGACCCUUCGAGUUAACACCAAA--ACAAA-- 150
MBFV-NC_015843.2 CC-----NNNNNNNN--GG--AGACCCUUCGAGUGAACACCAACA--A-GAAA-- 150
MBFV-NC_001563.2 CCGCG-----NNNNNNNNGAGG--AGACCCCGUGCCA--AAAACACCA--A-AAGAAA-- 150
MBFV-NC_009942.1 CCGCG-----NNNNNNNN--GG--AGACCCCGUGCCACAAACACCAACA--ACAAA-- 150
MBFV-NC_009028.2 CGUGU-----NNNNNNNNGUGG--AGACCCUUCAGCAC--CAAGCGCGAA--ACAAA-- 150
MBFV-NC_040776.1 CGUUU-----NNNNNNNN--GG--AGACCCUUGGCAACAAGCGCAAA--GACAAA-- 151
MBFV-NC_034151.1 CGCUA-----NNNNNNNN-----AGACCCUUGCGAGUGAAC--GCAAA-UAAAA-- 147
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MBFV-NC_006551.1 CCGCG-----NNNNNNNN-----ACCCCGCA-UCAUAAGCAUCA-----AAAAA-- 143
MBFV-NC_001437.1 CCGCG-----NNNNNNNN--U--AGAGGAGACCCCGCAUUGCA-----UCA-AA-- 144
MBFV-NC_007580.2 CCGCG-----NNNNNNNN--UU--AGAGGAGACCCUUGCCGUUAACGC--AAACAA-- 150
MBFV-NC_009029.2 CCGCG-----NNNNNNNNAGAGG--AGACCCUCCCAAGAAAGCGCAACCAAAAA-- 154
MBFV-NC_032088.1 CCGCG-----NNNNNNNNAGAGGUUAGAGGAGACCCCAACAUACCGCAAA--ACAAA-- 155
MBFV-NC_009026.2 CAACG-----NNNNNNNN-----CCCUUGGCAAAACAGUUAACCGCACCAAAAGAAA-- 151
ISFV-NC_017086.1 UCGGUCU-----NNNNNNNN-----AGAGGAGACCCCAAAAAUUG--AAGGG 144
ISFV-NC_016997.1 -----NNNNNNNN-----AGGAAACCCCAAAAAUUGUAUAGG 148
ISFV-NC_040610.1 CCGCU-----NNNNNNNN-----ACCCCUCAUUAUUUAUUAAG 134
ISFV-NC_024017.1 CGGUG-----NNNNNNNN-----CCCAUCUGCUGAGAG--CAAAA 137
TBFV-NC_018705.3 CC-----NNNNNNNN-----CCCGCGGAAAUCAAGCAAGCCCAACCCUGG 149
TBFV-NC_027709.1 CCGCAA-----NNNNNNNNUCUCUUCAGGAUUUUUCCUCCUUAUACAAA--UUCCCC 157
TBFV-NC_001672.1 CCGCAA-----NNNNNNNNUCUCUUCAGGAUUUUUCCUCCUUAUACAAA--UUCCCC 157
TBFV-NC_003690.1 CCGCAA-----NNNNNNNNUCUCUUCAGGAUUUUUCCUCCUUAUACAAA--UUCCCC 157
TBFV-NC_005062.1 CCGCUA-----NNNNNNNN--UCUUCAGGGUUUUUCCUCCUUAUACAAA--UUCCCC 157
TBFV-NC_001809.1 CCGCAAUAAGUNNNNNNNNNUC--UCCUGGGAUUUUUCCGCGUUAUACUAAAUUUCCCC 157
NKV-NC_003635.1 CUGGAAGGAAGUNNNNNNNNUUGGCCAAGAACCGCUCUGGCGUUUGCCUGUUAUUU--C 157
NKV-NC_004119.1 CUUGUCGAA--NNNNNNNUUGGCUAAGGUUACACAGCUUUUGCUGCCGCGUUUUCAA 158
NKV-NC_008718.1 UAAAAAG--NNNNNNNA-----UAAAGCAGGCGGAGCGGUCU 139
NKV-NC_005039.1 AAAAAAA--NNNNNNNC-----U-----CUACGACUGGAUUUUG 136
ISFV-NC_027817.1 UACAUAUCACAGNNNNNNNN-----AUGUG-----CAGGGCAACAAGUUCUA 140
ISFV-NC_034204.1 GGCUGGGGAAGANNNNNNNN-----CUC-----CAGAGCAAAACAGGGGAU 138
ISFV-NC_034017.1 GGUCGGCGAAGANNNNNNNN-----ACCUC-----CAGAGCAAAACAGGGGAGA 140
ISFV-NC_024299.2 UUAAGGAGAAANNNNNNNN-----ACCGCAAGGUGAGGGCGCACAGGACG 143
ISFV-NC_008604.2 ---CCGGGGCGCANNNNNNNN-----UCACCGCAAGGUGAGGGCGCACAGGAU 145
ISFV-NC_021069.1 ACCGUGGAGGAANNNNNNNN-----UACCGUAAGGUGAGGGCGCACAGGAUC 145
ISFV-NC_012671.1 AUCUGGAGGAGNNNNNNNN-----CACCCAAGGUGAGGGCGCACAGGAUC 144
ISFV-NC_027819.1 GGUUUUGAG--ANNNNNNN-----AAAGGCCAUACACGAGGGCAACAGGAA 145
ISFV-NC_001564.2 CGUUCUGGGGAANNNNNNNN-----UUUCAAACCGGACGGGCAACAGGGA 145
ISFV-NC_005064.1 UUGGACCGGCCGNNNNNNNN-----CUUCAAACCGGACGGGCAACAGGGA 143
ISFV-NC_012932.1 CCAGACCGCCGNNNNNNNN-----A--AAAUCGGCGGAGCAACAGGGA 141
20.....130.....140.....150.....160.....170.....1



MBFV-NC_008719.1 .))))))))) GACCAUAUUGACGCGUGGG--AAAGACCGGAGACACUCCUUGAUUUCUACC---UUUCUC 199
MBFV-NC_012735.1 GACCAUAUUGACGCGCAGGG--AAAGACCGGAGACACUCCUUGAUUUCUACC---UUUCUC 199
ISFV-NC_027999.1 CUUCAUAUUGACACCAAGGAAAGACCGGAGAAACUUCUUGCUUACUCGC---AGCAAC 197
MBFV-NC_002031.1 GACCAUAUUGACGCGCAGGG--AAAGACCGGAGUGGUUCUCUGCUUUUCCAC---CAGAG 197
MBFV-NC_012532.1 CAGCAUAUUGACG---UGGGA--AAGACCA--GAGACUCCAGUAGUUUCCAC---CAGCU 199
MBFV-NC_035889.1 CAGCAUAUUGACG---UGGGA--AAGACCA--GAGACUCCAGUAGUUUCCAC---CAGCU 199
MBFV-NC_012533.1 CAGCAUAUUGACACCUUGGGA--AAGACCG--GAGACUCUGUUGGUUUCC---CACACU 201
MBFV-NC_002640.1 CAGCAUAUUGACG---UGGGA--AAGACCA--GAGAUCCUGCU--GUCUCUGC---AACAU 203
MBFV-NC_001477.1 CAGCAUAUUGACG---UGGGA--AAGACCA--GAGAUCCUGCU--GUCUCUAC---AGCAUC 203
MBFV-NC_001475.2 CAGCAUAUUGACG---UGGGA--AAGACCA--GAGAUCCUGCU--GUCUCCUC---AGCAUC 203
MBFV-NC_001474.2 CAGCAUAUUGACG---UGGGA--AAGACCA--GAGAUCCUGCU--GUCUCCUC---AGCAUC 203
MBFV-NC_012534.1 CAGCAUAUUGACACCUUGGGA--GAGACUAGGAGACCCUUGUCU---UAAC---AACACC 202
MBFV-NC_015843.2 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGACCCUUGUCU---UAAC---AACACC 202
MBFV-NC_001563.2 CAGCAUAUUGACACCUUGGGA--UAGACUAGGGAUUCUUGUCU---CUGC---AACACC 201
MBFV-NC_009942.1 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGAUUCUUGUCU---CUGC---ACAACC 201
MBFV-NC_009028.2 CAGCAUAUUGACGCGCUUGGGA--AAGACCGGAGAUCCUUGUCU---UUC---AUACC 201
MBFV-NC_040776.1 CAGCAUAUUGACACCUUGGGA--AAGACCGGAGACCCUUGUCU---CUGC---AACACC 202
MBFV-NC_034151.1 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGACCCUUGUCU---AUUUC---AACACC 200
MBFV-NC_000943.1 CAGCAUAUUGACACCUUGGGA--AAGACUAGGAGAUUCUUGUCU---AUUUC---AACAU 199
MBFV-NC_001437.1 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGAUUCUUGUCU---AUUUC---AACAU 199
MBFV-NC_007580.2 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGAUUCUUGUCU---AUUUC---AACAU 199
MBFV-NC_009029.2 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGAUUCUUGUCU---AUUUC---AACACC 200
MBFV-NC_032088.1 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGAUUCUUGUCU---UUG---ACUCC 205
MBFV-NC_009026.2 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGAUUCUUGUCU---UUG---AACACC 202
ISFV-NC_017086.1 CAGCAUAUUGACACCUUGGGA--UAGACUAGGAGAUUCUUGUCU---UUG---AACACC 202
ISFV-NC_016997.1 UAUUAUAUCGACACCUAGGAAAGACUGGAGAUAC--CUUUGGUUCUUCGCAC---ACUAAC 199
ISFV-NC_040610.1 CAGCAUAUUGACACCUUGGGA--AUAGACCGGAGAAUAGCAAAUUCUGGCGACUAAACAA 197
ISFV-NC_024017.1 UAGCAUAUUGACACCUUGGGAAGAGACAGAGAAUAGUUGUUUGGUCAUUGGAGACAAC 197
TBFV-NC_018705.3 CAAAGCUGUAAACCGGGGAAGGACUAGAGGUUAGAGGAGACCCUUGCGAGUAAACACC 209
TBFV-NC_027709.1 CUACGAGUAGGGGGGCGG-----UUUCUUGUUCCUUGAGGCCACCAUC 201
TBFV-NC_001672.1 CUCGGUAGAGGGGGGGCGG-----UUUCUUGUUCCUUGAGGCCACCAUC 201
TBFV-NC_003690.1 CUCGUCAGAGGGGGGGCGG-----UUUCUUGUUCCUUGAGGCCACCAUC 201
TBFV-NC_005062.1 CUCAUCUAGAGGGGGGGCGG-----UUUCUUGUUCCUUGAGGCCACCAUC 201
TBFV-NC_001809.1 CUCGACAGAGGGGGGGCGG-----UUUCUUGUUCCUUGAGGCCACCAUC 201
TBFV-NC_003687.1 CAGGAAACUGGGGGGGCGG-----UUUCUUGUUCCUUGAGGCCACCAUC 201
NKV-NC_003635.1 CAAAUUCCCGUU--ACCG-----GGGUGGGGUGAUUAGCCAUUGGUCG 199
NKV-NC_004119.1 UUGCCUCAUCUUGAAUGG-----GGGCGCGUGAUUAUAGCAGGAC 202
NKV-NC_008718.1 AAAACCCGAGGCCUCGCGUGGAAACACGUCGACG-----GGGACUGAGGAUUAAGUCCAGC 196
NKV-NC_005039.1 CAAUAUGUUGGUAUCAGGGAAGACCGGGUGUUUGUGCGUUUCGGAGUCCGCGGAGGCC 196
ISFV-NC_027817.1 ACGAACUAGGGUGAGUAG--CGUACCCCGCGGU--UGUGUAAACGAUUGCGUACUAG--A 196
ISFV-NC_034204.1 UAUCUUUAAGGUGAUUUGACGACCACCCUUGAAUUGUUAUAAACUGUGCGGAA--AA 197
ISFV-NC_034017.1 AAUCCCU--AGGUGAGUUGGCGACCCACCCUCUGAAUUGUUAUAAAGUUGUGCGGAA--AA 198
ISFV-NC_024299.2 AAAGUCCAGGGUGAGU--GACGACACCCCGCG--AAAUGUUUAUAUAGGCC--AGUU--G 196
ISFV-NC_008604.2 GA--AUCCAGGUGAGU--GACGCCACCCCGG--AAUUGUUAUUGUAAACA--GAGU---- 196
ISFV-NC_012671.1 GAAUAUCCGGGUGAGU--GACGCCACCCCGG--AAUUGUUAUUGUAGACA--G-GCU---- 197
ISFV-NC_027819.1 GAGUAUCCGGGUGAGU--GACGCCACCCCGG--AAUUGUUAUUGUAGACA--G-GCU---- 196
ISFV-NC_001564.2 GAAAUUCGGGUGAGU--AGCCACACCCCGG--AAACUGUAUUUAGUGA--UGACA---- 198
ISFV-NC_005064.1 GAAAUCCCGGGG--UA--GCGAACCCUCCGUAAUUGUGAAAAAGUAG--GGG--AA--AGA 199
ISFV-NC_012932.1 -AAUUCGGGGGA--C-GCGUACCCUCCG--AAUUGUGAAAAAGUAUG--GGGAAA--AGA 196
GAAAUCCCGGGGAUU--GCGAACCCUCCG--AAUUGUGAAAAAUUAG--GGGAAA--AGU 197
80.....190.....200.....210.....220.....230.....2



MBFV-NC_008719.1 ACCCUUA--AGC-- 209
MBFV-NC_012735.1 CCGCUAA--AGC-- 209
ISFV-NC_027999.1 CACCGAA--AGCA 209
MBFV-NC_002031.1 GUCUGUG--AGCA 209
MBFV-NC_012532.1 GGCCGC--CAGG 209
MBFV-NC_035889.1 GGCCGC--CAGG 209
MBFV-NC_012533.1 AGUCCC--C-U 209
MBFV-NC_002640.1 AAUCC-----A 209
MBFV-NC_001477.1 AUUCC-----A 209
MBFV-NC_001475.2 AUUCC-----A 209
MBFV-NC_001474.2 AUUCC-----A 209
MBFV-NC_012534.1 AGCCAU--C-- 209
MBFV-NC_015843.2 AGCCAU--U-- 209
MBFV-NC_001563.2 AGCCAC--AC-- 209
MBFV-NC_009942.1 AGCCAC--AC-- 209
MBFV-NC_009028.2 AGCCAC--UA-- 209
MBFV-NC_040776.1 AGCCAC--U-- 209
MBFV-NC_034151.1 AGCCAC--UC 209
MBFV-NC_000943.1 AGUCAC--AAGG 209
MBFV-NC_006551.1 AACCCAC--AAG 209
MBFV-NC_001437.1 AGCUAC--UAGG 209
MBFV-NC_007580.2 AGCCAC--AA-G 209
MBFV-NC_009029.2 GGCU----- 209
MBFV-NC_032088.1 AG-U----- 209
MBFV-NC_009026.2 UCCCA-----C-- 209
ISFV-NC_017086.1 ACCUA-----CGG 209
ISFV-NC_016997.1 UCUA-----UGG 209
ISFV-NC_040610.1 UACAAGC--ACAGA 209
ISFV-NC_024017.1 AGCCAUG--GCACA 209
MBFV-NC_018705.3 ----- 209
TBFV-NC_027709.1 ACCCAG-----AC 209
TBFV-NC_001672.1 ACCCAG-----AC 209
TBFV-NC_003690.1 ACCUAG-----AC 209
TBFV-NC_005062.1 ACCCAG-----AC 209
TBFV-NC_001809.1 ACCCAG-----AC 209
TBFV-NC_003687.1 AUCCAG-----GC 209
NKV-NC_003635.1 ACAGAU-----CAAG 209
NKV-NC_004119.1 -CAGA-----AAA 209
NKV-NC_008718.1 CCGCGCGCCCAUA 209
NKV-NC_005039.1 AGGGCGCCGUUG 209
ISFV-NC_027817.1 UAAAGUCAGAGU 209
ISFV-NC_034204.1 UCCAAA--GACUG 209
ISFV-NC_034017.1 UCCAAA--GAUG 209
ISFV-NC_024299.2 AGCUUAACACA 209
ISFV-NC_008604.2 GCUUGACAGCA 209
ISFV-NC_021069.1 GCUCGACAGC 209
ISFV-NC_012671.1 GCUCCGACGCA 209
ISFV-NC_027819.1 GAUACGAGUG-- 209
ISFV-NC_001564.2 ACUCAUCUUA-- 209
ISFV-NC_005064.1 ACCCAGCUAAAU 209
ISFV-NC_012932.1 ACCCAUCU--AAGC 209
40.....250.

