

dISFV-NC_040610.1 --G-----AACAAUUUUUAAAGAGUCAAAACUAGAAAUUUA--UUUC---A---AUGG 44
dISFV-NC_024017.1 UCG-----CGCAUUUUGAUAGAGUU---GACUAGAUAAACGAAUUAUC---G---AUGG 44
dISFV-NC_017086.1 AU-----AACACGUUUUGAAUAGGUUUUAU-UGUGAAUCGGAAGA-UAAC-C-----AUGG 44
MBFV-NC_009029.2 UGAUUACAUAACACAGUGUGAACAAGUUUU-UUGAACAGCA-----AUGA 44
MBFV-NC_032088.1 UC-----UAUAACUCAGUGUGAACAAGUUUU-UUGAUCAGUGGA-U-----A---AUGA 44
MBFV-NC_001437.1 -U-----UAGUGCAGUUUAACAGUUUUU-UAGAACGGAAGA-UAAC-C-----AUGA 44
MBFV-NC_000943.1 -----UAACGCGGUUUUGAACAGUUUUU-UGGAGCUUUUGA-UUUCAA-----AUGU 44
MBFV-NC_001563.2 AU-----UAACACAGUGCGAGCUGUUUCU-UGGCAC-GAAGA-UCUC-G-----AUGU 44
MBFV-NC_009942.1 AU-----UAACACAGUGCGAGCUGUUUCU-UAGCAC-GAAGA-UCUC-G-----AUGU 44
MBFV-NC_006551.1 -U-----UAACACAGUGCGCGAGCUGUUUCU-UUGAGC-GUUGA-UUUUA-----AUGU 44
MBFV-NC_034151.1 -----UAACACAGUGUGAAUAGUUUUU-U-GAACAGAGGUGAAAACC-----AUGU 44
MBFV-NC_009028.2 UU-----UAACACAGUCUGAAUAGUUUUU-U--AGCAAAGGA-UUUC---AUGU 44
MBFV-NC_040776.1 UU-----UAACACAGUCUGAAUAGUUUUU-U--AGCAGAGGU-ACUACC-----AUGU 44
MBFV-NC_012534.1 CCGUA---A--AACACAGUUUGAAC--GUUUU-UUGGAGAGAG---AUUAUU-----AUGU 44
MBFV-NC_015843.2 ACGUA---AACACAGUUUGAAC--GUUUU-UUGGAUAGAG---ACAACU-----AUGU 44
MBFV-NC_007580.2 UA-----ACUUGACUGCGAACAGUUUUU-U--AGCAGGGA-AUUACCCA-----AUGU 44
MBFV-NC_009026.2 AG-----AAAGUUUUUGAGGAAAGACG-A---GAAGCGAA-UUCUCUGA---AUGG 44
MBFV-NC_012532.1 -----AACAGGUUUUA-----AUUUGGAUUUGGAAACGAGAGUUUCUGG--UCAUGA 44
MBFV-NC_035889.1 -----ACAGGUUUUA-----UUUUGGAUUUGGAAACGAGAGUUUCUGG--UCAUGA 44
MBFV-NC_012533.1 -----AACAGUUUUU-----GUGUUGGAAAGAAACAGAUUCUUCGG--AAUUGA 44
MBFV-NC_002640.1 -----UCUAACAGUUUGUUUGAAUAGAGAGCAGAUUCUCUGGAAAAAUG- 43
MBFV-NC_001474.2 -----CGUAGUUUCUAACAGUUU-UUUAAUUAGAGAGCAGAUUCUCUG-----AUGA 44
MBFV-NC_001477.1 -----ACGUAGUUUCUAACAGUUU-UUU-AUUAGAGAGCAGAUUCUCUG-----AUGA 44
MBFV-NC_001475.2 -----ACGUAGUGCUGACAGUUU-UUU-AUUAGAGAGCAGAUUCUCUG-----AUGA 44
MBFV-NC_002031.1 -----UAAUCGUUCGUUGAGCGAUUAG-CAGAGAACUGACCAG-AACAUGU 44
dISFV-NC_027999.1 -----GGAUUAAUUGUUGUUGAGAGAACACGAGAGAAGUACUA-CU-AUGG 44
MBFV-NC_008719.1 -----AUUUCUACUGAAAGG-GUAGAGAAAAGGAGUUUUGCUU-CUCAUGG 44
MBFV-NC_012735.1 -----UUUCUACUGAAAGGAGUAGAAGAAAGGAGAUUCAUUC-CCAUGG 44
dISFV-NC_016997.1 A---AACAUAAACGCAUUGAAUAGGUUUGAAAGAGUUGAAUCA-----AUGA 44
.....10.....20.....30.....40.....50.....6



dISFV-NC_040610.1 UUA---GACAACUUGGAAA-----GACCGUUGCAAGA--GGUCUGU--CAUAUUGCGAAAGC 95
dISFV-NC_024017.1 UGA---CUAAAUCAGAGAA-----GCCCCGCCGAAAGCGGGCUGU--UAAUAUUGCUAACAC 95
dISFV-NC_017086.1 CGA---AUAAACCCAGAGAA-----GCCCCG---AAGA--GGGCUA--CGAAUAUAGUGAGAC 92
MBFV-NC_009029.2 CCA---AAAAACCCAGGAAG-----GCCCCGUAGAAAU--GGGCCG--CAUAUUGCUAAAGC 95
MBFV-NC_032088.1 CUA---AAAAACCCAGGAAA-----GUCCCGGCAAUCGU--GGACUGU--CAUAUUGCUAAAGC 95
MBFV-NC_001437.1 CUA---AAAAACCCAGGAGG-----GCCCCGUAAAAAAC--GGGCUA--CAUAUUGCUGAAAC 95
MBFV-NC_000943.1 CUA---AAAAACCCAGGAGG-----ACCCGGGAAGCCCCGGGUCG--CAUAUUGCUAAAC 95
MBFV-NC_001563.2 CUA---AGAAACCCAGGAGG-----GCCCCGUAAAAAAC--GGGCUG--CAUAUUGCUAAAC 95
MBFV-NC_009942.1 CUA---AGAAACCCAGGAGG-----GCCCCGGAAGAGCC--GGGCUG--CAUAUUGCUAAAC 95
MBFV-NC_006551.1 CUA---AGAAACCCAGGAGG-----GCCCCGGAAGAAAC--GGGCCA--CAUAUUGCUGAAAC 95
MBFV-NC_034151.1 CUA---AAAAACCCAGGAGG-----ACCCGGAAGAAAC--GGGUCG--UAAUAUUGCUGAAGC 95
MBFV-NC_009028.2 CUA---AAAAACCCAGGAAA-----GUCCCGCUGCAAAG--GGACUGU--CAUAUUGCUAAAC 95
MBFV-NC_040776.1 CUA---AAAAACCCAGGAGG-----ACCCGCCCGGAAGG--GGGUUG--CAUAUUGCUGAAAC 95
MBFV-NC_012534.1 UUAACAAAAAACCCAGGAAA-----ACCCGGGGCAACC--GGGUUG--CAUAUUGCUAAAGC 98
MBFV-NC_015843.2 CUAACAAAAAACCCAGGAAAG-----ACCCGGCUCAGGC--GGGUUG--CAUAUUGCUAAAGC 98
MBFV-NC_007580.2 CUA---AAAAACCCAGGAAA-----ACCCGCUAGAAAC--GGGUUG--CAUAUUGCUAAAC 95
MBFV-NC_009026.2 CUA---GAAACCCAGGAAAG-----ACCCGGAGGAAAC--GGGUCG--CAUAUUGCUAAAGC 95
MBFV-NC_012532.1 AAAACCCCAAGAAAGAAAU-----CCGGAGGA-UC--CGGAUUG--CAUAUUGCUGAAAC 95
MBFV-NC_035889.1 AAAA-CCCAAAAAAGAAAU-----CCGGAGGAUUC--GGAUUG--CAUAUUGCUAAAC 95
MBFV-NC_012533.1 AAA-CCCCAAAAAGG-----GCCGCAUCG--GGCCUA--CAUAUUGCUGAAGC 89
MBFV-NC_002640.1 --AA-CCAACGAAAAAAG-----GUG--GUUAGAC--CACCUU--CAUAUUGCUGAAGC 89
MBFV-NC_001474.2 AUAA-CCAACGGAAAAAAG-----GCG--AAAAACACGCCUU--CAUAUUGCUGAAAC 92
MBFV-NC_001477.1 ACAA-CCAACGGAAAAAAG-----ACG--GGUCGAC--CGUCUU--CAUAUUGCUGAAGC 92
MBFV-NC_001475.2 ACAA-CCAACGGAAAGAG-----ACG--GGAACAC--CGUCUA--CAUAUUGCUGAAGC 92
MBFV-NC_002031.1 CU-----GGUCGUAAAGCUCACGGGAAAAACCCUGGGCG--CAUAUUGGUCAGAC 92
dISFV-NC_027999.1 UUGAGAAAAACUAGAGUAGG---AUCUCGGGUUAAAACCCGAGGUG--CAUAUUGAU----- 96
MBFV-NC_008719.1 C---AACAAAGAGGAGCAAGCAAGUCUCGGGUCACGACC--GGGGCG--CAUAUUGGU----- 96
MBFV-NC_012735.1 C---AACAAAGGGGAGAAUAGUUCUCGGGUCGAUCC--GAGGCG--CAUAUUGGU----- 96
dISFV-NC_016997.1 GAUCAUUGGUCUUUGCAGCUGAGAGGCCCGUUAAA---CGGGCGG--CGAUUAUUAUAAAC 101
0.....70.....80.....90.....100.....110.....1



dISFV-NC_040610.1 --GGAUUACCACCCG-CU---NNNNNNNCUCAUUUUUAU-A-UAACA--GCAUAUUGACA- 146
dISFV-NC_024017.1 --GCAUCCCAAGCG-UG---NNNNNNNCU- GCUGAGAGC-A-AAUAAG--GCAUAUUGACA- 145
dISFV-NC_017086.1 GUGCGUUGCCUCGCGUCU---NNNNNNNCCCAAAAAUGA--A-GGGCA--CUAAUUGCGACAC 146
MBFV-NC_009029.2 GCGGUGCGUCCCGCG-----NNNNNNNNA- GCGCAAACAC-A-AAACAG--GCAUAUUGACA- 145
MBFV-NC_032088.1 GCGGAGCAUCCCGCG-----NNNNNNNNU- ACCGCAAAAC-A-AAACAG--GCAUAUUGACA- 145
MBFV-NC_001437.1 GCGGCCUACCCCGCG-----NNNNNNNC- GCAUUUGCAU-C-AAACAG--GCAUAUUGACA- 145
MBFV-NC_000943.1 GCGGCAUACCCCGCG-----NNNNNNNNA- AAAGCAUCA--A-CAACAG--GCAUAUUGACA- 145
MBFV-NC_001563.2 GCGGUUAGCCCGCG-----NNNNNNNNA- AACACCAAAA-G-AAACAG--GCAUAUUGACA- 145
MBFV-NC_009942.1 GCGGAAUGCCCCGCG-----NNNNNNNNA- ACACCAAC-A-AAACAG--GCAUAUUGACA- 145
MBFV-NC_006551.1 GCGGCAUACCCCGCG-----NNNNNNNNU- AAGCAUCA--A-AAACAG--GCAUAUUGACA- 145
MBFV-NC_034151.1 GCACAUCCCGCGCUA-----NNNNNNNNG- AA- CGCAAU-AAAAACAG--GCAUAUUGACA- 145
MBFV-NC_009028.2 GCCUGGCUAGCGUGU-----NNNNNNNC- AAGCGGAA--ACAAACAG--GCAUAUUGACG- 145
MBFV-NC_040776.1 GCCAGCCAGCGUUU-----NNNNNNNN-- AAGCGCAAAG-ACAAACAG--GCAUAUUGACA- 145
MBFV-NC_012534.1 GCGGUGCAUCCC-----NNNNNNNN-- AACACCAAAA-CAAAACAG--GCAUAUUGACA- 145
MBFV-NC_015843.2 GCGGAACGUCCC-----NNNNNNNNG- AACACCAAA--GAAACAG--GCAUAUUGACA- 145
MBFV-NC_007580.2 GCGGCUAUGCCCGCG-----NNNNNNNCCGUUAACGCAA-AC-AAACAG--GCAUAUUGACA- 146
MBFV-NC_009026.2 GUACGGCGGCCAACG-----NNNNNNNACGC--ACCAA-AGAAACAG--GCAUAUUGACA- 145
MBFV-NC_012532.1 GCGGAGUAGCCCGUG-----NNNNNNNCCCGGA-AAACGCAAAACAG--GCAUAUUGACG- 147
MBFV-NC_035889.1 GCGGAGUAGCCCGUG-----NNNNNNN- CCCGGA-AAACGCAAAACAG--GCAUAUUGACG- 146
MBFV-NC_012533.1 GCUUUGGAUAGAGCGCUGGCGCCNNNNNNNA---UAACCAACUAAAAACAG--GCAUAUUGACAC 146
MBFV-NC_002640.1 GCGAGAGAAACCGCGUAUCAANNNNNNNCCCCCC--AACACAAAAACAG--GCAUAUUGACG- 146
MBFV-NC_001474.2 GCGGAGAGAAACCGCGUGU---NNNNNNNCCCCCC--AAACAAAAACAG--GCAUAUUGACG- 146
MBFV-NC_001477.1 GCGGAGAAACCGCGUGU---NNNNNNNCCCGA--CAACACAAACAG--GCAUAUUGACG- 146
MBFV-NC_001475.2 GCGUGAGAAACCGUGUGU---NNNNNNNCCCCCC--CAAUAAAAACAG--GCAUAUUGACG- 146
MBFV-NC_002031.1 GAGGAGUUCGCUCCUUGU---NNNNNNNNAAG- GAACAAU-AGUGGGA--GCAUAUUGACGC 147
dISFV-NC_027999.1 ---UAGCGCUACUGGAA---NNNNNNNCCA-UUGGAAUUUAGCU--UCAUAUUGACAC 146
MBFV-NC_008719.1 ---GACGGCAAGGCCA---NNNNNNNCC--GAGCAC-UAUAGCGGA--GCAUAUUGACGC 146
MBFV-NC_012735.1 ---AGCGGCUAGAGUGA---NNNNNNNCC--GAGCACAUAGCGGA--GCAUAUUGACGC 147
dISFV-NC_016997.1 GUAAGCUGC-----NNNNNNNC---AAAAUGUAUAGGCUA--UUAUAUCGACAC 146
20.....130.....140.....150.....160.....170.....1



dISFV-NC_040610.1 CCAGGG-AUAGACCGGAGAAAAUACACAUAUUC--- 177
dISFV-NC_024017.1 CUUGGGAAGAGACCAGAGAUUAG-AUGUUGUUU--- 177
dISFV-NC_017086.1 UUGGG--AAAGACCAGAGGUACUCGCUAUUCA--- 177
MBFV-NC_009029.2 CCUGGGA--AAGACUAGGGGAUU--UGCUGCUCUGG 177
MBFV-NC_032088.1 CCUGGGA--UAGACUAGGAGAU--CGCUGCUCUGG 177
MBFV-NC_001437.1 CCUGGGAA-UAGACUGGGGAGAU--UUCUGCUCUA- 177
MBFV-NC_000943.1 CCUGGGAA-AAGACUAGGAGAU--UUCUGCUCUA- 177
MBFV-NC_001563.2 CCUGGGA--UAGACUAGGGGAGAU--UUCUGCUCUGC 177
MBFV-NC_009942.1 CCUGGGA--UAGACUAGGAGAU--UUCUGCUCUGC 177
MBFV-NC_006551.1 CCUGGGAAUUGACUAGGAGAU--UUCUGCUCU- 177
MBFV-NC_034151.1 CCUGGGA--UAGACUGGGAGACC--CUCGCUUAUU 177
MBFV-NC_009028.2 CCUGGGA--AAGACCGGGAGAU--CUCGCUUUCC 177
MBFV-NC_040776.1 CCUGGGA--AAGACCGGGAGACC--CUCGCUUGC 177
MBFV-NC_012534.1 CCUGGGA--GAGACUAGGAGACC--CUCUGUCCUA 177
MBFV-NC_015843.2 CCUGGGA--UAGACUAGGAGACC--CUCUGUCCUA 177
MBFV-NC_007580.2 CCUGGAA--AGACAGGAGAUCC--CCUGCUUUUUC 177
MBFV-NC_009026.2 CCUGGGA--UAGACCGGAGAAU--UGCUGCCUCGC 177
MBFV-NC_012532.1 -UGGGAA---AGACCAGAGACUCCAUGAGUUUCC-- 177
MBFV-NC_035889.1 CUGGGAA---AGACCAGAGACUCCAUGAGUUUCC-- 177
MBFV-NC_012533.1 CUGGGAA---AGACCGGAGACUCUGUUGGCUUUC-- 177
MBFV-NC_002640.1 CUGGGAA---AGACCAGAGAUCCUGCUGUCUCUG-- 177
MBFV-NC_001474.2 CUGGGAA---AGACCAGAGAUCCUGCUGUCUCCU-- 177
MBFV-NC_001477.1 CUGGGAG---AGACCAGAGAUCCUGCUGUCUCUA-- 177
MBFV-NC_001475.2 CUGGGAG---AGACCAGAGAUCCUGCUGUCUCCU-- 177
MBFV-NC_002031.1 CAGGG-A--AAGACCGGAGUGGUUCUG-CUUU-- 177
dISFV-NC_027999.1 CAGGGAA--AAGACCGGAGAAACUUCUUG-CUUA-- 177
MBFV-NC_008719.1 CUGGG-A--AAGACCGGAGACACUCCUGAUUCU-- 177
MBFV-NC_012735.1 CAGGG-A--AAGACCGGAGACACUCCUUGAUUC-- 177
dISFV-NC_016997.1 CUAAGAA--AGACUGGAGAUAC--CUUGGUUUCU 177
80.....190.....200.....210.....

