

dISFV-NC_040610.1 -----AAAGAAGUCAAAACUAGAAAUUUAA-UUU---CA-----AUGGUU---AGACAA 42
dISFV-NC_024017.1 -----UGAU-AGAGUUUGACUAGAUACGAAUUU---CG-----AUGGUG---ACUAAA 42
dISFV-NC_017086.1 -----UGAAUAGGUUUUUAUUGGAAUCGAAA-UAC---CG-----AUGGCG---AAUAAA 42
MBFV-NC_009028.2 -----UCUGAAUAGUUUUUU---AGCAAGGGA-UUUC---AUGUCU---AAAAAA 42
MBFV-NC_040776.1 -----UCUGAAUAGUUUUUU---AGCAGAGGU-ACUACC---AUGUCU---AAAAAA 42
MBFV-NC_034151.1 -----UGAAUAGUUUUUU---GAACAGAGGUGAAAACC-----AUGUCU---AAAAAA 42
MBFV-NC_000943.1 -----UGAACAGUUUUUUGGAGCUUUUGAUUU---CAA-----AUGUCU---AAAAAA 42
MBFV-NC_006551.1 -----GCCGGCAGUUUCUUUGAGC-GUUGAUUU---UCA-----AUGUCU---AAGAAA 42
MBFV-NC_001563.2 -----UGCGAGCUGUUUCUUGGCAC-GAAGAUUU---C-G-----AUGUCU---AAGAAA 42
MBFV-NC_009942.1 -----UGCGAGCUGUUUCUUGGCAC-GAAGAUUU---C-G-----AUGUCU---AAGAAA 42
MBFV-NC_007580.2 -----GCGAACAGUUUUUU---AGCAGGGAAUACCCA-----AUGUCU---AAAAAA 42
MBFV-NC_009026.2 -----UCG-----AGGAAAAGCAGAGAAGCGAAUUCUCUGA-----AUGGCU---AGAAAA 42
MBFV-NC_009029.2 ACACAGUGUGAACAAGUUUUUUGAACACGCA-----AUG-----ACCAAAAAA 42
MBFV-NC_032088.1 -----AGUGUGAACAAGUUUUUUGAUCAGUG--GAUA-----AUG---ACUAAAAAA 42
MBFV-NC_012534.1 -----AGUUUGAAC--GUUUUUUGGAGAGAGAUUUU-----AUGUUUAACAAAAAA 45
MBFV-NC_015843.2 -----AGUUUGAAC--GUUUUUUGGAUAGAGACAACU-----AUGUCUAACAAAAAA 45
MBFV-NC_001437.1 -----UUAAACAGUUUUUUAGAACCGGAAGAUAAACC-----AUGACU---AAAAAA 42
MBFV-NC_012532.1 -----AUUUUGGAUUU---GGAAACGAGAG-UUUCUGG--UCAUGAAAAAACCCCAA 45
MBFV-NC_035889.1 -----UUUUUGGAUUU---GGAAACGAGAG-UUUCUGG--UCAUGAAAAA-CCCAA 44
MBFV-NC_002640.1 -----UGUUUGAAUAGAGAGCAGA-UCUCUGGAAAAAUG---AA-CCAAC 40
MBFV-NC_001477.1 -----AACAGUUUUUUUAUUGAGAGAGCAGA-UCUCUG-----AUGAACAA-CCAAC 43
MBFV-NC_001475.2 -----GACAGUUUUUUUAUUGAGAGAGCAGA-UCUCUG-----AUGAACAA-CCAAC 43
MBFV-NC_001474.2 -----ACAGUUUUUUUAUUGAGAGAGCAGA-UCUCUG-----AUGAAUA-CCAAC 43
MBFV-NC_012533.1 -----GUGUUGAGAAAAGAAAACAGAUUCUUCGGAA--AUGAA-----AAC 38
dISFV-NC_027999.1 -----UUGUUUGAGAGAACAGCGAGAAUACUACU-AUGGUUGAGAAAAACU 45
MBFV-NC_012735.1 -----AAGGAGUAGAAGAAAG-GAGAUUCAUUCCCAAUGGCAACAAAGGGG 45
MBFV-NC_008719.1 -----AAAGGUGAGAGAAAAG-GAGUUUGCUCUCUAGGCAACAAGAGGA 45
MBFV-NC_002031.1 -----UUGAGCGAUUAGCAGA-GAACUGACCAGAACAUUGUC-----U 36
dISFV-NC_016997.1 CAUUAGAAUAGGUUUGAAAGAGUUGAAUCA-----AUGAGAUCAAUGGUC 45
.....10.....20.....30.....40.....50.....6



(((((.....((((((((((((.....
dISFV-NC_040610.1 CUUGGAAAGACC---GUUGCAAGACGGUCUGGCAUAUUGCGAAAGC--GGAUUACCACCC 97
dISFV-NC_024017.1 UCAAGAAAGCCC---GCCGCAAAGCGGGCUGUAUAUUGCUAACAC--GCAUCACCAAGC 97
dISFV-NC_017086.1 CCCAAGAAAGCCC---GG---AAGACGGGCUACGUAUUGAGACGUGCGUUGCCUCGC 96
MBFV-NC_009028.2 CCAGGAAAGUCC---CGUCGAAAGCGGACUGUCAAUAUGCUAAAACGCCUGGCUAGCGUG 99
MBFV-NC_040776.1 CCAGGAGGACCC---GCCGGAAGGCGGGUUGUCAAUAUUGCUGAAACGCCAGCCAGCGUU 99
MBFV-NC_034151.1 CCAGGAGGACCC---GGAAAGAACC GGUGUCUAUAUUGCUGAAGCGCACAUCCCGCGCU 99
MBFV-NC_000943.1 CCAGGAGGACCC---GGGAAGCCCCGGGUCGCAUAUUGCUAAAACGCGGCAUACCCCGC 99
MBFV-NC_006551.1 CCAGGAGGGGCC---GGAAGAAACCGGGCCAUAUAUUGCUGAAACGCGGCAUACCCCGC 99
MBFV-NC_001563.2 CCAGGAGGGGCC---GGUAAAAACCGGGCUGUCAAUAUUGCUAAAACGCGGUAUGCCCGC 99
MBFV-NC_009942.1 CCAGGAGGGGCC---GGCAAGAGCCGGGCUUGUCAAUAUUGCUAAAACGCGGAAUGCCCGC 99
MBFV-NC_007580.2 CCAGGAAAACCC---GGUAGAAAACCGGGUUGUCAAUAUUGCUAAAACGCGGCGUAUCCCGC 99
MBFV-NC_009026.2 CCAGGAAGACCC---GGAGGAAAACCGGGUCGCAUAUUGGCUAAAGCGUACGGCGGCCAAC 99
MBFV-NC_009029.2 CCAGGAAGGCC---GGUAGAAAUCGGGCGCGCAUAUUGGCUAAAGCGCGGUGCGUCCCGC 99
MBFV-NC_032088.1 CCAGGAAAGUCC---GGCAAUCGUCGGACUGUCAAUAUUGCUAAAGCGCGGAGCAUCCCGC 99
MBFV-NC_012534.1 CCAGGAAAACCC---GGGGCAACCCGGGUUGUCAAUAUUGCUAAAGCGCGGUGCAUCC--- 100
MBFV-NC_015843.2 CCAGGAAGACCC---GGCUCAGGCCGGGUUGUCAAUAUUGCUAAAGCGCGGAAACGUCC--- 100
MBFV-NC_001437.1 CCAGGAGGGGCC---GGUAAAAACCGGGCUACUAUAUUGCUGAAACGCGGGCUACCCCGC 99
MBFV-NC_012532.1 GAAGAAAUC--C---GGAGA-UCCGGAUUGUCAAUAUUGCUAAAACGCGGAGUAGCCCGU 99
MBFV-NC_035889.1 AAAGAAAUC--C---GGAGGAUUCGGAUUGUCAAUAUUGCUAAAACGCGGAGUAGCCCGU 99
MBFV-NC_002640.1 GAAAAAAGG--U---GGUUGAGACC--ACCUUCAAUAUUGCUGAAACGCGAGAGAAACCGC 93
MBFV-NC_001477.1 GGAAAAAGA--C---GGGUCGACC--GUCUUCAAUAUUGCUGAAACGCGCGAGAAACCGC 96
MBFV-NC_001475.2 GGAAGAAGA--C---GGGAAAAAC--GUCUACUAUAUUGCUGAAACGCGGAGAGAAACCGU 96
MBFV-NC_001474.2 GGAAAAAGG--C---GAAAAACAC--GCCUUCAAUAUUGCUGAAACGCGAGAGAAACCGC 96
MBFV-NC_012533.1 CCAAAAAAG--G---GCCGCAUCGCGGCCUAUAUAUUGCUGAAGCGCUUUGGAUCUAGC 93
dISFV-NC_027999.1 AGAGUAGGAUUCUGGGGUAAAACCGGGUGUCAAUAUUGAU-----UAGCGCUACU 96
MBFV-NC_012735.1 AUGAAUAAGUCUCGGGCUCAUCCCGAGGCGCAUAUUGGU-----AGCGGCUAGA 96
MBFV-NC_008719.1 GCAAGCAAGUCUCGGGUCACGACCCGGGGCGCAUAUUGGU-----GACGGCCAAG 96
MBFV-NC_002031.1 GGUCGUAAGCUCAGGGAACCAACCCUGGGCGUCAAUAUUGGUACGACGAGGAGUUCGUCC 96
dISFV-NC_016997.1 UUUCGAGCUAGGAGGCCCGUAAAACGGGCGCGCAUAUAUAUAAAACGUAAGCUGC----- 100
0.....70.....80.....90.....100.....110.....1



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dISFV-NC_040610.1 G-CU---NNNNNNNNCUACUUAUUU-AUAUAACAGCAUAUUGACA-CCAGGG-AUAGACCG 150
dISFV-NC_024017.1 G-UG---NNNNNNNNCU-UCUGAGA-CAAAAUAAGCAUAUUGACA-CUUGGGAAGAGACCA 150
dISFV-NC_017086.1 GUCU---NNNNNNNCCAAAAAUG-A-AGGGCAUAUAUUGACACUUGGG--AAAGACCA 149
MBFV-NC_009028.2 U-----NNNNNNNNCAAGCGCGAAA--ACAAACAGCAUAUUGACG-CCUGGGA--AAGACC 148
MBFV-NC_040776.1 U-----NNNNNNNN-AAGCGCAA-GACAAACAGCAUAUUGACA-CCUGGGA--AAGACC 148
MBFV-NC_034151.1 A-----NNNNNNNGAA-CGCAAA-UAAAAACAGCAUAUUGACA-CCUGGGA--UAGACU 148
MBFV-NC_000943.1 G-----NNNNNNNNAAAAAGCAUC--AAACAACAGCAUAUUGACA-CCUGGGA--AAGACU 149
MBFV-NC_006551.1 G-----NNNNNNNN-UAAGCAUCA-AAAAAACAGCAUAUUGACA-CCUGGGAUUUAGACU 150
MBFV-NC_001563.2 G-----NNNNNNNNAAACACC-AA-AAGAAACAGCAUAUUGACA-CCUGGGA--UAGACU 148
MBFV-NC_009942.1 G-----NNNNNNNNAAACACCA-CA-ACAAACAGCAUAUUGACA-CCUGGGA--UAGACU 148
MBFV-NC_007580.2 G-----NNNNNNNNCCGUUAACGC-AAACAACAGCAUAUUGACA-CCUGGGA--AGACA 148
MBFV-NC_009026.2 G-----NNNNNNNN-ACGCACCAA-AAGAAACAGCAUAUUGACA-CCUGGGA--UAGACC 148
MBFV-NC_009029.2 G-----NNNNNNNN-AGCGCAAAC-ACAAAACAGCAUAUUGACA-CCUGGGA--AAGACU 148
MBFV-NC_032088.1 G-----NNNNNNNN-UACCGCAA-ACAAAACAGCAUAUUGACA-CCUGGGA--UAGACU 148
MBFV-NC_012534.1 -----NNNNNNNN-AACACCAAA-ACAAAACAGCAUAUUGACA-CCUGGGA--GAGACU 148
MBFV-NC_015843.2 -----NNNNNNNNGAACACCACA-A-GAAACAGCAUAUUGACA-CCUGGGA--UAGACU 148
MBFV-NC_001437.1 G-----NNNNNNNN-----CAUAUUGACA-CCUGGGA--UAGACU 131
MBFV-NC_012532.1 G-----NNNNNNNNCCCCGGAAAAACGCAAAACAGCAUAUUGAC--G-UGGGA--AAGACC 148
MBFV-NC_035889.1 G-----NNNNNNNN-CCCCGAAAACGCAAAACAGCAUAUUGAC--GCUGGGA--AAGACC 148
MBFV-NC_002640.1 GUAUCAANNNNNNNNCCCCCAACACA-AAAAACAGCAUAUUGAC--GCUGGGA--AAGACC 148
MBFV-NC_001477.1 GUGU---NNNNNNNNCCCCGCACAACAA-CAAACAGCAUAUUGAC--GCUGGGA--GAGACC 148
MBFV-NC_001475.2 GUGU---NNNNNNNNCCCCCGCAAAUA-AAAACAGCAUAUUGAC--GCUGGGA--GAGACC 148
MBFV-NC_001474.2 GUGU---NNNNNNNNCCCCCGAAACAA-AAAACAGCAUAUUGAC--GCUGGGA--AAGACC 148
MBFV-NC_012533.1 GCUGGCCNNNNNNNAUAACCAA--CAUAAAACAGCAUAUUGACA-CCUGGGA--AAGACC 148
dISFV-NC_027999.1 GGAA---NNNNNNNNCCAUUGGAAAUUAGCU--UCAUAUUGACA-CCAGGGAAAAGACCG 150
MBFV-NC_012735.1 GUGA---NNNNNNNNCC-GAGCACAUAGCGGACCAUAUUGACG-CCAGG-AAAGACCG 150
MBFV-NC_008719.1 GCCA---NNNNNNNNCC-GAGCAC-UAUAGCGGACCAUAUUGACG-CCUGGG-AAAGACCG 149
MBFV-NC_002031.1 UUGU---NNNNNNNNAGGGAACAAAU-AGUGGGACCAUAUUGACG-CCAGGG-AAAGACCG 150
dISFV-NC_016997.1 -----NNNNNNNNCAAA--AAUGUAUAGGCUAUUAUAUUGCA-CCUAGGAAAGACUGG 150
20.....130.....140.....150.....160.....170.....1



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dISFV-NC_040610.1 GAGAAAUACACAAUUUC----- 167
dISFV-NC_024017.1 GAGAU AUG-AUGUUGUU----- 167
dISFV-NC_017086.1 GAGGUACUCGCUGAUUCA----- 167
MBFV-NC_009028.2 GGGAGAU-CCUCUGCUUUCC----- 167
MBFV-NC_040776.1 GGGAGAC-CCUCUGCUCUCG----- 167
MBFV-NC_034151.1 GGGAGAC-CCUCUGCUUAU----- 167
MBFV-NC_000943.1 AGGAGAU-CUUCUGCUCUA----- 167
MBFV-NC_006551.1 AGGAGAU-CUUCUGCUCU----- 167
MBFV-NC_001563.2 AGGGGAU-CUUCUGCUCUG----- 167
MBFV-NC_009942.1 AGGAGAU-CUUCUGCUCUGC----- 167
MBFV-NC_007580.2 GGAGAU-CCCUGCUUUUU----- 167
MBFV-NC_009026.2 GGAGAAU-UUGCUGCCUCG----- 167
MBFV-NC_009029.2 AGGGGAU-UUGCUGCUCUG----- 167
MBFV-NC_032088.1 AGGAGAU-CCGUGCUCUG----- 167
MBFV-NC_012534.1 AGGAGAC-CCUCUGUCCUA----- 167
MBFV-NC_015843.2 AGGAGAC-CCUCUGUCCUA----- 167
MBFV-NC_001437.1 GGGAGAUUCUCUGCUCUAUCUAACAUAGCUACUA 167
MBFV-NC_012532.1 AGAGACUCCAUGAGUUUCC----- 167
MBFV-NC_035889.1 AGAGACUCCAUGAGUUUCC----- 167
MBFV-NC_002640.1 AGAGAUCCUGCUGUCUCUG----- 167
MBFV-NC_001477.1 AGAGAUCCUGCUGUCUCUA----- 167
MBFV-NC_001475.2 AGAGAUCCUGCUGUCUCU----- 167
MBFV-NC_001474.2 AGAGAUCCUGCUGUCUCU----- 167
MBFV-NC_012533.1 GGAGACUCUGUUGGCUU----- 167
dISFV-NC_027999.1 GAGAAACUUCUUGCUU-A----- 167
MBFV-NC_012735.1 GAGACACUCCUUGAUUC----- 167
MBFV-NC_008719.1 GAGACACUCCUUGAUUC----- 167
MBFV-NC_002031.1 GAGUGGUUCUCUGCUU-U----- 167
dISFV-NC_016997.1 AGAUACCUUUGGUUCU----- 167
80.....190.....200.....210.....

