

Supplemental Data S5: Alignment of the HSV-1 US11 Gene with the Length of Multiple 9 nt Longer Than HSV-1 Strain 17

NC_001806.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
OP297870.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
OQ102003.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTCTTAAAA	60
HM585510.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60

NC_001806.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
OP297870.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
OQ102003.1	GGCGCGCCGTCCACCGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
HM585510.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
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NC_001806.2	ATGATCTCCGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
OP297870.1	ATGATCTCCGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
OQ102003.1	ATGATCTCCGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
HM585510.2	ATGATCTCCGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180

NC_001806.2	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
OP297870.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
OQ102003.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
HM585510.2	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240

NC_001806.2	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCCGCGACCAACC	300
OP297870.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCCGCGACCAACC	300
OQ102003.1	CCGCCAACAAATCCCCAGGACGCGCGTGTTCGCCGGGAGCCCCGGGTTCCGCGACCAACC	300
HM585510.2	CCGCCAACAAATCCCCAGGACGCGCGTGTTCGCCGGGAGCCCCGGGTTCCGCGACCAACC	300
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NC_001806.2	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
OP297870.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
OQ102003.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
HM585510.2	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTCCCGCGTGAC	360

NC_001806.2	CCCAGGGATCCACGACAACCCCGGTCTCCCAGGGAGCCCCGGTCTCC-----CCGG	411
OP297870.1	CCCAGGGATCCACGACAACCCCGGGAGCCCCGGCCTCCCAGGGAGCCCCGGCCTCCCCGG	420
OQ102003.1	CCCAGGGATCCACGACAGTCCCGGTCTCCCAGGGAGCCCCGGGATCCACGACGCCCCGC	420
HM585510.2	CCCAGGGATCCACGACAACCCCGGGAGCCCCGGCCTCCCAGGGATCCACGACAACCCCGG	420
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NC_001806.2	GAG-----CCCCGGTCTCCC CGGG AGCCCCGACCCACGCACCCCC	453
OP297870.1	GAG-----CCCCGGCCTCCCAGGGAGCCCCGACCCACGCACCCCC	462
OQ102003.1	GAACCACGACAG-----CCCCGGTCTCCCAGGGAGCCCCGGGATCCACGACGCCCC	471
HM585510.2	GAGCCCCGGCCTCCCAGGGATCCACGACAACCCCGGGAGCCCCGACCCACGCACCCCC	480
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NC_001806.2	CGCGAACCACGTACGGCTCGCGGGTCTGTATAG	486
OP297870.1	CGCGAACCACGTACGGCTCGCGGGTCTGTATAG	495
OQ102003.1	CGCGAACCACGGACGGCTCGCGGGTCTGTATAG	504
HM585510.2	CGCGAACCACGTACGGCTCGCGGGTCTGTATAG	513
