

Supplemental Data S3: Alignment of the HSV-1 US11 Gene 9 nt Shorter Than HSV-1 Strain 17

NC_001806.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
OP297871.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
OQ658624.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MH160371.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
HM585507.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
HM585501.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
HM585503.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
HM585505.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60

NC_001806.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
OP297871.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
OQ658624.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MH160371.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
HM585507.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
HM585501.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
HM585503.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
HM585505.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120

NC_001806.2	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
OP297871.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
OQ658624.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
MH160371.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
HM585507.2	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
HM585501.2	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
HM585503.2	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
HM585505.2	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180

NC_001806.2	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
OP297871.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
OQ658624.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MH160371.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
HM585507.2	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
HM585501.2	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
HM585503.2	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
HM585505.2	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240

NC_001806.2	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCGCGGACCAACC	300
OP297871.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCGCGGACCAACC	300
OQ658624.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MH160371.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCGCGGACCAACC	300
HM585507.2	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCGCGGACCAACC	300
HM585501.2	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCGCGGACCAACC	300
HM585503.2	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCGCGGACCAACC	300
HM585505.2	CCGCCAACAAATCCCCAGGACACCGCGTGTTCGCCGGGAGCCCCGGGTTCGCGGACCAACC	300

NC_001806.2	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
OP297871.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
OQ658624.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
MH160371.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
HM585507.2	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
HM585501.2	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
HM585503.2	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
HM585505.2	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360

NC_001806.2	CCCAGGGATCCACGACAACCCCG GT CTCCAGGGAGCCCCGGTCTCC CG GGAGCCCCGG	420
OP297871.1	CCCAGGGATCCACGACAACCCCGGGA-----GCCCCGGCCTCCCCGGGAGCCCCGG	411
OQ658624.1	CCCAGGGATCCACGACAACCCCGGGA-----GCCCCGGCCTCCCCGGGAGCCCCGG	411
MH160371.1	CCCAGGGATCCACGACAACCCCGGGATCCACGACAA-----CCCCGGGAGCCCCGG	411
HM585507.2	CCCAGGGATCCACGACAACCCCGGGA-----GCCCCGGCCTCCCCGGGATCCACGA	411
HM585501.2	CCCAGGGATCCACGACAACCCCGGGA-----GCCCCGGCCTCCCCGGGATCCACGA	411
HM585503.2	CCCAGGGATCCACGACAACCCCGGGA-----GCCCCGGCCTCCCCGGGATCCACGA	411
HM585505.2	CCCAGGGATCCACGACAACCCCGGGA-----GCCCCGGCCTCCCCGGGATCCACGA	411

NC_001806.2	TCTCCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCACGTACGGCTCGCGGGTCT	480
OP297871.1	CCTCCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCACGTACGGCTCGCGGGTCT	471
OQ658624.1	CCTCCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCACGTACGGCTCGCGGGTCT	471
MH160371.1	CCTCCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCACGTACGGCTCGCGGGTCT	471
HM585507.2	CAACCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCACGTACGGCTCGCGGGTCT	471
HM585501.2	CAACCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCACGTACGGCTCGCGGGTCT	471
HM585503.2	CAACCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCACGTACGGCTCGCGGGTCT	471
HM585505.2	CAACCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCACGTACGGCTCGCGGGTCT	471

NC_001806.2	GTATAG	486
OP297871.1	GTATAG	477
OQ658624.1	GTATAG	477
MH160371.1	GTATAG	477
HM585507.2	GTATAG	477
HM585501.2	GTATAG	477
HM585503.2	GTATAG	477
HM585505.2	GTATAG	477
