

Supplemental Data S1: Alignment of the US11 Gene with the Same Gene Length of US11 Gene in HSV-1 Strain 17

NC_001806.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
X02138.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MH319852.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
OP297873.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
KR011283.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
X14112.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
KR011281.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MG646679.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
OP297879.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MH160384.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
JN420342.2	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MG999890.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MG999850.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MH999848.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MH160390.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
GU734772.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MG999839.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
JN420341.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
JN400093.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MG999872.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
JN420340.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
JN420339.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MN159383.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
JN420337.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
JN420338.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60
MH160388.1	ATGAGCCAGACCCAACCCCGGCCCCAGTTGGGCCGGGCGACCCAGATGTTTACTTAAAA	60

NC_001806.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
X02138.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MH319852.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
OP297873.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
KR011283.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
X14112.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
KR011281.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MG646679.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
OP297879.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MH160384.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
JN420342.2	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MG999890.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MG999850.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MH999848.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MH160390.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
GU734772.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MG999839.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
JN420341.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
JN400093.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MG999872.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
JN420340.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
JN420339.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MN159383.1	GGCATGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
JN420337.1	GGCATGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
JN420338.1	GGCATGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120
MH160388.1	GGCGTGCCGTCCGCCGGCATGCACCCAGAGGTGTTACGCACCTCGAGGACACCCGCGC	120

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MH319852.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
OP297873.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
KR011283.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
X14112.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
KR011281.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
MG646679.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
OP297879.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
MH160384.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
JN420342.2	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
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MG999850.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
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MH160390.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
GU734772.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
MG999839.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
JN420341.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
JN400093.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
MG999872.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
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JN420339.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
MN159383.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
JN420337.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
JN420338.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180
MH160388.1	ATGATCTCCGGACCCCCGCAACGGGGTGATAATGATCAAGCGGCGGGGCAATGTGGAGAT	180

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X02138.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MH319852.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
OP297873.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
KR011283.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
X14112.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
KR011281.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MG646679.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
OP297879.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MH160384.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
JN420342.2	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MG999890.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MG999850.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MH999848.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MH160390.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
GU734772.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MG999839.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
JN420341.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
JN400093.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MG999872.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
JN420340.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
JN420339.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
MN159383.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
JN420337.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
JN420338.1	TCGGGTCTACTACGAGTCGGTGCGGACACTACGATCTCGAAGCCATCTGAAGCCGTCCGA	240
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NC_001806.2	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
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MH319852.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
OP297873.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
KR011283.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
X14112.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
KR011281.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MG646679.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
OP297879.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MH160384.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
JN420342.2	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MG999890.1	CTGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MG999850.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MH999848.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MH160390.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
GU734772.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MG999839.1	CTGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
JN420341.1	CCGCCAACATTTCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
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MN159383.1	CCACCAACAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
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JN420338.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
MH160388.1	CCGCCAACAAATCCCCAGGACACCGCGTGTTCCTCCGGGAGCCCCGGGTTCGCGGACCAACC	300
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OP297873.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
KR011283.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
X14112.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
KR011281.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
MG646679.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
OP297879.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
MH160384.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
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GU734772.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
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MN159383.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTTCCAGAGACCCAGGGTACCGCGTGAC	360
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JN420338.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
MH160388.1	CGAGAACCTAGGGAACCCAGAGTACCGCGAGCTCCAGAGACCCAGGGTACCGCGTGAC	360
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MH319852.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCCCGGGAGCCCCGG	420
OP297873.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCCCGGGAGCCCCGG	420
KR011283.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCCCGGGAGCCCCGG	420
X14112.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCCCGGGAGCCCCGG	420
KR011281.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCCCGGGAGCCCCGG	420
MG646679.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCAGGGAGCCCCGG	420
OP297879.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCAGGGAGCCCCGG	420
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JN420342.2	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCAGGGAGCCCCGG	420
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GU734772.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCCCGGGAGCCCCGG	420
MG999839.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCCCGGGAGCCCCGG	420
JN420341.1	CCCAGGGATCCACGACAACCCCGGTCTCCAGGGAGCCCCGGTCTCCCCGGGAGCCCCGG	420
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JN420340.1	CCTCCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCAGTACGGCTCGCGGGTCT	480
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MN159383.1	TCTCCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCAGTACGGCTCGCGGGTCT	480
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JN420338.1	CCTCCCCGGGAGCCCCGGACCCACGCACCCCCCGCGAACCAGTACGGCTCGCGGGTCT	480
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MH319852.1	GTATAG	486
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MG646679.1	GTATAG	486
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MH160384.1	GTATAG	486
JN420342.2	GTATAG	486
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MH160390.1	GTATAG	486
GU734772.1	GTATAG	486
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