

## Electronic Supplementary Material

### **Reducing Viral Inhibition of Host Cellular Apoptosis Strengthens the Immunogenicity and Protective Efficacy of an Attenuated HSV-1 Strain**

Xingli Xu<sup>1</sup>, Yufeng He<sup>1</sup>, Shengtao Fan<sup>1</sup>, Min Feng<sup>1</sup>, Guorun Jiang<sup>1</sup>, Lichun Wang<sup>1</sup>, Ying Zhang<sup>1</sup>, Yun Liao<sup>1</sup>, Qihan Li<sup>1</sup>✉

1. Yunnan Key Laboratory of Vaccine Research and Development on Severe Infectious Diseases, Institute of Medical Biology, Chinese Academy of Medical Sciences and Peking Union Medical College, Kunming 650118, China

Supporting information to DOI: 10.1007/s12250-019-00156-7

**Table S1.** Primers used in plasmid and mutant strain construction

Primer name	Target	Assay	Sequence (5' to 3')
Us3-F	<i>Us3</i>	PCR	CGACCTGTATACCTATCTGAG
Us3-R	<i>Us3</i>	PCR	CGTCTATGTCCATCTTGTAGT
Us3-g-RNA-1F	<i>Us3</i>	PX330-g-RNA construction	CACCACCCCGAGGACATTTGCCT
Us3-g-RNA-1R	<i>Us3</i>	PX330-g-RNA construction	AAACAGGCAAATGTCCTCGGGGGT
Us3-g-RNA-2F	<i>Us3</i>	PX330-g-RNA construction	CACCACCGTCGACATTTGGAGCGC
Us3-g-RNA-2R	<i>Us3</i>	PX330-g-RNA construction	AAACGCGCTCCAAATGTGCGACGGT
Us5-F	<i>Us5</i>	PCR	AGAAACAGCACACGACTT
Us5-R	<i>Us5</i>	PCR	ACGGATTTTCCTGGTTAGC
Us5-g-RNA-1F	<i>Us5</i>	PX330-g-RNA construction	CACCGGGACCTGCGGCCAACACAA
Us5-g-RNA-1R	<i>Us5</i>	PX330-g-RNA construction	AAACTTGTGTTGGCCGCAGGTCCC
Us5-g-RNA-2F	<i>Us5</i>	PX330-g-RNA construction	CACCGGGGCGTTACCATCCCTACA
Us5-g-RNA-2R	<i>Us5</i>	PX330-g-RNA construction	AAACTGTAGGGATGGTAACGCCCC

**Table S2.** Primers used in RT-PCR reaction

Primer name	Target	Assay	Sequence (5' to 3')
Us3-sense1	<i>Us3</i> fragment1	PCR	CTCGTTGGTTGGCACTCA
Us3-AS1	<i>Us3</i> fragment1	PCR	ATCTGGATGGCTGCTGTC
Us3-sense2	<i>Us3</i> fragment2	PCR	GCAGCCATCCAGATTACC
Us3-AS2	<i>Us3</i> fragment2	PCR	GATACACCGACAAGAACCA
Us5-sense1	<i>Us5</i>	PCR	GAAACAGCACACGACTTG
Us5-AS1	<i>Us5</i>	PCR	GAGTTTGGACCCGACATC

**Table S3. Primers used in PCR reaction**

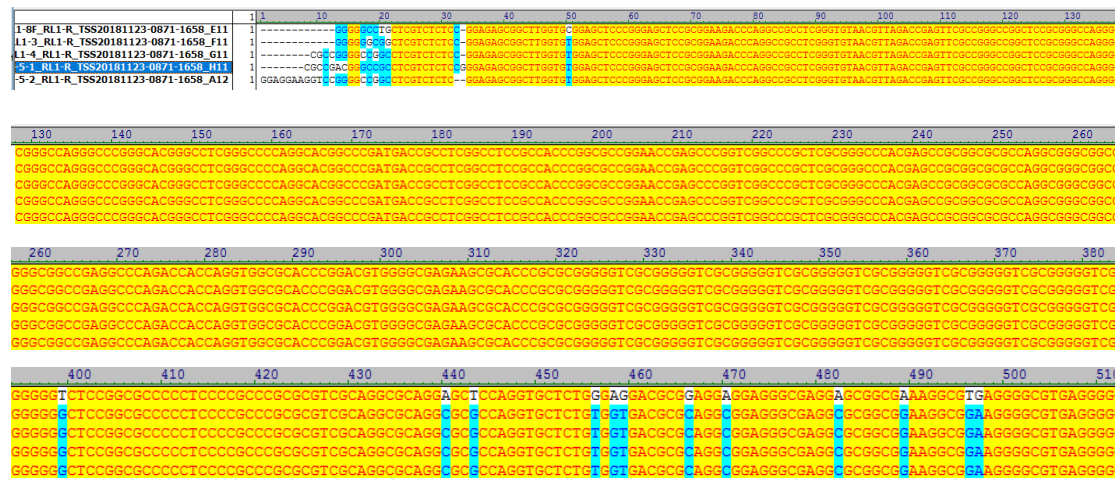
Primer name	Target	Assay	Sequence (5' to 3')
RL1-F	<i>RL1</i>	PCR	CCTTCTTGTTTCGCTGCTG
RL1-R	<i>RL1</i>	PCR	GCTGGCTCCAAGCGTATA
RL2-F	<i>RL2</i>	PCR	CGGATGTCTGGGTGTTTC
RL2-R	<i>RL2</i>	PCR	ATTGCCCGTCCAGATAAAG
RS1-F	<i>RS1</i>	PCR	ATGGCGTCGGAGAACAAG
RS1-R	<i>RS1</i>	PCR	ACGAGGACGAAGAGGATG
Us6-F	<i>Us6</i>	PCR	GCTCCTACAACAAGTCTCT
Us6-R	<i>Us6</i>	PCR	CGCATCCAGTACACAATTC
Us12-F	<i>Us12</i>	PCR	CACCTTCCTGGACACCAT
Us12-R	<i>Us12</i>	PCR	GCACCGACTCGTAGTAGA
UL5-F	<i>UL5</i>	PCR	CCATCAACACCATCTTTCAT
UL5-R	<i>UL5</i>	PCR	GTACTCCAGCACCTTCAT
UL15-F	<i>UL15</i>	PCR	CCTACTATAGCGTTCTGAATAC
UL15-R	<i>UL15</i>	PCR	GAGGCAAACACGATGGTA
UL23-F	<i>UL23</i>	PCR	CCGAGCCGATGACTTACT
UL23-R	<i>UL23</i>	PCR	TATACAGGTCGCCGTTGG
UL29-F	<i>UL29</i>	PCR	CGGACAAGGTAACCATAGG
UL29-R	<i>UL29</i>	PCR	ACGAGGAAGAAGCGGTAA
UL44-F	<i>UL44</i>	PCR	CCTCCAGATATGGCGTTAC
UL44-R	<i>UL44</i>	PCR	GGTAGAGACTGTGGTGAAC
UL48-F	<i>UL48</i>	PCR	TATGTACCATGCTCGATACC
UL48-R	<i>UL48</i>	PCR	ACAGAGGCAGTCAAACAG
UL49-F	<i>UL49</i>	PCR	CTTCAGGTATGGCGAGTC
UL49-R	<i>UL49</i>	PCR	CGTTGAGGTCTTCGTCTG

File S1. Sequence alignment results of *RS1*, *RL1*, *RL2*, *Us6*, *Us12*, *UL5*, *UL15*, *UL23*, *UL29*, *UL44*, *UL48*, and *UL49* genes in HSV-1 WT (8F), M3, M4, M5-P5, and M5-P15 strains.

RS1:



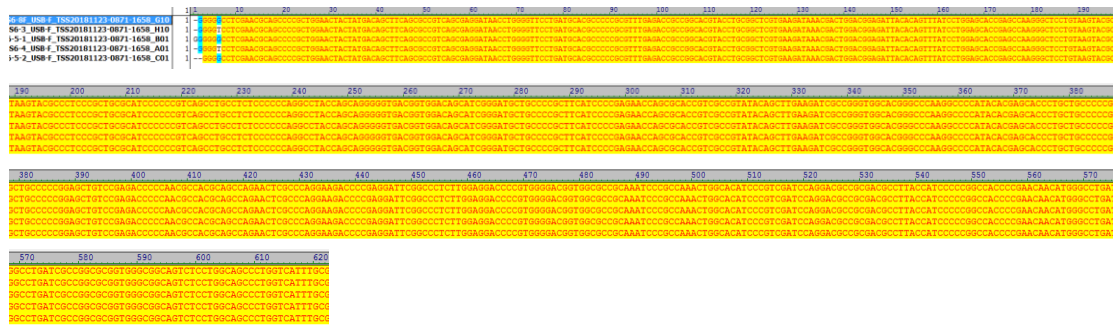
RL1:



RL2:



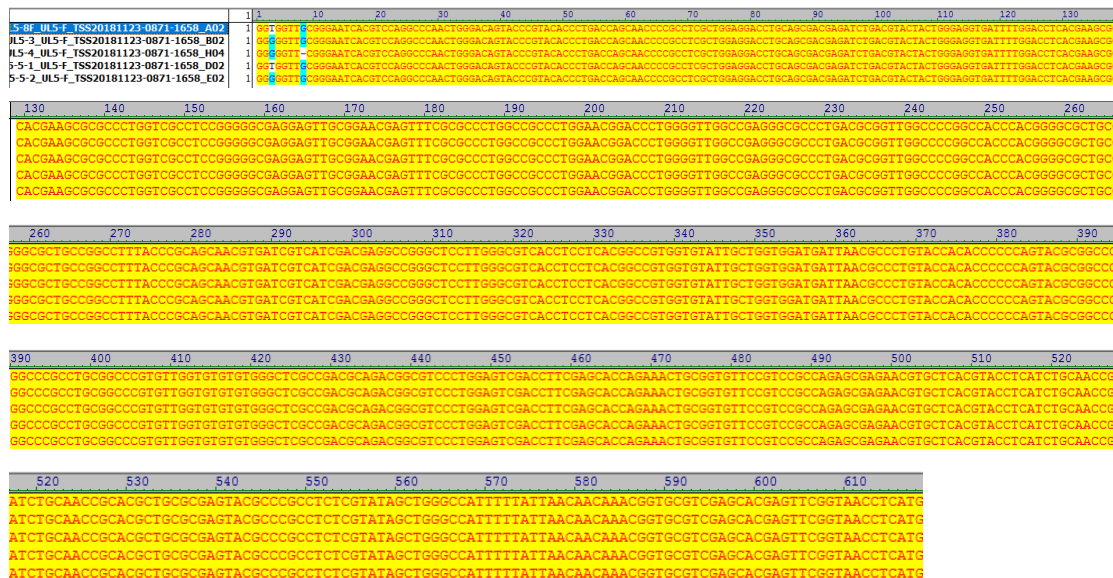
US6:



US12:



UL5



UL15:

15-8f_UL15-R_TSS20181123-0871-1658_F06	1	10	20	30	40	50	60	70	80	90	100	110	120	130
15-3_UL15-R_TSS20181123-0871-1658_G06	1	10	20	30	40	50	60	70	80	90	100	110	120	130
15-4_UL15-R_TSS20181123-0871-1658_H06	1	10	20	30	40	50	60	70	80	90	100	110	120	130
5-5-1_UL15-R_TSS20181123-0871-1658_A07	1	10	20	30	40	50	60	70	80	90	100	110	120	130
5-5-2_UL15-R_TSS20181123-0871-1658_B07	1	10	20	30	40	50	60	70	80	90	100	110	120	130

130	140	150	160	170	180	190	200	210	220	230	240	250	260
GTGGCCGCTG	AGCCGATCTT	GATCCCCGAAAGGAGG	CCAGGACAGGCGGAT	GAGGGCACCAGAAAC	CCAGGCTT	GGCGTGGCGCCGGGGAC	GAGAAAC	CCGTTGGCGGCT	GGCGAAAGTGGCCAC	GGC	GGCGGCT	GGCGAAAGTGGCCAC	GGC
GTGGCCGCTG	AGCCGATCTT	GATCCCCGAAAGGAGG	CCAGGACAGGCGGAT	GAGGGCACCAGAAAC	CCAGGCTT	GGCGTGGCGCCGGGGAC	GAGAAAC	CCGTTGGCGGCT	GGCGAAAGTGGCCAC	GGC	GGCGGCT	GGCGAAAGTGGCCAC	GGC
GTGGCCGCTG	AGCCGATCTT	GATCCCCGAAAGGAGG	CCAGGACAGGCGGAT	GAGGGCACCAGAAAC	CCAGGCTT	GGCGTGGCGCCGGGGAC	GAGAAAC	CCGTTGGCGGCT	GGCGAAAGTGGCCAC	GGC	GGCGGCT	GGCGAAAGTGGCCAC	GGC
GTGGCCGCTG	AGCCGATCTT	GATCCCCGAAAGGAGG	CCAGGACAGGCGGAT	GAGGGCACCAGAAAC	CCAGGCTT	GGCGTGGCGCCGGGGAC	GAGAAAC	CCGTTGGCGGCT	GGCGAAAGTGGCCAC	GGC	GGCGGCT	GGCGAAAGTGGCCAC	GGC

260	270	280	290	300	310	320	330	340	350	360	370	380	390
ACGGCCGCTG	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT
ACGGCCGCTG	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT
ACGGCCGCTG	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT
ACGGCCGCTG	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT	CTAAACAGGAGGAT

390	400	410	420	430	440	450	460	470	480	490	500	510	520
CTCCAGGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC
CTCCAGGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC
CTCCAGGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC
CTCCAGGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC	CGGCGCTG	GGCGTACGTC

520	530	540	550	560	570
CAAAGTGC	ACCAGCTGGCGAAAGGCTT	CGGAGCGGTGGAGGGCTT	GAACAGTATT	CAGG	
CAAAGTGC	ACCAGCTGGCGAAAGGCTT	CGGAGCGGTGGAGGGCTT	GAACAGTATT	CAGG	
CAAAGTGC	ACCAGCTGGCGAAAGGCTT	CGGAGCGGTGGAGGGCTT	GAACAGTATT	CAGG	
CAAAGTGC	ACCAGCTGGCGAAAGGCTT	CGGAGCGGTGGAGGGCTT	GAACAGTATT	CAGG	

UL23:

23-8f_UL23-f_TSS20181123-0871-1658_C03	1	10	20	30	40	50	60	70	80	90	100	110	120	130
L23-3_UL23-f_TSS20181123-0871-1658_D03	1	10	20	30	40	50	60	70	80	90	100	110	120	130
L23-4_UL23-f_TSS20181123-0871-1658_F03	1	10	20	30	40	50	60	70	80	90	100	110	120	130
P3-5-1_UL23-f_TSS20181123-0871-1658_F03	1	10	20	30	40	50	60	70	80	90	100	110	120	130
P3-5-2_UL23-f_TSS20181123-0871-1658_G03	1	10	20	30	40	50	60	70	80	90	100	110	120	130

130	140	150	160	170	180	190	200	210	220	230	240	250	260
CCGTGACCG	CGCGCTTCTGGCT	CTCATATCGGGGGGAGGCTGGGAGCT	CACATGCCCGCCCCCGCCCT	CACCTCATCTTCGACCGCCAT	CCCATGCCACCTT	CCTGTGTACCGGGCCGCGCAT							
CCGTGACCG	CGCGCTTCTGGCT	CTCATATCGGGGGGAGGCTGGGAGCT	CACATGCCCGCCCCCGCCCT	CACCTCATCTTCGACCGCCAT	CCCATGCCACCTT	CCTGTGTACCGGGCCGCGCAT							
CCGTGACCG	CGCGCTTCTGGCT	CTCATATCGGGGGGAGGCTGGGAGCT	CACATGCCCGCCCCCGCCCT	CACCTCATCTTCGACCGCCAT	CCCATGCCACCTT	CCTGTGTACCGGGCCGCGCAT							
CCGTGACCG	CGCGCTTCTGGCT	CTCATATCGGGGGGAGGCTGGGAGCT	CACATGCCCGCCCCCGCCCT	CACCTCATCTTCGACCGCCAT	CCCATGCCACCTT	CCTGTGTACCGGGCCGCGCAT							

260	270	280	290	300	310	320	330	340	350	360	370	380	390
GATACCTT	ATGGGCAGCATGAC	CCCCAGGCGCTGCTGGCGTT	CGCTTCCCTCAT	CCCGCCGACCTT	GCCCGGACAAACAT	CGTGTGGGGCCCTT	CCGAGGGGACAGACAT	CGACCGCT	GGCCAAACG				
GATACCTT	ATGGGCAGCATGAC	CCCCAGGCGCTGCTGGCGTT	CGCTTCCCTCAT	CCCGCCGACCTT	GCCCGGACAAACAT	CGTGTGGGGCCCTT	CCGAGGGGACAGACAT	CGACCGCT	GGCCAAACG				
GATACCTT	ATGGGCAGCATGAC	CCCCAGGCGCTGCTGGCGTT	CGCTTCCCTCAT	CCCGCCGACCTT	GCCCGGACAAACAT	CGTGTGGGGCCCTT	CCGAGGGGACAGACAT	CGACCGCT	GGCCAAACG				
GATACCTT	ATGGGCAGCATGAC	CCCCAGGCGCTGCTGGCGTT	CGCTTCCCTCAT	CCCGCCGACCTT	GCCCGGACAAACAT	CGTGTGGGGCCCTT	CCGAGGGGACAGACAT	CGACCGCT	GGCCAAACG				

390	400	410	420	430	440	450	460	470	480	490	500	510	520
ICGCCAGCC	CCCCGGCAGCGCTT	GACCTGGCTATGCTGGCCGCA	TTCGCCGCTT	ACGGCTGCTT	GCCAATACGGT	CGGATCT	TCAGGGCCGGCGGCT	CGTGGCGGAGGAT	GGGGACAGCTT	CGGGG			
ICGCCAGCC	CCCCGGCAGCGCTT	GACCTGGCTATGCTGGCCGCA	TTCGCCGCTT	ACGGCTGCTT	GCCAATACGGT	CGGATCT	TCAGGGCCGGCGGCT	CGTGGCGGAGGAT	GGGGACAGCTT	CGGGG			
ICGCCAGCC	CCCCGGCAGCGCTT	GACCTGGCTATGCTGGCCGCA	TTCGCCGCTT	ACGGCTGCTT	GCCAATACGGT	CGGATCT	TCAGGGCCGGCGGCT	CGTGGCGGAGGAT	GGGGACAGCTT	CGGGG			
ICGCCAGCC	CCCCGGCAGCGCTT	GACCTGGCTATGCTGGCCGCA	TTCGCCGCTT	ACGGCTGCTT	GCCAATACGGT	CGGATCT	TCAGGGCCGGCGGCT	CGTGGCGGAGGAT	GGGGACAGCTT	CGGGG			

520	530	540	550	560	570	580	590	600	610	620		
TTTCGGGG	ACGGCCGTGCCGCC	CCAGGGTGC	CCGAGCCCA	GAGCAAC	CGGGCCAC	GACCCCAT	ATCGGGGAC	ACGTTA	TTTACCCT	GTTTCGGGCC	CCCGAGTT	GCTGGCCC
TTTCGGGG	ACGGCCGTGCCGCC	CCAGGGTGC	CCGAGCCCA	GAGCAAC	CGGGCCAC	GACCCCAT	ATCGGGGAC	ACGTTA	TTTACCCT	GTTTCGGGCC	CCCGAGTT	GCTGGCCC
TTTCGGGG	ACGGCCGTGCCGCC	CCAGGGTGC	CCGAGCCCA	GAGCAAC	CGGGCCAC	GACCCCAT	ATCGGGGAC	ACGTTA	TTTACCCT	GTTTCGGGCC	CCCGAGTT	GCTGGCCC
TTTCGGGG	ACGGCCGTGCCGCC	CCAGGGTGC	CCGAGCCCA	GAGCAAC	CGGGCCAC	GACCCCAT	ATCGGGGAC	ACGTTA	TTTACCCT	GTTTCGGGCC	CCCGAGTT	GCTGGCCC

UL29:

29-8f_UL29-F_TSS20181123-0871-1658_H03	1	1	10	20	30	40	50	60	70	80	90	100	110	120	130
L29-3_UL29-F_TSS20181123-0871-1658_A04	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
L29-4_UL29-F_TSS20181123-0871-1658_B04	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19-5-1_UL29-F_TSS20181123-0871-1658_C04	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
19-5-2_UL29-F_TSS20181123-0871-1658_D04	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

130 140 150 160 170 180 190 200 210 220 230 240 250 260

260 270 280 290 300 310 320 330 340 350 360 370 380 390

390 400 410 420 430 440 450 460 470 480 490 500 510 520

520 530 540 550 560 570 580 590 600 610 620 630 640 650

UL44

14-8_UL44-F_TSS20181123-0871-1658_E04	54	60	70	80	90	100	110	120	130	140	150	160	170	180	190
14-3_UL44-F_TSS20181123-0871-1658_F04	54	54	54	54	54	54	54	54	54	54	54	54	54	54	54
14-4_UL44-F_TSS20181123-0871-1658_G04	54	54	54	54	54	54	54	54	54	54	54	54	54	54	54
5-2_UL44-F_TSS20181123-0871-1658_A01	60	60	60	60	60	60	60	60	60	60	60	60	60	60	60

190 200 210 220 230 240 250 260 270 280 290 300 310 320

320 330 340 350 360 370 380 390 400 410 420 430 440 450

450 460 470 480

UL48

8-8_UL48-F_TSS20181123-0871-1658_B01	116	120	130	140	150	160	170	180	190	200	210	220	230	240	250
8-3_UL48-F_TSS20181123-0871-1658_C01	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116
8-4_UL48-F_TSS20181123-0871-1658_D01	116	116	116	116	116	116	116	116	116	116	116	116	116	116	116
5-1_UL48-F_TSS20181123-0871-1658_E01	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117
5-2_UL48-F_TSS20181123-0871-1658_F01	118	118	118	118	118	118	118	118	118	118	118	118	118	118	118

260 270 280 290 300 310 320 330 340 350 360 370 380 390

390 400 410 420 430 440 450 460 470 480 490 500 510





**File S2.** Sequencing results of the full length mRNA of *Us3*–WT, *Us3*–MU, *Us5*–WT, and *Us5*–MU (the red marked areas are the deleted regions).

**Us3-WT:**

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1   ATGGCCTGTC GTAAGTTTTG TCGCGTTTAC GGGGGACAGG GCAGGAGGAA GGAGGAGGCC
61  GTCCC GCCG AGACAAAGCC GTCCCGGGTG TTTCTCATG GCCCCTTTA TACCCAGCC
121 GAGGACGCGT GCCTGGACTC CCCGCCCCG GAGACCCCA AACCTTCCA CACCACACCA
181 CCCGGCGATG CCGAGCGCCT GTGTCATCTG CAGGAGATCC TGGCCAGAT GTACGGAAAC
241 CAGGACTACC CCATAGAGGA CGACCCAGC GCGGATGCCG CGGACGATGT CGACGAGGAC
301 GCCCGGACG ACGTGGCCTA TCCGGAGGAA TACGCAGAGG AGCTTTTTCT GCCCGGGAC
361 GCGACCGGTC CCCTTATCGG GGCCAACGAC CACATCCCTC CCCCGCGTGG CGCATCTCCC
421 CCCGGTATAC GACGACGCAG CCGGGATGAG ATTGGGGCCA CGGGATTAC CGCGGAAGAG
481 CTGGACGCCA TGGACAGGGA GCGGCTCGA GCCATCAGCC GCGGCGGCAA GCCCCCTCG
541 ACCATGGCCA AGCTGGTGAC TGGCATGGG CTTACGATCC ACGGAGCGCT CACCCAGGA
601 TCGGAGGGGT GTGTCTTGA CAGCAGCCAT CCAGATTACC CCAACGGGT AATCGTGAAG
661 GCGGGGTGGT ACACGAGCAC GAGCCACGAG GCGGACTGC TGAGGCGACT GGACCACCCG
721 GCGATCCTGC CCTCCTGGA CCTGCATGTC GTCTCCGGG TCACGTGTCT GGTCTCCCC
781 AAGTACCAGG CCGACCTGTA TACCTATCTG AGTAGGCGCC TGAACCCACT GGGACGCCCG
841 CAGATCGCAG CGGTCTCCG GCAGCTCCTA AGCGCCGTTG ACTACATTCA CCGCCAGGGC
901 ATTATCCACC GCGACATTA GACCGAAAAT ATTTTATTA ACACCCCGA GGACATTTG
961 CTGGGGGACT TTGGTGCCG GTGCTTCGTG CAGGGTCCC GATCAAGCCC CTCCCTAC
1021 GGAATCGCCG GAACCATCGA CACCAACGCC CCCGAGGTCC TGGCCGGGGA TCCGTATACC
1081 ACGACCGTGG ACATTTGGAG CGCCGGTCTG GTGATCTTCG AACTGCCGT CCACAACGCG
1141 TCCTTGTCT CGCCCCCG CGGCCCAA AGGGGCCCGT GCGACAGTCA GATCACCCGC
1201 ATCATCCGAC AGGCCAGGT CCACGTTGAC GAGTTTTCC CGCATCCAGA ATCGCGCTC
1261 ACCTCGGCT ACCGCTCCG CGCGCCGGG AACAATCGC CGCCTTACAC CCGACCGGCC
1321 TGGACCGCT ACTACAAGAT GGACATAGAC GTCGAATATC TGGTTTGAA AGCCCTCACC
1381 TTCGACGGCG CGCTTCGCC CAGCGCCGA GAGCTGCTT GTTTGCCGCT GTTCAACAA
1441 AAATGA

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**Us3-MU:**

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1   ATGGCCTGTC GTAAGTTTTG TCGCGTTTAC GGGGGACAGG GCAGGAGGAA GGAGGAGGCC
61  GTCCC GCCG AGACAAAGCC GTCCCGGGTG TTTCTCATG GCCCCTTTA TACCCAGCC
121 GAGGACGCGT GCCTGGACTC CCCGCCCCG GAGACCCCA AACCTTCCA CACCACACCA
181 CCCGGCGATG CCGAGCGCCT GTGTCATCTG CAGGAGATCC TGGCCAGAT GTACGGAAAC
241 CAGGACTACC CCATAGAGGA CGACCCAGC GCGGATGCCG CGGACGATGT CGACGAGGAC
301 GCCCGGACG ACGTGGCCTA TCCGGAGGAA TACGCAGAGG AGCTTTTTCT GCCCGGGAC
361 GCGACCGGTC CCCTTATCGG GGCCAACGAC CACATCCCTC CCCCGCGTGG CGCATCTCCC
421 CCCGGTATAC GACGACGCAG CCGGGATGAG ATTGGGGCCA CGGGATTAC CGCGGAAGAG
481 CTGGACGCCA TGGACAGGGA GCGGCTCGA GCCATCAGCC GCGGCGGCAA GCCCCCTCG
541 ACCATGGCCA AGCTGGTGAC TGGCATGGG CTTACGATCC ACGGAGCGCT CACCCAGGA

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601 TCGGAGGGGT GTGTCTTTGA CAGCAGCCAT CCAGATTACC CCCAACGGGT AATCGTGAAG  
 661 GCGGGGTGGT ACACGAGCAC GAGCCACGAG GCGCGACTGC TGAGGCGACT GGACCACCCG  
 721 GCGATCCTGC CCCTCCTGGA CCTGCATGTC GTCTCCGGGG TCACGTGTCT GGTCTCCCC  
 781 AAGTACCAGG CCGACCTGTA TACCTATCTG AGTAGGCGCC TGAACCCACT GGGACGCCCC  
 841 CAGATCGCAG CGGTCTCCCG GCAGCTCCTA AGCGCCGTTG ACTACATTCA CCGCCAGGGC  
 901 ATTATCCACC GCGACATTAA GACCGAAAAT ATTTTATTA ACACCCCGA GGACATTTGG  
 961 TCTGGTGATC TTCGAGACTG CCGTCCACAA CGCGTCCTTG TTCTCGGCC CCCGCGGCC  
 1021 CAAAAGGGGC CCGTGCGACA GTCAGATCAC CCGCATCATC CGACAGGCC AGGTCCACGT  
 1081 TGACGAGTTT TCCCCGCATC CAGAATCGCG CCTCACCTCG CGTACCGCT CCCGCGCGGC  
 1141 CGGGAACAAT CGCCCGCTT ACACCCGACC GGCCTGGACC CGTACTACA AGATGGACAT  
 1201 AGACGTCGAA TATCTGGTTT GCAAAGCCCT CACCTTCGAC GGCGCGCTTC GCCCAGCGC  
 1261 CGCAGAGCTG CTTTGTTCG CGCTGTTCA ACAGAAATGA

**Us5-WT:**

1 ATGTCTCTGC GCGCAGTCTG GCATCTGGGG CTTTGGGAA GCCTCGTGGG GGCTGTTCTT  
 61 GCCGCCACCC ATCTGGGACC TGCGGCCAAC A**CAACGGACC CCTTAACGCA CGCCCCAGTG**  
**121 TCCCCTACC CCAGCCCCCT GGGGGGCTTT GCCGTCCCC TCGTAGTCGG TGGGCTGTGC**  
**181 GCCGTAGTCC TGGGGGCGGC GTGTCTGCTT GAGCTCTGC GTCGTACGTG CCGCGGGTGG**  
**241 GGGCGTTACC ATCCCTACAT GGACCCAGTT GTCGTATAA**

**Us5-MU:**

1 ATGTCTCTGC GCGCAGTCTG GCATCTGGGG CTTTGGGAA GCCTCGTGGG GGCTGTTCTT  
 61 GCCGCCACCC ATCGGGGACC TGCGGCCAAC A