

Supplementary Table 1 : Primer sequences and amplicon positions of the *UL69* HCMV-DB gene screened in CTH cells using qualitative and/or quantitative PCR.

Gene	Primers Sequence	Amplicon positions
UL69	FWD: 5' ATCATCACGCACAACACCCT 3' RVS: 5' AGACGACTCGGTGGTAATGC 3'	99368-99475
	FWD: 5' ATCATCACGCACAACACCCT 3' RVS: 5' TAACTTGATGACGCCGTCGC 3'	99368-99606
	FWD: 5' AGTCGGTACCCGAGTCGTCTTCTTGCGGTA 3' RVS: 5' CGGACGTGAATTCTTATCTTCCCTGAGCGAGCG 3'	99465-101580
	FWD: 5' CGAGTCGTCTTCTTGCGGTA 3' RVS: 5' TAACTTGATGACGCCGTCGC 3'	99466-99625
	FWD: 5' TGCCGTCGTACTGTGATTACC 3' RVS: 5' GGGACACCGTCGTCTACAAG 3'	99517-99710
	FWD: 5' GCGACGGCGTCATCAAGTTA 3' RVS: 5' CAACCACAGCAGCACTACTC 3'	99606-99807
	FWD: 5' TCTTGTAGACGACGGTGTCC 3' RVS: 5' CAACGCTGACAGCCTACGA 3'	99690-99902
	FWD: 5' GGGATGTCGATGACTCCCTTC 3' RVS: 5' GTCGCTATTGGATCTCACCGT 3'	99850-100048
	FWD: 5' TGTCAGCGTTGCTGGGTC 3' RVS: 5' CAGCAACCATGCCACTGC 3'	99892-100000
	FWD: 5' GAATTTGGTCTCCTCCCCGC 3' RVS: 5' AACCCGCACGATCCCTATCT 3'	99951-100542
	FWD: 5' GACTAACCGTTTGAGCGTGC 3' RVS: 5' GCAAGCTGGTGGTGAAAAG 3'	100402-100664
	FWD: 5' AGCCCAGGTCCAAGTTGTTG 3' RVS: 5' TTCGATTGGCTGGAGGAACC 3'	100461-100692
	FWD: 5' GCCCAGGTCCAAGTTGTTGA 3' RVS: 5' GCAAGCTGGTGGTGAAAAG 3'	100462-100664
	FWD: 5' AGCTGAGCGTTTCGTCGAT 3' RVS: 5' AGTCTACGTCTGGCACCCCT 3'	100578-100830
	FWD: 5' CTCGTCGTGTGAACAGCAGGATG 3' RVS: 5' GAACTACAGCAACTCAGCCGTTTGA 3'	100732-100959
	FWD: 5' CGATCAAACGGCTGAGTTGC 3' RVS: 5' ACATAGGGCGTCCTCCTCTT 3'	100932-101236
	FWD: 5' TCGCTTGAAAGAGGAGGACG 3' RVS: 5' GCGAATACCATCTCGCGGAA 3'	101209-101444
	FWD: 5' GGGGAGGAGGATAGTGGTCC 3' RVS: 5' TTATCTTCCCTGAGCGAGCG 3'	101313-101561
	FWD: 5' TCGCCTTCGGTATCATCGTC 3' RVS: 5' TTATCTTCCCTGAGCGAGCG 3'	101336-101580

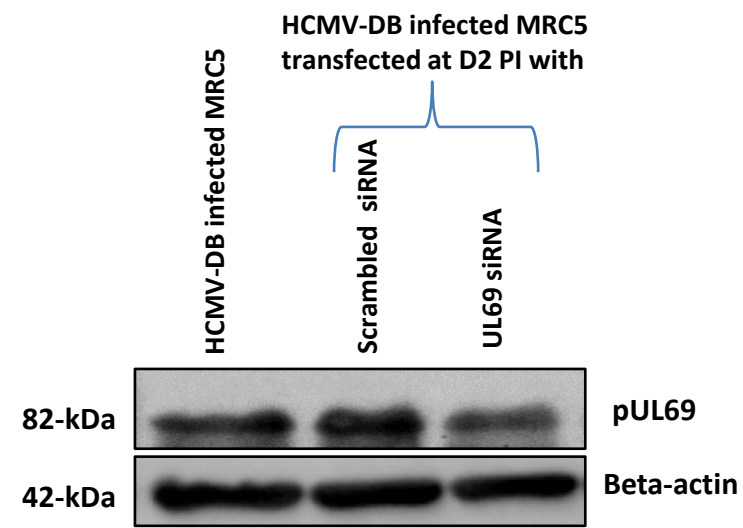
Human herpesvirus 5 strain DB, complete genome

Sequence ID: [KT959235.1](#) Length: 235512 Number of Matches: 1Range 1: 99397 to 101619 [GenBank](#) [Graphics](#)[Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
4050 bits(2193)	0.0	2213/2223(99%)	0/2223(0%)	Plus/Plus
Query 1	TTAGTCATCCATATCATCGCTGTAAACACAGCATGTCCTCGTAATCGGGCGTCTGGCAACG	68		
Sbjct 99397	TTAGTCATCCATATCATCGCTGTAAACACAGCATGTCCTCGTAATCGGGCGTCTGGCAACG	99456		
Query 61	CATTACCACCGAGTCGTCTTCTGCGGTACCGGTGGTGGCGCGGCTGCTGCTGGGT	120		
Sbjct 99457	CATTACCACCGAGTCGTCTTCTGCGGTACCGGTGGTGGCGCGGCTGCTGCTGGGT	99516		
Query 121	TGCCGTCGTACTGTGATTACCGTGGCGGATGCACCGGATGATGGGCTGCTGTGGGG	180		
Sbjct 99517	TGCCGTCGTACTGTGATTACCGTGGCGGATGCACCGGATGATGGGCTGCTGTGGGG	99576		
Query 181	AACCTGGGGTGGACTGCCGCCGTGAGAAGGCGACGGCGTCATCAAGTTAAGTCACCAACG	240		
Sbjct 99577	AACCTGGGGTGGACTGCCGCCGTGAGAAGGCGACGGCGTCATCAAGTTAAGTCACCAACG	99636		
Query 241	GTGACTCCGGACACCGGCGAGGGGCGCCGGGGGACTGGGAGGACCGCGGTCGTCTTGTA	300		
Sbjct 99637	GTGACTCCGGACACCGGCGAGGGGCGCCGGGGGACTGGGAGGACCGCGGTCGTCTTGTA	99696		
Query 301	GACGACGGTGTCCCCGTGCGATCCGTGGCTCGTACCAGATCTTGACTGCTAGCGTCGTC	360		
Sbjct 99697	GACGACGGTGTCCCCGTGCGATCCGTGGCTCGTACCAGATCTTGACTGCTAGCGTCGTC	99756		
Query 361	ACTGTCTTCGTCTCTTCCAGCTCGCCCTCAGAGTAGTGCTGCTGTGGTTGCGACGGTGG	420		
Sbjct 99757	ACTGTCTTCGTCTCTTCCAGCTCGCCCTCAGAGTAGTGCTGCTGTGGTTGCGACGGTGG	99816		
Query 421	CTGGCGGGAGGAGCGGCGGCGATCAATTGGAGAGGATGTGATGACTCCCTTCTCTGTC	480		
Sbjct 99817	CTGGCGGGAGGAGCGGCGGCGATCAATTGGAGAGGATGTGATGACTCCCTTCTCTGTC	99876		
Query 481	CTTTTATCGTAGGCTGTGAGCGTTGCTGGGTCGCTCTGCTTTCCATATTGCGCATTG	540		
Sbjct 99877	CTTTTATCGTAGGCTGTGAGCGTTGCTGGGTCGCTCTGCTTTCCATATTGCGCATTG	99936		
Query 541	CTCATCGGTGGGATGAATTTGGTCTCTCCCGCTGTGTGTCGCGGCGAGTGGGTGGTT	600		
Sbjct 99937	CTCATCGGTGGGATGAATTTGGTCTCTCCCGCTGTGTGTCGCGGCGAGTGGGTGGTT	99996		
Query 601	GCTGGCGGTGTGTTGTGTCGTAACGGCAAGACGGTGAGATCCAATAGCGACTGCTCGTC	660		
Sbjct 99997	GCTGGCGGTGTGTTGTGTCGTAACGGCAAGACGGTGAGATCCAATAGCGACTGCTCGTC	100056		
Query 661	GAAGGGACAGTACGCTATCATGAAACGATAGGGTGCCAAACGCGCGTTGGATGCGCAGTTC	720		
Sbjct 100057	GAAGGGACAGTACGCTATCATGAAACGATAGGGTGCCAAACGCGCGTTGGATGCGCAGTTC	100116		
Query 721	GCACATCTCGTTCTGACACTCGTGGCACTGCAGGGCGCCTAGGATCAGGTCCGAGACAGC	780		
Sbjct 100117	GCACATCTCGTTCTGACACTCGTGGCACTGCAGGGCGCCTAGGATCAGGTCCGAGACAGC	100176		
Query 781	GCCGACGCGGTAGGTACCATGGCGTTGTAGTATCGAACTGGTCAAAAAATTGGGGCGT	840		
Sbjct 100177	GCCGACGCGGTAGGTACCATGGCGTTGTAGTATCGAACTGGTCAAAAAATTGGGGCGT	100236		
Query 841	ACCGGTGACTTGCAACGCGCGACGGCGTAGCGAGACGGCCACGCGGAGAAGAGCACAC	900		
Sbjct 100237	ACCGGTGACTTGCAACGCGCGACGGCGTAGCGAGACGGCCACGCGGAGAAGAGCACAC	100296		
Query 901	GTAGGCCATGGCGCGGTGATGGGTGCGAGAAAGTCTCGGGCGGACGCTTCTGCAAGTC	960		
Sbjct 100297	GTAGGCCATGGCGCGGTGATGGGTGCGAGAAAGTCTCGGGCGGACGCTTCTGCAAGTC	100356		
Query 961	GCAGACGTCGTCGCGTAGCCAGGCGCTCATTTGACCGGGCTTCTGACTAACCGTTTGAG	1020		
Sbjct 100357	GCAGACGTCGTCGCGTAGCCAGGCGCTCATTTGACCGGGCTTCTGACTAACCGTTTGAG	100416		

Query 1021	CGTGTGCAATGGTCGCCCCAGCCGCTCTGGTGGTCCAGGATGCAGCCAGGTCCAGGTT	1080
Sbjct 100417	CGTGTGCAATGGTCGCCCCAGCCGCTCTGGTGGTCCAGGATGCAGCCAGGTCCAGGTT	100476
Query 1081	GTGAGTGTGTTGAAGAGCAGCTGACGCATGCCGCCACCCTCTCCAGATAGGGATCGTG	1140
Sbjct 100477	GTGAGTGTGTTGAAGAGCAGCTGACGCATGCCGCCACCCTCTCCAGATAGGGATCGTG	100536
Query 1141	CGGGTTGACGGGTAGCCCGTGCAAGTGGTGGTACTTCATGTAGCTGAGCGTTCTGTCGAT	1200
Sbjct 100537	CGGGTTGACGGGTAGCCCGTGCAAGTGGTGGTACTTCATGTAGCTGAGCGTTCTGTCGAT	100596
Query 1201	GATGGCCAGCAACGTGTGCAAGTGGGAGCGTTGTACACGGCGAAGATCTTCCACCAC	1260
Sbjct 100597	GATGGCCAGCAACGTGTGCAAGTGGGAGCGTTGTACACGGCGAAGATCTTCCACCAC	100656
Query 1261	CAGCTTGCAGCAGCAACGGTTCCTCCAGCAATCGAATGTTGACGGATGTGCAACAGGTA	1320
Sbjct 100657	CAGCTTGCAGCAGCAACGGTTCCTCCAGCAATCGAATGTTGACGGATGTGCAACAGGTA	100716
Query 1321	GTGCGTGTGCATGAGCTCGTCGTGTGACAGCAGGATGCGACCGCGCGGCTGATGATCTTG	1380
Sbjct 100717	GTGCGTGTGCATGAGCTCGTCGTGTGACAGCAGGATGCGACCGCGCGGCTGATGATCTTG	100776
Query 1381	CGGGAAGGCGGTGGGACCTTGAGATCGGCGGGGTAGGGTGCCAGACGTAGACTCTCGGC	1440
Sbjct 100777	CGGGAAGGCGGTGGGACCTTGAGATCGGCGGGGTAGGGTGCCAGACGTAGACTCTCGGC	100836
Query 1441	CGTGTAGCGCTGAAGGTGATAGACGGGCGAGGTAGAATCGGTGAGGTACCGGACGAGGC	1500
Sbjct 100837	CGTGTAGCGCTGAAGGTGATAGACGGGCGAGGTAGAATCGGTGAGGTACCGGACGAGGC	100896
Query 1501	GGCGCCGCGCTGCAGACGCGCTCTTTTTCGATCAAAACGGCTGAGTTGCTGTAG	1560
Sbjct 100897	GGCGCCGCGCTGCAGACGCGCTCTTTTTCGATCAAAACGGCTGAGTTGCTGTAG	100956
Query 1561	TTGTCCTCTGCTCATGGCGTCCAGTTGCTGTCGAATAAGCGCCAGCATCTGTTGTTG	1620
Sbjct 100957	TTGTCCTCTGCTCATGGCGTCCAGTTGCTGTCGAATAAGCGCCAGCATCTGTTGTTG	101016
Query 1621	CGGTCCGCGGACGATCCGTGATGATTATTGGCTGAGGAGGGGTGAGAAGAACCGAAAGT	1680
Sbjct 101017	CGGTCCGCGGACGATCCGTGATGATTATTGGCTGAGGAGGGGTGAGAAGAACCGAAAGT	101076
Query 1681	CGTAGGACAACCTGGGAACTCGGCGACGAAGATGCGTCAATCGCCGCGGTGATGGTCGG	1740
Sbjct 101077	CGTAGGACAACCTGGGAACTCGGCGACGAAGATGCGTCAATCGCCGCGGTGATGGTCGG	101136
Query 1741	TTGCGCGTCATCGTTGTGTAAGACTTACCGTAGTGGGGGTGAAGGGGACCGAGGCGGA	1800
Sbjct 101137	TTGCGCGTCATCGTTGTGTAAGACTTACCGTAGTGGGGGTGAAGGGGACCGAGGCGGA	101196
Query 1801	CGCGGCCACGCGTCGCTTGAAGAGGAGGACGCCCTATGTCGCGCACGGAAGCCGCGGT	1860
Sbjct 101197	CGCGGCCACGCGTCGCTTGAAGAGGAGGACGCCCTATGTCGCGCACGGAAGCCGCGGT	101256
Query 1861	GCCCATGATGATGTGTCGCGCGGTGCCCGGAGTGGCTGGCGGAGGAGGGTGAAGGGG	1920
Sbjct 101257	GCCCATGATGATGTGTCGCGCGGTGCCCGGAGTGGCTGGCGGAGGAGGGTGAAGGGG	101316
Query 1921	AGGAGGATAGTGGTCCGGATCGCTTCGGTATCATCGTCTTGTGTAGCGGGGTGTCG	1980
Sbjct 101317	AGGAGGATAGTGGTCCGGATCGCTTCGGTATCATCGTCTTGTGTAGCGGGGTGTCG	101376
Query 1981	TGCGGGGACGAGGGTCGGTGAATGAGGAGGCGGCCGACGGTATCTTCCGCGAGATG	2040
Sbjct 101377	TGCGGGGACGAGGGTCGGTGAATGAGGAGGCGGCCGACGGTATCTTCCGCGAGATG	101436
Query 2041	GTAATCGCTGGCGGCTGCTCCGTTCGGTGTGACGGCGAGGTGGACTTCGCTCGCGTCG	2100
Sbjct 101437	GTAATCGCTGGCGGCTGCTCCGTTCGGTGTGACGGCGAGGTGGACTTCGCTCGCGTCG	101496
Query 2101	GAATTCCTGGGACGGGTTCTGTAATCCAGACAGAAGCGCCGTGCGCGACGGGCGCGGG	2160
Sbjct 101497	GAATTCCTGGGACGGGTTCTGTAATCCAGACAGAAGCGCCGTGCGCGACGGGCGCGGG	101556
Query 2161	TTGCGCTCGCTCAGGGAAGATAACGACGGAGCGTGTGACGGCGCGGTGAGTGCAGCTC	2220
Sbjct 101557	TTGCGCTCGCTCAGGGAAGATAACGACGGAGCGTGTGACGGCGCGGTGAGTGCAGCTC	101616
Query 2221	CAT 2223	
Sbjct 101617	CAT 101619	

Mutation

A**B**