

Appendix 5. Rabbit HSV-1 Latent TG gene expression array means, their fold-changes with standard deviations and corresponding quantitative real-time PCR results of six selected genes.

Sample	Green Signal	Red Signal	Microarray value	Fold-change in gene expression	
				Array	qreal-time PCR
Immunoglobulin Joining Chain					
N1	3586.1	618.6	-2.54		
N2	2944	621.6	-2.24		
N3	2757.2	462.6	-2.58		
N4	2851.6	445.4	-2.68		
L1	2685.2	19493	2.86		
L2	3194.4	3562	0.16		
L3	3053	3863.3	0.34		
L4	4214.1	15934.8	1.92		
Mean \pm standard error			3.83 \pm 0.47	14.22 \pm 1.39	44.32
Human Lysozyme					
N1	18965.9	3446	-2.46		
N2	15564.1	4454.5	-1.8		
N3	10689.7	1607.2	-2.73		
N4	15941.4	1914.2	-3.06		
L1	15394	8469.4	-0.86		
L2	16913.6	47196.9	1.48		
L3	17548.7	17040.1	-0.04		
L4	4854	17001.3	1.81		
Mean \pm standard error			3.11 \pm 0.66	8.63 \pm 1.58	3.14
Ribosomal protein L27a					
N1	25459.3	14312.8	-0.83		
N2	24755.4	13698.6	-0.85		
N3	20070.6	9038	-1.15		
N4	20812.4	9126.3	-1.19		
L1	21105.8	25309.2	0.26		
L2	22647.4	16916.8	-0.42		
L3	24545.1	19007.4	-0.37		
L4	22422.1	36028.8	0.68		

Mean \pm standard error			1.04 \pm 0.12	2.06 \pm 1.09	1.93
Cysteine-rich Secretory Protein 3					
N1	345.2		-1.89		
N2	304.8		-1.2		
N3	203.8		-2.04		
N4	298.7		-2.21		
L1	206		-1.78		
L2	238.4		1.36		
L3	237.8		0.23		
L4	259.4		1.17		
Mean \pm standard error			2.08 \pm 0.93	4.23 \pm 1.91	4.38
Cathelicidin Antimicrobial Peptide					
N1	18178.4		-2.46		
N2	16312.5		-1.51		
N3	16192.7		-2.5		
N4	17480.4		-3.19		
L1	17061.3		-2.02		
L2	15903		1.7		
L3	16919.9		-0.39		
L4	16648.4		1.45		
Mean \pm standard error			2.6 \pm 1.27	6.06 \pm 2.41	3.05
Interleukin-1 b					
N1	398.8		-2.29		
N2	403.4		-1.51		
N3	330.7		-2.18		
N4	286		-2.56		
L1	283.7		-1.87		
L2	213.7		0.64		
L3	308		0.04		
L4	449.7		0.94		
Mean \pm standard error			2.07 \pm 0.70	4.20 \pm 1.62	2.68

Change in gene expression of six selected genes in HSV-1 latent rabbit trigeminal ganglia (TG) were compared to naive TG (control) based on microarrays (Array) and quantitative

real-time polymerase chain reaction. The mean log₂ difference and standard error of mean log₂ difference (Microarray value) for each of the selected genes is logarithmic and was obtained by the averaging the difference between microarray values for infected (L) and microarray values for naive (N) of each gene before conversion. Listed are the corresponding processed red and green signal values from the microarrays. The fold change in gene expression (Array and Quantitative real-time polymerase chain reaction) is arithmetic. Relative quantitative expression levels were determined for each gene. All results are expressed as an expression ratio of the HSV-1 latent trigeminal ganglia to naive trigeminal ganglia, normalized against housekeeping GAPDH expression levels using the $2^{-\Delta\Delta C_T}$ method [31]. All signal values of the arrays are distinguishable from background values, and most are high. The raw red and green signal values for the approximately 3,000 genes, 55,000 values are available on the Interdisciplinary Center for Biotechnology Research website.