

Appendix 4. Gene expression significantly altered by more than twofold in the HSV-1 latent rabbit trigeminal ganglia.

Probe name	p-value	Mean log2 difference	Hit definition	GO Biologic Process	E-value
UF_Mm_31438	0.0014	-1.63	Open Reading Frame		0
UF_Oc_r_30690	0.0008	-1.58	Melanotransferrin		0.058
UF_Oc_c_40672	0.0113	-1.56	Ltap		0.832
UF_Oc_r_30235	0.0008	-1.51	“Collagen, Type VIII, Alpha 1”	“cell adhesion, phosphate transport”	0
UF_Oc_r_30194	0.0016	-1.49	“Tubulin, Beta 2”	microtubule-based process	0
UF_Oc_r_30458	0.0172	-1.49	rRNA Promoter Binding Protein	“rRNA transcription, cell proliferation”	0
UF_Oc_r_30513	0.018	-1.49	Hypothetical Protein		0
UF_Oc_r_30049	0.0066	-1.46	Kinesin Family Member 5A	“electron transport, synaptic transmission, microtubule-based movement”	0
UF_Oc_r_31122	0.0023	-1.42	Human BAC clone RP11-655A7		0
UF_Oc_r_30197	0.0096	-1.39	Aldolase A	“fructose metabolism, glycolysis, striated muscle contraction”	0
UF_Oc_r_30547	0.0136	-1.38	ribosomal protein S2		0
UF_Oc_n_41120	0.0112	-1.36	“CAMP-dependent, Regulatory, Type II, Alpha”	“protein amino acid phosphorylation, intracellular signaling cascade, signal transduction”	0
UF_Oc_r_30246	0.0058	-1.32	Aldolase A	“fructose metabolism, glycolysis, striated muscle contraction”	0
UF_Oc_c_41074	0.0038	-1.31	Human clone RP11-61L4		0
UF_Oc_c_40213	0.0052	-1.27	Lumican	“collagen fibril organization, visual perception”	0

UF_Oc_c_40419	0.0005	-1.24	Lumican		0
UF_Oc_n_41454	0.0004	-1.22	Tissue Inhibitor of Metalloproteinase 3	“visual perception, induction of apoptosis by extracellular signals, sensory perception”	0
UF_Oc_c_41003	0.0006	-1.22	Lumican		0
UF_Oc_r_30143	0.0267	-1.2	“Guanine Nucleotide Binding Protein, Alpha Activating Activity Polypeptide O”	“neurogenesis, G-protein coupled receptor protein signaling pathway, muscle Contraction, signal transduction, axon guidance”	0
UF_Oc_c_40586	0.002	-1.17	Human cDNA clone		0
UF_Oc_n_41166	0.0015	-1.14	“Calpain, Small Subunit 1”	positive regulation of cell proliferation	0
UF_Oc_r_30003	0.0168	-1.12	“Collagen, Type III, Alpha 1”	“organogenesis, phosphate transport, circulation”	0
UF_Oc_c_40942	0.0179	-1.11	Human DNA sequence		0
UF_Oc_m_30346	0.0046	-1.1	Alpha Enolase	“transcription, glycolysis, regulation of transcription, DNA-dependent”	0
UF_Oc_n_41394	0.0054	-1.09	Annexin A2	skeletal development	0
UF_Oc_c_40392	0.0008	-1.09	Anterior Gradient 2 Homolog		0
UF_Oc_m_41039	0.0046	-1.09	Human non-neuronal splice variant (PTBP2)		0
UF_Oc_n_41226	0.0489	-1.08	Upstream Transcription Factor 2	“transcription, regulation of transcription, DNA-dependent”	0
UF_Oc_r_30798	0.0043	-1.08	Human neuron navigator 1		0
UF_Oc_m_40304	0.014	-1.07	Alpha Enolase	“Transcription, glycolysis, regulation of transcription, DNA-dependent”	0
UF_Oc_r_30254	0.0144	-1.06	Calsyntenin 1	“cell adhesion, homophilic cell	0

				adhesion”	
UF_Oc_r_30383	0.0172	-1.05	Triosephosphate Isomerase 1	“pentose-phosphate shunt, gluconeogenesis, metabolism, fatty acid biosynthesis, glycolysis”	0
UF_Oc_r_30561	0	-1.05	src homology 2 domain-containing transforming protein 2 protein		0.002
UF_Oc_n_31493	0.0169	-1.04	Calcium/calmodulin-dependent Protein Kinase II Gamma	“autophosphorylation, protein amino acid phosphorylation, G1/S transition of mitotic cell cycle, calcium ion transport”	0
UF_Mm_31288	0.022	-1.04	“COP9 Homolog, Subunit 7a”		0
UF_Oc_n_41334	0.0044	-1.03	“Adaptor-related Protein Complex 3, Beta 2 Subunit”	“protein transport, endocytosis, post-Golgi transport”	0
UF_Oc_c_40385	0.0097	-1.01	Rho-GTPase-activating Protein 5	“Rho protein signal transduction, cell adhesion”	0
UF_Oc_r_30858	0.0065	-1.01	Human ARP1 actin-related protein 1 homolog A		0
UF_Oc_r_30594	0.0216	-1.01	unspecific monooxygenase		0.008
UF_Oc_n_41347	0.0166	-1	Carnitine Palmitoyltransferase 1C	“fatty acid metabolism, lipid metabolism”	0
UF_Oc_r_31090	0.0175	1	Human chromosome 1 clone RP4-809J13		0
UF_Oc_c_41058	0.0194	1.02	HIV-1 Rev binding protein		0
UF_Oc_c_40260	0.01	1.04	Ribosomal Protein L27a	protein biosynthesis	0
UF_Oc_r_30051	0.0003	1.04	“Acid Phosphatase 6,”		0
UF_Oc_c_40883	0.0173	1.04	Human DNA sequence		0
UF_Oc_n_31488	0.0101	1.07	Adenylate Kinase 3	“nucleobase, nucleoside,	0

				nucleotide and nucleic acid metabolism, amino acid biosynthesis”	
UF_Oc_c_40432	0.0431	1.07	NADH Dehydrogenase Subunit 4L		0
UF_Oc_r_31092	0.0158	1.12	Human chemokine ligand 12		0
UF_Oc_r_30069	0.0099	1.14	Adenylate Kinase 2	“nucleobase, nucleoside, nucleotide and nucleic acid metabolism”	0
UF_Oc_c_40013	0.0008	1.17	Cathepsin K	proteolysis and peptidolysis	0
UF_Oc_n_41305	0.0072	1.18	antibody variable domain		0
UF_Oc_c_40313	0.032	1.26	Ankyrin Repeat Domain 22	“regulation of transcription, DNA-dependent”	0
UF_Oc_n_41285	0.0469	1.35	Amyloid A Protein	acute-phase response	0
UF_Oc_r_30126	0.0013	1.52	“Potassium Inwardly-rectifying Channel, Subfamily J, Member 13”	“ion transport, potassium ion transport”	0
UF_Oc_c_40323	0.0027	1.53	“Major Histocompatibility Complex, Class II, DQ Alpha 1”	“immune response, antigen processing, exogenous antigen via major histocompatibility complex class II, antigen presentation, exogenous antigen”	0
UF_Oc_n_41565	0.0212	2.07	“Interleukin 1, Beta”	“cell-cell signaling, apoptosis, cell proliferation, negative regulation of cell proliferation, signal transduction, inflammatory response, regulation of cell cycle, antimicrobial humoral response”	0
UF_Oc_c_40416	0.0326	2.08	Cysteine-rich Secretory Protein 3	“Fertilization, innate immune response, cell-	0

				cell adhesion, spermatogenesis, defense response”	
UF_Oc_n_41508	0.0321	2.6	Cathelicidin Antimicrobial Peptide	“response to pest, pathogen or parasite, defense response to bacteria”	0
UF_Oc_c_40194	0.0039	3.11	Lysozyme C	“cell wall catabolism, carbohydrate metabolism, cytolysis, defense response to bacteria”	0
UF_Oc_c_40190	0.0011	3.83	Immunoglobulin Joining Chain	humoral immune response	0

Gene expression significantly ($p \leq 0.05$) altered by more than twofold in the HSV-1 latent rabbit TG. Mean log₂ difference is the level of gene expression in HSV-1 latent trigeminal ganglia. The p-value represents the level of significance in treatment means. Hit definition is the name of the most homologous gene. E-value is the level of confidence that the matched name is incorrect. Also listed are the Gene Ontology Consortium terms for biologic process associated with the most homologous gene.