

Appendix 3. GENES SIGNIFICANTLY ALTERED IN RABBIT HSV-1 LATENT TG ACCORDING TO THEIR GO FOR BIOLOGICAL PROCESS.

Genes significantly altered in rabbit HSV-1 latent TG according to their GO for biological process. The most heavily populated biological processes included protein transport, protein biosynthesis, protein folding, protein modification, proteolysis and peptidolysis, carbohydrate metabolism and energy metabolism, cell adhesion, apoptosis and immune and defensive responses.

ProbeName	Mean log2 Difference	p-value	E-Value	Hit definition	GO Biological Process
<i>Protein Biosynthesis: Ribosomal</i>					
UF_Oc_c_40256	0.23	0.018	0.000	Ribosomal Protein L32	protein biosynthesis
UF_Oc_c_40473	0.24	0.034	0.000	40S Ribosomal Protein SA	protein biosynthesis
UF_Oc_m_30161	0.25	0.036	0.000	Ribosomal Protein L9	protein biosynthesis
UF_Oc_m_40231	0.29	0.009	0.000	Ribosomal Protein, Large, P0	ribosome biogenesis and assembly, protein biosynthesis
UF_Oc_c_40145	0.30	0.029	0.000	Ribosomal Protein L6	protein biosynthesis
UF_Oc_m_40336	0.33	0.001	0.000	Ribosomal Protein S27	protein biosynthesis
UF_Oc_m_40308	0.33	0.017	0.000	Ribosomal Protein L10	protein biosynthesis
UF_Oc_m_30165	0.34	0.020	0.000	Ribosomal Protein, Large, P0	ribosome biogenesis and assembly, protein biosynthesis
UF_Oc_m_30380	0.36	0.009	0.000	Ribosomal Protein S27	protein biosynthesis
UF_Oc_c_40351	0.42	0.004	0.000	Ribosomal Protein S27-like Protein	protein biosynthesis
UF_Oc_m_30350	0.42	0.019	0.000	Ribosomal Protein L10	protein biosynthesis
UF_Oc_c_40149	0.43	0.027	0.000	Ribosomal Protein S15a	protein biosynthesis
UF_Oc_c_40171	0.44	0.009	0.000	Large Subunit Ribosomal Protein L36a	protein biosynthesis
UF_Oc_c_40085	0.45	0.015	0.000	Ribosomal Protein L11	protein biosynthesis
UF_Oc_m_40302	0.45	0.016	0.000	Ribosomal Protein S3	protein biosynthesis
UF_Oc_m_40327	0.47	0.004	0.000	Ribosomal Protein L29	protein biosynthesis
UF_Oc_c_40398	0.48	0.004	0.000	Ribosomal Protein L34	protein biosynthesis
UF_Oc_m_40242	0.48	0.005	0.000	Ribosomal Protein S12	protein biosynthesis, ribosome biogenesis
UF_Oc_m_30176	0.50	0.021	0.000	Ribosomal Protein S12	protein biosynthesis, ribosome biogenesis
UF_Oc_m_30374	0.52	0.015	0.000	Ribosomal Protein L29	protein biosynthesis
UF_Mm_31305	0.61	0.003	0.000	Ribosomal Protein L13	protein biosynthesis, ribosome biogenesis
UF_Oc_m_40310	0.67	0.021	0.000	Ribosomal Protein S16	protein biosynthesis, ribosome biogenesis
UF_Oc_c_40260	1.04	0.010	0.000	Ribosomal Protein L27a	protein biosynthesis
<i>Protein Biosynthesis: Translation</i>					

Table S2.1

ProbeName	Mean log2 Difference	p-value	E-Value	Hit definition	GO Biological Process
UF_Oc_c_40257	-0.83	0.027	0.000	Eukaryotic Translation Initiation Factor 3 Subunit 7	protein biosynthesis, regulation of translational initiation
UF_Oc_n_41313	-0.68	0.046	0.000	Eukaryotic Translation Elongation Factor 1 Delta Isoform 1	translational elongation, protein biosynthesis
UF_Oc_m_40251	-0.67	0.029	0.000	Eukaryotic Translation Initiation Factor 5A; EIF5AI	protein biosynthesis, translational initiation
UF_Oc_m_30185	-0.53	0.038	0.000	Eukaryotic Translation Initiation Factor 5A; EIF5AI	protein biosynthesis, translational initiation
UF_Oc_m_40365	-0.33	0.005	0.000	Eukaryotic Translation Initiation Factor 4 Gamma, 2	regulation of translational initiation
UF_Oc_m_30407	-0.27	0.002	0.000	Eukaryotic Translation Initiation Factor 4 Gamma, 2	regulation of translational initiation
UF_Oc_c_40265	0.30	0.014	0.000	RIKEN CDNA 1200009C21	protein biosynthesis, translational initiation
UF_Oc_r_30108	0.39	0.028	0.000	Eukaryotic Translation Initiation Factor 4A, Isoform 2	protein biosynthesis, regulation of translational initiation
UF_Oc_r_30788	0.47	0.048	0.000	LOC464141	regulation of protein biosynthesis, protein biosynthesis, translational initiation
UF_Mm_31396	0.74	0.009	0.000	Eukaryotic Translation Initiation Factor 3, Subunit 5	protein biosynthesis
<i>Protein Folding</i>					
UF_Oc_r_30315	-0.93	0.006	0.000	Calreticulin	protein folding
UF_Oc_r_30320	-0.90	0.016	0.000	Cell Division Cycle 37 Homolog	protein folding
UF_Oc_r_30217	-0.69	0.027	0.000	NIMA-interacting 1Protein	protein folding
UF_Oc_r_30271	-0.62	0.006	0.000	Heat Shock Protein 1, Beta	response to unfolded protein, protein folding
UF_Oc_n_41550	-0.59	0.001	0.000	FK506-binding Protein	protein folding
UF_Oc_c_40268	-0.54	0.021	0.000	Parkinson Disease 7	protein folding
UF_Oc_r_30152	-0.53	0.003	0.000	Chaperonin Containing TCP1, Subunit 3	protein folding
UF_Oc_c_40414	-0.36	0.012	0.000	Heat Shock 10kD Protein	response to unfolded protein, protein folding
UF_Oc_c_40442	-0.30	0.008	0.000	MHC Class II Region Expressed Gene KE2	protein folding
UF_Oc_r_30212	-0.21	0.014	0.000	Cytoskeleton Associated Protein 1	protein folding

Table S2.2

ProbeName	Mean log2 Difference	p-value	E-Value	Hit definition	GO Biological Process
UF_Oc_c_40384	-0.19	0.041	0.000	60 KDa Protein 1-like Protein	response to unfolded protein, protein folding
UF_Oc_n_41162	0.22	0.011	0.000	Ubiquitously-expressed Transcript	protein folding
UF_Oc_r_30139	0.29	0.009	0.000	DnaJ Homolog, Subfamily B, Member 6	response to unfolded protein, protein folding
UF_Oc_n_31540	0.54	0.010	0.000	DnaJ Homolog, Subfamily B, Member 11	protein folding
UF_Oc_c_40396	0.66	0.014	0.000	Heat Shock Protein 2	response to unfolded protein, protein folding
<i>Protein Modification</i>					
UF_Oc_n_41120	-1.36	0.011	0.000	Protein Kinase, CAMP-dependent, Regulatory, Type II, Alpha	protein amino acid phosphorylation
UF_Oc_n_31493	-1.04	0.017	0.000	Calcium/calmodulin-dependent Protein Kinase II Gamma	protein amino acid phosphorylation
UF_Oc_r_30324	-0.75	0.036	0.000	RAD23 Homolog A	protein modification
UF_Oc_n_41417	-0.70	0.033	0.000	Protein Kinase C, Zeta	protein amino acid phosphorylation
UF_Oc_c_40121	-0.60	0.004	0.000	Ubiquitin-conjugating Enzyme E2L 3 Isoform 1	protein modification
UF_Oc_r_30310	-0.54	0.001	0.000	Lysyl Oxidase-like 1	protein modification
UF_Oc_c_40293	-0.52	0.028	0.000	EPH Receptor B3	protein amino acid phosphorylation
UF_Oc_c_40061	-0.39	0.025	0.000	Inhibitor Of Kappa Light Polypeptide Gene Enhancer In B-cells	protein amino acid phosphorylation
UF_Oc_c_40154	0.34	0.011	0.000	nitiation Factor 2-associated 67kDa Protein	protein modification
UF_Oc_c_40484	0.35	0.022	0.000	LOC478757	protein amino acid phosphorylation
UF_Oc_c_40507	0.36	0.050	0.000	TANK-binding Kinase 1	protein amino acid phosphorylation
UF_Oc_r_30144	0.42	0.006	0.000	Ataxia Telangiectasia And Rad3 Related	protein amino acid phosphorylation
UF_Mm_31251	0.44	0.050	0.000	Budding Uninhibited By Benzimidazoles 1 Homolog, Beta	protein amino acid phosphorylation
UF_Oc_c_40206	0.52	0.005	0.000	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	N-linked glycosylation
UF_Oc_r_30474	0.59	0.005	0.000	Hypothetical Protein FLJ22313	protein modification
<i>Protein Transport</i>					

Table S2.3

ProbeName	Mean log2 Difference	p-value	E-Value	Hit definition	GO Biological Process
UF_Oc_n_41334	-1.03	0.004	0.000	Adaptor-related Protein Complex 3, Beta 2 Subunit	protein transport, ER to Golgi transport
UF_Oc_r_30234	-0.52	0.016	0.000	Dullard Homolog	protein transport
UF_Oc_r_30292	0.26	0.007	0.000	Importin 9	protein transport
UF_Oc_c_40445	0.38	0.019	0.000	Translocation Protein 1	protein transport
UF_Oc_r_30762	0.43	0.029	0.000	LOC545522	protein transport, intracellular protein transport
UF_Oc_r_30504	0.48	0.011	0.000	Transmembrane Trafficking Protein	protein transport, ER to Golgi transport
UF_Oc_r_30071	0.50	0.018	0.000	SAR1a Gene Homolog 2	protein transport, intracellular protein transport
UF_Oc_c_40376	0.59	0.008	0.000	Sec61 Beta Subunit	protein transport
UF_Oc_r_30081	0.72	0.003	0.000	Nucleoporin 133kDa	protein transport
UF_Oc_n_41178	0.94	0.027	0.000	Syndet	protein transport, intracellular protein transport
<i>Proteolysis and Peptidolysis</i>					
UF_Oc_n_41478	-0.95	0.012	0.000	Protease, Serine, 11	proteolysis and peptidolysis
UF_Oc_r_30153	-0.83	0.014	0.000	Ubiquitin-activating Enzyme E1	ubiquitin cycle
UF_Oc_r_30360	-0.71	0.016	0.000	Leucine Rich Repeat Containing 41	ubiquitin cycle
UF_Oc_r_30211	-0.64	0.006	0.000	RIKEN CDNA 1300002A08 Gene	proteolysis and peptidolysis
UF_Oc_c_40121	-0.60	0.004	0.000	Ubiquitin-conjugating Enzyme E2L 3 Isoform 1	ubiquitin cycle, ubiquitin-dependent protein catabolism
UF_Oc_c_40139	-0.54	0.018	0.000	Ubiquitin-conjugating Enzyme E2 Variant 2	ubiquitin cycle
UF_Oc_r_30438	-0.47	0.022	0.000	Neural Precursor Cell Expressed, Developmentally Down-regulated Gene 8	ubiquitin cycle
UF_Oc_r_30469	-0.43	0.022	0.000	Secernin 1	proteolysis and peptidolysis
UF_Oc_r_30132	-0.43	0.008	0.000	Ubiquitin Protein Ligase E3A	proteolysis and peptidolysis, ubiquitin cycle, ubiquitin-dependent protein catabolism
UF_Oc_c_40153	-0.37	0.018	0.000	Hypothetical Protein	ubiquitin cycle
UF_Oc_c_40040	-0.28	0.006	0.000	Ubiquitin C-terminal Hydrolase	ubiquitin cycle, ubiquitin-dependent protein catabolism

Table S2.4

ProbeName	Mean log2 Difference	p-value	E-Value	Hit definition	GO Biological Process
UF_Oc_r_30417	-0.25	0.045	0.000	Protein Inhibitor Of Activated STAT Protein 1	ubiquitin cycle
UF_Oc_r_30482	0.31	0.043	0.000	Ring Finger Protein 167	protein ubiquitination, proteolysis and peptidolysis
UF_Oc_c_40021	0.49	0.038	0.000	Fibroblast Activation Protein, Alpha	proteolysis and peptidolysis
UF_Oc_n_41457	0.57	0.019	0.000	Leucine Aminopeptidase 3	proteolysis and peptidolysis
UF_Mm_31245	0.64	0.032	0.000	Poly Polymerase Family, Member 2	proteolysis and peptidolysis
UF_Oc_c_40012	0.66	0.002	0.000	Ubiquitin-like 2 Activating Enzyme E1B	ubiquitin cycle
<i>Carbohydrate & Energy: Glycolysis</i>					
UF_Oc_r_30197	-1.39	0.010	0.000	Aldolase A, Fructose-bisphosphate	glycolysis
UF_Oc_r_30246	-1.32	0.006	0.000	Aldolase A, Fructose-bisphosphate	glycolysis
UF_Oc_m_30346	-1.10	0.005	0.000	Alpha Enolase	glycolysis
UF_Oc_m_40304	-1.07	0.014	0.000	Alpha Enolase	glycolysis
UF_Oc_r_30383	-1.05	0.017	0.000	Triosephosphate Isomerase 1	glycolysis, gluconeogenesis
UF_Oc_n_41453	-0.76	0.012	0.000	Malate Dehydrogenase 2, NAD	glycolysis, tricarboxylic acid cycle
UF_Oc_r_30286	-0.56	0.019	0.000	Pyruvate Kinase M	glycolysis
UF_Oc_r_30016	-0.27	0.044	0.000	Glucose Phosphate Isomerase	glycolysis, gluconeogenesis
UF_Oc_c_40146	0.18	0.041	0.000	Pyruvate Dehydrogenase E1 Component Beta Subunit	glycolysis, tricarboxylic acid cycle
<i>Carbohydrate & Energy: Electron Transport</i>					
UF_Oc_r_30049	-1.46	0.007	0.000	Kinesin Family Member 5A	electron transport
UF_Oc_c_40553	-0.95	0.018	0.019	NADH dehydrogenase subunit 3	
UF_Oc_r_30228	-0.80	0.036	0.000	Open Reading Frame	electron transport
UF_Oc_r_30295	-0.78	0.001	0.000	Fatty Acid Desaturase 3	electron transport
UF_Oc_n_41505	-0.67	0.016	0.000	Cytochrome C Oxidase Subunit VIa Polypeptide 1	electron transport
UF_Oc_c_40354	-0.57	0.029	0.000	Cytochrome C Oxidase Subunit VIIa Polypeptide 2	electron transport
UF_Mm_31362	-0.56	0.004	0.000	Cytochrome C Oxidase Polypeptide VIb	electron transport
UF_Oc_c_40409	-0.50	0.000	0.000	NADH Dehydrogenase 1 Alpha Subcomplex, 4	
UF_Mm_31429	-0.48	0.033	0.000	NADH Dehydrogenase Fe-S Protein 2	electron transport

Table S2.5

ProbeName	Mean log2 Difference	p-value	E-Value	Hit definition	GO Biological Process
UF_Oc_c_40039	-0.46	0.012	0.000	CDNA Sequence	electron transport
UF_Oc_c_40140	-0.39	0.021	0.000	NADH Dehydrogenase Fe-S Protein 4,	electron transport
UF_Oc_c_40086	-0.38	0.000	0.000	NADH Dehydrogenase	mitochondrial electron transport, NADH to ubiquinone
UF_Oc_c_40007	-0.37	0.018	0.000	NADH:ubiquinone Oxidoreductase B17.2 Subunit	electron transport
UF_Oc_c_40202	-0.37	0.030	0.000	Ubiquinol-cytochrome C Reductase Binding Protein	electron transport
UF_Oc_c_40370	-0.36	0.010	0.000	DKFZP434I092 Protein	electron transport
UF_Oc_c_40387	-0.34	0.033	0.000	NADH Dehydrogenase	
UF_Oc_n_41159	-0.27	0.021	0.000	Cytochrome B-5	electron transport
UF_Oc_c_40170	-0.26	0.037	0.000	NADH Dehydrogenase 1 Alpha Subcomplex, 6	electron transport
UF_Mm_31361	0.27	0.015	0.000	Cytochrome C-1	electron transport
UF_Oc_c_40468	0.36	0.048	0.000	NADH Dehydrogenase 1 Alpha Subcomplex, 8	
UF_Oc_c_40185	0.39	0.042	0.000	Electron Transfer Flavoprotein-ubiquinone Oxidoreductase	electron transport
UF_Oc_c_40483	0.44	0.027	0.000	NADH Dehydrogenase Subunit 6	
UF_Oc_c_40076	0.89	0.010	0.000	Thioredoxin Domain Containing	electron transport
<i>Carbohydrate & Energy: Proton Transport</i>					
UF_Oc_n_41527	-0.64	0.031	0.000	ATP Synthase, H+ Transporting, Mitochondrial F0 Complex, Subunit D	proton transport, ATP synthesis coupled proton transport
UF_Oc_c_40321	-0.54	0.027	0.000	ATP Syntase Subunit F6	proton transport, ATP synthesis coupled proton transport
UF_Oc_r_30237	-0.52	0.024	0.000	Vacuolar ATPase 16kDa Subunit C	proton transport, ATP synthesis coupled proton transport, ATP biosynthesis
UF_Oc_c_40273	-0.52	0.027	0.000	Ubiquitination Factor E4A	proton transport, ATP synthesis coupled proton transport, ATP biosynthesis
UF_Oc_r_30343	-0.45	0.032	0.000	ATP Synthase, H+ Transporting, Mitochondrial F1 Complex, Beta Polypeptide	proton transport, ATP synthesis coupled proton transport

Table S2.6

ProbeName	Mean log2 Difference	p-value	E-Value	Hit definition	GO Biological Process
UF_Oc_c_40333	-0.21	0.013	0.000	ATP Synthase, H+ Transporting, Mitochondrial F0 Complex, Subunit F, Isoform 2	proton transport, ATP biosynthesis
UF_Oc_n_31495	-0.18	0.032	0.000	ATPase, H+ Transporting, Lysosomal V0 Subunit A Isoform 1	proton transport
<i>Cell Adhesion</i>					
UF_Oc_r_30235	-1.51	0.001	0.000	Collagen, Type VIII, Alpha 1	cell adhesion
UF_Oc_r_30254	-1.06	0.014	0.000	Calsyntenin 1	cell adhesion
UF_Oc_c_40385	-1.01	0.010	0.000	Rho-GTPase-activating Protein 5	cell adhesion
UF_Oc_n_41419	-0.87	0.015	0.000	Acetylcholinesterase	cell adhesion
UF_Mm_31323	-0.75	0.027	0.000	Lutheran Blood Group	cell adhesion
UF_Oc_n_41473	-0.47	0.028	0.000	Scavenger Receptor Class B Member 1	cell adhesion
UF_Oc_c_40465	-0.46	0.023	0.000	RIKEN CDNA 2200001I15	cell adhesion
UF_Oc_r_30213	-0.24	0.017	0.000	Hypothetical Gene	cell adhesion
UF_Mm_31347	0.24	0.017	0.000	Junction Adhesion Molecule 3	cell adhesion
UF_Oc_c_40016	0.32	0.027	0.000	Procollagen, Type XII, Alpha 1	cell adhesion
UF_Oc_n_41257	0.49	0.024	0.000	Amyloid Beta Protein	cell adhesion
<i>Apoptosis</i>					
UF_Oc_n_41417	-0.70	0.033	0.000	Protein Kinase C, Zeta	anti-apoptosis
UF_Oc_n_41473	-0.47	0.028	0.000	Scavenger Receptor Class B Member 1	apoptosis
UF_Oc_n_31521	-0.39	0.034	0.000	Sulfatase 1	apoptosis
UF_Oc_n_41393	-0.24	0.045	0.000	BCL2-like 1	regulation of apoptosis, anti-apoptosis
UF_Mm_31338	0.34	0.010	0.000	Transformation Related Protein 53 Inducible Nuclear Protein 1	apoptosis, induction of apoptosis
UF_Oc_r_30088	0.44	0.004	0.000	SON DNA Binding Protein	anti-apoptosis
UF_Oc_c_40347	0.48	0.027	0.000	Autophagy Protein 5-like	apoptosis, autophagy
UF_Oc_n_41257	0.49	0.024	0.000	Amyloid Beta Protein	apoptosis
UF_Oc_c_40215	0.57	0.027	0.000	Bax Inhibitor-1	negative regulation of apoptosis, apoptosis
UF_Oc_c_40076	0.89	0.010	0.000	Thioredoxin Domain Containing	anti-apoptosis
UF_Oc_n_41565	2.07	0.021	0.000	Interleukin 1, Beta	apoptosis
<i>Immune Response</i>					

Table S2.7

ProbeName	Mean log2 Difference	p-value	E-Value	Hit definition	GO Biological Process
UF_Oc_c_40061	-0.39	0.025	0.000	Inhibitor Of Kappa Light Polypeptide Gene Enhancer In B-cells	protein amino acid phosphorylation, Immune response, protein complex assembly
UF_Oc_r_30016	-0.27	0.044	0.000	Glucose Phosphate Isomerase	neurogenesis, gluconeogenesis, humoral immune response, carbohydrate metabolism, glycolysis, hemostasis
UF_Oc_n_41451	0.54	0.004	0.000	antibody variable domain	
UF_Oc_n_41541	0.82	0.049	0.000	Interleukin 1 Receptor Antagonist	cell surface receptor linked signal transduction, Immune response, lipid metabolism, insulin secretion
UF_Oc_n_41212	0.83	0.025	0.000	antibody variable domain	
UF_Oc_n_41256	0.99	0.046	0.000	antibody variable domain	
UF_Oc_n_41305	1.18	0.007	0.000	antibody variable domain	
UF_Oc_c_40323	1.53	0.003	0.000	MHCClass II, DQ Alpha 1	Immune response, antigen processing, exogenous antigen via MHC class II, antigen presentation, exogenous antigen
UF_Oc_c_40190	3.83	0.001	0.000	Immunoglobulin Joining Chain	humoral immune response
<i>Host Defense</i>					
UF_Oc_r_30332	-0.70	0.036	0.000	HMT1 HnRNP Methyltransferase-like 2	Defense response
UF_Oc_c_40267	-0.69	0.005	0.000	LOC459361	response to pest, pathogen or parasite
UF_Oc_r_30421	-0.44	0.025	0.000	MHC Class I Protein	Defense response
UF_Oc_r_30382	0.75	0.003	0.000	Ceruloplasmin	acute-phase response
UF_Oc_n_41285	1.35	0.047	0.000	Amyloid A Protein	acute-phase response
UF_Oc_c_40416	2.08	0.033	0.000	Cysteine-rich Secretory Protein 3	Defense response
UF_Oc_n_41508	2.60	0.032	0.000	Cathelicidin Antimicrobial Peptide	response to pest, pathogen or parasite, Defense response to bacteria
UF_Oc_c_40194	3.11	0.004	0.000	Lysozyme C	Defense response to bacteria

Table S2.8