## Table S1: Twenty nine genes significantly upregulated in the HSV-1 17Syn⁺ latent TG relative to 17ΔPst(LAT⁻) latent TG 1 hour after mouse hyperthermic stress

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<thead>
<tr>
<th>Gene name (Genbank accession number)</th>
<th>Gene symbol (description)</th>
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<th>Real-time PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td>1427837_at (U25103)</td>
<td>IgK-V32 [immunoglobulin kappa chain variable 32 (V32)]</td>
<td>immune response</td>
<td>+7.9</td>
<td>+1.51</td>
</tr>
<tr>
<td>1424931_s_at (M94350)</td>
<td>IgL-V1 (immunoglobulin lambda chain, variable 1)</td>
<td>humoral immune response; antigen processing and presentation of peptide antigen via MHC class I</td>
<td>+3.6</td>
<td>+13.59</td>
</tr>
<tr>
<td>1430523_s_at (AK008145)</td>
<td>IgL-V1 homolog (immunoglobulin lambda chain, variable 1)</td>
<td>humoral immune response; antigen processing and presentation of peptide antigen via MHC class I</td>
<td>+3.4</td>
<td>+2.17</td>
</tr>
<tr>
<td>1425324_x_at (AF466769)</td>
<td>IgH-4 (serum IgG1) [immunoglobulin heavy chain 4 (serum IgG1)]</td>
<td>humoral immune/defense response; antibody-dependent cellular cytotoxicity; positive regulation of type I /IIa hypersensitivity; phagocytosis, recognition/engulfment; complement activation</td>
<td>+2.9</td>
<td>+8.40</td>
</tr>
<tr>
<td>1416111_at (AF001036)</td>
<td>CD83 (CD83) antigen</td>
<td>immune response/ immune modulation</td>
<td>+3.3</td>
<td>+17.39</td>
</tr>
<tr>
<td>1444078_at (BB154331)</td>
<td>CD8A (CD8 antigen, alpha chain)</td>
<td>immune response/suppressor; T cell mediated immunity/activation/ cytotoxic differentiation; tyrosine kinase signaling pathway; positive regulation of calcium-mediated signaling; cell surface receptor linked signal transduction</td>
<td>+2.9</td>
<td>+2.95</td>
</tr>
<tr>
<td>1419684_at</td>
<td>CCL8 [chemokine (C-C motif) ligand 8]</td>
<td>immune/inflammatory response; Chemotaxis; signal</td>
<td>+3.0</td>
<td>+3.05</td>
</tr>
</tbody>
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Upregulation of Immune Genes in HSV-1 Reactivation

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<tr>
<td>1417976_at (AF483481)</td>
<td>ADA (adenosine deaminase)†</td>
<td>immune response; purine nucleotide/purine ribonucleoside monophosphate metabolism; metal ion binding</td>
<td>+5.3</td>
<td>+9.65</td>
</tr>
<tr>
<td>1428719_at (AK008551)</td>
<td>2010309G21RikIgL (RIKEN cDNA 2010309G21 gene immunoglobulin lambda chain complex)</td>
<td>cDNA; antigen binding</td>
<td>+3.0</td>
<td>+1.04</td>
</tr>
<tr>
<td>1418549_at (AF307151)</td>
<td>CGA (glycoprotein hormones, alpha subunit)</td>
<td>hormone activity</td>
<td>+3.8</td>
<td>ND</td>
</tr>
<tr>
<td>1436127_at (AI854101)</td>
<td>CRHBP (corticotropin releasing hormone binding protein)</td>
<td>hormone metabolism; adrenocorticotropin-releasing hormone binding</td>
<td>+3.8</td>
<td>ND</td>
</tr>
<tr>
<td>1450795_at (NM_008497)</td>
<td>LHB (luteinizing hormone beta)</td>
<td>hormone activity</td>
<td>+2.8</td>
<td>ND</td>
</tr>
<tr>
<td>1437522_x_at (BB025253)</td>
<td>GH (growth hormone)</td>
<td>hormone activity; regulation of steroid hormone receptor signaling pathway; glucose transport</td>
<td>+2.7</td>
<td>ND</td>
</tr>
<tr>
<td>1460668_at (NM_010253)</td>
<td>GAL (galanin)</td>
<td>hormone activity; neuropeptide signaling/nervous system development</td>
<td>+2.8</td>
<td>ND</td>
</tr>
<tr>
<td>1418735_at (NM_008475)</td>
<td>KRT2-4 (keratin complex 2, basic, gene 4)</td>
<td>cytoskeleton organization and biogenesis; epithelial cell differentiation; negative regulation of epithelial cell proliferation</td>
<td>+16.7</td>
<td>ND</td>
</tr>
<tr>
<td>1438394_x_at (AV082644)</td>
<td>KRT2-4 homolog (keratin complex 2, basic, gene 4)</td>
<td>cytoskeleton organization and biogenesis; epithelial cell differentiation; negative regulation of epithelial cell proliferation</td>
<td>+7.7</td>
<td>ND</td>
</tr>
<tr>
<td>1448745_s_at (BC026781)</td>
<td>LOR (loricrin)</td>
<td>cytoskeleton structural activity; bridging;</td>
<td>+4.7</td>
<td>ND</td>
</tr>
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</tr>
<tr>
<td>1449363_at (BC019946)</td>
<td>ATF3 (activating transcription factor 3) †</td>
<td>DNA-dependent regulation of transcription; gluconeogenesis transcription; sequence-specific DNA binding protein dimerization activity</td>
<td>+3.2</td>
<td>ND</td>
</tr>
<tr>
<td>1422134_at (NM_008036)</td>
<td>FOSB (FBJ osteosarcoma oncogene B)</td>
<td>DNA-dependent regulation of transcription; regulation of progression through cell cycle; DNA-dependent proteolysis</td>
<td>+3.0</td>
<td>ND</td>
</tr>
<tr>
<td>1418197_at (BC012701)</td>
<td>UCP1 [uncoupling protein 1 (mitochondrial, proton carrier)]†</td>
<td>mitochondrial transport; oxidative phosphorylation uncoupler activity; brown fat cell differentiation; protein binding</td>
<td>+4.6</td>
<td>ND</td>
</tr>
<tr>
<td>1456248_at (AV076385)</td>
<td>2310002A05Rik (RIKEN cDNA 2310002A05 gene)</td>
<td>cDNA</td>
<td>+5.2</td>
<td>ND</td>
</tr>
<tr>
<td>1428909_at (BI683916)</td>
<td>A130040M12Rik (RIKEN cDNA A130040M12 gene)</td>
<td>cDNA</td>
<td>+2.7</td>
<td>ND</td>
</tr>
<tr>
<td>1416756_at (AK002290)</td>
<td>DNAJB1 (HSP40) [DNAJ (HSP40) homolog, subfamily B, member 1]</td>
<td>heat shock protein folding; chaperone cofactor-dependent protein folding</td>
<td>+3.1</td>
<td>ND</td>
</tr>
<tr>
<td>1416755_at (AB028272)</td>
<td>DNAJB1 (HSP40) homolog [DNAJ (HSP40) homolog, subfamily B, member 1]</td>
<td>heat shock protein folding; chaperone cofactor-dependent protein folding</td>
<td>+3.0</td>
<td>ND</td>
</tr>
<tr>
<td>1423285_at (BB731671)</td>
<td>COCH (coagulation factor C homolog)</td>
<td>coagulation</td>
<td>+3.6</td>
<td>ND</td>
</tr>
<tr>
<td>1456112_at (AW554765)</td>
<td>TPR (translocated promoter region)</td>
<td>nuclear export of mRNAs; serine-tRNA ligase activity; ATP binding</td>
<td>+2.7</td>
<td>ND</td>
</tr>
<tr>
<td>1449939_s_at (NM_010052)</td>
<td>DLK1 (delta-like 1 homolog)</td>
<td>calcium ion/protein binding</td>
<td>+3.1</td>
<td>ND</td>
</tr>
<tr>
<td>1448749_at</td>
<td>PLEK (pleckstrin)</td>
<td>intracellular signaling</td>
<td>+3.0</td>
<td>ND</td>
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<tr>
<td>(AF181829)</td>
<td></td>
<td>cascade; calcium ion binding</td>
<td>+3.0</td>
<td>+6.77</td>
<td></td>
</tr>
<tr>
<td>1426193_at (AY078071)</td>
<td>OTOS (otospiralin)</td>
<td>sensory perception of sound</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

†Pathways: Ada; purine nucleotide metabolism, Atf3; smooth muscle contraction, and Ucp1; electron transport chain
ND: Not Determined

Fold change values of expression of 29 genes based on microarrays (Microarray) in the 17Syn⁺ high phenotypic reactivator latent TG relative to a LAT negative recombinant, 17ΔPst low phenotypic reactivator latent TG 1 hour after mouse hyperthermic stress. Controls were non-heat-treated 17Syn⁺ and 17ΔPst(LAT⁺) infected TG. Relative quantitative expression levels were determined for each of the 9 adaptive immunity genes and 1 gene selected randomly from the remaining 20 genes. All results are expressed as an expression ratio of the latent 17Syn⁺ latent TG to the 17ΔPst(LAT⁺) latent TG of heat-treated mice, normalized against β-actin expression levels using the $2^{-\Delta\Delta C_T}$ method.†Pathways for Ada, Atf3 and Ucp1.