Supplementary Information

Supplementary Methods

Evaluation of the Affymetrix Rhesus Macaque GeneChip for use on Sooty Mangabey Samples

Gene expression in rhesus macaques and sooty mangabeys was monitored using the Affymetrix Rhesus Genome Array which contains probesets for ~47, 000 transcripts (1) and has been tested rigorously by independent primate centers (2) These arrays were designed using rhesus cDNA and genomic rhesus sequences from multiple sources (1). Prior to the availability of rhesus macaque arrays, several groups, including our own, have published microarray studies hybridizing samples from various non-human primates on arrays with probes specific for human sequences, however a central concern has been cross-species specificity of these arrays. At the onset of this study, we were concerned with the ability of the Rhesus Genome Array to accurately hybridize cRNA derived from SMs, and whether data from the arrays would allow meaningful comparison between RM and SM samples. The design of probesets for this array employed an algorithm in which macaque subsequences most orthologous between human and macaque were utilized; to further reduce the effect of polymorphisms, 16 probes per probeset (rather than the customary 11) were used for ~15,000 probesets (1). A recent study comparing 1,180 transcripts between rhesus macaques and humans have estimated the average degree of nucleotide identity to be 97.79±1.78% in the coding region, and 95.10±4.15% in the 3' UTR (3), with less than 1% of genes having lower than 88% homology. To minimize the effect of individual probes with sequence mismatches due to interpecies variation, we used the Robust Multi-Array analysis for normalization and probeset summarization of the dataset. We feel that RMA normalization is the most appropriate method for interspecies comparisons for two reasons: (i) the global background adjustment (as opposed to background correction at the probe level, ie. Perfect Match – Mismatch correction) will reduce the effect of mismatches on expression measurements at the probe level, and (ii) the use of median polish to summarize individual probes into probeset measurements is robust and the effect of individual probes with sequence variation due to interspecies differences is minimized. Lastly, as described in detail below, we limited our analysis to include only genes for which (i) a two-fold change in expression relative to uninfected samples could be detected, and (ii) the gene expression change was determined to be statistically significant. Including the requirement of a two-fold ratio cut-off in our analysis, rather than direct comparison of probeset intensities, would further reduce false-negative comparisons between the species. Based on the high degree of cDNA transcript identity between SMs and RMs, the probe design of the Rhesus GeneChip towards orthologous sequences, and our data analysis approach, we reasoned that the Rhesus GeneChip would be able to accurately detect changes in sooty mangabey transcript levels, and that our analysis would be focused on genes that could be meaningfully compared between species. Nevertheless, to confirm the utililty of the array for our analysis, we employed *in silico* analyses prior to hybridization and post-analysis validation experiments of our results from the main study.

To predict the overall binding ability of the Rhesus GeneChip with SM cDNAs, we performed an *in silico* analysis of perfect and mismatch binding based on SM sequences in GenBank and individual probes on the array. Due to the variation in annotation of probesets on the Affymetrix RM Array, probesets were matched to genes based on the presence of at least one perfect match within the gene sequence. In some cases multiple genes matched with a single probeset due to the presence of multiple alleles or orthologs of particular genes within the set of sequences. The resultant probesets were then aligned using Clustal to the available sequence and probes within each set were binned based on the number of mismatches and/or indels between the probe and the sequence. Probes with >5 mismatches or containing indels are likely not contained within the query sequence. As detailed in Supplementary Table S2, 54 of the 100 sequences were successfully aligned with probesets on the Affymetrix RM array. These 54 sequences represent 42 unique genes. In almost all cases where probesets aligned with their intended gene (e.g. not a close paralog), the number of perfect match probes outnumbered the probes containing mismatches. Because of the median polish summarization employed by the RMA algorithm, and our estimate that most probesets have a majority of probes that match perfectly with SM sequences, we felt any effect due to interspecies sequence variation on the arrays would be minimal. An independent analysis by (C. Davies, Affymetrix, Inc., pers. communication) verified our findings.

To verify that hybridization efficiency was similar between RMs and SMs, we calculated the global statistics of the log10 intensity on all 94 arrays described in this study. The array data was pre-filtered to exclude all probesets representing control sequences, viral genomes or reporter genes. As summarized in Supplementary Table S1, the means, medians, ranges and standard deviations on arrays hybridized with total RNA from SMs (33 arrays) or RMs (61 arrays) were nearly identical, and were very similar to the cumulative statistics from all 94 arrays. The distribution of log10 intensities on each individual array is depicted in Supplementary Figure S1. Similar to the global statistics for each species, the RM arrays have a slightly larger range of expression values compared to those hybridized with SM RNA, and arrays hybridized with SM samples have a moderately higher median intensity; however no gross differences were apparent between species hybridization statistics. Collectively, these data validate our *in silico* model of hybridization of SM RNA on the Rhesus GeneChips. More importantly, these data indicate that gene expression measurements obtained from hybridizing SM RNA samples to the Rhesus GeneChips is directly comparable to data obtained from RM samples.

Microarray data analysis – normalization, principal components analysis, hierarchical clustering

Arrays were scanned using the Affymetrix GeneChip Scanner 3000 7G, and visual inspection and evaluation of overall intensity was used to judge the quality of the hybridization; 2 of 96 total arrays were judged to be of low quality and removed from the analysis. .CEL files from the remaining Rhesus GeneChip arrays were imported into Partek Genomics Suite v.6.4 (Partek, Inc. St. Louis, MO) and RMA pre-processing was used to perform global background correction, quantile normalization and median polish probeset summarization. Probeset annotation was based on NetAffx Annotation Release 27 (November 2008, Affymetrix, Inc.) which utilizes the most update-to-date build of the rhesus macaque genome (Unigene Macaca mulatta Build #13, September, 2008). After generation of smaller gene lists (ie. One-way ANOVA to define SIV-inducible genes in SMs), probeset annotations were further updated using the DAVID annotation tool (http://david.abcc.ncifcrf.gov/) (3-4). For probesets with no Unigene rhesus macaque identifier, the Gene Symbol for the human orthologue was used. Similarity between samples was estimated using principal component analysis was used to reduce the log10 intensities on individual arrays and using a covariance dispersion matrix and normalized eigenvector scaling. PC#1 (37.4%), PC#2 (11.7%) and PC#3 (7.8%) accounted for 56.9% of the variance in the dataset. Hierarchical clusters between samples or between genes were assembled using Euclidean metric and average linkage to determine distance between datasets and clusters, respectively.

Identification of genes induced by SIV infection and genes with differential SIV regulation between species

One-way ANOVA was used to test for differences in the log10 intensities of individual probesets in the sooty mangabey group (33 arrays) after infection, and the P-value was corrected for multiple hypothesis testing using the Benjamini-Hochberg False Discovery Rate method. This corrected P-value was 0.0008342 was used in combination with a second criteria, a two-fold change up or down, in the average gene expression relative to pre-infected samples ($\log_{10}$ *time X* – Log_{10} *time 0* > 0.301 or < -0.301) to define differentially expressed genes. The same algorithm was used to identify differentially expressed genes in the SIVmac239-infected RM group (36 arrays, corrected P-value = 0.00746). Although fairly stringent by current standards, this approach allowed us to have a high degree of confidence in probesets/genes defined as differential. The utility of our approach in identifying genes with SIV-inducible expression in SMs and RMs was supported by the high degree of overlap between our SM/RM dataset and concurrent, independent, studies detailing SIV infection in AGMs (5) and previously published observations from our group in SHIV89.6P infected cynomolgus macaques (6).

Because of the differences in sample sizes between the SIVsmm SM (33 arrays), SIVsmm RM (25 arrays) and SIVmac239 RM (36 arrays) groups, a direct Boolean analysis to determine SIV-regulated genes that differed between species would not be appropriate; exclusion of a gene from one group and not another may be due to differing P-values rather than underlying biology. Instead, we employed a two-layered approach. In the first step, we used a two-way ANOVA to define genes with expression that differed (i) between the three infection groups, and (ii) over time after infection. This gene list was further reduced by a post-hoc filter to include only genes that also exhibited significantly different expression values between SMs and both RM groups. This initial gene list was large (>20,000 probesets) and we reasoned that it included genes with differential expression due to (i) species-specific differences in constitutive expression, (ii) differing hybridization efficiency of genes with sequence disparity, or (iii) distinct patterns of transcription in response to SIV infection. To focus our analysis on the latter, we added a second step to the analysis: only genes that were defined as SIV-inducible for each individual infection group by the initial filter (one-way ANOVA, and a 2-fold average change) were included. This reduced the dataset considerably, such that the list of genes that were SIV-inducible in SMs and differed from RMs was comprised of 239 individual probesets. Supporting the efficacy of this approach was the observation that the probesets representing CCR5 and MKI67, two genes with well-described differences in SIV induction *in vivo* between RMs and SMs (7-8), were identified by this analysis (Supplemental Table S6).

Identifying genes that correlate with immune activation

To identify genes correlated with T cell activation in SIVmac239-infected RMs, we correlated gene expression measured the arrays with proliferation/activation marker expression measure by flow cytometry. The appearance of markers of immune activation on CD4+ and CD8+ T cells have been comprehensively demonstrated to be an accurate indicator of disease progression in HIV infection (9-10). As a preliminary step, we compared the Pearson correlation between the percentage of various activation markers on CD3+CD4+ and CD3+CD8+ T lymphocytes and their normalized log10 intensity measured by the array for individual SIVmac239 animals. This analysis was performed for CD38, HLA-DR, CD69, CD25 and Ki-67; we found that the percentage of Ki-67 on CD3+CD8+ T cells had the strongest, and most significant correlation (r = 0.6854, P = 5.70x10-5). Because Ki-67 has also been reported to be the most reliable marker of immune activation in SIV-infected non-human primates (11), we reasoned that it would be the best marker to identify novel genes potentially regulating pathogenic immune activation. We performed Pearson correlations between the percentage of Ki-67+CD3+CD8+ cells of individual SIVmac239 infected animals and the normalized Log10 intensity values of 830 probesets determined to be SIV-induced by ANOVA, the P-value was adjusted using Benjamini-Hochberg FDR to a cutoff value of 0.0106, filtering the list to 177 probesets (Supplementary Table S9). Inspection of the gene list provided support that this analysis was capable of identifying factors involved in the pathogenic activation and cell proliferation observed in SIV infection, as the majority of genes with significant correlation were involved in cell-cycle progression. Additionally, the analysis identified CCR5 and TIM3, which have both been positively correlated to activation marker expression in HIV/SIV disease progression (12) provided independent validation of this approach.

Lymph node biopsies and RNA extraction

Axillary or inguinal lymph node biopsies that had been obtained from two SMs prior to infection; two SMs at the peak of viral replication at 14 dpi; and two SMs at 30 dpi as viral loads were decreasing to set point. We analyzed axillary or inguinal LNs from 4 RMs without SIV infection and LNs from four RMs infected intravaginally with 2x105 TCID50 of SIVmac239 and sacrificed at 14 days p.i., the peak of viral replication; these animals were from two cross-sectional studies described in (13). For lymph node (LN) biopsies, animals were anesthetized with Ketamine or Telazol; the skin over the axillary or inguinal region was clipped and surgically prepped. An incision was made over the LN, which was exposed by blunt dissection and excised over clamps. A portion of the lymph node biopsy for microarray analysis was snap frozen in liquid N2. All animals were housed and cared for at the Yerkes National Primate Research Center in Atlanta, Georgia in accordance with the regulations of the American Association of Accreditation of Laboratory Animal Care standards.

Identifying genes differentially expressed in LNs in SMs and RMs

RNA extractions, synthesis of biotin-labeled cRNA probes, microarray hybridization, and data analysis for LNs followed previously published procedures (14). Briefly, snap-frozen lymph node was homogenized in TRIzol. Total RNA was isolated and further purified. Double stranded cDNA and biotin-labeled cRNA probes were synthesized, column purified and fragmented. Fifteen micrograms of fragmented cRNA was hybridized to an Affymetrix GeneChip® Rhesus Macaque Genome Array. After hybridization, chips were washed, stained with streptavidin-phycoerythrin, and scanned with GeneChip Operating Software at the Biomedical Genomics Center at the University of Minnesota. Preparation of cRNA probes and microarray hybridizations were done in duplicate for each RNA sample. Cel. files were uploaded into the Expressionist program (Genedata, Pro version 5.1) and the expression level for each of the 47,000 transcripts in the arrays were analyzed using the RMA algorithm. The expression levels from duplicate microarrays of the same animal's RNA were correlated and averaged. Tests for differences between the before and after infection at various time points were conducted using the 2-sample Wilcoxon signed-rank test. Fold differences in the level of gene expression between after infection and before infection were calculated with the ratio of the means. After statistical analysis, data was sorted based on these transcript cutoffs: p-value of < 0.05 and fold change ≥ 2.0. Significantly changed genes and transcripts were uploaded into NetAffix Analysis Center (http://www.affymetrix.com/analysis/index.affx) to query gene ontology information and into Ingenuity Pathways Analysis (Ingenuity® Systems, www.ingenuity.com) for gene annotation and pathway analysis. Hierarchical clustering analysis side-by-side with whole blood data was carried out by using Partek Genomics Suite software (Partek, Inc.).

RNA Purification and Real-time PCR

RNA was purified from whole blood using PAXgene as described in the Methods. RNA was purified from PBMCs using QIAGEN RNeasy columns, utilizing QIAShredder columns for homogenization and on-column DNAse digestion, according to manufacturer's protocols (QIAGEN, Inc.). Quantitative real time PCR was performed on total RNA using an ABI-PRISM 7900HT Sequence Detection System and SYBR green PCR Master Mix (Applied Biosystems). 200-1000 ng of RNA was reverse transcribed in a 10-20 μl reaction under the following conditions: 6.25 μM dN6 random hexanucleotide primer (Applied Biosystems), 50 mM TrisHCl pH 8.3, 3 mM $MgCl_2$, 75 mM KCl, 500 μM of dATP, dGTP, dTTP, and dCTP, 10 mM DTT and 200 U SuperScript II RNAse H^- reverse transcriptase at 42 ºC for 1 hr. Each qPCR reaction was performed in a volume of 10 μl with 0.1 μl of cDNA, primer pair and 5 μl of SYBR green PCR MasterMix in ABI-PRISM optical 386 well plates. Each primer pair was tested with a logarithmic dilution of cDNA to generate a standard curve, which was used to calculate the starting quantity of target RNA. Primers specific for GAPDH mRNA was used as an endogenous standard to normalize samples. Fold-change was calculated by dividing the normalized post-infected sample quantity with the normalized pre-infected control quantity. (Primer sequences are in Supplementary Table S10).

IFNα Stimulation of PBMCs

PBMCs purified from SM venous blood by density gradient centrifugation. $5x10^6$ PBMCs were cultured for 24 hrs in RPMI media supplemented with 10% heat inactivated fetal calf serum at 37 º C and varying concentrations of IFNα diluted in PBS, or PBS alone. PBMCs from uninfected SMs (Animal IDs: FEa1, FUa1, FJa1 FKa1) were treated with recombinant IFNα2a (kindly provided by Francois Villinger, Emory University) at 5,000 IU/ml. SIV-infected SMs (FUv, FSs, FRs, FWv) were the same animals used for microarray analysis and were SIV+ for 3.5 yrs; PBMCs from these animals were stimulated overnight with InterferonαA/D, a recombinant interferon with demonstrated activity on macaques (Sigma-Aldrich, St. Louis, MO, USA) at indicated concentrations. After stimulation, PBMCs were centrifuged for 5 min at 1500 rpm, media was aspirated and cells were lysed in 650 ml of RLT buffer with 1% β-mercaptoethanol. RNA was purified using RNeasy and qPCR for ISG expresseion performed as described above.

References

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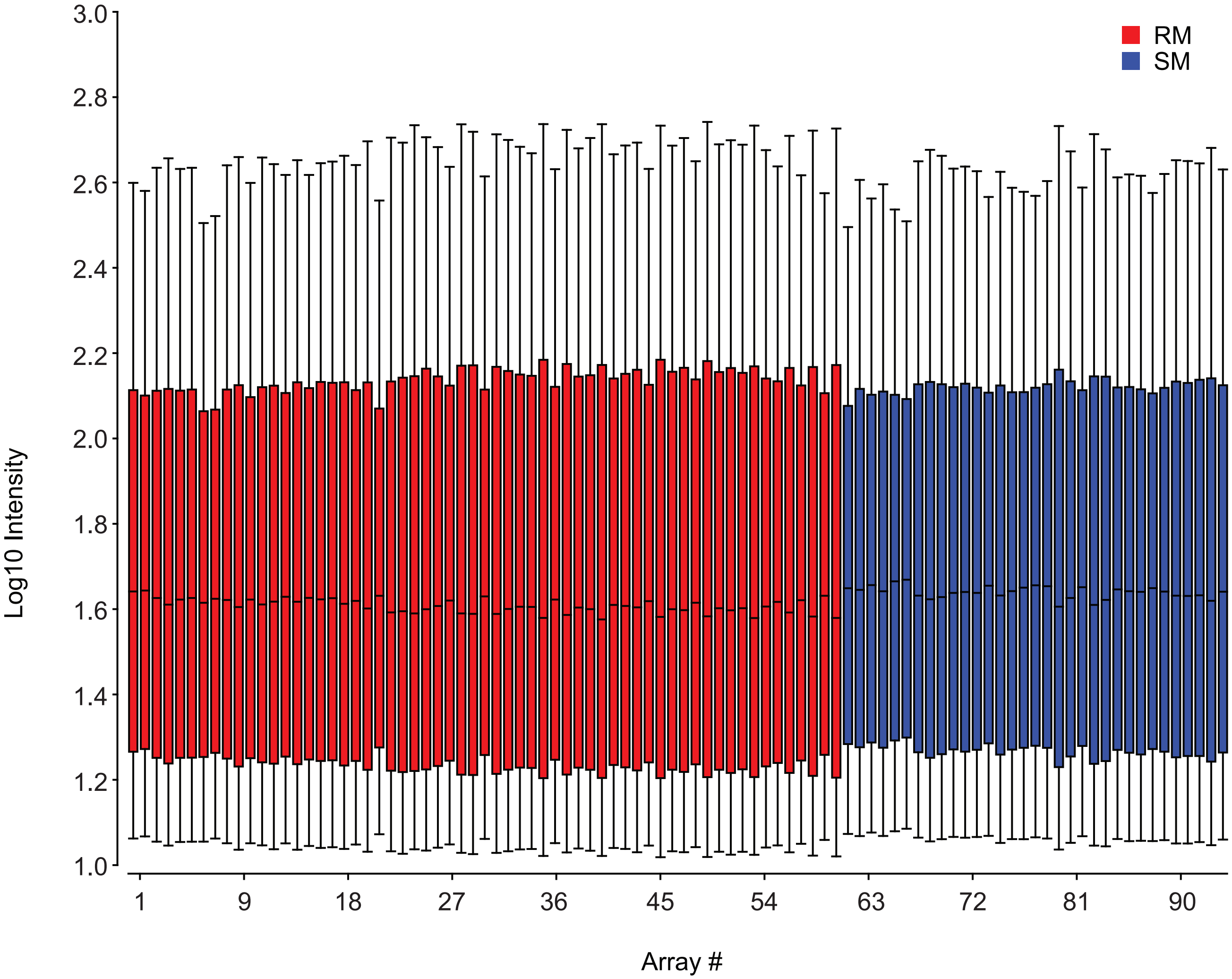


Supplementary Figure S1: Probeset intensities of Affymetrix arrays hybridized with RNA from rhesus macaques and sooty mangabeys are equivalent. Raw hybridization intensities from .CEL files were RMA normalized and log10 transformed. Box plots depict the median, 1st and 3rd quartiles of measured intensities over 52,865 probesets. Whiskers range to the top 90% and bottom 10% of the data range.

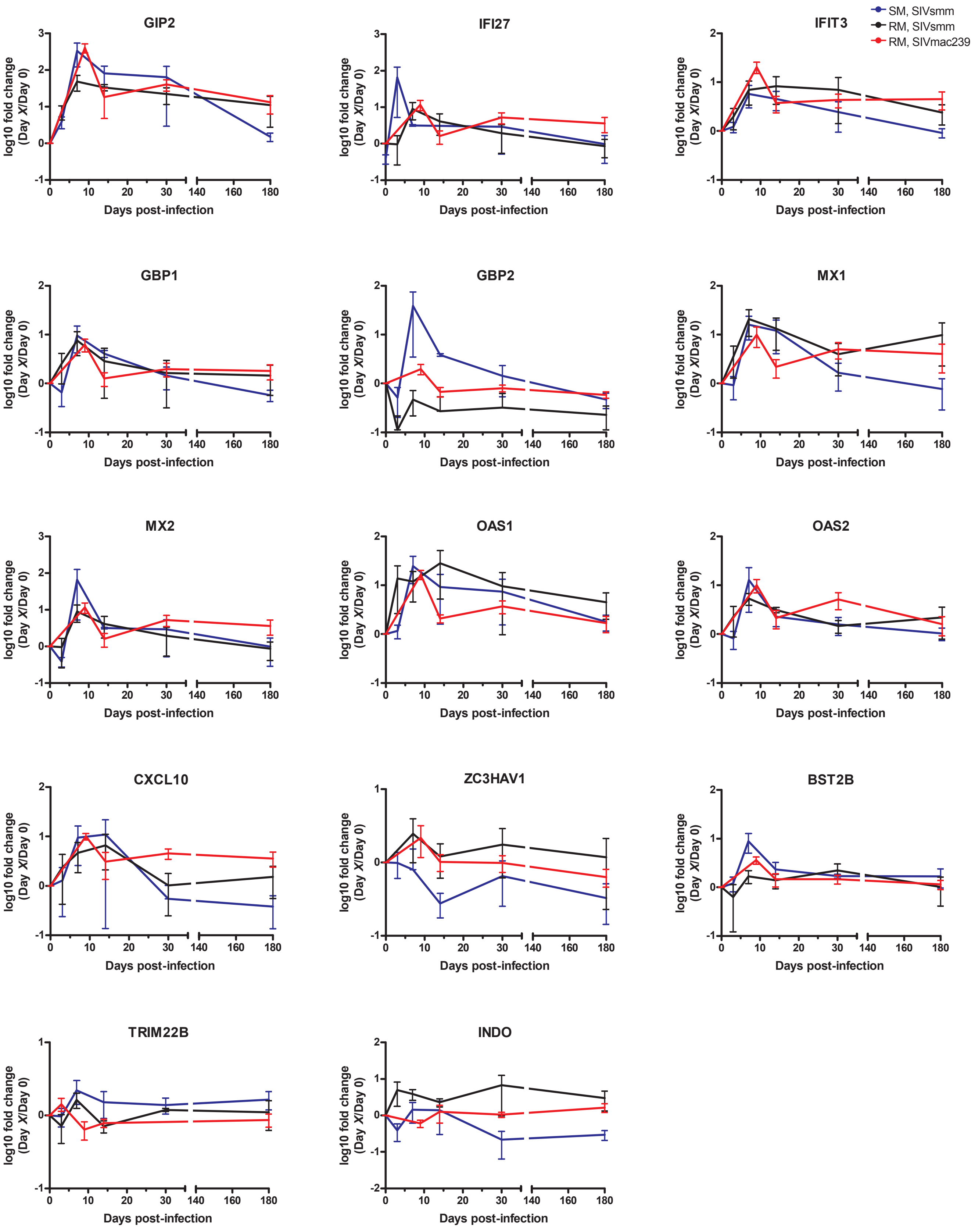
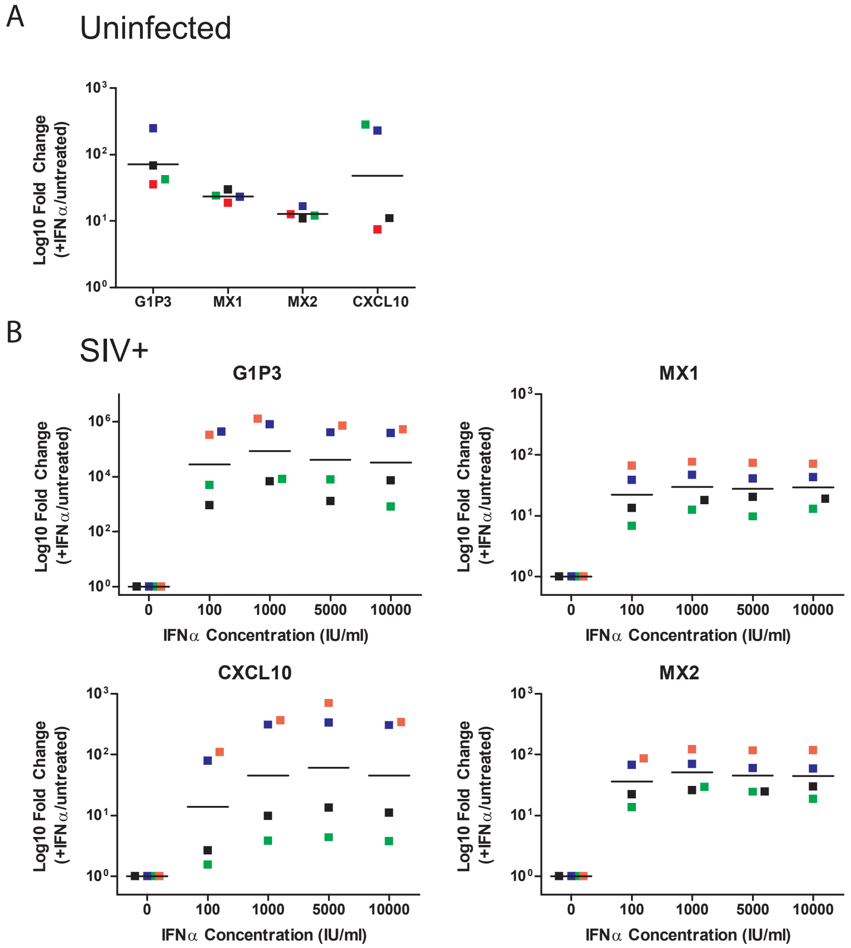
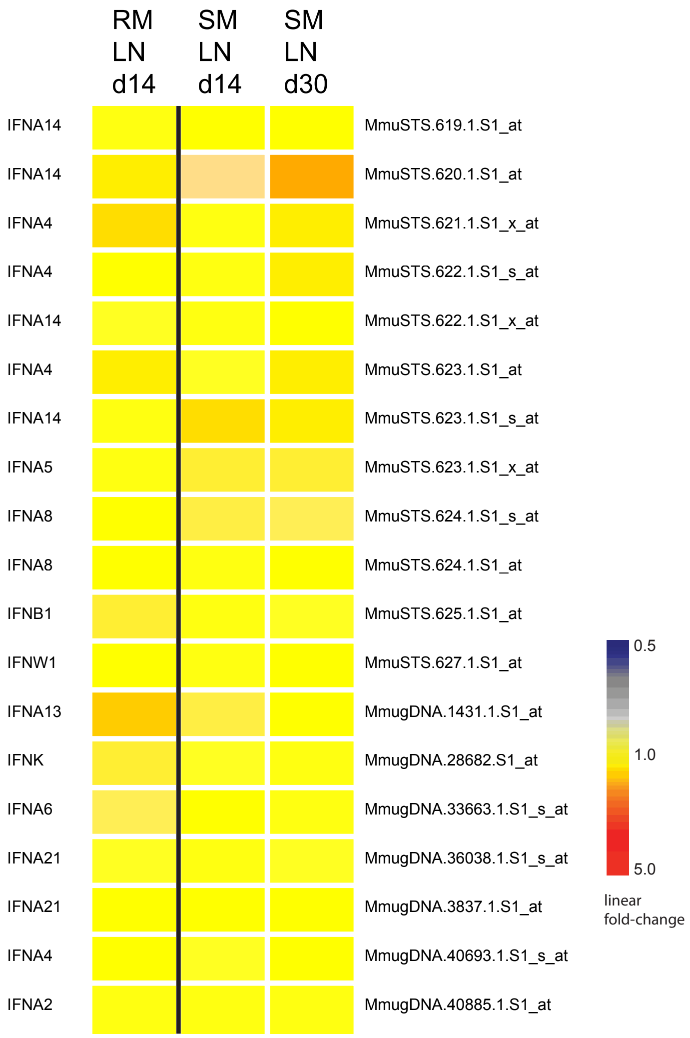


Figure S2. Real-time PCR validation of microarray gene expression. cDNA was generated from RNA samples used for microarray analysis. HUGO gene names are above resprective line graphs, x-axis indicates time after infection, y-axis represents log10 fold-change assessed by real-time PCR. Fold-changes are expressed as mean±SEM. Blue lines indicate SIV$_{smm}$-infected SMs, black- SIV$_{smm}$-infected RMs and red- SIV$_{mac239}$-infected RMs. Primer sequences are indicated Supplementary Table S10.



Supplementary Figure S3. ISG induction in response to IFNα in SM PBMCs. PBMCs from four uninfected (A) and four of the five SIVsmm-infected SMs used for the array analysis (B) were stimulated for 24 hr with IFNα. PBMCs from uninfected animals were treated with 5,000 IU/ml recombinant SM IFNα; PBMCs from infected animals were treated for 24 hrs with recombinant consensus IFNα at the concentration indicated on the *x* axis. Coloured squares indicate individual animal, horizontal lines indicate the mean fold-change



Supplementary Figure S4. Heat map of Type I and II IFNs expressed in lymph nodes during SIV infection in SMs and RMs. Gene symbol indicated at left, probeset ID indicated at right. Colour scale is indicated at right.

Supplementary Table S1. Global log10 intensity statistics of *Cercocebus atys* and *Macaca mulatta* total RNA hybridized on Affymetrix GeneChip Rhesus Macaque Genome Arrays.

		Cercocebus atys	***Macaca mulatta***	***All samples***
Animals (n)		5	12	17
# arrays		33	61	94
Log10 Probeset Intensity†	Mean	1.76	1.75	1.75
	Median	1.65	1.62	1.63
	Range	0.77-4.50	0.75-4.51	0.75-4.51
	Std. Dev.	0.61	0.64	0.63

† Intensity statistics determined using 52,024 probesets; probesets representing control, reporter or viral sequences were excluded from analysis.

Supplementary Table S2. In silico analysis of Rhesus GeneChip probesets with known SM cDNAs.

					# of probes in each set with the given number of mismatches							proportion of probes in each set with the given number of mismatches						
GenBank Accession *	GenBank Definition *	Affymetrix Probeset ID	Probeset Gene Symbol	# probes	0	1	2	3	4	5	>5	0	1	2	3	4	5	>5 or indel
DQ645390.1	Cercocebus torquatus atys interleukin 13 mRNA, complete cds	Mmu.5696.1.S1_at	IL13	11	9	1	1	0	0	0	0	0.82	0.09	0.09	0	0	0	0
DQ863275.1	Cercocebus torquatus atys tumor necrosis factor alpha mRNA, complete cds	Mmu.14298.1.S1_at	TNF-ALPHA	11	9	2	0	0	0	0	0	0.82	0.18	0	0	0	0	0
EF113920.1	Cercocebus torquatus atys tripartite motif-containing 5 alpha isoform (TRIM5) mRNA, TRIM5-Ceat-1 allele, complete cds	Mmu.13018.2.S1_a_at	TRIM5	11	8	3	0	0	0	0	0	0.73	0.27	0	0	0	0	0
EF113921.1	Cercocebus torquatus atys tripartite motif-containing 5 alpha isoform (TRIM5) mRNA, TRIM5-Ceat-2 allele, complete cds	Mmu.13018.1.S1_at	TRIM5	11	8	2	1	0	0	0	0	0.73	0.18	0.09	0	0	0	0
EF113922.1	Cercocebus torquatus atys tripartite motif-containing 5 alpha isoform (TRIM5) mRNA, TRIM5-Ceat-3 allele, complete cds	Mmu.13018.2.S1_a_at	TRIM5	11	8	3	0	0	0	0	0	0.73	0.27	0	0	0	0	0
EF113923.1	Cercocebus torquatus atys tripartite motif-containing 5 alpha isoform (TRIM5) mRNA, TRIM5-Ceat-4 allele, complete cds	Mmu.13018.2.S1_a_at	TRIM5	11	9	2	0	0	0	0	0	0.82	0.18	0	0	0	0	0
EF113923.1	Cercocebus torquatus atys tripartite motif-containing 5 alpha isoform (TRIM5) mRNA, TRIM5-Ceat-4 allele, complete cds	Mmu.13018.1.S1_at	TRIM5	11	9	1	1	0	0	0	0	0.82	0.09	0.09	0	0	0	0
EF444798.1	Cercocebus torquatus atys clone SMPDL2 programmed cell death ligand 2 mRNA, complete cds, alternatively spliced	MmugDNA.36670.1.S1_at	---	11	4	4	0	0	1	0	2	0.36	0.36	0	0	0.09	0	0.18
EF444801.1	Cercocebus torquatus atys clone FDNJQPDL2 programmed cell death ligand 2 mRNA, complete cds, alternatively spliced	MmugDNA.36670.1.S1_at	---	11	3	6	2	0	0	0	0	0.27	0.55	0.18	0	0	0	0
EF444804.1	Cercocebus torquatus atys clone FECBBPDL2 programmed cell death ligand 2 mRNA, complete cds, alternatively spliced	MmugDNA.36670.1.S1_at	---	11	7	4	0	0	0	0	0	0.64	0.36	0	0	0	0	0
AF344839.1	AF344839 Cercocebus torquatus atys CD80 protein (MnB71) mRNA, complete cds	MmugDNA.16293.1.S1_at	CD80	11	5	3	0	0	0	0	3	0.46	0.27	0	0	0	0	0.27
"	"	MmugDNA.29916.1.S1_at	CD80	11	4	0	0	0	0	0	7	0.36	0	0	0	0	0	0.64
AF344840.1	AF344840 Cercocebus torquatus atys CD86 protein precursor, mRNA, complete cds	MmugDNA.32699.1.S1_at	CD86	11	9	2	0	0	0	0	0	0.82	0.18	0	0	0	0	0
"	"	MmugDNA.6272.1.S1_at	CD86	11	2	0	0	0	0	0	9	0.18	0	0	0	0	0	0.82
AF344841.1	AF344841 Cercocebus torquatus atys CD154 protein mRNA, complete cds	Mmu.4194.1.S1_at	CD40LG	11	11	0	0	0	0	0	0	1.00	0	0	0	0	0	0
"	"	MmuSTS.4670.1.S1_s_at	CD40LG	16	1	0	0	0	0	0	15	0.06	0	0	0	0	0	0.94
AF344842.1	AF344842 Cercocebus torquatus atys CD28 protein mRNA, complete cds	MmugDNA.27546.1.S1_s_at	CD28	11	10	0	1	0	0	0	0	0.91	0	0.09	0	0	0	0
"	"	MmugDNA.27543.1.S1_at	CD28	11	9	0	1	1	0	0	0	0.82	0	0.09	0.09	0	0	0
AF344843.1	AF344843 Cercocebus torquatus atys FAS antigen CD95 mRNA, complete cds	MmugDNA.18450.1.S1_s_at	FAS	11	8	3	0	0	0	0	0	0.73	0.27	0	0	0	0	0
"	"	MmuSTS.4665.1.S1_at	FAS	16	5	0	0	0	0	0	11	0.31	0	0	0	0	0	0.69
AF344847.1	AF344847 Cercocebus torquatus atys CD95L protein (CD95L) mRNA, complete cds	MmugDNA.8857.1.S1_at	LOC574159	11	9	1	0	0	0	0	1	0.82	0.09	0	0	0	0	0.09
AF344848.1	AF344848 Cercocebus torquatus atys clone MNCTLA4 CD152 protein (CTLA-4) mRNA, complete cds	MmugDNA.5921.1.S1_s_at	CTLA-4	11	11	0	0	0	0	0	0	1.00	0	0	0	0	0	0
"	"	MmugDNA.30020.1.S1_at	CTLA-4	11	10	1	0	0	0	0	0	0.91	0.09	0	0	0	0	0
"	"	MmugDNA.25217.1.S1_at	CTLA-4	11	3	2	0	0	0	0	6	0.27	0.18	0	0	0	0	0.55
EU131369.1	Cercocebus torquatus atys clone FEa1 sialic acid binding Ig-like lectin 5 (SIGLEC5) mRNA, complete cds	MmugDNA.14326.1.S1_at	SIGLEC5	16	5	3	1	0	0	0	7	0.31	0.19	0.06	0	0	0	0.44
EU131370.1	Cercocebus torquatus atys clone FHaI sialic acid binding Ig-like lectin 5 (SIGLEC5) mRNA, complete cds	MmugDNA.14326.1.S1_at	SIGLEC5	16	7	1	1	0	0	0	7	0.44	0.06	0.06	0	0	0	0.44
EU124695.1	Cercocebus torquatus atys TRIM22 (TRIM22) mRNA, complete cds	Mmu.2142.1.S1_at	TRIM22	11	3	0	0	0	0	0	8	0.27	0	0	0	0	0	0.73
EU204916.1	Cercocebus torquatus atys interferon regulatory factor 7 mRNA, complete cds	MmugDNA.29625.1.S1_at	LOC699578	16	10	5	1	0	0	0	0	0.63	0.31	0.06	0	0	0	0
EU204918.1	Cercocebus torquatus atys interferon regulatory factor 3 mRNA, complete cds	Mmu.5468.1.S1_at	IRF3	11	9	1	1	0	0	0	0	0.82	0.09	0.09	0	0	0	0
EU204918.1	Cercocebus torquatus atys interferon regulatory factor 3 mRNA, complete cds	MmugDNA.21023.1.S1_at	IRF3	16	11	2	0	0	0	0	3	0.69	0.13	0	0	0	0	0.19
EU204920.1	Cercocebus torquatus atys interferon regulatory factor 2 mRNA, complete cds	Mmu.11885.2.S1_at	IRF2	11	10	0	0	0	0	0	1	0.91	0	0	0	0	0	0.09
EU204931.1	Cercocebus torquatus atys Toll-like receptor 1 mRNA, complete cds	MmuSTS.4595.1.S1_at	TLR1	16	13	3	0	0	0	0	0	0.81	0.19	0	0	0	0	0
EU204932.1	Cercocebus torquatus atys Toll-like receptor 2 mRNA, complete cds	MmuSTS.1204.1.S1_at	TLR2	16	16	0	0	0	0	0	0	1.00	0	0	0	0	0	0
EU204935.1	Cercocebus torquatus atys Toll-like receptor 3 mRNA, complete cds	MmugDNA.5783.1.S1_at	TLR3	16	12	4	0	0	0	0	0	0.75	0.25	0	0	0	0	0
EU204937.1	Cercocebus torquatus atys Toll-like receptor 4 mRNA, complete cds	Mmu.3422.1.A1_at	---	11	9	0	0	0	0	0	2	0.82	0	0	0	0	0	0.18
EU204937.1	Cercocebus torquatus atys Toll-like receptor 4 mRNA, complete cds	MmugDNA.19245.1.S1_at	TLR4	11	6	5	0	0	0	0	0	0.55	0.46	0	0	0	0	0
EU204938.1	Cercocebus torquatus atys Toll-like receptor 5 mRNA, complete cds	MmuSTS.4033.1.S1_at	TLR5	16	15	0	0	0	0	0	1	0.94	0	0	0	0	0	0.06
EU204942.1	Cercocebus torquatus atys Toll-like receptor 7 mRNA, complete cds	MmugDNA.37911.1.S1_at	TLR7	11	9	0	0	0	0	0	2	0.82	0	0	0	0	0	0.18
EU204945.1	Cercocebus torquatus atys Toll-like receptor 8 mRNA, partial cds	MmuSTS.4034.1.S1_at	TLR8	16	16	0	0	0	0	0	0	1.00	0	0	0	0	0	0
EU204946.1	Cercocebus torquatus atys Toll-like receptor 9 mRNA, complete cds	MmuSTS.4035.1.S1_at	TLR9	16	11	5	0	0	0	0	0	0.69	0.31	0	0	0	0	0
U75385.1	CTU75385 Cercocebus torquatus atys prion protein (PrP) gene, partial cds	MmugDNA.29782.1.S1_at	LOC699249	11	6	0	0	0	0	0	5	0.55	0	0	0	0	0	0.46
EU204956.1	Cercocebus torquatus atys interferon alpha 2 gene, promoter region and complete cds	MmugDNA.40885.1.S1_at	LOC709948	16	4	1	0	0	0	0	11	0.25	0.06	0	0	0	0	0.69
EU204957.1	Cercocebus torquatus atys interferon beta 1 gene, promoter region and complete cds	MmuSTS.625.1.S1_at	IFNB1	16	8	2	1	0	0	0	5	0.50	0.13	0.06	0	0	0	0.31
EU204940.1	Cercocebus torquatus atys Toll-like receptor 6 mRNA, complete cds	MmugDNA.38658.1.S1_at	TLR6	16	4	3	0	0	0	0	9	0.25	0.19	0	0	0	0	0.56
EU204925.1	Cercocebus torquatus atys interleukin 1 receptor-associated kinase 1 mRNA, partial cds	MmugDNA.29193.1.S1_at	LOC696602	11	11	0	0	0	0	0	0	1.00	0	0	0	0	0	0
U76920.1	CTU76920 Cercocebus torquatus atys lysozyme c precursor (LZM) mRNA, complete cds	MmugDNA.22297.1.S1_at	LYZ	11	11	0	0	0	0	0	0	1.00	0	0	0	0	0	0
AF480026.1	Cercocebus torquatus atys isolate B400 CD209L2 gene, partial sequence	Mmu.5240.1.S1_at	CD209L2	11	3	2	0	0	0	0	6	0.27	0.18	0	0	0	0	0.55
AF051902.1	AF051902 Cercocebus torquatus atys 079 chemokine receptor CCR5 gene, complete cds	Mmu.14249.1.S1_at	CCR5	11	7	3	1	0	0	0	0	0.64	0.27	0.09	0	0	0	0
AF051903.1	AF051903 Cercocebus torquatus atys 085 chemokine receptor CCR5 gene, complete cds	Mmu.14249.1.S1_at	CCR5	11	8	3	0	0	0	0	0	0.73	0.27	0	0	0	0	0
AF051904.1	AF051904 Cercocebus torquatus atys 087 chemokine receptor CCR5 gene, complete cds	Mmu.14249.1.S1_at	CCR5	11	8	1	2	0	0	0	0	0.73	0.09	0.18	0	0	0	0
AF051905.1	AF051905 Cercocebus torquatus atys 089 chemokine receptor CCR5 gene, complete cds	Mmu.14249.1.S1_at	CCR5	11	8	3	0	0	0	0	0	0.73	0.27	0	0	0	0	0
AF051906.1	AF051906 Cercocebus torquatus atys PJG chemokine receptor CXCR4 mRNA, complete cds	MmuSTS.4017.1.S1_at	CXCR4	16	13	1	1	0	0	0	1	0.81	0.06	0.06	0	0	0	0.06
AY544576.1	Cercocebus torquatus atys immunoglobulin gamma-1 heavy chain constant region (IGHG1) gene, partial cds	MmuSTS.4348.1.S1_at	IGHG1	16	10	3	3	0	0	0	0	0.63	0.19	0.19	0	0	0	0
AY544577.1	Cercocebus torquatus atys immunoglobulin gamma-2 heavy chain constant region (IGHG2) gene, partial cds	MmuSTS.4348.1.S1_at	IGHG1	16	4	9	3	0	0	0	0	0.25	0.56	0.19	0	0	0	0
AY544578.1	Cercocebus torquatus atys immunoglobulin gamma-3 heavy chain constant region (IGHG3) gene, partial cds	MmuSTS.4348.1.S1_at	IGHG1	16	6	5	3	2	0	0	0	0.38	0.31	0.19	0.13	0	0	0
AY544579.1	Cercocebus torquatus atys immunoglobulin gamma-4 heavy chain constant region (IGHG4) gene, partial cds	MmuSTS.4348.1.S1_at	IGHG1	16	5	6	4	1	0	0	0	0.31	0.38	0.25	0.06	0	0	0
AY544580.1	Cercocebus torquatus atys immunoglobulin alpha heavy chain (IGHA) mRNA, IGHA-1 allele, partial cds	MmugDNA.41975.1.S1_at	---	11	6	1	1	1	1	0	1	0.55	0.09	0.09	0.09	0.09	0	0.09
"	"	MmugDNA.42358.1.S1_s_at	---	11	6	0	0	0	0	0	5	0.55	0	0	0	0	0	0.46
"	"	Mmu.15103.2.S1_at	---	11	5	2	3	0	0	1	0	0.46	0.18	0.27	0	0	0.09	0
AY544581.1	Cercocebus torquatus atys immunoglobulin alpha heavy chain (IGHA) mRNA, IGHA-2 allele, partial cds	MmugDNA.41975.1.S1_at	---	11	6	2	1	0	0	1	1	0.55	0.18	0.09	0	0	0.09	0.09
AY552755.1	Cercocebus torquatus atys haptoglobin gene, exon 5 and partial cds	MmuSTS.598.1.S1_at	HP	16	8	4	0	0	0	0	4	0.50	0.25	0	0	0	0	0.25
AY552413.1	Cercocebus torquatus atys haptoglobin-related protein (Hpr) mRNA, partial cds	MmuSTS.598.1.S1_at	HP	16	6	2	1	1	0	2	4	0.38	0.13	0.06	0.06	0	0.13	0.25
AY686135.1	Cercocebus torquatus atys isolate G078 cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial	Mmu.15402.10.S1_s_at	---	11	5	1	3	1	1	0	0	0.455	0.09	0.27	0.09	0.09	0	0

* " indicates matched SM cDNA to multiple probesets; " denotes the cDNA above.

Supplementary Table S3. Hemoglobin RNA blocking Peptide-Nucleic Acid (PNA) oligonucleotide sequences.

Name	**Sequence**[†]	**Concentration (nM)**	**Target**
huPNA1	5'-Ac-TAA CGG TAT TTG GAG-3'	290	HBA
rhPNA2	5'-Ac-GTA GTT GGA CTT TGG-3'	580	HBB
huPNA3	5'-Ac-GCC CTT CAT AAT ATC-3'	580	HBB
rhPNA4	5'-Ac- ATC CAG ATC CTC AAG-3'	580	HBB
simconPNA	5'Ac- TGA GCT TAG TGG TAC-3'	580	HBB

[†] Ac - Acetylated

Supplemental Table S4. 428 probesets detected as differential after SIVsmm infection of SMs in RNA derived from total blood. The Affymetrix Gene Symbol refers to the annotation of the Affymetrix Rhesus Genome Array provided by Affymetrix, Inc. (v.27) which is based on the most recent build of the Unigene Rhesus Macaque genome (Build #13). The Corrected Gene Symbol column refers to updates to the annotation by cross-referencing Probeset IDs with human orthologues using the DAVID database (http://david.abcc.ncifcrf.gov/list.jsp). The DX /D0 columns describe the linear ratio of overexpressed (red >+2-fold) and underexpressed (green <-2-fold) genes. Gene Description were obtained from the DAVID database based on human annotation.

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	Gene Description
MmugDNA.41706.1.S1_at	---	RSAD2	1.07E-12	1.71	91.63	74.94	29.27	5.52	1.30	radical s-adenosyl methionine domain containing 2
MmuSTS.1497.1.S1_at	---	RSAD2	5.34E-09	1.74	49.95	49.42	17.85	4.93	1.32	radical s-adenosyl methionine domain containing 2
MmuSTS.4748.1.S1_at	---	USP18	8.36E-16	1.61	50.45	44.75	9.22	3.54	1.39	ubiquitin specific peptidase 18
MmuSTS.1612.1.S1_at	LOC698943	OASL	1.87E-10	1.44	27.76	35.26	6.49	3.10	1.09	2'-5'-oligoadenylate synthetase-like
MmugDNA.21336.1.S1_at	LOC708602	CMPK2	1.58E-08	1.46	53.66	32.50	10.57	3.38	1.39	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
MmugDNA.17118.1.S1_at	LOC700141	ISG15	2.44E-08	1.23	28.51	30.54	5.19	2.70	1.21	interferon, alpha-inducible protein (clone ifi-15k)
MmugDNA.38910.1.S1_at	AMBP	HERC5	6.07E-10	1.92	39.08	29.87	13.20	6.55	1.18	hect domain and rld 5
MmuSTS.3006.1.S1_at	MX1	MX1	8.61E-09	1.90	32.27	27.07	7.94	5.03	1.87	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
MmugDNA.12892.1.S1_at	LOC707854	IFI44	1.93E-08	1.82	45.84	24.30	18.22	5.86	1.43	interferon-induced protein 44
MmuSTS.4655.1.S1_at	OAS1	OAS1	2.74E-14	1.25	18.11	23.84	5.52	2.29	1.35	2',5'-oligoadenylate synthetase 1, 40/46kda
MmugDNA.19594.1.S1_at	LOC695344	IFIT3	9.14E-13	1.67	27.27	20.60	6.68	2.93	1.07	interferon-induced protein with tetratricopeptide repeats 3
MmuSTS.3682.1.S1_x_at	LOC707854	IFI44	1.51E-07	1.89	37.34	18.85	17.04	5.28	1.27	interferon-induced protein 44
MmugDNA.27193.1.S1_at	LOC693567	FLJ20035	2.00E-08	1.73	28.90	18.47	9.16	2.98	1.14	hypothetical protein flj10787
MmuSTS.1893.1.S1_s_at	---	CXCL10	2.76E-10	1.24	16.60	17.93	4.12	1.36	1.15	chemokine (c-x-c motif) ligand 10
MmuSTS.1579.1.S1_at	IFIT1	IFIT1	7.67E-07	1.06	17.74	17.45	5.63	2.61	-1.43	interferon-induced protein with tetratricopeptide repeats 1
MmugDNA.11735.1.S1_at	---	DDX58	2.61E-10	1.61	18.95	16.99	5.45	2.99	1.16	dead (asp-glu-ala-asp) box polypeptide 58
MmuSTS.4428.1.S1_at	LOC702381	IFI6	5.65E-11	1.40	10.70	16.84	5.93	3.88	1.63	interferon, alpha-inducible protein (clone ifi-6-16)
MmuSTS.713.1.S1_at	LOC697698	TTLL6	1.18E-09	1.55	18.81	15.08	5.03	2.84	1.27	Similar to tubulin tyrosine ligase-like family, member 6
MmugDNA.5747.1.S1_at	IFIT2	IFIT2	6.82E-12	1.64	23.93	14.42	8.01	3.38	-1.00	Similar to tubulin tyrosine ligase-like family, member 6
MmugDNA.22912.1.S1_s_at	GBP1	GBP1	4.24E-08	1.78	14.10	14.41	5.19	2.32	1.10	guanylate binding protein 1, interferon-inducible, 67kda
MmugDNA.36433.1.S1_at	LOC694684	GBP2	1.75E-09	1.32	12.46	14.37	2.76	1.96	1.11	guanylate binding protein 2, interferon-inducible
MmugDNA.6512.1.S1_at	LOC699458	LOC26010	9.66E-07	1.29	9.40	13.36	3.41	1.56	1.56	dna polymerase-transactivated protein 6
MmugDNA.20819.1.S1_at	LOC712342	OAS3	3.30E-10	1.31	15.14	13.24	3.41	2.20	1.24	2'-5'-oligoadenylate synthetase 3, 100kda
MmugDNA.35740.1.S1_at	IFIT2	IFIT2	6.40E-10	1.10	17.31	12.52	4.61	2.79	-1.49	interferon-induced protein with tetratricopeptide repeats 2
MmuSTS.713.1.S1_x_at	LOC697698	TTLL6	1.43E-10	1.35	14.04	12.10	3.95	2.45	1.08	Similar to tubulin tyrosine ligase-like family, member 6
MmugDNA.30921.1.S1_at	LOC705525	HERC6	1.72E-12	1.26	10.83	11.23	3.71	1.95	1.12	Similar to tubulin tyrosine ligase-like family, member 6
MmuSTS.2397.1.S1_s_at	LOC694684	GBP2	2.63E-08	1.22	8.23	11.05	2.57	1.78	1.10	guanylate binding protein 2, interferon-inducible
MmugDNA.8486.1.S1_at	LOC712401	OAS2	3.10E-09	1.34	15.72	11.01	3.32	1.84	1.26	2'-5'-oligoadenylate synthetase 2, 69/71kda
MmugDNA.20634.1.S1_at	LOC697698	DHX58	8.96E-11	1.22	13.08	10.32	3.04	2.18	1.17	likely ortholog of mouse d11lgp2
MmugDNA.25674.1.S1_at	LOC699580	KCTD14	5.11E-09	1.22	5.12	10.29	2.53	1.40	1.34	potassium channel tetramerisation domain containing 14
MmugDNA.41315.1.S1_at	GBP1	GBP1	1.02E-09	1.54	10.93	10.11	5.81	2.10	1.25	guanylate binding protein 1, interferon-inducible, 67kda
MmugDNA.208.1.S1_at	---	SECTM1	6.06E-08	1.26	4.84	9.52	2.64	1.74	1.12	secreted and transmembrane 1
MmugDNA.32616.1.S1_at	LOC713425	XAF1	1.10E-07	1.14	6.38	9.52	2.93	1.95	1.20	xiap associated factor-1
Mmu.10088.2.S1_at	MX2	MX2	6.48E-07	1.32	11.46	9.28	2.83	2.10	1.24	myxovirus (influenza virus) resistance 2 (mouse)
MmuSTS.1377.1.S1_at	LOC695971	BCL2L14	9.65E-10	1.15	5.26	9.11	2.28	1.21	1.28	bcl2-like 14 (apoptosis facilitator)
MmugDNA.1672.1.S1_at	LOC694699	TNFAIP6	2.58E-09	-1.22	4.74	8.65	2.18	1.16	-2.44	tumor necrosis factor, alpha-induced protein 6
Mmu.3779.1.S1_at	LOC695344	IFIT3	6.47E-10	-1.10	7.23	8.30	2.06	1.57	-1.31	interferon-induced protein with tetratricopeptide repeats 3
MmuSTS.2737.1.S1_at	ADAMDEC1	ADAMDEC1	2.11E-06	1.56	2.56	8.26	4.20	1.73	1.10	adam-like, decysin 1
MmugDNA.29625.1.S1_at	LOC699578	IRF7	5.15E-09	1.14	5.10	8.04	2.41	1.84	1.07	interferon regulatory factor 7
MmugDNA.33882.1.S1_at	---	TRIM14	1.82E-08	1.51	7.38	7.99	3.93	2.27	1.34	tripartite motif-containing 14
Mmu.865.1.S1_at	OAS1	OAS1	5.58E-11	-1.05	4.98	7.91	1.80	1.34	1.04	2',5'-oligoadenylate synthetase 1, 40/46kda
MmugDNA.8521.1.S1_at	GOT2	GOT2	2.31E-09	1.01	6.35	7.79	2.64	1.84	-1.09	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
MmuSTS.1927.1.S1_at	MX2	MX2	7.21E-08	1.32	9.07	7.55	3.62	2.18	1.21	myxovirus (influenza virus) resistance 2 (mouse)
MmugDNA.20819.1.S1_s_at	LOC712342	OAS3	1.01E-10	1.09	8.32	7.54	2.70	1.92	1.06	2'-5'-oligoadenylate synthetase 3, 100kda
MmugDNA.7695.1.S1_at	---	IFIT5	5.13E-11	1.14	7.15	7.34	2.93	1.77	-1.08	interferon-induced protein with tetratricopeptide repeats 5
MmugDNA.31670.1.S1_at	PTPRA	FAM70A	1.77E-08	1.14	13.45	7.26	2.75	1.39	1.30	family with sequence similarity 70, member a
MmugDNA.22278.1.S1_at	---	DDX58	5.17E-10	1.12	7.24	7.19	2.52	1.63	1.02	dead (asp-glu-ala-asp) box polypeptide 58
MmugDNA.19136.1.S1_at	---	CCDC75	2.60E-06	1.69	9.42	7.08	3.62	2.21	1.16	coiled-coil domain containing 75
MmuSTS.4660.1.S1_at	LOC694699	TNFAIP6	9.21E-07	-1.05	4.08	7.06	1.89	1.04	-2.21	tumor necrosis factor, alpha-induced protein 6
MmugDNA.40648.1.S1_at	LOC707769	JUP	1.59E-08	-1.03	3.61	7.03	1.29	1.04	1.05	junction plakoglobin
MmuSTS.1778.1.S1_at	SCIN	SCIN	1.70E-08	1.19	3.30	6.94	1.40	1.20	-1.12	scinderin
MmugDNA.23571.1.S1_at	---	EPSTI1	2.95E-07	1.24	6.52	6.79	2.36	2.12	1.09	epithelial stromal interaction 1 (breast)
MmugDNA.33861.1.S1_at	LOC713425	XAF1	2.81E-07	1.13	7.59	6.70	3.24	1.97	1.08	xiap associated factor-1
MmugDNA.15476.1.S1_at	LOC700208	EPSTI1	2.94E-08	1.30	6.90	6.66	2.71	1.90	1.18	epithelial stromal interaction 1 (breast)
MmugDNA.24962.1.S1_at	LOC695344	IFIT3	5.35E-12	1.49	7.62	6.30	4.78	2.34	-1.01	interferon-induced protein with tetratricopeptide repeats 3
MmugDNA.16654.1.S1_at	---	GBP2	2.47E-07	1.15	5.82	6.17	2.13	1.18	1.03	guanylate binding protein 2, interferon-inducible
MmugDNA.8893.1.S1_at	LOC715369	CORO2A	1.33E-06	1.12	3.48	6.16	1.40	1.38	1.29	coronin, actin binding protein, 2a
Mmu.11584.1.S1_at	LOC719092	BST2	4.56E-07	1.27	4.31	6.14	2.43	1.72	1.07	bone marrow stromal cell antigen 2
MmugDNA.19189.1.S1_at	DDX58	DDX58	3.41E-08	-1.11	3.75	6.09	1.29	1.02	-1.10	dead (asp-glu-ala-asp) box polypeptide 58
MmuSTS.1439.1.S1_at	LGALS3BP	LGALS3BP	6.01E-08	1.06	3.74	5.96	1.55	1.37	1.13	lectin, galactoside-binding, soluble, 3 binding protein
MmugDNA.36297.1.S1_at	IFIH1	IFIH1	2.41E-08	1.58	7.95	5.76	3.17	1.81	-1.03	interferon induced with helicase c domain 1
Mmu.12633.1.S1_at	LOC715591	PARP14	6.11E-08	1.38	5.86	5.36	2.52	1.56	1.04	poly (adp-ribose) polymerase family, member 14
MmugDNA.23544.1.S1_s_at	LOC694225	FCGR2C	6.42E-11	1.26	3.29	5.35	1.53	1.40	-1.10	fc fragment of igg, low affinity iic, receptor for (cd32)
MmugDNA.13092.1.S1_at	---	SHROOM4	1.20E-05	1.06	4.19	5.26	1.99	1.24	1.00	kiaa1202 protein
MmugDNA.20321.1.S1_at	LOC719142	HIRA	0.000536686	1.51	3.84	5.18	1.53	1.75	1.46	hir histone cell cycle regulation defective homolog a (s. cerevisiae)
Mmu.11961.1.S1_x_at	GBP1	GBP1	0.000491867	1.02	3.89	5.05	2.01	1.17	-1.29	guanylate binding protein 1, interferon-inducible, 67kda
MmugDNA.27480.1.S1_s_at	LOC710375	LGALS8	6.46E-06	1.04	5.80	5.01	1.76	1.38	-1.11	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.8112.1.S1_at	---	RNF213	5.92E-07	1.37	5.13	4.99	2.29	1.68	1.14	chromosome 17 open reading frame 27
Mmu.13018.2.S1_a_at	TRIM5	TRIM5	3.36E-07	-1.04	2.65	4.98	1.25	1.25	-1.30	tripartite motif-containing 5
MmugDNA.28694.1.S1_s_at	---	ZCCHC2	8.95E-07	1.19	6.31	4.97	2.94	1.83	-1.11	zinc finger, cchc domain containing 2
Mmu.11960.1.S1_at	GBP1	GBP1	0.000185398	1.00	3.01	4.91	1.55	1.39	1.01	guanylate binding protein 1, interferon-inducible, 67kda
MmugDNA.35760.1.S1_at	LOC708404	RTP4	1.37E-06	1.15	4.41	4.78	2.26	1.42	-1.00	receptor transporter protein 4
MmugDNA.29993.1.S1_s_at	LOC694225	FCGR2B	8.84E-10	1.33	3.31	4.78	1.67	1.41	1.10	fc fragment of igg, low affinity iib, receptor (cd32)
MmugDNA.5999.1.S1_at	---	ZCCHC2	9.24E-08	1.30	4.01	4.73	1.68	1.86	1.06	zinc finger, cchc domain containing 2
MmugDNA.32611.1.S1_s_at	LOC715462	SLFN5	0.000110836	1.14	4.62	4.63	1.26	1.44	-1.18	likely ortholog of mouse schlafen 5
MmugDNA.14170.1.S1_at	---	ZCCHC2	5.52E-08	-1.02	3.43	4.62	1.58	1.55	-1.25	zinc finger, cchc domain containing 2
MmugDNA.19098.1.S1_at	---	LOC100130123	5.60E-07	1.19	3.14	4.58	1.51	1.39	1.15	---
MmugDNA.3353.1.S1_at	LOC700215		1.34E-05	1.05	2.53	4.56	1.27	1.13	-1.23	similar to NmrA-like family domain containing 1
MmugDNA.8379.1.S1_at	LOC715462	SLFN5	0.000130493	1.04	4.08	4.51	1.43	1.24	-1.22	similar to Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)
MmuSTS.2042.1.S1_at	---	PML	3.17E-10	1.14	3.63	4.48	1.41	1.35	1.24	promyelocytic leukemia
MmugDNA.17877.1.S1_s_at	---	PML	3.19E-09	1.11	3.69	4.40	1.41	1.16	1.12	promyelocytic leukemia
MmuSTS.603.1.S1_at	LOC720054	HSPA1B	0.000441505	1.11	3.30	4.39	2.30	-1.19	-1.69	heat shock 70kda protein 1a
MmugDNA.31005.1.S1_at	---	NANS	1.10E-06	1.11	3.50	4.32	1.87	1.62	1.01	n-acetylneuraminic acid synthase (sialic acid synthase)
MmugDNA.13932.1.S1_at	---	RNF213	1.54E-08	1.02	3.98	4.29	1.49	1.37	-1.11	chromosome 17 open reading frame 27
MmugDNA.23425.1.S1_at	IL1RN	IL1RN	3.26E-06	1.09	2.01	4.28	-1.08	-1.36	1.01	interleukin 1 receptor antagonist
MmuSTS.3702.1.S1_at	---	EIF2AK2	1.48E-08	-1.10	2.83	4.27	1.55	1.34	-1.08	eukaryotic translation initiation factor 2-alpha kinase 2
MmugDNA.8115.1.S1_at	---	RNF213	6.12E-08	1.11	4.65	4.26	1.95	1.41	1.05	chromosome 17 open reading frame 27
MmugDNA.36196.1.S1_at	---	STAT2	1.01E-07	1.19	3.22	4.16	1.59	1.36	1.06	signal transducer and activator of transcription 2, 113kda

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	Gene Description
MmugDNA.34622.1.S1_at	PARP9	PARP9	9.32E-09	1.41	5.39	4.16	2.30	1.74	1.16	poly (adp-ribose) polymerase family, member 9
MmugDNA.20352.1.S1_at	---	DDX60L	1.21E-08	-1.02	3.59	4.11	1.11	-1.07	-1.16	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like
MmugDNA.32611.1.S1_at	LOC715462	SLFN5	0.000120016	1.19	3.61	4.08	1.42	1.46	-1.06	likely ortholog of mouse schlafen 5
Mmu.11960.1.S1_x_at	GBP1	GBP1	3.66E-05	-1.05	2.68	4.06	1.33	1.05	1.06	guanylate binding protein 1, interferon-inducible, 67kda
MmuSTS.602.1.S1_at	LOC715638	HSPA1A	5.27E-05	1.02	2.89	4.05	1.79	1.08	-1.18	similar to Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)
MmugDNA.23497.1.S1_at	STAT1	STAT1	1.19E-06	1.39	3.49	4.02	2.05	1.64	1.20	signal transducer and activator of transcription 1, 91kda
MmugDNA.28694.1.S1_at	---	ZCCHC2	5.86E-06	1.15	3.10	4.01	1.69	1.43	-1.07	zinc finger, cchc domain containing 2
MmuSTS.1082.1.S1_at	LOC712674	PDE8B	6.86E-07	1.33	4.02	4.00	2.52	1.78	1.22	phosphodiesterase 8b
MmugDNA.15286.1.S1_at	LOC715591	PARP14	4.50E-09	1.23	5.00	4.00	2.22	1.53	-1.08	poly (adp-ribose) polymerase family, member 14
MmugDNA.23196.1.S1_at	---	STAT1	1.31E-07	1.20	3.41	3.99	1.48	1.41	1.13	signal transducer and activator of transcription 1, 91kda
MmuSTS.1513.1.S1_at	IFI35	IFI35	5.74E-06	1.28	4.38	3.96	2.16	1.29	1.02	interferon-induced protein 35
MmugDNA.19523.1.S1_at	CD164	CD164	0.000315465	1.21	2.32	3.93	1.84	1.51	-1.01	cd164 antigen, sialomucin
MmuSTS.4666.1.S1_at	TNFSF10	TNFSF10	7.77E-07	1.17	4.21	3.92	1.50	-1.01	1.36	tumor necrosis factor (ligand) superfamily, member 10
MmugDNA.43291.1.S1_at	LOC712401	OAS2	9.79E-09	-1.03	2.62	3.90	1.22	-1.02	-1.05	2'-5'-oligoadenylate synthetase 2, 69/71kda
MmugDNA.19588.1.S1_at	---	TIFA	1.16E-07	1.32	2.00	3.88	1.94	-1.21	-1.49	traf-interacting protein with a forkhead-associated domain
MmugDNA.21105.1.S1_at	LOC721995	LIG1	0.000371967	1.24	4.33	3.87	2.06	1.84	1.16	ligase i, dna, atp-dependent
Mmu.13018.1.S1_at	TRIM5	TRIM5	5.75E-05	1.25	3.17	3.85	1.52	1.30	1.11	tripartite motif-containing 5
MmuAffx.10.1.A1_x_at	---	---	0.000163111	-1.20	3.92	3.83	2.83	2.18	-1.72	---
MmugDNA.19278.1.S1_at	LOC693527	PHACTR2	3.63E-07	1.21	3.82	3.82	1.77	1.55	1.11	phosphatase and actin regulator 2
MmuSTS.4678.1.S1_at	---	TREX1	7.39E-07	1.15	2.78	3.81	1.26	1.27	1.21	three prime repair exonuclease 1
MmuSTS.2890.1.S1_at	---	TRIM14	5.15E-05	1.05	3.73	3.81	2.79	2.01	-1.24	tripartite motif-containing 14
MmuSTS.1560.1.S1_at	---	MGC20410	9.85E-08	-1.01	1.91	3.71	1.48	1.08	1.19	---
MmugDNA.16432.1.S1_at	DHX8	PRIC285	3.07E-07	-1.00	2.68	3.69	1.39	1.20	1.10	peroxisomal proliferator-activated receptor a interacting complex 285
MmunewRS.936.1.S1_at	LOC695158	GBP6	9.87E-08	1.10	3.72	3.69	2.06	1.30	-1.17	guanylate binding protein family, member 6
Mmu.7639.1.S1_at	STAT1	STAT1	9.85E-08	1.54	4.54	3.68	2.14	1.35	1.26	signal transducer and activator of transcription 1, 91kda
MmugDNA.34026.1.S1_at	LOC718510	PLA2G4C	9.94E-05	1.02	2.09	3.68	1.14	1.12	1.07	phospholipase a2, group ivc (cytosolic, calcium-independent)
MmugDNA.9803.1.S1_at	---	PML	3.93E-06	1.33	4.21	3.67	1.80	1.47	1.21	promyelocytic leukemia
MmunewRS.20.1.S1_at	LOC719253	IFI16	6.72E-05	1.24	3.67	3.66	1.63	1.45	-1.09	interferon, gamma-inducible protein 16
MmuSTS.1789.1.S1_at	LOC720679	SCO2	6.75E-07	1.14	3.09	3.65	1.64	1.33	-1.14	sco cytochrome oxidase deficient homolog 2 (yeast)
MmugDNA.9650.1.S1_at	LOC714914	DTX3L	1.03E-09	1.19	3.57	3.63	1.80	1.38	1.08	deltex 3-like (drosophila)
MmuSTS.2101.1.S1_at	LOC702775	RIN2	0.000570969	1.29	3.30	3.61	1.66	-1.01	1.23	ras and rab interactor 2
MmugDNA.19992.1.S1_at	TRIM5	TRIM5	1.04E-06	1.16	3.31	3.59	1.69	1.41	-1.07	tripartite motif-containing 5
MmugDNA.24620.1.S1_at	---	---	0.00134118	1.47	3.51	3.57	1.59	1.82	-1.08	---
MmugDNA.2176.1.S1_at	ISG20	ISG20	8.12E-07	1.10	3.06	3.55	1.83	1.40	1.07	interferon stimulated exonuclease gene 20kda
MmugDNA.7052.1.S1_at	LOC705561	UBE2L6	4.46E-06	1.29	3.21	3.52	1.90	1.37	1.24	ubiquitin-conjugating enzyme e2l 6
MmugDNA.9266.1.S1_at	LOC716161	ECGF1	0.000236943	1.41	3.79	3.51	1.81	1.85	1.23	endothelial cell growth factor 1 (platelet-derived)
MmugDNA.41833.1.S1_at	LOC719092	BST2	0.000272929	1.18	3.21	3.50	2.22	1.43	-1.08	bone marrow stromal cell antigen 2
MmuSTS.3349.1.S1_at	LOC713715	CCRL2	1.33E-07	1.06	4.67	3.49	1.24	-1.11	-1.69	chemokine (c-c motif) receptor-like 2
MmugDNA.19523.1.S1_s_at	CD164	CD164	3.83E-05	1.24	2.25	3.49	1.45	1.39	-1.14	cd164 antigen, sialomucin
MmugDNA.8695.1.S1_at	---	CORO2A	3.24E-07	1.04	2.87	3.48	1.59	1.18	1.09	coronin, actin binding protein, 2a
Mmu.11980.1.S1_at	GNPAT	GNPAT	3.81E-06	1.26	3.30	3.46	1.78	1.70	1.12	glyceronephosphate o-acyltransferase
MmugDNA.42778.1.S1_at	LOC711660	PARP12	2.84E-12	1.20	3.74	3.44	1.58	1.32	1.12	poly (adp-ribose) polymerase family, member 12
MmugDNA.8251.1.S1_at	LOC707359	TMEM140	3.58E-08	-1.01	2.45	3.41	1.26	1.03	-1.36	hypothetical protein flj11000
MmugDNA.20774.1.S1_at	---	CD274	5.04E-07	1.05	3.06	3.40	1.43	-1.01	-1.53	cd274 antigen
MmugDNA.4421.1.S1_at	LOC696886	MAFB	0.000479046	1.20	2.97	3.39	1.81	1.50	1.16	v-maf musculoaponeurotic fibrosarcoma oncogene homolog b (avian)
MmugDNA.9176.1.S1_at	ATP5G1	CNP	3.29E-09	1.10	2.80	3.38	1.64	1.23	1.20	2',3'-cyclic nucleotide 3' phosphodiesterase
MmugDNA.38530.1.S1_at	LOC717470	SIGLEC1	2.19E-06	1.08	2.73	3.37	1.44	1.27	-1.07	sialic acid binding ig-like lectin 1, sialoadhesin
MmuSTS.1204.1.S1_at	TLR2	TLR2	1.43E-05	1.28	2.00	3.36	1.31	1.10	-1.30	toll-like receptor 2
MmugDNA.3158.1.S1_at	CCL8	CCL8	5.07E-06	-1.10	1.99	3.35	1.28	-1.10	-1.01	chemokine (c-c motif) ligand 8
MmugDNA.25388.1.S1_at	---	RIN2	1.32E-05	1.22	2.12	3.33	1.19	1.35	1.12	ras and rab interactor 2
MmugDNA.13395.1.S1_at	LOC719253	IFI16	0.000539609	-1.32	2.75	3.33	1.75	1.44	-1.83	interferon, gamma-inducible protein 16
MmugDNA.21377.1.S1_at	LOC705910	MOV10	2.68E-05	1.08	2.83	3.32	1.32	1.23	1.09	mov10, moloney leukemia virus 10, homolog (mouse)
MmugDNA.5661.1.S1_at	LOC719402	KIAA0082	2.33E-11	1.22	3.68	3.30	1.93	1.52	1.20	kiaa0082
MmugDNA.3485.1.S1_at	---	EPSTI1	7.57E-07	1.27	4.30	3.26	2.06	1.61	1.18	epithelial stromal interaction 1 (breast)
MmugDNA.18432.1.S1_at	INDO	INDO	0.00465945	1.19	3.31	3.20	2.06	1.41	1.40	indoleamine-pyrrole 2,3 dioxygenase
MmuSTS.4059.1.S1_at	TRIM21	TRIM21	1.30E-07	1.09	2.64	3.18	1.19	1.19	1.02	tripartite motif-containing 21
MmugDNA.19224.1.S1_at	LOC710375	LGALS8	1.01E-07	1.28	3.26	3.14	1.35	1.37	1.08	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.38658.1.S1_at	TLR6	TLR6	0.00163381	1.11	2.53	3.13	1.36	1.18	-1.62	toll-like receptor 6
MmugDNA.3343.1.S1_at	---	SOCS3	0.00235681	1.02	1.36	3.13	1.63	-1.48	-1.97	suppressor of cytokine signaling 3
MmuSTS.3554.1.S1_at	LOC705554	DHRS9	1.28E-08	1.02	2.75	3.07	1.35	1.05	-1.14	dehydrogenase/reductase (sdr family) member 9
Mmu.11363.1.S1_at	CXCL10	CXCL10	2.19E-05	-1.23	1.42	3.05	1.02	-1.21	-1.16	chemokine (c-x-c motif) ligand 10
Mmu.2142.1.S1_at	TRIM22	TRIM22	4.55E-05	1.36	3.52	3.02	1.44	1.31	1.09	tripartite motif-containing 22
MmuSTS.2728.1.S1_at	LOC706004	GCN5L2	7.17E-12	-1.14	2.72	3.01	-1.10	-1.08	-1.18	gcn5 general control of amino-acid synthesis 5-like 2 (yeast)
MmugDNA.34119.1.S1_at	FGL2	FGL2	1.57E-06	1.31	2.49	2.98	1.81	1.09	1.07	fibrinogen-like 2
MmugDNA.25916.1.S1_at	LOC713232	PLSCR1	1.10E-06	1.52	4.32	2.98	1.98	1.30	1.36	phospholipid scramblase 1
MmugDNA.12946.1.S1_at	---	PML	3.53E-08	1.02	2.22	2.97	1.36	1.25	-1.02	promyelocytic leukemia
MmugDNA.11328.1.S1_at	ATF3	ATF3	4.52E-12	-1.07	3.30	2.96	1.10	-1.15	1.03	activating transcription factor 3
MmugDNA.40745.1.S1_at	LOC710316	MLKL	5.01E-11	1.14	3.22	2.95	1.44	1.16	-1.08	mixed lineage kinase domain-like
MmugDNA.42826.1.S1_at	LOC710406	C21ORF91	0.00010876	-1.02	2.36	2.92	1.51	-1.03	-1.16	chromosome 21 open reading frame 91
MmugDNA.4767.1.S1_at	---	LOC441108	7.59E-06	1.04	1.88	2.91	-1.05	1.29	1.13	hypothetical gene supported by ak128882
MmugDNA.10146.1.S1_at	LOC712588	TRIM25	1.39E-06	1.09	2.03	2.90	1.37	1.35	-1.26	tripartite motif-containing 25
MmugDNA.22619.1.S1_x_at	LOC710928	UNC93B1	9.84E-05	1.16	2.69	2.90	1.41	1.39	1.25	unc-93 homolog b1 (c. elegans)
MmugDNA.1812.1.S1_at	LOC696090	ZBP1	0.00337309	1.08	1.97	2.88	1.44	1.41	1.16	z-dna binding protein 1
MmugDNA.31841.1.S1_at	TNFSF13B	TNFSF13B	9.49E-07	1.48	3.12	2.88	1.90	1.61	-1.15	tumor necrosis factor (ligand) superfamily, member 13b
MmugDNA.28886.1.S1_at	LOC717665	C6ORF150	0.000460982	-1.08	2.31	2.87	1.47	1.02	-1.18	chromosome 6 open reading frame 150
MmuSTS.3639.1.S1_at	---	EXT1	3.25E-05	1.22	2.01	2.85	1.39	1.30	1.17	exostoses (multiple) 1
MmuSTS.4171.1.S1_at	MSRA	MSRA	5.93E-06	1.06	2.78	2.84	1.30	1.21	-1.12	methionine sulfoxide reductase a
MmugDNA.22619.1.S1_at	LOC710928	UNC93B1	1.24E-05	1.11	2.59	2.83	1.45	1.29	1.28	unc-93 homolog b1 (c. elegans)
MmugDNA.11115.1.S1_s_at	LOC707033	LOC707033	6.19E-06	1.22	2.74	2.81	1.41	1.26	1.23	---
MmugDNA.11765.1.S1_at	LOC694240	ANKRD22	5.46E-05	1.62	4.45	2.81	2.24	1.51	-1.04	ankyrin repeat domain 22
MmugDNA.4964.1.S1_at	LOC707625	SPTLC2	5.25E-09	1.11	2.41	2.77	1.11	-1.09	1.16	serine palmitoyltransferase, long chain base subunit 2
MmugDNA.6326.1.S1_at	---	SLFN5	0.000409565	-1.07	2.80	2.77	1.93	1.49	-1.61	likely ortholog of mouse schlafen 5
Mmu.12096.1.S1_at	LOC694225	DCP2	1.02E-08	1.19	2.09	2.77	1.58	1.07	-1.02	dcp2 decapping enzyme homolog (s. cerevisiae)
MmugDNA.27375.1.S1_at	---	PHACTR2	3.44E-06	1.03	4.08	2.76	1.50	1.51	-1.03	phosphatase and actin regulator 2
MmugDNA.17749.1.S1_at	---	XAF1	0.000347691	-1.11	2.69	2.75	1.73	1.11	-1.11	xiap associated factor-1
MmuSTS.1188.1.S1_at	LOC713232	PLSCR1	1.30E-05	1.40	3.97	2.74	1.96	1.39	1.41	phospholipid scramblase 1
MmugDNA.36516.1.S1_at	GNPAT	IRF9	4.15E-06	1.16	2.50	2.73	1.75	1.52	1.08	interferon-stimulated transcription factor 3, gamma 48kda
MmuSTS.1659.1.S1_at	LOC707072	RPL4	0.000493846	1.47	2.58	2.73	1.72	1.30	1.30	ribosomal protein l4
MmuSTS.3489.1.S1_at	LOC715923	CD68	0.000148034	1.33	2.18	2.72	1.72	1.14	1.20	cd68 antigen
Mmu.8122.1.A1_at	LOC712588	TRIM25	1.87E-07	1.07	1.94	2.72	1.29	1.03	-1.40	tripartite motif-containing 25
Mmu.11961.1.S1_at	GBP1	GBP1	0.000165902	-1.15	1.86	2.71	1.01	-1.04	-1.03	guanylate binding protein 1, interferon-inducible, 67kda
MmugDNA.29290.1.S1_at	---	PHACTR2	4.37E-06	1.24	4.14	2.71	2.16	1.53	-1.03	phosphatase and actin regulator 2
MmugDNA.37307.1.S1_at	LOC699295	LBA1	8.27E-06	1.03	1.70	2.70	-1.01	1.15	1.03	lupus brain antigen 1
MmugDNA.14153.1.S1_at	LOC710375	LGALS8	3.89E-07	1.24	3.31	2.70	1.62	1.27	-1.02	lectin, galactoside-binding, soluble, 8 (galectin 8)

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	Gene Description
MmugDNA.30463.1.S1_at	NMI	NMI	1.86E-07	1.25	3.04	2.69	1.81	1.28	-1.23	n-myc (and stat) interactor
MmugDNA.31960.1.S1_at	---	XRN1	4.36E-07	1.17	1.78	2.69	1.30	-1.06	-1.09	5'-3' exoribonuclease 1
MmuSTS.3917.1.S1_at	STAT1	STAT1	7.80E-10	1.40	3.37	2.69	2.00	1.23	1.17	signal transducer and activator of transcription 1, 91kda
MmugDNA.38197.1.S1_at	LOC720683	LOC440836	0.000104084	1.38	3.51	2.68	1.85	1.80	1.01	similar to mgc52679 protein
MmugDNA.22837.1.S1_at	WARS	WARS	0.00748293	1.49	2.36	2.66	1.61	1.19	1.42	interferon-induced protein 53
MmugDNA.685.1.S1_at	LOC716161	ECGF1	0.0117046	-1.04	2.23	2.66	1.60	1.48	-1.09	endothelial cell growth factor 1 (platelet-derived)
MmugDNA.36872.1.S1_at	LOC694916	LYSMD2	0.000500459	1.10	2.74	2.65	1.54	1.15	1.19	lysm, putative peptidoglycan-binding, domain containing 2
MmuSTS.3115.1.S1_at	---	MXD1	0.000464429	1.01	1.63	2.62	1.24	1.18	1.01	max dimerization protein 1
MmugDNA.19097.1.S1_at	---	SHROOM4	5.14E-06	-1.06	1.82	2.62	1.24	1.04	1.08	kiaa1202 protein
MmugDNA.24210.1.S1_at	---	ATF6	1.84E-05	1.22	2.61	2.58	1.30	1.16	-1.27	activating transcription factor 6
MmugDNA.42447.1.S1_s_at	LOC719253	IFI16	6.19E-05	1.44	2.86	2.58	1.99	1.54	1.28	interferon, gamma-inducible protein 16
MmugDNA.28999.1.S1_at	LOC718036	KIAA1618	1.35E-07	1.07	2.31	2.58	1.64	1.33	-1.20	kiaa1618
MmugDNA.33090.1.S1_at	---	RNF213	0.132418	1.10	1.61	2.57	1.22	1.29	1.12	chromosome 17 open reading frame 27
MmunewRS.902.1.S1_at	LOC702068	EMB	0.00152003	1.34	2.13	2.56	1.70	1.20	-1.07	embigin homolog (mouse)
MmugDNA.29742.1.S1_at	LOC715410	CD163	0.0499426	1.76	2.37	2.53	1.60	1.61	1.25	cd163 antigen
MmugDNA.17877.1.S1_at	---	PML	0.0033246	1.09	2.03	2.53	1.11	1.25	1.22	promyelocytic leukemia
MmuSTS.1580.1.S1_at	---	IFIT5	0.0001136	1.10	3.41	2.51	1.59	1.39	-1.00	interferon-induced protein with tetratricopeptide repeats 5
MmugDNA.2761.1.S1_at	SP100	SP100	3.15E-08	1.20	2.66	2.51	1.82	1.27	1.02	sp100 nuclear antigen
MmugDNA.5794.1.S1_at	MT2A	MT2A	0.000324057	1.28	3.04	2.50	1.50	1.42	1.36	metallothionein 2a
MmugDNA.34145.1.S1_at	LOC704928	DYNLT1	2.17E-07	1.22	2.82	2.50	1.44	1.29	-1.04	dynein, light chain, tctex-type 1
MmugDNA.22222.1.S1_at	---	NBN	0.00303202	-1.13	1.77	2.49	1.40	-1.09	-1.35	nibrin
MmugDNA.5950.1.S1_at	LOC708132	PARP10	8.32E-06	1.03	1.98	2.49	1.10	1.21	1.11	poly (adp-ribose) polymerase family, member 10
MmugDNA.35965.1.S1_at	LOC704259	CXORF21	0.000265535	1.25	2.53	2.48	1.73	1.55	-1.27	chromosome x open reading frame 21
MmugDNA.25634.1.S1_at	WARS	WARS	0.00076498	1.38	2.22	2.48	1.67	1.20	1.30	interferon-induced protein 53
MmugDNA.29385.1.S1_at	LOC711648	MIRN21	5.04E-05	1.28	2.01	2.47	2.04	1.32	-1.32	microrna 21
MmugDNA.9703.1.S1_at	TREM1	TREM1	0.00187869	1.22	1.92	2.47	1.16	1.34	-1.17	triggering receptor expressed on myeloid cells 1
MmugDNA.13391.1.S1_at	LILRAD	LILRA3	2.24E-05	1.05	1.47	2.47	1.03	-1.06	-1.27	leukocyte immunoglobulin-like receptor, subfamily a (without tm domain), member 3
MmugDNA.9495.1.S1_at	---	PHACTR2	2.50E-05	1.02	2.29	2.46	1.45	1.08	-1.01	phosphatase and actin regulator 2
MmunewRS.633.1.S1_s_at	APOBEC3H	APOBEC3H	2.14E-05	1.04	1.90	2.45	1.28	1.07	1.13	arp10 protein
MmuSTS.4535.1.S1_at	LOC700118	ERAP2	0.00010459	1.23	2.00	2.45	1.21	1.12	1.14	leukocyte-derived arginine aminopeptidase
MmugDNA.3988.1.S1_at	LOC694240	ANKRD22	1.12E-06	1.28	2.56	2.45	2.08	1.08	-1.03	ankyrin repeat domain 22
MmugDNA.635.1.S1_at	TNFSF13B	TNFSF13B	2.00E-07	1.35	3.42	2.44	1.98	1.31	-1.30	tumor necrosis factor (ligand) superfamily, member 13b
MmugDNA.36766.1.S1_at	TOR1B	TOR1B	1.33E-05	1.33	2.77	2.44	1.42	1.19	1.03	torsin family 1, member b (torsin b)
MmugDNA.32890.1.S1_at	LOC717355	NAPA	7.38E-06	1.05	2.36	2.44	1.43	1.14	1.04	n-ethylmaleimide-sensitive factor attachment protein, alpha
Mmu.4440.1.S1_at	LOC693561	PI4K2B	8.55E-06	-1.01	2.14	2.44	1.06	1.25	1.16	phosphatidylinositol 4-kinase type 2 beta
MmugDNA.19.1.S1_at	SCIN	SCIN	0.00208969	1.10	1.89	2.44	1.38	1.10	-1.02	scinderin
MmugDNA.252.1.S1_at	P2RY2	P2RY2	0.0313536	1.39	2.18	2.44	1.68	1.35	1.28	purinergic receptor p2y, g-protein coupled, 2
MmunewRS.254.1.S1_at	IFI27	IFI27	0.0739484	1.31	4.27	2.43	2.94	1.62	1.35	interferon, alpha-inducible protein 27
MmugDNA.41043.1.S1_at	---	NBN	0.00100475	-1.15	1.79	2.43	1.46	1.10	-1.87	nibrin
MmugDNA.30432.1.S1_at	---	MSRA	0.000505459	1.01	1.82	2.43	-1.02	1.14	1.11	methionine sulfoxide reductase a
MmugDNA.41060.1.S1_at	---	PHF11	5.54E-07	1.09	2.17	2.43	1.09	1.11	1.01	phd finger protein 11
MmugDNA.41044.1.S1_at	---	NBN	0.00107677	-1.06	1.74	2.42	1.47	-1.17	-1.38	nibrin
MmugDNA.27150.1.S1_at	LOC699207	PATL1	0.000441782	-1.09	2.04	2.42	1.02	1.07	-1.04	flj36874 protein
MmugDNA.9795.1.S1_at	LOC715418	TRIM14	7.79E-07	-1.07	1.88	2.42	1.09	1.14	-1.05	tripartite motif-containing 14
MmugDNA.39691.1.S1_s_at	TRIM38	TRIM38	0.00013425	1.21	2.45	2.42	1.20	1.15	1.06	tripartite motif-containing 38
MmugDNA.29151.1.S1_at	---	SPTLC2	1.29E-05	1.17	1.95	2.41	1.29	1.18	-1.07	serine palmitoyltransferase, long chain base subunit 2
MmugDNA.8672.1.S1_at	LOC704374	SDC3	9.27E-07	-1.03	1.50	2.41	1.13	1.04	-1.09	syndecan 3 (n-syndecan)
MmugDNA.22615.1.S1_s_at	---		7.30E-08	1.08	2.08	2.40	-1.01	1.11	-1.05	---
MmugDNA.40394.1.S1_at	LY6E	LY6E	6.11E-05	1.17	1.93	2.40	1.25	1.32	1.54	lymphocyte antigen 6 complex, locus e
MmugDNA.36105.1.S1_at	LOC697051	AMDHD2	0.0105833	1.29	1.74	2.40	1.45	1.47	1.24	amidohydrolase domain containing 2
MmugDNA.28553.1.S1_at	LOC705017	PIK3AP1	7.19E-06	1.02	2.26	2.40	-1.08	-1.01	-1.03	phosphoinositide-3-kinase adaptor protein 1
MmugDNA.12091.1.S1_at	BAK1	BCL2L7P1	1.61E-05	1.10	1.92	2.39	1.41	1.31	1.19	bcl2-like 7 pseudogene 1
MmugDNA.9235.1.S1_s_at	---	ADAR	1.56E-06	1.15	2.64	2.39	1.28	1.22	-1.05	adenosine deaminase, rna-specific
MmugDNA.32046.1.S1_at	LOC720688	KLHDC7B	0.000202604	1.00	1.45	2.38	1.20	1.13	1.03	kelch domain containing 7b
MmugDNA.1987.1.S1_at	SLC2A5	SLC2A5	0.000245713	1.13	1.89	2.36	1.71	1.22	1.09	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
MmugDNA.222.1.S1_at	---	EMB	0.000691604	1.26	2.09	2.35	1.48	1.28	-1.24	embigin homolog (mouse)
MmugDNA.2075.1.S1_at	LOC710877	SMCHD1	3.08E-05	1.23	2.84	2.35	1.50	1.12	-1.11	structural maintenance of chromosomes flexible hinge domain containing 1
MmugDNA.13466.1.S1_at	LOC720056	ATF6	0.000386833	1.04	1.85	2.34	1.18	1.04	-1.24	activating transcription factor 6
Mmu.13989.1.S1_at	LOC719212	LOC719212	0.000231713	1.24	1.86	2.34	1.44	1.32	1.11	---
MmugDNA.27352.1.S1_at	ZNFX1	ZNFX1	2.20E-08	1.01	2.08	2.34	1.10	-1.05	-1.22	zinc finger, nfx1-type containing 1
MmugDNA.2972.1.S1_at	---	SP140	0.000254037	1.00	1.74	2.33	-1.10	1.16	1.05	sp140 nuclear body protein
MmuSTS.1849.1.S1_at	DTX1	DTX1	2.41E-05	-1.00	1.79	2.33	2.95	1.37	1.20	deltex homolog 1 (drosophila)
Mmu.7836.1.S1_x_at	CFLAR	CFLAR	0.00394086	1.38	2.01	2.33	1.15	1.32	-1.10	casp8 and fadd-like apoptosis regulator
MmuSTS.3660.1.S1_at	POR	POR	0.000851062	1.13	1.85	2.32	1.14	1.28	1.06	p450 (cytochrome) oxidoreductase
MmugDNA.33437.1.S1_s_at	LOC713517	ZNF313	8.80E-08	1.06	2.13	2.32	1.08	1.11	-1.16	zinc finger protein 313
MmugDNA.35809.1.S1_at	---	HIRA	0.000412482	1.16	1.86	2.31	1.05	1.08	1.05	hir histone cell cycle regulation defective homolog a (s. cerevisiae)
MmugDNA.10692.1.S1_at	LOC702542	SCOTIN	1.27E-05	1.14	2.33	2.29	1.31	1.23	1.16	scotin
MmugDNA.27480.1.S1_at	LOC710375	LGALS8	0.00393605	-1.02	2.54	2.29	1.27	1.27	1.11	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.20995.1.S1_at	---	CCR1	3.99E-05	1.14	2.36	2.29	1.32	-1.08	-1.31	chemokine (c-c motif) receptor 1
MmugDNA.34302.1.S1_at	GBP1	GBP1	0.000763536	1.13	1.80	2.28	1.07	1.16	1.15	guanylate binding protein 1, interferon-inducible, 67kda
MmugDNA.15480.1.S1_at	---	ZC3HAV1	5.80E-06	1.13	2.08	2.28	1.19	1.07	-1.05	zinc finger ccch-type, antiviral 1
MmuSTS.2931.1.S1_at	LOC693427	KCNJ15	0.0136841	1.04	1.14	2.28	1.31	-1.04	-1.25	potassium inwardly-rectifying channel, subfamily j, member 15
MmugDNA.14810.1.S1_at	LOC711784	TRAFD1	3.04E-07	1.10	2.13	2.27	1.14	1.03	1.06	traf-type zinc finger domain containing 1
MmugDNA.3702.1.S1_at	LOC702068	EMB	3.32E-05	1.27	2.31	2.25	1.83	1.09	-1.21	embigin homolog (mouse)
MmugDNA.9213.1.S1_at	---	FLJ11286	2.64E-06	-1.07	1.81	2.25	1.02	1.14	1.01	hypothetical protein flj11286
MmugDNA.12018.1.S1_at	LOC712342	OAS3	7.06E-06	-1.24	1.70	2.25	1.03	-1.04	-1.07	2'-5'-oligoadenylate synthetase 3, 100kda
MmugDNA.27315.1.S1_at	---	SAMD9	1.88E-06	1.15	2.46	2.25	1.96	1.37	-1.33	sterile alpha motif domain containing 9
MmugDNA.40942.1.S1_at	---	SAMD4A	0.00715835	1.15	2.38	2.24	1.42	-1.27	-1.01	sterile alpha motif domain containing 4a
MmugDNA.4403.1.S1_at	---	---	0.000410364	-1.09	1.48	2.24	1.06	1.28	-1.26	---
MmugDNA.7816.1.S1_at	LOC696542	CYBB	0.00683444	1.20	1.88	2.23	1.47	1.27	-1.00	cytochrome b-245, beta polypeptide (chronic granulomatous disease)
MmugDNA.21968.1.S1_at	LOC707687	LOC707687	0.000235047	1.12	2.10	2.22	1.55	1.33	1.03	---
MmuSTS.805.1.S1_at	ATP5G1	ATP5G1	0.0071991	1.06	1.86	2.22	1.21	1.28	1.24	atp synthase, h+ transporting, mitochondrial f0 complex, subunit c1 (subunit 9)
MmugDNA.6653.1.S1_at	PCTAIRE2BP	TDRD7	1.59E-06	1.25	2.67	2.21	1.46	1.26	1.15	tudor domain containing 7
MmugDNA.43121.1.S1_at	---	CLEC7A	0.00114384	1.70	2.41	2.21	1.76	1.39	1.17	c-type lectin domain family 7, member a
MmugDNA.1096.1.S1_at	LOC695727	MVP	0.000131212	1.06	1.56	2.20	1.03	1.13	-1.07	major vault protein
MmugDNA.1519.1.S1_at	---	KIAA1618	3.72E-07	1.13	1.79	2.20	-1.02	1.30	-1.03	kiaa1618
MmugDNA.12648.1.S1_at	---	TRIM22	1.39E-07	1.31	2.89	2.19	1.59	1.31	1.10	tripartite motif-containing 22
MmugDNA.42437.1.S1_at	LOC717355	NAPA	7.39E-05	1.20	2.09	2.19	1.30	1.24	1.18	n-ethylmaleimide-sensitive factor attachment protein, alpha
MmugDNA.26949.1.S1_at	---	TRIM26	8.34E-09	1.11	1.83	2.18	1.14	1.13	1.20	tripartite motif-containing 26
MmugDNA.32362.1.S1_at	---	MAFB	0.00169912	1.44	2.93	2.18	1.99	1.10	1.08	v-maf musculoaponeurotic fibrosarcoma oncogene homolog b (avian)
MmugDNA.15107.1.S1_at	LILRBC	ARG2	0.00222308	1.32	1.93	2.17	1.23	1.12	-1.57	arginase, type ii
MmuSTS.733.1.S1_at	LOC700400	AGRN	0.000126773	1.06	1.89	2.17	1.35	1.17	1.04	agrin
MmugDNA.31098.1.S1_at	---	PCGF5	0.000346193	1.13	2.61	2.17	1.34	-1.03	-1.39	polycomb group ring finger 5
MmugDNA.10888.1.S1_at	---	---	0.00189018	1.10	2.16	2.17	1.25	1.09	1.03	---

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	Gene Description
MmugDNA.1081.1.S1_at	LOC717726	TAP1	0.000147782	1.15	2.02	2.17	1.29	1.21	1.09	transporter 1, atp-binding cassette, sub-family b (mdr/tap)
MmuSTS.1444.1.S1_at	LMO2	LMO2	5.25E-06	1.17	2.37	2.15	1.43	1.15	-1.02	lim domain only 2 (rhombotin-like 1)
MmugDNA.10606.1.S1_at	LOC714244	SP110	0.00261161	-1.13	1.68	2.14	1.15	1.49	-1.18	sp110 nuclear body protein
MmugDNA.25884.1.S1_at	---	SLC26A11	0.00270576	1.11	1.74	2.14	1.28	1.09	1.13	solute carrier family 26, member 11
MmugDNA.1574.1.S1_at	---	---	2.95E-08	-1.08	1.44	2.14	1.03	-1.15	1.14	---
MmugDNA.17449.1.S1_at	LOC704124	TFEC	2.77E-05	1.60	2.86	2.13	2.82	1.20	1.09	transcription factor ec
MmugDNA.1639.1.S1_at	LILRBC	ARG2	0.000390904	1.07	1.43	2.12	-1.09	-1.04	-1.52	arginase, type ii
MmugDNA.23750.1.S1_at	---	PARP11	7.61E-06	1.32	2.42	2.12	1.52	1.16	1.19	poly (adp-ribose) polymerase family, member 11
MmugDNA.39346.1.S1_at	LOC710518	SLC25A37	0.0160744	1.05	1.81	2.11	1.02	1.00	-1.61	solute carrier family 25, member 37
MmugDNA.22222.1.S1_s_at	---	NBN	0.0167091	-1.07	1.57	2.11	1.32	1.00	-1.41	nibrin
MmuSTS.4763.1.S1_at	LOC722740	FBXO6	0.00106064	1.13	1.75	2.09	1.32	1.10	1.04	f-box protein 6
MmugDNA.2776.1.S1_at	SP100	SP100	1.58E-05	1.03	1.49	2.09	1.27	1.10	1.05	sp100 nuclear antigen
MmugDNA.16901.1.S1_at	LOC709760	STAT5B	0.000222646	1.02	1.23	2.09	-1.15	1.00	-1.38	signal transducer and activator of transcription 5b
MmugDNA.36869.1.S1_at	---	DBF4B	1.38E-06	1.02	2.87	2.09	1.35	1.04	1.01	dbf4 homolog b (s. cerevisiae)
MmugDNA.41250.1.S1_at	---	PAQR8	0.00024372	1.23	2.94	2.08	1.41	1.19	1.04	progestin and adipoq receptor family member viii
MmugDNA.17638.1.S1_at	---	SPTLC2	5.80E-05	1.32	2.65	2.08	1.38	1.05	1.10	serine palmitoyltransferase, long chain base subunit 2
MmugDNA.8141.1.S1_at	UPP1	UPP1	0.00393546	1.26	1.70	2.08	1.18	-1.08	-1.09	uridine phosphorylase 1
MmuSTS.1158.1.S1_at	PHF11	PHF11	8.81E-06	1.26	2.56	2.07	1.62	1.23	1.02	phd finger protein 11
MmugDNA.7313.1.S1_at	LOC694589	PAPD5	5.66E-07	1.28	1.86	2.06	1.09	1.14	1.17	pap associated domain containing 5
MmugDNA.28698.1.S1_x_at	---	SAMD9	0.00029096	1.19	2.32	2.06	1.74	1.14	-1.12	sterile alpha motif domain containing 9
MmuSTS.3742.1.S1_at	PTX3	PTX3	2.01E-05	-1.18	1.67	2.05	1.64	-1.03	-1.43	pentraxin-related gene, rapidly induced by il-1 beta
MmugDNA.16397.1.S1_s_at	LOC700880	GRN	0.000952245	1.18	1.75	2.05	1.07	1.23	1.02	granulin
MmugDNA.22157.1.S1_at	---	PCGF5	0.000393579	-1.03	1.84	2.05	1.02	1.10	-1.11	polycomb group ring finger 5
MmuSTS.354.1.S1_at	LOC705061	NFE2	0.0019449	-1.06	1.40	2.04	1.06	-1.03	-1.41	nuclear factor (erythroid-derived 2), 45kda
MmuSTS.2830.1.S1_at	LOC715866	APOL3	6.22E-05	1.27	1.96	2.04	1.41	1.06	1.09	tnf-inducible protein cg12-1
MmugDNA.27554.1.S1_at	---	C17ORF60	3.51E-05	1.11	2.25	2.04	1.48	1.14	-1.21	chromosome 17 open reading frame 60
MmugDNA.27093.1.S1_at	A2M	A2M	0.00836289	1.13	1.81	2.04	1.21	1.27	1.10	alpha-2-macroglobulin
MmugDNA.42970.1.S1_at	LOC710928	UNC93B1	0.000106533	1.05	1.66	2.04	1.05	1.17	1.21	unc-93 homolog b1 (c. elegans)
MmugDNA.9155.1.S1_s_at	LOC697427	DRAM	1.06E-08	1.10	2.29	2.03	1.64	1.07	-1.25	hypothetical protein flj11259
MmugDNA.2077.1.S1_at	---	SMCHD1	0.000442218	1.29	2.90	2.03	1.64	1.07	-1.20	structural maintenance of chromosomes flexible hinge domain containing 1
MmugDNA.27936.1.S1_s_at	---	CFLAR	0.000137649	-1.01	1.31	2.01	-1.04	1.04	-1.03	casp8 and fadd-like apoptosis regulator
MmugDNA.28698.1.S1_at	---	SAMD9	0.000161518	1.19	2.26	2.01	1.73	1.12	-1.16	sterile alpha motif domain containing 9
MmugDNA.32458.1.S1_at	ZAN	NAGK	0.000245246	1.32	1.81	2.01	1.26	1.20	1.07	n-acetylglucosamine kinase
MmuSTS.1185.1.S1_at	LOC712705	PLA1A	1.93E-07	-1.11	1.32	2.01	1.05	-1.15	-1.03	phospholipase a1 member a
MmuSTS.4033.1.S1_at	TLR5	TLR5	0.000129629	1.02	1.29	2.01	1.02	-1.11	-1.75	toll-like receptor 5
MmuSTS.864.1.S1_at	LOC710375	LGALS8	8.67E-08	-1.02	2.05	1.95	1.17	1.05	-1.04	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.13798.1.S1_s_at	LOC711784	TRAFD1	6.12E-06	1.13	2.04	1.94	1.21	1.08	1.10	traf-type zinc finger domain containing 1
MmugDNA.228.1.S1_at	LOC708518	C6ORF192	4.70E-05	1.31	2.41	1.91	1.65	-1.00	-1.02	chromosome 6 open reading frame 192
MmugDNA.11097.1.S1_at	LOC704579	SRGAP2	2.71E-06	1.09	2.04	1.91	1.01	1.16	1.20	slit-robo rho gtpase activating protein 2
MmugDNA.25587.1.S1_at	LOC693561	PI4K2B	2.00E-05	1.28	2.82	1.90	1.75	1.06	-1.00	phosphatidylinositol 4-kinase type 2 beta
Mmu.10941.2.S1_at	LOC712466	LOC712466	0.0168533	1.54	2.15	1.86	1.47	1.13	1.07	---
MmugDNA.494.1.S1_at	---	RAB8A	0.00291461	1.36	2.08	1.85	1.34	1.16	1.20	rab8a, member ras oncogene family
Mmu.16290.1.S1_at	LOC722935	PDCL3	0.000141681	1.21	3.12	1.84	1.81	1.10	1.09	phosducin-like 3
MmugDNA.35036.1.S1_at	---	PHACTR2	0.00420145	1.07	3.66	1.79	1.50	1.33	-1.07	phosphatase and actin regulator 2
MmugDNA.30129.1.S1_at	TNFSF10	TNFSF10	0.00054178	-1.25	2.38	1.76	1.35	1.00	-1.85	tumor necrosis factor (ligand) superfamily, member 10
MmugDNA.28010.1.S1_at	LOC710375	LGALS8	4.79E-05	-1.02	2.17	1.76	1.06	1.03	-1.11	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.31377.1.S1_s_at	LOC706568	CASP1	0.000193287	1.51	2.41	1.71	1.99	1.10	1.03	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
MmugDNA.27612.1.S1_at	LOC709414	ANKMY2	1.33E-05	1.17	2.14	1.69	1.52	1.05	-1.08	ankyrin repeat and mynd domain containing 2
MmuSTS.1595.1.S1_at	---	NT5C	0.000155709	1.31	2.22	1.64	1.74	1.07	-1.27	5', 3'-nucleotidase, cytosolic
MmugDNA.34184.1.S1_at	LOC722935	TMEM123	0.00266049	1.29	2.48	1.62	1.79	1.14	1.11	transmembrane protein 123
MmugDNA.2078.1.S1_at	---	SMCHD1	0.001154	1.36	2.36	1.61	1.43	1.13	1.01	structural maintenance of chromosomes flexible hinge domain containing 1
MmugDNA.12043.1.S1_at	---	SAMD9L	0.00034117	-1.23	1.89	1.57	1.52	1.26	-2.33	sterile alpha motif domain containing 9-like
MmugDNA.22862.1.S1_at	---	PAQR8	4.54E-07	1.03	2.05	1.55	1.07	1.02	1.04	progestin and adipoq receptor family member viii
MmuSTS.4665.1.S1_s_at	FAS	FAS	0.00513186	1.34	2.17	1.51	1.60	1.11	1.07	fas (tnf receptor superfamily, member 6)
MmuSTS.608.1.S1_at	CHMP5	CHMP5	1.97E-05	1.27	2.52	1.45	1.73	1.07	-1.22	chromatin modifying protein 5
MmugDNA.10394.1.S1_at	---	RNASEL	0.00611785	1.49	2.08	1.45	1.30	1.28	1.02	ribonuclease l (2',5'-oligoisoadenylate synthetase-dependent)
MmugDNA.13052.1.S1_at	LOC705017	PIK3AP1	0.00010822	1.19	2.07	1.44	1.14	1.06	-1.03	phosphoinositide-3-kinase adaptor protein 1
Mmu.11047.2.S1_s_at	LOC711303	LOC711303	0.00996233	-1.16	1.10	1.41	4.40	2.44	1.03	---
MmuSTS.2164.1.S1_at	LOC708293	DDX10	7.42E-06	-1.18	1.02	1.32	3.80	2.08	1.16	dead (asp-glu-ala-asp) box polypeptide 10
MmugDNA.42067.1.S1_at	LOC701100	UBE2J1	0.00760671	1.02	1.16	1.29	2.34	1.31	1.09	ubiquitin-conjugating enzyme e2, j1 (ubc6 homolog, yeast)
MmugDNA.3247.1.S1_at	LOC704341	HIST2H4B	0.000920491	1.31	1.23	1.27	3.22	1.96	1.52	h4 histone, family 2
MmugDNA.3247.1.S1_s_at	LOC704341	HIST2H4B	0.000122818	1.05	1.11	1.26	2.23	1.62	1.26	h4 histone, family 2
MmuSTS.4348.1.S1_at	IGHG1 /// LOC71130	IGHG1	0.000313979	-1.22	1.06	1.26	5.77	2.81	1.06	immunoglobulin heavy constant gamma 1 (g1m marker)
MmuSTS.1283.1.S1_at	LOC711236	DTL	3.85E-06	1.23	1.50	1.25	3.09	1.57	1.11	denticleless homolog (drosophila)
MmugDNA.15862.1.S1_at	LOC697324	CKS2	2.75E-05	1.05	-1.10	1.25	4.38	1.68	-1.19	cdc28 protein kinase regulatory subunit 2
MmugDNA.11614.1.S1_at	LY96	LY96	0.000441484	1.31	1.32	1.23	1.49	1.13	-2.12	lymphocyte antigen 96
MmugDNA.14099.1.S1_at	PDIA5	PDIA5	9.22E-06	1.07	-1.01	1.22	2.71	1.51	1.26	protein disulfide isomerase family a, member 5
MmugDNA.32941.1.S1_at	LOC711569	C16ORF75	0.00456631	-1.08	2.21	1.21	2.07	-1.14	-1.34	hypothetical protein mgc24665
MmugDNA.34901.1.S1_at	SDF2L1	SDF2L1	0.314152	1.54	1.32	1.18	2.07	1.64	1.35	stromal cell-derived factor 2-like 1
MmuSTS.2164.1.S1_s_at	LOC708293	DDX10	0.000944551	1.12	1.16	1.17	2.41	1.83	1.28	dead (asp-glu-ala-asp) box polypeptide 10
MmugDNA.24653.1.S1_at	LOC708576	HMMR	4.11E-06	-1.07	-1.07	1.17	2.65	1.28	-1.05	hyaluronan-mediated motility receptor (rhamm)
MmuSTS.3275.1.S1_at	LOC700582	RRM2	8.50E-08	-1.33	-1.19	1.14	4.92	2.31	1.18	ribonucleotide reductase m2 polypeptide
MmugDNA.12895.1.S1_s_at	LOC693572	MGC29506	0.000341322	-1.09	-1.05	1.13	3.96	1.79	1.03	proapoptotic caspase adaptor protein
Mmu.15507.1.S1_x_at	---	IMPACT	0.000124248	-1.21	1.02	1.11	2.04	1.41	-1.02	impact homolog (mouse)
MmuSTS.911.1.S1_at	LOC695383	ALDH9A1	0.00403658	1.18	1.12	1.11	2.37	1.43	1.07	aldehyde dehydrogenase 9 family, member a1
MmugDNA.6277.1.S1_at	LOC708293	BUB1	4.13E-05	1.15	1.21	1.11	2.29	1.96	1.36	bub1 budding uninhibited by benzimidazoles 1 homolog (yeast)
MmugDNA.31059.1.S1_at	PTTG1	PTTG1	0.000101362	1.22	1.05	1.09	2.82	1.95	1.43	pituitary tumor-transforming 1
MmugDNA.18794.1.S1_at	---	CDC20	3.23E-05	-1.02	1.10	1.08	2.61	1.82	1.29	cdc20 cell division cycle 20 homolog (s. cerevisiae)
MmugDNA.21289.1.S1_at	LOC707717	NME1	0.000981783	1.34	1.08	1.08	2.45	1.59	1.18	non-metastatic cells 1, protein (nm23a) expressed in
MmugDNA.39863.1.S1_at	---	C18ORF24	0.00728521	1.18	1.19	1.06	2.55	1.71	1.27	chromosome 18 open reading frame 24
MmuSTS.4685.1.S1_at	TYMS	TYMS	1.58E-06	1.14	1.00	1.06	3.43	2.65	1.23	thymidylate synthetase
MmugDNA.25384.1.S1_at	UBE2C	UBE2C	1.65E-07	-1.12	-1.05	1.05	2.99	1.95	1.28	ubiquitin-conjugating enzyme e2c
MmugDNA.7056.1.S1_s_at	LOC701579	UCHL1	6.51E-05	-1.01	1.11	1.04	2.82	1.56	1.16	ubiquitin carboxyl-terminal esterase l1 (ubiquitin thiolesterase)
MmugDNA.35877.1.S1_s_at	LOC700659	ARMET	0.00453604	1.30	1.12	1.03	2.10	1.42	1.23	arginine-rich, mutated in early stage tumors
MmugDNA.22076.1.S1_at	LOC693572	MGC29506	0.000237491	-1.01	-1.05	1.01	5.43	2.50	1.00	proapoptotic caspase adaptor protein
MmugDNA.4124.1.S1_at	LOC721995	CDCA5	2.51E-05	-1.01	1.16	1.00	2.04	1.55	1.14	cell division cycle associated 5
MmugDNA.38781.1.S1_at	LOC698390	LOC698390	0.000297984	-1.13	-1.01	-1.03	7.79	2.09	-1.10	---
MmugDNA.4085.1.S1_at	LOC700589	CCNE1	0.000866619	1.10	1.05	-1.03	2.28	1.52	1.24	cyclin e1
MmugDNA.40742.1.S1_at	LOC702184	CCNB2	3.91E-09	1.01	1.04	-1.04	4.79	2.43	1.37	cyclin b2
Mmu.11962.1.S1_at	LMAN1	LMAN1	5.56E-06	-1.13	1.05	-1.05	3.16	1.41	1.17	lectin, mannose-binding, 1
MmuSTS.3327.1.S1_at	OIP5	OIP5	0.00109518	1.21	1.19	-1.05	2.17	1.57	1.23	opa interacting protein 5
MmugDNA.30433.1.S1_at	LOC716009	SHCBP1	2.35E-07	1.00	-1.14	-1.05	5.10	1.82	1.08	shc sh2-domain binding protein 1
MmugDNA.5663.1.S1_at	PLS3	PLS3	6.47E-06	1.26	-1.07	-1.06	3.90	-1.19	-1.18	plastin 3 (t isoform)
Mmu.15443.1.S1_x_at	---	IGKV1-5	0.0403676	-1.31	1.02	-1.07	2.99	1.80	-1.17	immunoglobulin kappa variable 1-5

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	Gene Description
MmugDNA.18451.1.S1_at	LOC697635	PRDX4	0.000322219	1.25	-1.09	-1.07	2.57	1.47	1.17	peroxiredoxin 4
MmuSTS.3576.1.S1_at	CCNA2	CCNA2	0.000200609	1.16	1.05	-1.07	2.96	1.80	1.26	cyclin a2
MmugDNA.2427.1.S1_at	LOC705385	TXNDC5	8.28E-05	1.03	-1.20	-1.08	3.01	1.63	1.16	thioredoxin domain containing 5
MmugDNA.10778.1.S1_at	LOC694877	CDKN3	6.78E-08	1.23	1.04	-1.10	4.35	1.73	1.09	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)
Mmu.4398.1.S1_s_at	CYCS	CYCS	0.000104998	1.40	1.26	-1.11	2.60	1.34	1.27	cytochrome c, somatic
MmugDNA.26033.1.S1_at	LOC713624	CENPN	0.000611871	1.03	1.15	-1.12	2.06	1.56	1.22	chromosome 16 open reading frame 60
MmugDNA.32060.1.S1_s_at	---	SPCS3	0.000265663	1.42	1.29	-1.13	2.58	1.40	-1.12	signal peptidase complex subunit 3 homolog (s. cerevisiae)
MmugDNA.38346.1.S1_at	LOC711486 /// LOC7	PSAT1	0.000181536	1.01	-1.12	-1.16	2.33	1.29	1.11	phosphoserine aminotransferase 1
MmugDNA.28902.1.S1_at	---	GAB1	1.88E-06	1.13	1.21	-1.16	2.12	1.06	-1.27	grb2-associated binding protein 1
MmugDNA.12273.1.S1_at	TOP2A	TOP2A	3.25E-06	-1.02	-1.01	-1.17	2.80	2.42	1.19	topoisomerase (dna) ii alpha 170kda
MmugDNA.29315.1.S1_at	LOC701888	DEPDC1	5.18E-07	-1.03	-1.10	-1.19	3.18	1.57	-1.03	dep domain containing 1
MmugDNA.32729.1.S1_at	MKI67	MKI67	0.00263865	1.38	1.25	-1.19	2.21	1.76	1.33	antigen identified by monoclonal antibody ki-67
MmugDNA.2975.1.S1_at	LOC707526	POLE2	9.22E-08	1.14	1.12	-1.20	2.35	1.56	1.12	polymerase (dna directed), epsilon 2 (p59 subunit)
MmugDNA.15250.1.S1_at	---	CENPA	1.46E-06	1.07	1.11	-1.22	3.01	1.80	1.21	centromere protein a, 17kda
MmugDNA.31369.1.S1_at	---	RRM2	2.30E-07	1.16	1.16	-1.24	7.31	3.50	1.54	ribonucleotide reductase m2 polypeptide
MmugDNA.1969.1.S1_at	LOC714686	MCM4	0.0116049	-1.03	-1.04	-1.24	2.01	1.44	1.00	mcm4 minichromosome maintenance deficient 4 (s. cerevisiae)
MmugDNA.21403.1.S1_at	LOC722088	CDCA3	3.32E-05	1.09	1.01	-1.24	2.11	1.26	1.09	cell division cycle associated 3
MmuSTS.1653.1.S1_at	TMPRSS3	TMPRSS3	3.12E-05	1.28	-1.06	-1.24	2.15	1.56	1.16	serine protease tadg12
MmuSTS.1779.1.S1_at	---	NEK2	4.23E-05	1.18	1.21	-1.26	2.59	1.82	1.15	nima (never in mitosis gene a)-related kinase 2
MmugDNA.25197.1.S1_at	ASPM	ASPM	0.000173751	1.03	1.02	-1.27	2.11	1.50	1.03	hypothetical protein flj10517
MmuSTS.2700.1.S1_at	LOC694423	E2F7	2.15E-06	1.15	1.08	-1.27	2.58	1.57	1.26	e2f transcription factor 7
MmugDNA.17376.1.S1_at	S100A8	S100A8	0.000412813	1.33	1.17	-1.28	1.81	1.13	-2.26	s100 calcium binding protein a8 (calgranulin a)
MmugDNA.14075.1.S1_at	RSN	BUB1B	3.01E-06	1.08	-1.00	-1.28	2.26	1.66	1.30	bub1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
MmugDNA.6706.1.S1_at	LOC693531	CKAP2	9.79E-06	1.22	1.13	-1.29	2.49	1.77	1.20	cytoskeleton associated protein 2
MmugDNA.33823.1.S1_s_at	---	KIAA0101	4.16E-08	1.00	-1.02	-1.30	5.24	2.60	1.27	kiaa0101
MmugDNA.38956.1.S1_at	---	NUSAP1	5.92E-08	-1.01	-1.20	-1.31	3.08	1.73	1.06	nucleolar and spindle associated protein 1
MmugDNA.14322.1.S1_at	TFDP1	TFDP1	9.46E-06	1.34	-1.00	-1.33	2.50	1.64	1.37	transcription factor dp-1
MmugDNA.5873.1.S1_at	---	CEP55	8.08E-06	1.04	1.08	-1.36	2.47	1.63	1.18	centrosomal protein 55kda
MmugDNA.12490.1.S1_at	LOC702368	E2F8	0.000588763	1.04	1.04	-1.37	2.20	1.28	1.15	e2f transcription factor 8
MmugDNA.10186.1.S1_at	---	CASC5	4.42E-07	1.24	1.01	-1.39	2.24	1.55	1.33	cancer susceptibility candidate 5
MmugDNA.21515.1.S1_at	---	PRC1	1.31E-06	-1.09	-1.07	-1.42	2.05	1.49	-1.03	protein regulator of cytokinesis 1
MmugDNA.11557.1.S1_at	LOC715235	NCAPG	0.000129006	1.18	1.10	-1.43	2.81	1.68	1.09	chromosome condensation protein g
MmunewRS.816.1.S1_s_at	LOC706650	IGJ	8.83E-06	-1.20	-1.51	-1.47	4.07	1.72	-1.23	immunoglobulin j polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
MmugDNA.5879.1.S1_at	TNFRSF17	TNFRSF17	3.09E-05	-1.20	-1.25	-1.48	3.81	1.76	-1.07	tumor necrosis factor receptor superfamily, member 17
MmuSTS.64.1.S1_at	GMNN	GMNN	0.000100361	1.27	1.08	-1.49	2.91	1.46	-1.07	geminin, dna replication inhibitor
MmugDNA.19768.1.S1_at	LOC709006	CENPM	3.58E-05	-1.02	-1.30	-1.50	2.17	1.44	1.01	chromosome 22 open reading frame 18
MmugDNA.13565.1.S1_at	---	KIF11	2.20E-05	1.23	1.11	-1.51	2.31	1.57	1.17	kinesin family member 11
MmugDNA.3201.1.S1_at	---	BACH2	0.102604	-1.34	-1.63	-1.61	-2.42	-1.41	-1.17	btb and cnc homology 1, basic leucine zipper transcription factor 2
MmugDNA.15585.1.S1_at	HSF4	KIF15	0.0050633	1.01	-1.00	-1.64	2.09	1.37	1.04	kinesin family member 15
MmuSTS.4157.1.S1_at	LOC708574	MAD2L1	6.23E-05	1.29	1.09	-1.69	3.71	1.57	1.13	mad2 mitotic arrest deficient-like 1 (yeast)
MmugDNA.36434.1.S1_at	---	GZMA	9.48E-06	1.34	1.48	-1.75	6.15	1.70	1.00	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)
MmugDNA.3270.1.S1_at	---	YY1	0.000315189	1.21	-1.46	-2.00	-1.26	-1.02	1.08	yy1 transcription factor
MmugDNA.41216.1.S1_at	---	NUDT3	0.00179829	1.11	-1.83	-2.02	-1.68	-1.14	-1.10	diphosphoinositol polyphosphate phosphohydrolase
MmugDNA.16608.1.S1_at	---	ELL2	4.71E-05	1.36	-1.43	-2.03	1.46	1.06	-1.04	elongation factor, rna polymerase ii, 2
MmugDNA.10260.1.S1_at	---	GLS	5.59E-05	1.13	-2.18	-2.05	-1.26	-1.12	1.17	glutaminase
MmugDNA.621.1.S1_at	---	RPL35	3.60E-05	1.35	-1.60	-2.05	-1.41	1.07	1.07	ribosomal protein l35
MmugDNA.29893.1.S1_at	---	ANKRD28	0.00038183	-1.05	-1.47	-2.08	-1.19	-1.17	-1.26	ankyrin repeat domain 28
MmugDNA.4894.1.S1_at	---	GSK3B	0.000461024	1.14	-1.53	-2.26	-1.25	-1.13	-1.03	glycogen synthase kinase 3 beta
MmugDNA.30329.1.S1_at	PABPC4	PABPC4	0.00144765	1.28	-1.63	-2.37	-1.25	-1.10	1.18	poly(a) binding protein, cytoplasmic 4 (inducible form)
MmugDNA.13458.1.S1_at	---	NAP1L1	0.00112975	-1.09	-1.52	-2.50	-1.13	-1.49	-1.49	nucleosome assembly protein 1-like 1
MmugDNA.12660.1.S1_at	---	FAM101B	0.0021112	1.16	-1.67	-2.58	-1.45	1.05	1.13	family with sequence similarity 101, member b
MmugDNA.21136.1.S1_at	LOC709607	LTBP1	0.0386331	-1.13	-1.82	-2.59	-2.19	-1.57	-1.62	latent transforming growth factor beta binding protein 1
MmugDNA.21770.1.S1_at	LOC704306		3.04E-08	1.06	-1.12	-2.64	-1.19	1.10	-1.06	hypothetical protein LOC704306
MmugDNA.29351.1.S1_at	LOC706985	SNCA	0.584629	-1.73	-1.56	-2.64	-1.28	-1.49	-1.38	synuclein, alpha (non a4 component of amyloid precursor)
MmugDNA.23281.1.S1_at	---	PELO	0.00253498	-1.10	-2.39	-2.72	-1.62	-1.70	-1.39	pro1770 protein
MmugDNA.36739.1.S1_at	---	CR1	1.17E-05	1.12	-1.87	-2.82	-1.41	-1.25	-1.10	complement component (3b/4b) receptor 1 (knops blood group)
MmugDNA.21074.1.S1_at	LOC698536	IRS2	0.000103729	1.01	-2.02	-2.93	-1.46	-1.23	-1.35	insulin receptor substrate 2
MmuSTS.1081.1.S1_at	PDE6H	PDE6H	2.60E-05	-1.06	-2.62	-3.03	-2.31	-1.52	-1.45	phosphodiesterase 6h, cgmp-specific, cone, gamma

Supplemental Table S5. 830 probesets determined to be differential after SIVmac239 infection of RMs in RNA from total blood. The Affymetrix Gene Symbol refers to the annotation provided by Affymetrix, Inc. for the Rhesus Genome Array (v.27), based on the Unigene Rhesus Macaque genome Build #13. In cases of missing or provisional annotation, gene symbols were annotated from existing human orthologues based on the DAVID database and are listed in the Corrected Gene Symbol column. X/D0 columns refer to the linear ratio of average gene expression relative to pre-infected average values (red = ratios > +2-fold, green = ratios <-2-fold). Gene Descriptions were based off DAVID annotation where available or Affymetrix annotation.

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/DO	Gene Description
MmugDNA.17118.1.S1_at	LOC700141	ISG15	4.46E-03	32.08	4.95	7.84	2.73	interferon, alpha-inducible protein (clone ifi-15k)
MmuSTS.4748.1.S1_at	---	USP18	2.10E-04	28.96	3.91	5.12	3.46	ubiquitin specific peptidase 18
MmuSTS.1893.1.S1_s_at	---	CXCL10	1.47E-07	19.58	2.57	3.49	2.13	chemokine (c-x-c motif) ligand 10
MmuSTS.4655.1.S1_at	OAS1	OAS1	3.25E-07	16.88	4.37	3.50	1.59	2',5'-oligoadenylate synthetase 1, 40/46kda
MmugDNA.35740.1.S1_at	IFIT2	IFIT2	2.93E-03	16.76	1.73	3.76	2.40	interferon-induced protein with tetratricopeptide repeats 2
MmugDNA.30775.1.S1_at	LOC722182	LOC722182	5.49E-04	15.82	2.51	3.77	1.43	similar to HRAS-like suppressor 2
MmugDNA.19594.1.S1_at	LOC695344	IFIT3	7.09E-03	14.97	2.18	4.48	2.35	interferon-induced protein with tetratricopeptide repeats 3
MmuSTS.1612.1.S1_at	LOC698943	OASL	5.36E-03	14.06	2.76	3.78	2.27	2'-5'-oligoadenylate synthetase-like
MmugDNA.34026.1.S1_at	LOC718510	PLA2G4C	5.39E-06	13.76	1.79	2.22	1.95	phospholipase a2, group ivc (cytosolic, calcium-independent)
MmuSTS.2101.1.S1_at	LOC702775	RIN2	8.68E-07	11.81	2.62	1.84	1.19	ras and rab interactor 2
Mmu.3779.1.S1_at	LOC695344	IFIT3	1.18E-04	11.37	1.56	3.06	1.53	interferon-induced protein with tetratricopeptide repeats 3
MmugDNA.31670.1.S1_at	PTPRA	FAM70A	1.33E-03	11.29	3.42	2.86	1.48	family with sequence similarity 70, member a
MmugDNA.8486.1.S1_at	LOC712401	OAS2	2.71E-03	11.10	2.17	3.33	2.01	2'-5'-oligoadenylate synthetase 2, 69/71kda
MmuSTS.603.1.S1_at	LOC720054	HSPA1B	5.23E-04	10.29	2.25	1.91	1.81	heat shock 70kda protein 1a
MmugDNA.23425.1.S1_at	IL1RN	IL1RN	2.20E-08	9.86	1.86	1.37	1.11	interleukin 1 receptor antagonist
MmuSTS.681.1.S1_at	IL1RN	IL1RN	1.43E-09	9.55	1.42	1.27	1.03	interleukin 1 receptor antagonist
MmugDNA.6512.1.S1_at	LOC699458	LOC26010	2.36E-06	9.07	4.00	3.31	1.36	dna polymerase-transactivated protein 6
Mmu.11363.1.S1_at	CXCL10	CXCL10	2.06E-08	8.98	1.66	1.72	1.44	chemokine (c-x-c motif) ligand 10
MmugDNA.11735.1.S1_at	---	DDX58	6.22E-03	8.45	1.74	2.68	2.00	dead (asp-glu-ala-asp) box polypeptide 58
MmugDNA.20819.1.S1_s_at	LOC712342	OAS3	4.32E-03	8.38	2.08	2.80	1.73	2'-5'-oligoadenylate synthetase 3, 100kda
MmuSTS.4428.1.S1_at	LOC702381	IFI6	1.98E-03	8.35	2.88	4.89	1.88	interferon, alpha-inducible protein (clone ifi-6-16)
MmugDNA.19189.1.S1_at	DDX58	DDX58	4.50E-04	8.32	1.73	1.83	1.52	dead (asp-glu-ala-asp) box polypeptide 58
MmuSTS.713.1.S1_at	LOC697698	TTLL6	5.13E-03	8.21	2.39	3.09	1.80	Similar to tubulin tyrosine ligase-like family, member 6
MmuSTS.1377.1.S1_at	LOC695971	BCL2L14	6.80E-05	8.13	3.83	2.96	1.54	bcl2-like 14 (apoptosis facilitator)
MmugDNA.43291.1.S1_at	LOC712401	OAS2	2.74E-05	7.95	1.61	2.17	1.42	2'-5'-oligoadenylate synthetase 2, 69/71kda
Mmu.10088.2.S1_at	MX2	MX2	7.36E-03	7.94	1.98	2.98	2.18	myxovirus (influenza virus) resistance 2 (mouse)
MmuSTS.713.1.S1_x_at	LOC697698	TTLL6	2.96E-03	7.89	2.25	2.99	1.73	Similar to tubulin tyrosine ligase-like family, member 6
MmuSTS.1580.1.S1_at	---	IFIT5	2.09E-03	7.71	2.17	2.71	1.81	interferon-induced protein with tetratricopeptide repeats 5
MmugDNA.30921.1.S1_at	LOC705525	HERC6	8.90E-04	7.23	1.80	3.34	1.47	hect domain and rld 6
MmugDNA.20634.1.S1_at	LOC697698	DHX58	3.21E-03	7.13	2.07	2.47	1.63	likely ortholog of mouse d11lgp2
MmugDNA.29625.1.S1_at	LOC699578	IRF7	4.78E-03	6.96	2.34	2.55	1.71	interferon regulatory factor 7
MmuSTS.1560.1.S1_at	---	MGC20410	1.03E-05	6.92	2.90	1.70	1.26	---
MmuSTS.2010.1.S1_at	PCDH20	PCDH20	1.35E-08	6.87	1.83	1.48	1.18	protocadherin 20
MmugDNA.25674.1.S1_at	LOC699580	KCTD14	1.60E-04	6.83	5.45	2.19	1.20	potassium channel tetramerisation domain containing 14
MmugDNA.1672.1.S1_at	LOC694699	TNFAIP6	1.47E-03	6.75	4.07	2.25	1.59	tumor necrosis factor, alpha-induced protein 6
MmugDNA.41339.1.S1_at	GCH1	GCH1	5.60E-06	6.61	2.80	1.92	1.44	GTP cyclohydrolase 1
MmuSTS.4660.1.S1_at	LOC694699	TNFAIP6	3.16E-03	5.94	3.66	2.28	1.54	tumor necrosis factor, alpha-induced protein 6
MmugDNA.22278.1.S1_at	---	DDX58	5.91E-03	5.92	1.55	2.45	1.68	dead (asp-glu-ala-asp) box polypeptide 58
MmugDNA.40942.1.S1_at	---	SAMD4A	3.72E-05	5.83	2.40	1.82	1.37	sterile alpha motif domain containing 4a
Mmu.11960.1.S1_at	GBP1	GBP1	6.62E-03	5.75	1.76	2.18	1.96	guanylate binding protein 1, interferon-inducible, 67kda
MmugDNA.19865.1.S1_s_at	IFITM3	IFITM3	4.25E-04	5.64	2.52	1.29	1.18	interferon induced transmembrane protein 3 (1-8U)
MmugDNA.20352.1.S1_at	---	DDX60L	2.59E-04	5.30	1.26	1.53	1.42	---
MmugDNA.25492.1.S1_s_at	LOC719412	LOC719412	2.32E-03	5.25	3.75	2.63	1.75	similar to Probable DNA dC->dU-editing enzyme APOBEC-3A (Phorbolin-1)
MmugDNA.14074.1.S1_at	---	---	2.14E-05	5.25	2.02	2.31	1.21	---
Mmu.865.1.S1_at	OAS1	OAS1	1.10E-09	5.10	1.60	1.80	1.15	2',5'-oligoadenylate synthetase 1, 40/46kda
MmugDNA.36297.1.S1_at	IFIH1	IFIH1	1.58E-04	5.02	1.56	2.06	1.49	interferon induced with helicase c domain 1
Mmu.11961.1.S1_at	GBP1	GBP1	5.57E-04	4.94	1.33	1.96	1.73	guanylate binding protein 1, interferon-inducible, 67kda
MmuAffx.23.23.S1_s_at	S100P	S100P	1.02E-03	4.93	5.31	2.65	1.26	S100 calcium binding protein P
MmuSTS.3702.1.S1_at	---	EIF2AK2	1.48E-04	4.91	1.65	2.20	1.36	eukaryotic translation initiation factor 2-alpha kinase 2
MmugDNA.13099.1.S1_at	---	---	1.88E-08	4.88	1.02	1.45	1.46	---
MmugDNA.19136.1.S1_at	---	CCDC75	4.46E-03	4.84	1.72	2.49	1.49	coiled-coil domain containing 75
MmugDNA.11328.1.S1_at	ATF3	ATF3	4.51E-08	4.82	1.18	1.35	1.08	activating transcription factor 3
MmuSTS.2397.1.S1_s_at	LOC694684	GBP2	6.32E-03	4.81	2.06	1.78	1.66	guanylate binding protein 2, interferon-inducible
MmugDNA.8379.1.S1_at	LOC715462	SLFN5	1.38E-04	4.76	1.62	1.97	1.18	likely ortholog of mouse schlafen 5
MmugDNA.15907.1.S1_at	---	---	3.98E-04	4.74	2.81	1.71	1.45	---
MmugDNA.3353.1.S1_at	LOC700215	LOC700215	2.67E-03	4.72	1.85	1.45	1.32	similar to NmrA-like family domain containing 1
MmugDNA.33242.1.S1_at	---	---	5.34E-04	4.69	2.48	2.05	1.41	---
MmuSTS.2728.1.S1_at	LOC706004	GCN5L2	1.43E-07	4.50	1.17	1.15	1.05	gcn5 general control of amino-acid synthesis 5-like 2 (yeast)
MmugDNA.3747.1.S1_at	LOC693771	LOC693771	6.14E-04	4.48	2.62	1.76	1.40	similar to Transmembrane protein 51
MmuSTS.602.1.S1_at	LOC715638	HSPA1A	1.91E-03	4.32	1.90	1.69	1.21	similar to Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)
MmugDNA.3485.1.S1_at	---	EPSTI1	1.53E-04	4.32	1.67	1.83	1.42	epithelial stromal interaction 1 (breast)
MmugDNA.38053.1.S1_at	TFPI2	TFPI2	8.10E-04	4.27	2.16	1.56	1.07	tissue factor pathway inhibitor 2
MmugDNA.38530.1.S1_at	LOC717470	SIGLEC1	4.84E-06	4.26	1.71	2.28	1.12	sialic acid binding ig-like lectin 1, sialoadhesin
MmugDNA.2176.1.S1_at	ISG20	ISG20	1.70E-06	4.17	1.73	1.51	1.50	interferon stimulated exonuclease gene 20kda
MmugDNA.40434.1.S1_at	LOC714928	LOC714928	2.03E-03	4.14	1.72	1.84	1.61	similar to ataxin-1 ubiquitin-like interacting protein
MmugDNA.5120.1.S1_at	---	---	2.06E-05	4.03	1.97	1.52	1.15	---
MmuSTS.1778.1.S1_at	SCIN	SCIN	7.29E-03	4.02	4.29	1.67	1.04	scinderin
MmuSTS.2042.1.S1_at	---	PML	4.09E-05	4.01	1.63	1.95	1.32	promyelocytic leukemia
MmugDNA.35760.1.S1_at	LOC708404	RTP4	8.63E-05	3.94	1.93	1.74	1.35	receptor transporter protein 4
MmugDNA.31716.1.S1_s_at	LOC715633	LOC715633	6.58E-04	3.85	3.21	1.66	1.48	similar to molybdenum cofactor sulfurase
MmugDNA.17877.1.S1_s_at	---	PML	1.44E-05	3.84	1.39	1.58	1.30	promyelocytic leukemia
MmugDNA.27480.1.S1_at	LOC710375	LGALS8	3.99E-05	3.83	1.46	1.96	1.33	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.17449.1.S1_at	LOC704124	TFEC	5.09E-03	3.82	2.34	1.88	2.01	transcription factor ec
MmugDNA.27315.1.S1_at	---	SAMD9	4.65E-03	3.76	1.73	1.83	1.52	sterile alpha motif domain containing 9
MmugDNA.3158.1.S1_at	CCL8	CCL8	2.36E-07	3.75	1.32	1.28	1.02	chemokine (c-c motif) ligand 8
MmugDNA.8115.1.S1_at	---	RNF213	5.72E-03	3.75	1.77	1.87	1.46	chromosome 17 open reading frame 27
MmuSTS.1439.1.S1_at	LGALS3BP	LGALS3BP	5.48E-04	3.74	1.85	1.88	1.49	lectin, galactoside-binding, soluble, 3 binding protein
MmugDNA.1812.1.S1_at	LOC696090	ZBP1	4.29E-07	3.74	2.26	1.73	1.17	z-dna binding protein 1
MmugDNA.34497.1.S1_at	LOC715706	LOC715706	3.51E-04	3.73	1.73	1.34	-1.06	similar to schlafen family member 13
MmugDNA.20774.1.S1_at	---	CD274	2.45E-03	3.70	1.34	1.08	1.39	cd274 antigen
MmugDNA.5885.1.S1_at	LOC701429	LOC701429	1.01E-06	3.69	1.38	1.21	1.00	Similar to 40S ribosomal protein S17
MmugDNA.27480.1.S1_s_at	LOC710375	LGALS8	3.84E-04	3.68	1.49	1.87	1.37	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.33882.1.S1_at	---	TRIM14	1.44E-03	3.66	2.10	1.79	1.18	tripartite motif-containing 14
MmugDNA.13395.1.S1_at	LOC719253	IFI16	2.30E-04	3.65	1.61	1.55	1.24	interferon, gamma-inducible protein 16
Mmu.11584.1.S1_at	LOC719092	BST2	6.02E-06	3.59	2.08	1.51	1.16	bone marrow stromal cell antigen 2
MmugDNA.22032.1.S1_at	---	---	1.27E-04	3.59	-1.16	1.42	1.19	---
MmugDNA.25587.1.S1_at	LOC693561	PI4K2B	1.06E-05	3.54	1.50	1.58	1.35	phosphatidylinositol 4-kinase type 2 beta
MmugDNA.8893.1.S1_at	LOC715369	CORO2A	1.63E-04	3.51	2.40	1.31	-1.20	coronin, actin binding protein, 2a
MmugDNA.38006.1.S1_s_at	S100P	S100P	1.40E-03	3.48	4.15	1.93	1.31	S100 calcium binding protein P

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/ DO	Gene Description
MmuAffx.10.1.A1_x_at	---	---	9.19E-04	3.48	1.68	1.76	1.21	---
MmugDNA.32046.1.S1_at	LOC720688	KLHDC7B	7.69E-05	3.47	2.01	2.19	1.24	kelch domain containing 7b
MmugDNA.32611.1.S1_at	LOC715462	SLFN5	3.77E-03	3.45	1.75	1.44	1.14	likely ortholog of mouse schlafen 5
MmugDNA.9803.1.S1_at	---	PML	3.64E-04	3.44	1.40	1.59	1.36	promyelocytic leukemia
MmugDNA.18184.1.S1_at	---	---	1.27E-04	3.40	1.51	1.07	1.36	---
MmugDNA.36196.1.S1_at	---	STAT2	4.17E-03	3.39	1.69	1.76	1.38	signal transducer and activator of transcription 2, 113kda
Mmu.12633.1.S1_at	LOC715591	PARP14	7.08E-03	3.37	1.23	1.56	1.60	poly (adp-ribose) polymerase family, member 14
MmugDNA.23367.1.S1_at	LOC715967	LOC715967	1.05E-03	3.36	1.68	1.86	1.37	hypothetical protein LOC715967
MmugDNA.28010.1.S1_at	LOC710375	LGALS8	2.48E-03	3.35	1.25	1.68	1.15	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.42826.1.S1_at	LOC710406	C21ORF91	7.26E-07	3.34	1.36	1.30	1.28	chromosome 21 open reading frame 91
MmugDNA.8672.1.S1_at	LOC704374	SDC3	2.02E-06	3.32	1.30	1.60	1.18	syndecan 3 (n-syndecan)
MmugDNA.42778.1.S1_at	LOC711660	PARP12	1.27E-04	3.32	1.47	1.39	1.22	poly (adp-ribose) polymerase family, member 12
MmugDNA.28698.1.S1_x_at	---	SAMD9	4.10E-03	3.32	1.55	1.76	1.31	sterile alpha motif domain containing 9
MmugDNA.13723.1.S1_at	LOC714371	LOC714371	2.93E-04	3.32	1.66	2.04	1.09	Similar to polypeptide N-acetylgalactosaminyltransferase 2
MmuSTS.1283.1.S1_at	LOC711236	DTL	2.43E-03	3.31	6.52	2.61	1.86	denticleless homolog (drosophila)
MmugDNA.28886.1.S1_at	LOC717665	C6ORF150	1.41E-03	3.29	1.53	1.30	1.47	chromosome 6 open reading frame 150
MmugDNA.7800.1.S1_at	---	---	2.60E-04	3.28	1.44	1.47	1.36	---
MmugDNA.28698.1.S1_at	---	SAMD9	4.54E-03	3.28	1.52	1.80	1.32	sterile alpha motif domain containing 9
MmugDNA.22615.1.S1_at	---	---	5.89E-05	3.24	1.01	1.52	1.23	---
MmunewRS.843.1.S1_at	LOC721635	LOC721635	2.19E-05	3.21	1.20	1.32	1.22	hypothetical protein LOC721635
MmugDNA.10435.1.S1_at	LOC693306	LOC693306	6.33E-05	3.21	1.19	1.24	1.21	similar to family with sequence similarity 46, member A
MmugDNA.13723.1.S1_s_at	LOC714371	LOC714371	8.64E-04	3.19	1.56	1.87	1.06	Similar to polypeptide N-acetylgalactosaminyltransferase 2
MmugDNA.9534.1.S1_at	LOC715706	LOC715706	6.95E-04	3.19	1.50	1.09	1.03	similar to schlafen family member 13
MmuSTS.2890.1.S1_at	---	TRIM14	1.09E-03	3.17	1.68	1.47	1.19	tripartite motif-containing 14
MmugDNA.14170.1.S1_at	---	ZCCHC2	7.05E-03	3.17	1.29	1.39	1.34	zinc finger, cchc domain containing 2
MmugDNA.38074.1.S1_at	---	---	4.96E-05	3.17	1.20	1.18	-1.14	---
MmugDNA.23196.1.S1_at	---	STAT1	3.62E-04	3.15	1.19	1.47	1.33	signal transducer and activator of transcription 1, 91kda
MmugDNA.12946.1.S1_at	---	PML	9.95E-04	3.14	1.49	1.55	1.45	promyelocytic leukemia
MmuSTS.549.1.S1_at	BARD1	BARD1	1.87E-04	3.13	2.64	1.70	1.42	BRCA1 associated RING domain 1
MmugDNA.4351.1.S1_at	---	---	3.66E-07	3.13	1.15	1.13	-1.04	---
MmugDNA.19126.1.S1_at	---	---	6.06E-03	3.12	1.34	1.27	1.05	---
MmuSTS.3349.1.S1_at	LOC713715	CCRL2	4.33E-03	3.11	1.29	1.37	1.14	chemokine (c-c motif) receptor-like 2
MmuSTS.3569.1.S1_at	---	---	3.27E-06	3.11	1.08	1.31	1.14	---
MmugDNA.9650.1.S1_at	LOC714914	DTX3L	5.72E-04	3.10	1.36	1.51	1.38	deltex 3-like (drosophila)
Mmu.13018.2.S1_a_at	TRIM5	TRIM5	1.79E-04	3.10	1.18	1.31	1.31	tripartite motif-containing 5
MmugDNA.1805.1.S1_at	---	---	8.45E-04	3.09	1.52	-1.04	1.34	---
MmugDNA.7109.1.S1_at	SP100	SP100	5.42E-04	3.09	1.54	1.54	1.21	SP100 nuclear antigen
MmugDNA.28813.1.S1_at	LOC702789	LOC702789	1.28E-03	3.08	1.60	1.92	1.38	similar to phorbol-12-myristate-13-acetate-induced protein 1
MmugDNA.10434.1.S1_at	LOC693306	LOC693306	7.28E-04	3.02	1.29	1.24	1.31	similar to family with sequence similarity 46, member A
MmunewRS.20.1.S1_at	LOC719253	IFI16	4.48E-03	3.01	1.76	1.22	1.60	interferon, gamma-inducible protein 16
MmuSTS.4763.1.S1_at	LOC722740	FBXO6	2.41E-04	2.97	2.24	1.57	1.28	f-box protein 6
MmugDNA.40394.1.S1_at	LY6E	LY6E	2.17E-04	2.97	1.59	1.50	1.49	lymphocyte antigen 6 complex, locus e
MmugDNA.8695.1.S1_at	---	CORO2A	4.81E-04	2.95	2.48	1.35	-1.23	coronin, actin binding protein, 2a
MmugDNA.41833.1.S1_at	LOC719092	BST2	4.17E-04	2.94	2.19	1.29	1.07	bone marrow stromal cell antigen 2
MmugDNA.19865.1.S1_x_at	IFITM3	IFITM3	1.07E-05	2.93	1.56	1.02	1.01	interferon induced transmembrane protein 3 (1-8U)
MmugDNA.15595.1.S1_at	HTRA1	HTRA1	1.58E-04	2.91	5.74	1.72	1.29	HtrA serine peptidase 1
MmugDNA.269.1.S1_at	---	---	3.42E-05	2.91	1.19	-1.04	1.07	---
MmuSTS.4059.1.S1_at	TRIM21	TRIM21	2.94E-07	2.84	1.31	1.40	1.20	tripartite motif-containing 21
Mmu.4440.1.S1_at	LOC693561	PI4K2B	8.60E-07	2.82	1.14	1.21	1.25	phosphatidylinositol 4-kinase type 2 beta
MmugDNA.9495.1.S1_at	---	PHACTR2	1.35E-03	2.82	1.63	1.43	1.14	phosphatase and actin regulator 2
Mmu.13989.1.S1_at	LOC719212	LOC719212	6.63E-06	2.81	1.76	1.42	1.32	---
MmugDNA.11097.1.S1_at	LOC704579	SRGAP2	4.37E-04	2.81	1.15	1.30	1.61	slit-robo rho gtpase activating protein 2
MmugDNA.19098.1.S1_at	---	LOC100130123	7.57E-04	2.80	1.57	1.29	1.21	---
MmuSTS.1185.1.S1_at	LOC712705	PLA1A	3.58E-05	2.78	1.39	1.30	1.11	phospholipase a1 member a
MmugDNA.7052.1.S1_at	LOC705561	UBE2L6	7.14E-05	2.78	1.72	1.47	1.27	ubiquitin-conjugating enzyme e2l 6
MmugDNA.42856.1.S1_at	---	---	2.05E-06	2.77	1.37	1.40	1.11	---
MmugDNA.34787.1.S1_at	HTRA1	HTRA1	3.12E-05	2.76	4.27	1.69	1.16	HtrA serine peptidase 1
MmugDNA.36766.1.S1_at	TOR1B	TOR1B	2.64E-03	2.75	1.74	1.44	1.41	torsin family 1, member b (torsin b)
MmugDNA.10146.1.S1_at	LOC712588	TRIM25	7.10E-03	2.75	1.51	1.44	1.41	tripartite motif-containing 25
MmugDNA.9841.1.S1_at	---	---	3.87E-05	2.74	1.50	1.23	1.15	---
MmugDNA.22391.1.S1_at	LOC715533	LOC715533	1.65E-07	2.73	1.32	1.09	1.28	similar to poly (ADP-ribose) polymerase family, member 15
MmugDNA.12043.1.S1_at	---	SAMD9L	1.05E-03	2.72	1.56	1.20	1.37	sterile alpha motif domain containing 9-like
Mmu.7639.1.S1_at	STAT1	STAT1	2.83E-04	2.71	1.41	1.38	1.38	signal transducer and activator of transcription 1, 91kda
MmugDNA.21377.1.S1_at	LOC705910	MOV10	9.14E-06	2.71	1.34	1.19	1.01	mov10, moloney leukemia virus 10, homolog (mouse)
MmugDNA.5452.1.S1_at	FPR3	FPR3	3.53E-04	2.67	1.38	1.49	1.33	formyl peptide receptor 3
MmugDNA.24297.1.S1_s_at	SOCS1	SOCS1	3.32E-05	2.66	1.78	1.17	1.29	suppressor of cytokine signaling 1
MmugDNA.22619.1.S1_x_at	LOC710928	UNC93B1	2.39E-03	2.65	1.31	1.46	1.46	unc-93 homolog b1 (c. elegans)
MmuSTS.1513.1.S1_at	IFI35	IFI35	6.37E-04	2.65	1.78	1.19	1.27	interferon-induced protein 35
Mmu.12603.1.S1_at	LOC721956	LOC721956	2.88E-03	2.65	1.39	-1.01	1.62	hypothetical protein LOC721956
MmugDNA.22619.1.S1_at	LOC710928	UNC93B1	3.41E-03	2.64	1.33	1.44	1.43	unc-93 homolog b1 (c. elegans)
MmugDNA.23681.1.S1_at	---	---	9.58E-06	2.64	1.03	1.24	-1.48	---
MmuSTS.4521.1.S1_at	STAT2	STAT2	1.55E-04	2.62	1.13	1.51	1.16	signal transducer and activator of transcription 2
MmunewRS.644.1.S1_at	---	---	4.76E-03	2.61	1.33	1.44	1.09	---
MmugDNA.8251.1.S1_at	LOC707359	TMEM140	4.47E-03	2.57	1.23	1.00	1.23	hypothetical protein flj11000
MmuSTS.864.1.S1_at	LOC710375	LGALS8	9.48E-04	2.56	1.26	1.55	1.25	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.15997.1.S1_s_at	LILRA1 /// LILRAA	LILRA1 /// LILRAA	6.75E-04	2.56	1.27	1.28	1.14	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 /
MmuSTS.4666.1.S1_at	TNFSF10	TNFSF10	1.38E-05	2.55	1.28	1.06	-1.25	tumor necrosis factor (ligand) superfamily, member 10
MmuSTS.2164.1.S1_at	LOC708293	DDX10	1.92E-03	2.55	5.33	3.74	1.71	dead (asp-glu-ala-asp) box polypeptide 10
MmuSTS.3131.1.S1_at	LOC712754	LOC712754	9.75E-05	2.55	1.15	-1.10	2.19	similar to Regulator of G-protein signaling 1 (RGS1) (Early response protein 1R2
MmugDNA.30129.1.S1_at	TNFSF10	TNFSF10	3.72E-06	2.52	1.30	1.06	-1.23	tumor necrosis factor (ligand) superfamily, member 10
MmugDNA.7480.1.S1_at	GLRX	GLRX	7.10E-05	2.52	1.81	1.35	1.12	glutaredoxin (thioltransferase)
Mmu.8122.1.A1_at	LOC712588	TRIM25	5.42E-03	2.51	1.81	1.18	1.41	tripartite motif-containing 25
MmugDNA.14047.1.S1_at	---	---	1.15E-03	2.51	1.33	1.16	1.18	---
MmugDNA.2622.1.S1_at	LOC702384	LOC702384	2.97E-07	2.50	1.14	1.06	1.20	similar to abhydrolase domain containing 6
MmugDNA.9176.1.S1_at	ATP5G1	CNP	3.17E-06	2.47	1.48	1.22	1.34	2',3'-cyclic nucleotide 3' phosphodiesterase
MmugDNA.12374.1.S1_at	LOC708936	LOC708936	1.11E-05	2.46	-1.08	1.23	1.02	Similar to protein phosphatase 1, regulatory (inhibitor) subunit 2
MmugDNA.10601.1.S1_at	EHD4	EHD4	8.89E-07	2.46	1.09	-1.04	1.34	EH-domain containing 4
MmugDNA.5661.1.S1_at	LOC719402	KIAA0082	6.82E-03	2.46	1.37	1.29	1.27	kiaa0082
MmugDNA.13670.1.S1_at	DNPEP	DNPEP	3.84E-05	2.45	1.58	1.32	1.12	aspartyl aminopeptidase
MmugDNA.7797.1.S1_at	FCN1	FCN1	7.02E-04	2.44	2.35	1.57	1.20	ficolin (collagen/fibrinogen domain containing) 1
MmuSTS.3554.1.S1_at	LOC705554	DHRS9	2.65E-03	2.43	1.38	1.37	-1.08	dehydrogenase/reductase (sdr family) member 9
MmugDNA.19523.1.S1_at	CD164	CD164	2.08E-05	2.42	1.53	1.23	1.20	cd164 antigen, sialomucin
MmugDNA.28999.1.S1_at	LOC718036	KIAA1618	5.14E-03	2.42	1.81	1.45	1.18	kiaa1618
MmugDNA.36872.1.S1_at	LOC694916	LYSMD2	3.54E-06	2.41	1.19	1.14	1.31	lysm, putative peptidoglycan-binding, domain containing 2
MmuSTS.4535.1.S1_at	LOC700118	ERAP2	3.11E-07	2.41	1.47	1.04	1.03	leukocyte-derived arginine aminopeptidase

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/DO	Gene Description
MmugDNA.31375.1.S1_s_at	LOC706568	LOC706568	8.54E-04	2.40	1.76	1.12	1.06	similar to caspase 1 isoform alpha precursor
MmugDNA.6326.1.S1_at	---	SLFN5	9.70E-05	2.40	1.78	1.25	1.08	likely ortholog of mouse schlafen 5
MmunewRS.902.1.S1_at	LOC702068	EMB	5.50E-03	2.39	1.82	1.29	1.35	embigin homolog (mouse)
MmugDNA.2972.1.S1_at	---	SP140	4.74E-05	2.39	-1.08	1.14	1.25	sp140 nuclear body protein
MmugDNA.22615.1.S1_s_at	---	---	1.84E-04	2.38	1.01	1.18	1.19	---
MmuSTS.4678.1.S1_at	---	TREX1	3.70E-08	2.38	1.22	1.27	1.22	three prime repair exonuclease 1
MmugDNA.19343.1.S1_s_at	HBG2	HBG2	1.48E-03	2.38	-1.40	5.35	-1.08	hemoglobin, gamma G
MmugDNA.2761.1.S1_at	SP100	SP100	8.00E-05	2.37	1.42	1.38	1.27	sp100 nuclear antigen
MmugDNA.41220.1.S1_at	LOC715533	LOC715533	1.84E-05	2.37	1.20	1.01	1.28	similar to poly (ADP-ribose) polymerase family, member 15
Mmu.13018.1.S1_at	TRIM5	TRIM5	2.75E-04	2.36	1.23	1.44	1.18	tripartite motif-containing 5
MmugDNA.19523.1.S1_s_at	CD164	CD164	2.75E-05	2.36	1.47	1.23	1.21	cd164 antigen, sialomucin
MmugDNA.17877.1.S1_at	---	PML	2.43E-06	2.35	1.03	1.35	1.12	promyelocytic leukemia
MmuSTS.1659.1.S1_at	LOC707072	RPL4	2.96E-04	2.35	1.80	1.39	1.40	ribosomal protein l4
Mmu.11980.1.S1_at	GNPAT	GNPAT	6.37E-03	2.35	1.25	1.68	1.25	glyceronephosphate o-acyltransferase
MmugDNA.12018.1.S1_at	LOC712342	OAS3	1.26E-03	2.35	1.12	1.31	1.20	2'-5'-oligoadenylate synthetase 3, 100kda
MmugDNA.21968.1.S1_at	LOC707687	LOC707687	2.55E-03	2.35	1.49	1.34	1.18	---
MmuSTS.92.1.S1_at	---	---	8.90E-04	2.33	1.54	1.28	1.40	---
MmugDNA.6224.1.S1_at	LOC718484	LOC718484	1.31E-06	2.32	-1.02	1.28	1.12	similar to calcium binding protein 5
MmugDNA.39691.1.S1_s_at	TRIM38	TRIM38	7.70E-04	2.32	1.35	1.10	1.40	tripartite motif-containing 38
MmugDNA.8321.1.S1_at	LOC711898	LOC711898	3.19E-03	2.32	1.34	1.15	-1.04	Similar to slingshot 2
MmugDNA.9213.1.S1_at	---	FLJ11286	1.09E-05	2.31	1.28	1.30	1.04	hypothetical protein flj11286
MmugDNA.14283.1.S1_at	---	---	1.13E-03	2.31	1.26	1.32	1.01	---
MmuSTS.2830.1.S1_at	LOC715866	APOL3	4.90E-04	2.30	1.84	1.16	1.15	tnf-inducible protein cg12-1
MmugDNA.8389.1.S1_at	---	---	8.77E-04	2.30	1.91	1.51	1.25	---
MmugDNA.24620.1.S1_at	---	---	1.32E-04	2.30	1.61	1.41	-1.02	---
MmugDNA.5950.1.S1_at	LOC708132	PARP10	2.35E-05	2.29	1.24	1.30	1.32	poly (adp-ribose) polymerase family, member 10
MmuSTS.927.1.S1_at	LOC693955	LOC693955	1.05E-03	2.29	-2.01	2.07	-1.11	similar to fem-1 homolog b
MmuSTS.3917.1.S1_at	STAT1	STAT1	2.80E-03	2.28	1.45	1.43	1.29	signal transducer and activator of transcription 1, 91kda
MmugDNA.1057.1.S1_at	DNAJA1	DNAJA1	8.63E-04	2.28	1.32	1.19	1.23	DnaJ (Hsp40) homolog, subfamily A, member 1
MmuSTS.1158.1.S1_at	PHF11	PHF11	7.41E-04	2.28	1.36	1.30	1.23	phd finger protein 11
Mmu.10506.1.S1_s_at	DNAJA1	DNAJA1	7.33E-03	2.28	-1.06	1.53	1.37	DnaJ (Hsp40) homolog, subfamily A, member 1
MmugDNA.19435.1.S1_s_at	DNAJA1 /// LOC696406	DNAJA1 /// LOC696406	2.66E-03	2.28	-1.01	1.51	1.41	DnaJ (Hsp40) homolog, subfamily A, member 1 /// similar to DnaJ-like protein 2
MmugDNA.25388.1.S1_at	---	RIN2	1.93E-03	2.27	1.24	1.47	1.27	ras and rab interactor 2
MmugDNA.13798.1.S1_at	LOC711784	LOC711784	2.48E-04	2.27	1.26	1.08	1.09	Similar to aconitase 2, mitochondrial
MmugDNA.34145.1.S1_at	LOC704928	DYNLT1	4.97E-04	2.27	1.47	1.31	1.26	dynein, light chain, tctex-type 1
Mmu.12603.1.S1_a_at	LOC721956	LOC721956	1.51E-03	2.26	1.16	1.15	1.23	hypothetical protein LOC721956
MmugDNA.16432.1.S1_at	DHX8	PRIC285	2.95E-04	2.25	1.07	1.31	1.19	peroxisomal proliferator-activated receptor a interacting complex 285
MmugDNA.2279.1.S1_at	TNK2	TNK2	4.95E-03	2.25	1.28	1.35	1.22	tyrosine kinase, non-receptor, 2
MmugDNA.32890.1.S1_at	LOC717355	NAPA	1.65E-07	2.24	1.30	1.27	1.12	n-ethylmaleimide-sensitive factor attachment protein, alpha
MmugDNA.37123.1.S1_at	---	---	5.55E-05	2.24	1.06	1.34	1.19	---
MmugDNA.23324.1.S1_at	LOC719898	LOC719898	5.98E-05	2.23	1.18	1.16	1.12	similar to Carcinoembryonic antigen-related cell adhesion molecule 1 precursor (
MmugDNA.19992.1.S1_at	TRIM5	TRIM5	4.19E-04	2.21	1.24	1.23	1.17	tripartite motif-containing 5
MmugDNA.42104.1.S1_at	---	---	4.61E-07	2.21	1.09	1.14	1.14	---
MmugDNA.5794.1.S1_at	MT2A	MT2A	5.03E-04	2.21	1.46	1.31	1.26	metallothionein 2a
MmunewRS.633.1.S1_s_at	APOBEC3H	APOBEC3H	8.58E-05	2.20	1.05	1.68	1.06	arp10 protein
MmugDNA.31960.1.S1_at	---	XRN1	3.80E-05	2.19	1.07	1.18	1.07	5'-3' exoribonuclease 1
MmuSTS.3184.1.S1_at	LOC710061	LOC710061	4.04E-04	2.18	1.42	1.23	1.05	similar to MAP kinase interacting serine/threonine kinase 1 isoform 1
MmugDNA.37307.1.S1_at	LOC699295	LBA1	4.44E-04	2.18	1.06	1.04	1.07	lupus brain antigen 1
MmugDNA.27150.1.S1_at	LOC699207	PATL1	1.12E-04	2.18	1.26	1.21	1.09	flj36874 protein
MmuSTS.4171.1.S1_at	MSRA	MSRA	1.67E-03	2.18	1.52	1.27	-1.00	methionine sulfoxide reductase a
MmugDNA.32531.1.S1_at	LOC708143	LOC708143	1.16E-06	2.17	1.15	1.18	-1.12	similar to protein phosphatase 1J (PP2C domain containing)
MmuSTS.4540.1.S1_at	LOC694358	LOC694358	5.73E-06	2.17	-1.07	-1.08	1.47	similar to leucine-rich repeat kinase 1
MmugDNA.22157.1.S1_at	---	PCGF5	9.87E-07	2.17	1.20	1.35	1.12	polycomb group ring finger 5
MmugDNA.41577.1.S1_at	---	---	8.56E-07	2.17	1.32	1.09	-1.03	---
MmugDNA.43065.1.S1_at	LOC714549	LOC714549	4.58E-05	2.17	1.34	1.27	1.12	similar to pregnancy-induced growth inhibitor isoform 1
MmuSTS.3274.1.S1_at	LOC709733	LOC709733	1.25E-04	2.16	1.44	1.22	1.23	similar to ribosomal protein S6 kinase, 52kDa, polypeptide 1
MmuSTS.805.1.S1_at	ATP5G1	ATP5G1	2.95E-07	2.14	1.00	1.14	1.24	atp synthase, h+ transporting, mitochondrial f0 complex, subunit c1 (subunit 9)
MmugDNA.19435.1.S1_at	LOC696406	LOC696406	1.88E-03	2.14	-1.10	1.58	1.23	similar to DnaJ-like protein 2
MmugDNA.32966.1.S1_at	LOC704374	LOC704374	2.54E-04	2.14	1.25	1.29	1.09	similar to Syndecan-3 (SYND3)
MmugDNA.23750.1.S1_at	---	PARP11	3.23E-06	2.13	1.62	1.17	1.02	poly (adp-ribose) polymerase family, member 11
MmugDNA.30612.1.S1_at	SOX30	SOX30	2.70E-03	2.13	1.41	1.24	1.20	SRY (sex determining region Y)-box 30
MmugDNA.951.1.S1_at	---	---	9.64E-05	2.12	1.42	1.08	1.10	---
MmugDNA.1081.1.S1_at	LOC717726	TAP1	7.30E-04	2.11	1.46	1.08	1.26	transporter 1, atp-binding cassette, sub-family b (mdr/tap)
MmugDNA.19224.1.S1_at	LOC710375	LGALS8	1.83E-03	2.11	1.31	1.32	1.04	lectin, galactoside-binding, soluble, 8 (galectin 8)
MmugDNA.18626.1.S1_at	LOC699759	LOC699759	1.34E-04	2.11	1.28	1.10	1.11	Similar to zinc finger protein 33B
MmugDNA.41043.1.S1_at	---	NBN	1.95E-05	2.11	-1.87	1.44	1.03	nibrin
MmugDNA.2776.1.S1_at	SP100	SP100	9.66E-05	2.11	1.21	1.40	1.03	sp100 nuclear antigen
MmugDNA.4767.1.S1_at	---	LOC441108	5.28E-03	2.10	1.21	1.07	1.10	hypothetical gene supported by ak128882
MmuSTS.2164.1.S1_s_at	LOC708293	DDX10	4.38E-04	2.10	6.45	2.91	1.73	dead (asp-glu-ala-asp) box polypeptide 10
MmugDNA.4964.1.S1_at	LOC707625	SPTLC2	1.44E-07	2.09	1.35	1.15	1.04	serine palmitoyltransferase, long chain base subunit 2
MmugDNA.40112.1.S1_at	---	---	1.18E-03	2.08	-1.08	1.12	1.06	---
Mmu.5363.1.S1_at	LOC710966	LOC710966	7.59E-04	2.08	1.27	1.14	-1.08	similar to tribbles homolog 2
MmugDNA.13502.1.S1_at	---	---	4.31E-03	2.08	1.00	1.34	1.70	---
MmugDNA.15515.1.S1_at	LOC698143	LOC698143	8.77E-04	2.07	1.52	1.22	1.05	Similar to 60S ribosomal protein L12
MmugDNA.20483.1.S1_at	LOC703758	LOC703758	6.71E-03	2.07	1.80	1.48	1.23	similar to Protein KIAA0280
MmunewRS.165.1.S1_at	LOC719654	LOC719654	1.63E-03	2.07	1.12	1.09	1.07	similar to sialic acid binding immunoglobulin-like lectin-like protein 1 isoform
MmugDNA.14810.1.S1_at	LOC711784	TRAFD1	1.81E-04	2.06	1.28	1.06	1.10	traf-type zinc finger domain containing 1
MmugDNA.31377.1.S1_s_at	LOC706568	CASP1	4.06E-03	2.06	1.49	1.32	1.18	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
MmuSTS.4111.1.S1_at	EGF	EGF	6.12E-04	2.06	2.19	1.25	-1.06	epidermal growth factor (beta-urogastrone)
MmugDNA.21986.1.S1_at	---	---	7.35E-03	2.05	1.19	-1.07	1.26	---
MmugDNA.23383.1.S1_at	LOC710466	LOC710466	5.44E-03	2.05	1.35	1.25	-1.05	hypothetical protein LOC710466
MmuSTS.4836.1.S1_at	LOC718197	LOC718197	1.65E-05	2.05	1.41	1.15	1.10	Similar to GPI-anchored metastasis-associated protein homolog
MmuSTS.3400.1.S1_at	LOC719199	LOC719199	1.09E-03	2.05	1.50	1.22	1.19	similar to cyclin-dependent kinase inhibitor 1A
MmugDNA.9141.1.S1_at	---	---	2.16E-03	2.05	-1.59	2.20	-1.22	---
MmugDNA.20995.1.S1_at	---	CCR1	6.61E-03	2.05	1.49	1.26	-1.09	chemokine (c-c motif) receptor 1
MmugDNA.8510.1.S1_s_at	LOC722189	LOC722189	5.90E-04	2.05	1.47	1.15	1.16	similar to Retinoic acid receptor responder protein 3 (Tazarotene-induced gene 3
MmuSTS.646.1.S1_at	---	---	2.20E-04	2.05	1.50	1.48	1.11	---
MmugDNA.10601.1.S1_s_at	EHD4	EHD4	3.53E-06	2.04	1.22	1.03	1.23	EH-domain containing 4
MmugDNA.40682.1.S1_at	---	---	3.72E-05	2.04	1.04	-1.10	1.12	---
MmugDNA.599.1.S1_at	LOC700921	LOC700921	6.65E-03	2.03	1.40	1.10	1.19	similar to dpy-19-like 3
MmugDNA.28970.1.S1_at	IL1RN	IL1RN	8.62E-05	2.03	-1.03	1.08	-1.06	interleukin 1 receptor antagonist
MmugDNA.1574.1.S1_at	---	---	7.36E-05	2.02	1.07	1.08	1.03	---
MmuSTS.379.1.S1_at	LOC715096	LOC715096	6.42E-06	2.02	1.14	1.22	1.03	similar to Galectin-9 (HOM-HD-21) (Ecalectin)
MmugDNA.3087.1.S1_at	---	---	1.52E-04	2.02	1.27	-1.09	1.15	---
MmugDNA.6764.1.S1_at	GMIP	GMIP	2.89E-06	2.02	1.40	1.26	1.03	GEM interacting protein

Supplementary Table S5. part 3 of 9

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/ DO	Gene Description
MmugDNA.6653.1.S1_at	PCTAIRE2BP	TDRD7	4.33E-03	2.02	1.52	1.12	1.21	tudor domain containing 7
MmugDNA.22923.1.S1_at	---	---	6.53E-05	2.01	1.32	1.17	-1.05	---
MmugDNA.228.1.S1_at	LOC708518	C6ORF192	5.23E-03	2.01	1.40	1.45	1.10	chromosome 6 open reading frame 192
MmugDNA.33437.1.S1_s_at	LOC713517	ZNF313	3.03E-05	2.00	1.17	1.02	1.11	zinc finger protein 313
MmugDNA.41579.1.S1_at	LOC719732	LOC719732	1.09E-03	1.97	2.29	1.23	-1.12	similar to triggering receptor expressed on myeloid cells-like 1
MmugDNA.9141.1.S1_x_at	---	---	2.34E-03	1.96	-1.53	2.09	-1.25	---
MmugDNA.1987.1.S1_at	SLC2A5	SLC2A5	6.61E-04	1.92	3.27	1.78	1.11	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
MmugDNA.7502.1.S1_at	LOC701123	LOC701123	8.19E-05	1.91	3.56	1.25	-1.26	similar to tumor suppressor candidate 3 isoform a
MmugDNA.22222.1.S1_s_at	---	NBN	4.83E-06	1.89	-2.21	1.35	-1.00	nibrin
MmugDNA.7952.1.S1_at	---	---	8.95E-04	1.89	2.73	1.20	-1.27	---
MmugDNA.6277.1.S1_at	LOC708293	BUB1	2.78E-04	1.89	5.88	2.47	1.69	bub1 budding uninhibited by benzimidazoles 1 homolog (yeast)
MmuSTS.869.1.S1_at	DYSF	DYSF	5.41E-05	1.88	5.77	1.22	1.07	dysferlin
MmunewRS.500.1.S1_at	FABP5	FABP5	3.09E-03	1.86	2.34	1.72	1.13	fatty acid binding protein 5 (psoriasis-associated)
MmugDNA.38800.1.S1_at	SLC45A2	SLC45A2	2.54E-03	1.85	2.02	1.14	-1.20	Membrane-associated transporter protein
MmugDNA.21855.1.S1_s_at	---	---	6.32E-04	1.84	-1.52	2.88	-1.09	---
MmugDNA.25040.1.S1_at	LOC701799	LOC701799	9.85E-04	1.83	2.94	1.73	1.03	Hypothetical protein LOC701799
MmugDNA.30620.1.S1_at	---	---	6.76E-04	1.77	2.29	1.20	-1.40	---
MmugDNA.18674.1.S1_at	LOC704872	LOC704872	7.70E-06	1.76	2.77	1.31	-1.49	similar to C-type lectin superfamily 4, member G
MmugDNA.34150.1.S1_s_at	LOC701028	LOC701028	3.79E-03	1.74	1.95	2.40	1.46	hypothetical protein LOC701028
MmugDNA.32941.1.S1_at	LOC711569	C16ORF75	1.82E-07	1.73	3.65	2.11	1.27	hypothetical protein mgc24665
MmuSTS.3508.1.S1_at	LOC700467	LOC700467	2.69E-03	1.73	-2.67	1.55	-1.00	similar to complement component 5
MmuSTS.4208.1.S1_at	LOC702754	LOC702754	4.32E-03	1.73	2.31	1.32	-1.33	similar to glucosaminyl (N-acetyl) transferase 3, mucin type
MmugDNA.28421.1.S1_at	---	---	4.59E-03	1.73	-2.45	1.72	-1.15	---
MmugDNA.36470.1.S1_at	LOC709220	LOC709220	1.28E-03	1.69	3.35	1.90	1.56	Similar to zinc finger protein 587
MmugDNA.29385.1.S1_at	LOC711648	MIRN21	6.97E-03	1.66	2.15	1.34	1.05	microrna 21
MmugDNA.8645.1.S1_at	---	---	8.15E-05	1.65	-6.23	1.09	-1.48	---
MmugDNA.33886.1.S1_at	LOC722264	LOC722264	2.02E-03	1.64	-2.07	1.64	1.02	conserved gene telomeric to alpha globin cluster
MmunewRS.483.1.S1_at	LOC719807	LOC719807	9.84E-04	1.64	-3.56	1.75	-1.49	similar to intelectin
MmugDNA.8645.1.S1_x_at	---	---	1.45E-04	1.63	-5.52	1.15	-1.52	---
MmugDNA.43348.1.S1_at	---	---	4.55E-05	1.60	3.01	2.68	1.40	---
MmugDNA.19842.1.S1_at	CA13	CA13	5.68E-04	1.60	2.85	1.05	-1.45	carbonic anhydrase XIII
MmugDNA.14465.1.S1_at	---	---	4.17E-03	1.59	2.08	1.27	-1.47	---
MmuSTS.2361.1.S1_at	LOC715264	LOC715264	2.26E-03	1.59	2.25	1.41	1.14	similar to Protein S100-A2 (S100 calcium-binding protein A2) (Protein S-100L) (C
MmugDNA.41044.1.S1_at	---	NBN	1.89E-05	1.58	-3.11	1.10	1.01	nibrin
MmuSTS.4045.1.S1_at	LOC710925	LOC710925	2.60E-03	1.58	-1.15	1.30	2.45	similar to SP140 nuclear body protein isoform 1
MmuSTS.598.1.S1_at	HP	HP	4.27E-04	1.56	9.67	2.41	-1.92	haptoglobin
MmugDNA.22222.1.S1_at	---	NBN	3.51E-05	1.56	-3.92	1.18	1.03	nibrin
MmugDNA.9253.1.S1_at	LOC706102	LOC706102	3.38E-05	1.54	-3.43	1.19	-1.30	similar to muscleblind-like 3 isoform G
MmuSTS.4685.1.S1_at	TYMS	TYMS	4.13E-05	1.53	7.85	3.29	1.90	thymidylate synthetase
AFFX-Mmu-gapdh-M_s_at	GAPDH	GAPDH	1.26E-03	1.53	2.32	1.29	1.02	Glyceraldehyde-3-phosphate dehydrogenase
AFFX-Mmu-gapdh-5_at	GAPDH	GAPDH	2.66E-03	1.53	3.30	1.12	1.05	Glyceraldehyde-3-phosphate dehydrogenase
Mmu.11151.1.S1_at	LTB4DH /// LTB4DH	LTB4DH /// LTB4DH	3.93E-04	1.51	-2.37	1.25	-1.05	NADP-dependent leukotriene B4 12-hydroxydehydrogenase /// similar to NADP-depend
MmugDNA.36695.1.S1_at	LOC715070	LOC715070	6.70E-04	1.51	-2.04	1.91	1.05	similar to UBX domain containing 1
MmugDNA.26846.1.S1_at	---	---	4.08E-03	1.50	2.20	1.18	-1.25	---
MmuSTS.4311.1.S1_x_at	LOC697235	LOC697235	1.16E-04	1.49	7.58	1.93	1.16	similar to Histone H2A type 1-D (H2A.3)
MmugDNA.2191.1.S1_at	LOC715562	LOC715562	1.04E-03	1.49	-3.39	1.19	-1.38	similar to hemogen
MmugDNA.24936.1.S1_at	LTB4DH	LTB4DH	4.42E-04	1.49	-2.27	1.27	-1.03	NADP-dependent leukotriene B4 12-hydroxydehydrogenase
MmugDNA.42241.1.S1_at	LOC719669	LOC719669	6.84E-03	1.49	-2.25	1.60	-1.17	similar to benzodiazapine receptor (peripheral)-like 1
MmugDNA.38010.1.S1_at	---	---	1.06E-04	1.48	3.20	1.15	-1.57	---
MmuSTS.4311.1.S1_at	LOC697235	LOC697235	9.83E-06	1.48	9.43	1.95	1.16	similar to Histone H2A type 1-D (H2A.3)
MmugDNA.25123.1.S1_s_at	RNASE2	RNASE2	7.72E-04	1.47	3.53	1.41	-1.04	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)
MmugDNA.9683.1.S1_at	DNAI2	DNAI2	1.01E-04	1.47	-3.34	1.49	-1.07	dynein, axonemal, intermediate chain 2
MmugDNA.42981.1.S1_at	---	---	2.49E-03	1.46	2.11	1.12	-1.09	---
MmuSTS.2616.1.S1_at	ERAF	ERAF	1.50E-03	1.45	-2.85	1.52	-1.20	erythroid associated factor
AFFX-Mmu-gapdh-M_x_at	GAPDH	GAPDH	2.08E-03	1.45	3.04	1.11	1.04	Glyceraldehyde-3-phosphate dehydrogenase
MmuSTS.4200.1.S1_x_at	LOC711691	LOC711691	1.35E-03	1.45	4.23	1.63	1.32	Similar to pre-B-cell leukemia transcription factor 3
MmuSTS.4740.1.S1_at	F13A1	F13A1	8.79E-04	1.45	2.28	1.30	-1.04	coagulation factor XIII, A1 polypeptide
Mmu.11151.1.S1_s_at	LTB4DH	LTB4DH	6.09E-04	1.45	-2.22	1.21	-1.04	NADP-dependent leukotriene B4 12-hydroxydehydrogenase
MmugDNA.37366.1.S1_at	LOC696622	LOC696622	2.77E-04	1.44	-5.77	1.05	-1.22	similar to SA hypertension-associated homolog isoform 1
MmuSTS.1343.1.S1_at	TFDP1	TFDP1	1.20E-03	1.44	3.81	1.67	1.25	Similar to Transcription factor Dp-1 (E2F dimerization partner 1) (DRTF1-polypep
MmugDNA.13271.1.S1_at	---	---	2.55E-03	1.41	-2.25	1.92	-1.30	---
MmugDNA.30227.1.S1_at	LOC705063	LOC705063	1.25E-04	1.41	-6.07	1.21	1.11	similar to nitric oxide synthase trafficking isoform 1
MmuSTS.1209.1.S1_at	TMOD1	TMOD1	1.19E-03	1.39	-3.77	1.42	-1.11	tropomodulin 1
MmugDNA.21439.1.S1_at	LOC701889	LOC701889	1.44E-03	1.39	4.17	2.05	-1.18	Similar to 60S ribosomal protein L7a
MmugDNA.11078.1.S1_at	---	---	5.16E-04	1.38	-2.32	1.80	-1.00	---
MmugDNA.38008.1.S1_at	LOC718871	LOC718871	3.09E-03	1.38	-1.12	1.07	2.28	similar to asparaginase-like 1 protein
MmuSTS.4200.1.S1_at	LOC711691	LOC711691	1.85E-03	1.38	4.71	1.74	1.35	Similar to pre-B-cell leukemia transcription factor 3
MmugDNA.11842.1.S1_at	---	---	2.50E-03	1.37	-2.15	1.77	-1.07	---
MmugDNA.3866.1.S1_s_at	LOC714071	LOC714071	5.94E-05	1.37	-2.16	1.06	-1.29	hypothetical protein LOC714071
MmugDNA.5830.1.S1_at	TMOD1	TMOD1	7.41E-04	1.37	-4.28	1.44	-1.17	tropomodulin 1
MmugDNA.6851.1.S1_at	LOC695554	LOC695554	5.57E-03	1.37	-2.11	1.34	-1.06	hypothetical protein LOC695554
MmugDNA.8597.1.S1_at	---	---	2.06E-03	1.37	-3.35	1.84	-1.03	---
MmugDNA.39221.1.S1_at	---	---	2.34E-06	1.36	3.32	1.34	1.22	---
MmugDNA.34587.1.S1_s_at	GAPDH	GAPDH	7.17E-04	1.36	2.25	1.15	1.02	glyceraldehyde-3-phosphate dehydrogenase
MmugDNA.6249.1.S1_at	NFIX	NFIX	1.05E-03	1.36	-2.84	1.39	-1.21	nuclear factor I/X (CCAAT-binding transcription factor)
MmuSTS.3368.1.S1_at	LOC722330	LOC722330	9.55E-04	1.36	2.11	-1.02	1.06	similar to phosphofructokinase, platelet
MmuSTS.2452.1.S1_at	LOC696407	LOC696407	2.01E-03	1.36	-3.06	1.72	-1.32	similar to McLeod syndrome-associated, Kell blood group protein
MmugDNA.35516.1.S1_at	CTSD	CTSD	1.55E-04	1.35	2.35	1.10	-1.00	cathepsin D
MmuSTS.2026.1.S1_at	LOC712474	LOC712474	6.19E-04	1.35	-2.14	1.30	1.38	similar to cAMP-dependent protein kinase inhibitor gamma
MmuSTS.4002.1.S1_at	THBD	THBD	1.05E-03	1.35	2.21	1.23	-1.05	thrombomodulin
MmugDNA.20179.1.S1_at	LOC714802	LOC714802	4.07E-04	1.35	-2.73	1.40	1.01	similar to C16C10.1
MmugDNA.8879.1.S1_at	SESN3	SESN3	5.08E-04	1.35	-4.52	1.66	-1.03	sestrin 3
MmuSTS.4725.1.S1_at	LOC705323	LOC705323	4.50E-03	1.34	1.29	2.26	-1.34	Similar to vacuolar protein sorting 13A isoform A
MmugDNA.17219.1.S1_at	LOC703889	LOC703889	1.13E-09	1.34	3.97	1.76	1.11	similar to histone 1, H2ai (predicted)
MmuAffx.23.14.S1_at	---	---	8.18E-04	1.33	-2.04	1.42	-1.09	---
MmuSTS.144.1.S1_at	LOC710888	LOC710888	3.17E-04	1.33	2.28	1.85	1.33	similar to minichromosome maintenance protein 2
MmugDNA.35069.1.S1_at	RAB6B	RAB6B	3.12E-03	1.33	2.27	1.12	-1.15	RAB6B, member RAS oncogene family
MmuSTS.2757.1.S1_at	LOC702959	LOC702959	9.24E-04	1.32	-2.18	1.45	-1.25	similar to interferon-related developmental regulator 2
MmugDNA.30056.1.S1_at	TYMS	TYMS	1.29E-05	1.32	4.35	2.31	1.51	thymidylate synthetase
MmuSTS.4597.1.S1_at	LOC703271	LOC703271	8.60E-04	1.32	-2.88	1.53	-1.14	similar to hyaluronoglucosaminidase 3
MmugDNA.30746.1.S1_at	LOC713737	LOC713737	2.68E-04	1.32	3.07	1.69	1.31	similar to lymphocyte-activation protein 3 precursor
MmugDNA.23156.1.S1_s_at	LOC701134	LOC701134	1.76E-03	1.31	-3.76	1.23	-1.25	Similar to faciogenital dysplasia protein
MmugDNA.37873.1.S1_at	PCDHA11	PCDHA11	2.64E-04	1.30	2.89	1.13	-1.18	Protocadherin alpha 11
MmugDNA.23761.1.S1_at	LOC708579	LOC708579	6.13E-06	1.30	4.71	2.68	1.48	similar to RAD51 homolog protein isoform 1
MmugDNA.29213.1.S1_at	LOC697235	LOC697235	5.75E-05	1.29	6.22	1.75	1.17	similar to Histone H2A type 1-D (H2A.3)

Supplementary Table S5. part 4 of 9

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/DO	Gene Description
MmugDNA.33823.1.S1_s_at	---	KIAA0101	3.83E-05	1.29	6.44	3.89	2.12	kiaa0101
MmugDNA.28101.1.S1_at	ST3GAL5	ST3GAL5	1.12E-03	1.29	1.20	1.15	2.24	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
MmugDNA.3046.1.S1_at	CLIC1	CLIC1	4.02E-03	1.29	2.23	1.15	1.18	chloride intracellular channel 1
MmugDNA.22473.1.S1_at	---	---	2.61E-03	1.29	2.06	-1.01	1.01	---
Mmu.5875.1.S1_at	GYPA	GYPA	4.78E-04	1.28	-7.26	-1.06	-1.33	glycophorin A
Mmu.14041.1.S1_at	USP15	USP15	4.57E-03	1.28	-2.04	1.13	1.23	ubiquitin specific peptidase 15
MmugDNA.43560.1.S1_at	LOC693642	LOC693642	1.88E-05	1.28	2.15	1.30	-1.19	similar to RNA binding motif protein 9 isoform 1
MmugDNA.7137.1.S1_s_at	LOC696622	LOC696622	3.20E-03	1.27	-3.37	1.12	-1.21	similar to SA hypertension-associated homolog isoform 1
MmugDNA.2512.1.S1_at	LOC695836	LOC695836	4.66E-04	1.27	2.01	1.52	1.26	hypothetical protein LOC695836
MmugDNA.31369.1.S1_at	---	RRM2	2.58E-04	1.27	8.14	3.57	2.20	ribonucleotide reductase m2 polypeptide
MmugDNA.40252.1.S1_at	LOC717262	LOC717262	3.46E-03	1.27	-1.70	2.15	1.00	similar to zyg-11 homolog B (C. elegans)-like
MmugDNA.39863.1.S1_at	---	C18ORF24	2.74E-03	1.27	3.73	2.48	1.75	chromosome 18 open reading frame 24
MmugDNA.37537.1.S1_at	LOC704626	LOC704626	3.97E-04	1.27	-2.55	1.40	-1.02	similar to adiponectin receptor 1
MmuSTS.3275.1.S1_at	LOC700582	RRM2	7.87E-04	1.26	6.11	2.81	1.89	ribonucleotide reductase m2 polypeptide
MmuSTS.616.1.S1_at	LOC712354	LOC712354	1.79E-03	1.26	-2.20	1.42	-1.15	similar to Intercellular adhesion molecule 4 precursor (ICAM-4) (Landsteiner-Wie
MmugDNA.4124.1.S1_at	LOC721995	CDCA5	1.32E-05	1.25	3.74	2.22	1.45	cell division cycle associated 5
MmugDNA.20685.1.S1_at	LOC715117	LOC715117	1.30E-03	1.24	-2.14	1.53	-1.05	similar to activating signal cointegrator 1 complex subunit 2
MmugDNA.20333.1.S1_at	IL12RB2	IL12RB2	1.80E-03	1.23	2.84	1.11	1.22	interleukin 12 receptor, beta 2
Mmu.6559.1.S1_s_at	LOC701387	LOC701387	8.24E-04	1.22	3.45	1.46	1.09	similar to Adipophilin (Adipose differentiation-related protein) (ADRP)
MmugDNA.16154.1.S1_at	LOC711305	LOC711305	6.19E-05	1.22	2.05	1.44	1.13	similar to Methionine-R-sulfoxide reductase B2
MmugDNA.8160.1.S1_at	UQCRC1	UQCRC1	7.32E-04	1.21	2.26	1.16	-1.06	ubiquinol-cytochrome c reductase core protein I
MmuSTS.1558.1.S1_at	MELK	MELK	2.59E-05	1.21	5.76	2.49	1.85	maternal embryonic leucine zipper kinase
MmugDNA.38920.1.S1_at	LOC713371	LOC713371	1.71E-04	1.20	-4.42	1.14	-1.04	similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candida
MmugDNA.42453.1.S1_at	LOC695372	LOC695372	2.15E-03	1.20	2.22	1.20	1.03	hypothetical protein LOC695372
MmugDNA.20581.1.S1_at	---	---	5.04E-03	1.20	-2.55	1.53	-1.34	---
MmugDNA.3956.1.S1_at	LOC715562	LOC715562	5.87E-04	1.20	-6.18	1.10	-1.43	similar to hemogen
MmuSTS.3327.1.S1_at	OIP5	OIP5	3.85E-04	1.20	3.70	2.25	1.53	opa interacting protein 5
MmugDNA.24523.1.S1_at	LOC711581	LOC711581	3.43E-04	1.20	2.62	1.61	1.37	similar to cell division cycle associated 2
MmugDNA.9770.1.S1_at	LOC714207	LOC714207	9.44E-05	1.19	3.43	2.03	1.38	similar to G-2 and S-phase expressed 1
MmugDNA.9497.1.S1_at	KIFC1	KIFC1	3.01E-06	1.19	2.72	1.66	1.32	kinesin family member C1
MmugDNA.25384.1.S1_at	UBE2C	UBE2C	4.85E-06	1.19	4.65	2.68	1.46	ubiquitin-conjugating enzyme e2c
MmuSTS.4420.1.S1_at	TPX2	TPX2	1.15E-04	1.18	2.13	1.61	1.29	TPX2, microtubule-associated, homolog (Xenopus laevis)
MmugDNA.18716.1.S1_at	TFDP2	TFDP2	1.89E-04	1.18	-6.18	1.11	1.06	transcription factor Dp-2 (E2F dimerization partner 2)
MmuSTS.1276.1.S1_at	---	---	1.96E-03	1.18	-3.14	1.06	-1.60	---
MmugDNA.8585.1.S1_at	---	---	1.18E-03	1.18	2.40	1.23	-1.13	---
MmugDNA.29514.1.S1_at	---	---	4.72E-04	1.18	2.09	1.20	-1.06	---
MmugDNA.21462.1.S1_at	KIF4A	KIF4A	3.67E-05	1.18	2.41	1.46	1.13	kinesin family member 4
MmugDNA.8836.1.S1_at	LOC695568	LOC695568	2.38E-04	1.18	4.24	2.35	1.57	similar to minichromosome maintenance protein 10 isoform 2
MmugDNA.37946.1.S1_s_at	ABCC13	ABCC13	3.48E-03	1.18	-2.25	1.14	-1.11	ATP-binding cassette transporter 13
MmugDNA.27310.1.S1_at	LOC717131	LOC717131	1.06E-03	1.18	-2.07	1.10	-1.15	hypothetical protein LOC717131
MmugDNA.6936.1.S1_at	SOX6	SOX6	2.64E-03	1.18	-3.72	1.28	-1.37	SRY (sex determining region Y)-box 6
MmugDNA.3867.1.S1_at	LOC714071	LOC714071	4.43E-03	1.18	-2.03	1.13	-1.28	hypothetical protein LOC714071
MmugDNA.4085.1.S1_at	LOC700589	CCNE1	4.89E-04	1.18	2.84	1.95	1.48	cyclin e1
MmugDNA.20407.1.S1_at	---	---	1.13E-03	1.18	2.91	1.41	-1.12	---
MmuSTS.3165.1.S1_at	---	---	2.86E-04	1.17	-4.06	1.41	-1.05	---
MmuSTS.2138.1.S1_at	B4GALT4	B4GALT4	3.56E-03	1.17	2.10	-1.00	1.14	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4
MmunewRS.494.1.S1_at	---	---	5.50E-03	1.17	-2.02	1.26	1.00	---
MmugDNA.2768.1.S1_at	LOC693637	LOC693637	7.28E-05	1.17	3.25	1.51	1.35	similar to cell division cycle associated 1
MmugDNA.30331.1.S1_at	LOC697733	LOC697733	1.61E-03	1.17	2.12	1.26	-1.31	similar to multiple C2-domains with two transmembrane regions 1 isoform S
MmugDNA.10778.1.S1_at	LOC694877	CDKN3	1.96E-05	1.17	4.34	2.34	1.59	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)
MmugDNA.28002.1.S1_at	LOC709195	LOC709195	2.66E-05	1.17	4.53	2.22	1.50	Hypothetical protein LOC709195
Mmu.2556.1.S1_at	TFDP2	TFDP2	1.61E-04	1.17	-3.84	1.10	1.07	transcription factor Dp-2 (E2F dimerization partner 2)
MmugDNA.15549.1.S1_s_at	LOC718841	LOC718841	1.02E-03	1.16	-2.62	1.19	-1.19	Similar to Fc receptor-like 1
MmugDNA.20669.1.S1_at	LOC701182	LOC701182	8.15E-05	1.16	2.87	1.24	1.17	hypothetical protein LOC701182
MmugDNA.40091.1.S1_at	TFDP2	TFDP2	3.23E-04	1.16	-4.41	1.25	-1.11	transcription factor Dp-2 (E2F dimerization partner 2)
MmugDNA.8456.1.S1_at	KDELR3	KDELR3	3.15E-04	1.16	2.26	1.49	1.18	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
Mmu.1387.1.A1_at	---	---	2.74E-04	1.16	-2.15	1.66	-1.29	---
MmugDNA.41887.1.S1_at	MYBL2	MYBL2	3.00E-03	1.16	2.33	1.63	1.25	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
MmugDNA.27464.1.S1_at	LOC709427	LOC709427	2.58E-03	1.15	-4.96	1.61	-1.08	similar to erythrocyte membrane protein band 4.2
MmuSTS.1534.1.S1_at	---	---	3.25E-05	1.15	2.11	1.64	1.18	---
MmugDNA.7301.1.S1_s_at	LOC703530	LOC703530	2.59E-03	1.14	-2.14	1.42	-1.04	Similar to speedy homolog 1 isoform 2
MmuSTS.450.1.S1_at	LOC708158	LOC708158	3.62E-03	1.14	-2.85	1.08	-1.48	similar to hypoxia-inducible factor prolyl 4-hydroxylase isoform a
MmugDNA.2559.1.S1_at	LOC706506	LOC706506	1.85E-03	1.14	-4.52	1.11	-1.24	similar to leucine rich repeat containing 35
MmugDNA.43386.1.S1_at	LOC713911	LOC713911	3.10E-05	1.14	2.86	1.16	1.06	similar to mammary tumor virus receptor 2 isoform-like
MmugDNA.38940.1.S1_at	LOC714763	LOC714763	3.45E-04	1.14	-3.53	1.01	-1.25	similar to CG1998-PA
MmugDNA.11364.1.S1_at	LOC708805	LOC708805	2.73E-04	1.14	2.87	2.01	1.44	similar to forkhead box M1 isoform 3
MmugDNA.33387.1.S1_at	HIP2	HIP2	1.37E-03	1.14	2.41	1.72	1.29	Huntingtin interacting protein 2
MmugDNA.15754.1.S1_at	LOC713358	LOC713358	7.27E-05	1.13	3.51	1.76	1.25	similar to CHK1 checkpoint homolog
MmugDNA.7866.1.S1_at	LOC711530	LOC711530	1.46E-03	1.13	2.23	1.45	1.24	similar to DNA replication factor
MmuSTS.2066.1.S1_at	GINS2	GINS2	1.56E-04	1.13	2.74	1.76	1.30	GINS complex subunit 2 (Psf2 homolog)
MmugDNA.22810.1.S1_at	LOC716842	LOC716842	2.16E-03	1.13	-6.29	1.40	1.04	similar to Kruppel-like factor 1 (erythroid)
MmugDNA.35559.1.S1_at	LOC698238	LOC698238	1.83E-05	1.13	3.91	2.22	1.33	similar to Histone H1.2 (H1d)
MmuSTS.3544.1.S1_at	LOC694416	LOC694416	1.82E-03	1.13	-2.96	1.38	-1.12	similar to Pre-B-cell leukemia transcription factor 1 (Homeobox protein PBX1)
MmugDNA.3701.1.S1_at	NR4A2	NR4A2	1.50E-04	1.13	1.13	-1.31	3.01	nuclear receptor subfamily 4, group A, member 2
MmugDNA.26033.1.S1_at	LOC713624	CENPN	1.71E-04	1.13	2.56	1.70	1.28	chromosome 16 open reading frame 60
MmuSTS.636.1.S1_s_at	LOC699182	LOC699182	2.10E-03	1.12	-3.78	1.37	-1.06	similar to tripartite motif-containing 58
MmugDNA.29488.1.S1_at	HIPK1	HIPK1	1.00E-03	1.12	-3.57	1.33	-1.23	homeodomain interacting protein kinase 1
MmuSTS.1736.1.S1_at	---	---	8.09E-05	1.12	4.49	1.80	-1.27	---
MmuSTS.673.1.S1_s_at	LOC721861	LOC721861	5.97E-06	1.12	3.75	1.94	1.40	similar to chromatin assembly factor 1, subunit A (p150)
MmugDNA.13724.1.S1_at	---	---	8.17E-04	1.12	-3.32	1.22	-1.07	---
MmugDNA.2976.1.S1_at	LOC718180	LOC718180	5.62E-07	1.12	2.18	1.48	1.10	hypothetical protein LOC718180
MmugDNA.30971.1.S1_at	---	---	4.28E-04	1.12	2.14	1.33	-1.12	---
MmugDNA.30164.1.S1_at	LOC710328	LOC710328	4.29E-04	1.12	2.71	1.48	1.31	similar to timeless-interacting protein
MmugDNA.36182.1.S1_at	---	---	6.42E-03	1.12	-3.43	1.24	-1.56	---
MmugDNA.24379.1.S1_at	TFPI	TFPI	4.01E-03	1.12	2.10	1.11	-1.03	tissue factor pathway inhibitor
MmugDNA.22775.1.S1_at	DIAPH3	DIAPH3	2.66E-04	1.11	2.70	1.83	1.27	diaphanous homolog 3
MmugDNA.7726.1.S1_at	LOC704669	LOC704669	2.50E-04	1.11	-2.73	1.07	-1.03	Similar to sorting nexin associated golgi protein 1
MmugDNA.3020.1.S1_at	LOC710680	LOC710680	3.55E-04	1.11	2.12	1.45	1.31	similar to Zwilch
MmugDNA.8986.1.S1_at	---	---	8.62E-04	1.11	-2.01	1.06	-1.07	---
MmugDNA.5873.1.S1_at	---	CEP55	2.63E-05	1.11	5.24	2.57	1.81	centrosomal protein 55kda
MmuSTS.1535.1.S1_at	KIF2C	KIF2C	3.61E-08	1.10	4.09	2.18	1.45	kinesin family member 2C
MmugDNA.14990.1.S1_at	---	---	5.17E-04	1.10	-1.08	-1.08	2.00	---
MmugDNA.29315.1.S1_at	LOC701888	DEPDC1	4.97E-05	1.10	2.89	2.12	1.28	dep domain containing 1
MmugDNA.39841.1.S1_at	LOC698314	LOC698314	7.72E-04	1.10	-2.96	1.11	-1.22	hypothetical protein LOC698314
MmuSTS.64.1.S1_at	GMNN	GMNN	5.65E-04	1.09	2.39	1.61	1.60	geminin, dna replication inhibitor

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/DO	Gene Description
MmuSTS.3714.1.S1_at	LOC713222	LOC713222	5.26E-06	1.09	2.09	1.33	-1.05	similar to four and a half LIM domains 2
MmugDNA.19464.1.S1_at	LOC695531	LOC695531	1.86E-06	1.09	4.94	2.13	1.42	similar to ubiquitin-like, containing PHD and RING finger domains, 1
MmugDNA.27780.1.S1_at	---	---	6.73E-06	1.09	-1.65	-1.15	2.04	---
MmugDNA.28020.1.S1_at	---	---	8.14E-05	1.09	2.69	2.07	1.27	---
MmugDNA.23509.1.S1_at	LOC702987	LOC702987	1.31E-04	1.09	-2.28	1.08	1.00	similar to protein phosphatase 1A isoform 1
MmugDNA.39718.1.S1_at	MKRN1	MKRN1	5.62E-04	1.09	-3.24	1.17	-1.10	makorin ring finger protein 1
MmugDNA.12988.1.S1_s_at	LOC703598	LOC703598	3.06E-04	1.09	2.52	1.78	1.44	similar to high-mobility group box 3
MmugDNA.42307.1.S1_s_at	GYPA	GYPA	8.33E-05	1.08	-6.06	-1.27	-1.16	glycophorin A
MmugDNA.40742.1.S1_at	LOC702184	CCNB2	4.76E-06	1.08	5.88	2.74	1.66	cyclin b2
MmuSTS.3302.1.S1_at	RWDD3	RWDD3	7.09E-04	1.08	-3.69	-1.26	-1.31	RWD domain containing 3
MmugDNA.14322.1.S1_at	TFDP1	TFDP1	2.22E-03	1.08	2.35	1.76	1.39	transcription factor dp-1
Mmu.14249.1.S1_at	CCR5	CCR5	1.46E-03	1.08	2.84	1.51	1.56	chemokine (C-C motif) receptor 5
MmugDNA.11557.1.S1_at	LOC715235	NCAPG	8.19E-06	1.08	4.49	2.43	1.85	chromosome condensation protein g
MmugDNA.42135.1.S1_at	FBXO5	FBXO5	4.22E-04	1.08	2.01	1.32	1.27	F-box protein 5
MmugDNA.12490.1.S1_at	LOC702368	E2F8	2.11E-05	1.08	4.53	2.14	1.55	e2f transcription factor 8
MmuSTS.1955.1.S1_at	RTN4	RTN4	7.90E-06	1.08	2.24	1.57	1.17	Reticulon 4
MmuSTS.4250.1.S1_at	RAD51AP1	RAD51AP1	1.79E-05	1.08	2.87	1.75	1.59	RAD51 associated protein 1
MmuSTS.911.1.S1_at	LOC695383	ALDH9A1	2.10E-04	1.08	2.62	1.59	1.72	aldehyde dehydrogenase 9 family, member a1
MmugDNA.21403.1.S1_at	LOC722088	CDCA3	1.58E-04	1.08	3.03	2.06	1.28	cell division cycle associated 3
MmugDNA.39842.1.S1_s_at	LOC698314	LOC698314	1.06E-03	1.08	-3.42	1.05	-1.15	hypothetical protein LOC698314
MmuSTS.2109.1.S1_at	LOC709167	LOC709167	2.67E-06	1.08	-1.47	-1.26	2.51	similar to ADP-ribosylation factor-like 4D
MmugDNA.20818.1.S1_s_at	NR4A2	NR4A2	4.18E-04	1.07	-1.02	-1.21	2.07	nuclear receptor subfamily 4, group A, member 2
Mmu.8739.1.S1_at	LOC701021	LOC701021	4.29E-04	1.07	-2.11	1.06	-1.16	similar to cellular repressor of E1A-stimulated genes
MmugDNA.1969.1.S1_at	LOC714686	MCM4	7.37E-05	1.07	4.04	1.92	1.40	mcm4 minichromosome maintenance deficient 4 (s. cerevisiae)
MmugDNA.16923.1.S1_at	NF-AT	NF-AT	4.48E-04	1.07	1.00	1.31	2.25	transmembrane activator
MmugDNA.30751.1.S1_s_at	LOC693614	LOC693614	1.85E-03	1.07	-2.62	1.03	-1.24	similar to CG14209-PD, isoform D
MmugDNA.18794.1.S1_at	---	CDC20	3.77E-05	1.07	5.16	2.57	1.64	cdc20 cell division cycle 20 homolog (s. cerevisiae)
MmuSTS.3320.1.S1_at	LOC700382	LOC700382	4.49E-05	1.07	3.88	1.83	1.52	similar to cyclin E2 isoform 1
MmugDNA.23023.1.S1_at	---	---	2.09E-05	1.07	2.45	1.54	1.21	---
MmugDNA.9920.1.S1_at	---	---	2.42E-03	1.07	-2.27	1.13	-1.15	---
MmugDNA.12791.1.S1_at	LIPF	LIPF	2.22E-03	1.07	-4.22	1.11	-1.19	Lipase, gastric
MmuSTS.3707.1.S1_at	PSMD9	PSMD9	3.01E-03	1.07	-3.33	1.15	-1.48	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
MmuSTS.636.1.S1_at	LOC699182	LOC699182	3.22E-03	1.07	-3.08	1.24	-1.11	similar to tripartite motif-containing 58
MmugDNA.22284.1.S1_at	LOC704611	LOC704611	1.10E-03	1.07	-1.56	-1.13	2.12	similar to junctophilin 3
MmugDNA.19272.1.S1_s_at	LOC709633	LOC709633	3.43E-04	1.06	3.37	1.72	1.37	Hypothetical protein LOC709633
MmuSTS.3576.1.S1_at	CCNA2	CCNA2	2.51E-04	1.06	3.45	1.94	1.57	cyclin a2
MmugDNA.41567.1.S1_at	LOC718784	LOC718784	4.73E-03	1.06	1.01	1.32	2.36	similar to Fc receptor-like 4
MmugDNA.35455.1.S1_at	---	---	3.40E-06	1.06	-1.30	-1.28	2.11	---
MmugDNA.12273.1.S1_at	TOP2A	TOP2A	2.10E-06	1.06	3.77	2.32	1.56	topoisomerase (dna) ii alpha 170kda
MmugDNA.14959.1.S1_at	CDC2	CDC2	2.89E-04	1.06	2.11	1.40	1.30	cell division cycle 2, G1 to S and G2 to M
MmugDNA.38956.1.S1_at	---	NUSAP1	9.61E-07	1.05	3.81	2.34	1.60	nucleolar and spindle associated protein 1
MmuSTS.1462.1.S1_at	LOC707432	LOC707432	1.57E-03	1.05	-2.42	1.51	-1.47	similar to PDZ domain protein GIPC2
MmugDNA.38659.1.S1_at	CDIPT	CDIPT	3.99E-04	1.05	-2.42	-1.03	-1.07	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol syn
MmugDNA.8691.1.S1_at	LOC706985	LOC706985	1.00E-03	1.05	-4.39	1.36	-1.11	similar to alpha-synuclein isoform NACP140
MmugDNA.42865.1.S1_at	CDC2	CDC2	7.13E-06	1.05	2.57	1.49	1.25	cell division cycle 2, G1 to S and G2 to M
MmuSTS.3401.1.S1_s_at	LOC717153	LOC717153	4.95E-05	1.05	2.05	1.19	-1.14	similar to CCAAT/enhancer-binding protein alpha (C/EBP alpha)
MmugDNA.10448.1.S1_at	PRPF18	PRPF18	4.65E-03	1.05	-2.47	1.20	-1.07	PRP18 pre-mRNA processing factor 18 homolog
MmugDNA.5568.1.S1_at	LOC701134	LOC701134	3.42E-04	1.05	-3.07	-1.08	-1.11	Similar to faciogenital dysplasia protein
MmugDNA.2444.1.S1_at	LOC699723	LOC699723	6.20E-03	1.05	-2.46	1.31	-1.24	similar to CG17712-PA
MmugDNA.25436.1.S1_at	MCM3	MCM3	2.05E-04	1.04	3.18	1.64	1.42	minichromosome maintenance complex component 3
MmugDNA.602.1.S1_at	LOC717799	LOC717799	2.95E-04	1.04	2.01	-1.06	-1.10	similar to neural stem cell-derived dendrite regulator
MmugDNA.20683.1.S1_at	---	---	2.09E-04	1.04	2.01	1.20	1.04	---
MmugDNA.5308.1.S1_at	LOC709463	LOC709463	4.45E-03	1.04	2.10	1.05	1.03	similar to tetraspan 2
MmuSTS.2509.1.S1_at	LOC701863	LOC701863	1.12E-04	1.04	2.04	1.34	1.13	similar to H2A histone family, member J isoform 1
MmugDNA.2951.1.S1_at	LOC706404	LOC706404	8.26E-06	1.04	2.31	1.51	1.15	similar to anillin, actin binding protein (scraps homolog, Drosophila)
MmugDNA.3614.1.S1_at	LOC719817	LOC719817	4.07E-03	1.04	-2.28	1.44	1.08	similar to sudD suppressor of bimD6 homolog isoform 1
MmugDNA.19989.1.S1_at	LOC702520	LOC702520	5.87E-03	1.03	3.07	1.63	1.35	similar to defective in sister chromatid cohesion homolog 1
MmuSTS.3129.1.S1_at	RGS8	RGS8	3.80E-09	1.03	-1.00	-1.17	2.77	regulator of G-protein signaling 8
MmugDNA.39842.1.S1_at	LOC698314	LOC698314	4.43E-04	1.03	-2.78	1.03	-1.15	hypothetical protein LOC698314
MmuSTS.2070.1.S1_s_at	MICB	MICB	6.41E-05	1.03	2.66	1.61	1.22	MHC class I polypeptide-related sequence B
MmugDNA.10186.1.S1_at	---	CASC5	6.54E-04	1.03	2.36	1.60	1.83	cancer susceptibility candidate 5
MmuSTS.1554.1.S1_at	---	---	2.22E-04	1.03	1.00	-1.11	2.52	---
MmugDNA.24430.1.S1_at	LOC710858	LOC710858	1.30E-04	1.03	3.16	1.99	1.54	similar to cell division cycle 25A isoform a
MmugDNA.27170.1.S1_at	LOC715385	LOC715385	1.37E-03	1.02	-3.01	1.34	-1.09	similar to nudix-type motif 4 isoform alpha
MmuSTS.2698.1.S1_at	LOC698482	LOC698482	3.39E-04	1.02	2.07	1.68	1.17	similar to Histone H2B F (H2B 291A)
MmunewRS.760.1.S1_at	LOC717153	LOC717153	1.19E-05	1.02	2.02	1.32	-1.10	similar to CCAAT/enhancer-binding protein alpha (C/EBP alpha)
Mmu.7460.4.S1_a_at	KIR2DL4 /// KIR3DH5	KIR2DL4 /// KIR3DH5	8.70E-04	1.02	3.20	1.31	1.05	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4
MmugDNA.30535.1.S1_at	ANKRD6	ANKRD6	1.01E-03	1.02	-3.11	1.28	-1.10	ankyrin repeat domain 6
MmugDNA.26592.1.S1_at	EPB41	EPB41	2.29E-03	1.02	-3.63	1.26	-1.17	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)
MmugDNA.25197.1.S1_at	ASPM	ASPM	1.06E-04	1.02	2.44	1.78	1.22	hypothetical protein flj10517
MmugDNA.3558.1.S1_at	AURKA	AURKA	1.42E-06	1.02	2.17	1.60	1.15	serine/threonine protein kinase 6
MmugDNA.22893.1.S1_at	---	---	1.08E-04	1.02	-1.27	1.01	2.26	---
MmuSTS.3643.1.S1_at	CHIT1	CHIT1	6.07E-04	1.02	5.20	1.39	-1.39	chitinase 1 (chitotriosidase)
MmugDNA.31059.1.S1_s_at	PTTG1	PTTG1	1.92E-04	1.02	2.45	1.46	1.23	pituitary tumor-transforming 1
MmuSTS.2303.1.S1_s_at	LOC696772	LOC696772	5.49E-05	1.01	2.59	1.34	1.23	similar to discs large homolog 7
MmuSTS.4324.1.S1_at	ENTPD3	ENTPD3	4.20E-03	1.01	2.53	1.03	-1.12	ectonucleoside triphosphate diphosphohydrolase 3
MmugDNA.6172.1.S1_at	---	---	1.33E-03	1.01	-4.69	1.52	1.04	---
MmugDNA.14956.1.S1_at	LOC700081	LOC700081	1.70E-06	1.01	2.28	1.47	1.22	similar to CDC6 homolog
MmuSTS.220.1.S1_at	LOC710099	LOC710099	2.09E-04	1.01	2.26	1.50	1.43	similar to SCL/TAL1 interrupting locus
MmugDNA.12081.1.S1_at	---	---	3.40E-03	1.01	2.32	1.43	1.10	---
MmugDNA.38891.1.S1_at	ATPIF1	ATPIF1	2.99E-04	1.01	2.40	1.17	1.12	ATPase inhibitory factor 1
MmugDNA.3918.1.S1_at	DCLRE1A	DCLRE1A	6.28E-03	1.01	-2.63	1.13	-1.07	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)
MmugDNA.31383.1.S1_at	SESN3	SESN3	3.23E-03	1.01	-3.60	1.62	1.06	sestrin 3
MmuSTS.2071.1.S1_at	RAD54L	RAD54L	2.94E-05	1.01	2.17	1.44	1.09	RAD54-like protein
MmuSTS.3510.1.S1_at	---	---	8.08E-04	1.01	-5.23	-1.05	-1.18	---
MmuSTS.4399.1.S1_at	LOC719808	LOC719808	1.51E-05	1.01	2.16	1.36	1.21	similar to cell division cycle associated 8
MmugDNA.43588.1.S1_at	LOC712570	LOC712570	1.80E-07	1.01	2.38	1.58	1.24	hypothetical protein LOC712570
Mmu.7460.4.S1_x_at	KIR2DL4	KIR2DL4	1.02E-03	1.01	2.88	1.26	-1.04	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4
MmugDNA.15236.1.S1_at	TIMM17A	TIMM17A	9.47E-07	1.01	-1.16	-1.36	4.85	Translocase of inner mitochondrial membrane 17 A-like protein
MmugDNA.40365.1.S1_at	LOC716378	LOC716378	3.05E-06	1.01	-1.42	1.57	4.32	similar to activation-induced cytidine deaminase
Mmu.9793.1.S1_at	LOC703475	LOC703475	4.98E-03	1.00	-3.08	1.11	1.10	similar to chloride intracellular channel 2
MmuSTS.3146.1.S1_s_at	MCM5	MCM5	6.36E-05	1.00	2.94	1.56	1.49	minichromosome maintenance deficient protein 5
MmugDNA.31878.1.S1_at	GYPA	GYPA	6.13E-04	1.00	-5.97	-1.02	-1.13	glycophorin A
MmugDNA.8306.1.S1_at	---	---	4.91E-06	1.00	-1.37	1.09	2.33	---
MmugDNA.3247.1.S1_s_at	LOC704341	HIST2H4B	2.54E-03	1.00	2.07	1.53	1.23	h4 histone, family 2

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/ DO	Gene Description
MmugDNA.34901.1.S1_at	SDF2L1	SDF2L1	1.59E-03	1.00	2.05	1.30	1.30	stromal cell-derived factor 2-like 1
MmugDNA.14606.1.S1_at	LOC699334	LOC699334	1.13E-03	1.00	2.24	-1.02	1.16	similar to prohibitin
Mmu.11047.2.S1_s_at	LOC711303	LOC711303	1.17E-03	-1.00	2.03	1.83	1.96	---
MmuSTS.4348.1.S1_at	IGHG1 /// LOC711303	IGHG1	7.27E-04	-1.00	3.04	2.37	2.74	immunoglobulin heavy constant gamma 1 (g1m marker)
MmuSTS.1653.1.S1_at	TMPRSS3	TMPRSS3	1.18E-05	-1.01	2.33	1.79	1.32	serine protease tadg12
MmugDNA.2975.1.S1_at	LOC707526	POLE2	8.84E-06	-1.01	2.50	1.64	1.46	polymerase (dna directed), epsilon 2 (p59 subunit)
MmugDNA.35622.1.S1_at	---	---	2.20E-04	-1.01	2.39	1.56	1.17	---
MmugDNA.14691.1.S1_at	LOC703475	LOC703475	1.30E-03	-1.01	-5.72	1.01	-1.10	similar to chloride intracellular channel 2
MmugDNA.31030.1.S1_at	LOC703497	LOC703497	3.07E-05	-1.01	2.13	1.21	1.13	similar to prematurely terminated mRNA decay factor-like
MmuSTS.644.1.S1_at	SDHD	SDHD	7.32E-06	-1.01	2.61	1.63	1.23	Succinate dehydrogenase complex, subunit D, integral membrane protein
MmugDNA.8750.1.S1_at	LOC704050	LOC704050	6.71E-04	-1.01	2.86	1.34	1.21	similar to PHD finger protein 19 isoform a
MmugDNA.2951.1.S1_s_at	LOC706404	LOC706404	2.95E-05	-1.01	4.27	2.07	1.30	similar to anillin, actin binding protein (scraps homolog, Drosophila)
MmugDNA.31188.1.S1_at	LOC718626	LOC718626	1.27E-04	-1.02	-1.50	-1.26	2.24	similar to leucine zipper protein 1
MmuSTS.3934.1.S1_at	LOC713447	LOC713447	1.52E-06	-1.03	-1.66	-1.15	2.37	similar to collagen, type VIII, alpha 2
MmugDNA.6734.1.S1_at	LOC711291	LOC711291	4.34E-04	-1.03	3.57	1.18	-1.45	similar to CD177 antigen
MmugDNA.7117.1.S1_at	LOC714792	LOC714792	4.82E-03	-1.03	2.69	1.29	-1.20	hypothetical protein LOC714792
MmugDNA.5663.1.S1_at	PLS3	PLS3	7.93E-05	-1.03	2.14	1.29	1.11	plastin 3 (t isoform)
MmuSTS.3773.1.S1_at	RNF11	RNF11	5.15E-03	-1.03	-2.72	1.20	1.00	ring finger protein 11
MmugDNA.20354.1.S1_at	LOC712046	LOC712046	3.86E-05	-1.04	4.64	1.05	-1.20	similar to interleukin 18 receptor accessory protein precursor
MmuSTS.2645.1.S1_at	LOC708959	LOC708959	2.77E-06	-1.04	2.51	1.47	1.28	Similar to Protein KIAA0329/KIAA0297
MmuSTS.4762.1.S1_at	FBXO5	FBXO5	2.71E-04	-1.04	2.14	1.39	1.31	F-box protein 5
MmugDNA.19008.1.S1_at	LOC710142	LOC710142	4.86E-04	-1.04	2.23	1.06	1.06	similar to solute carrier family 39 (zinc transporter), member 8
MmuSTS.4722.1.S1_at	LOC709328	LOC709328	1.53E-03	-1.05	2.73	1.85	1.30	similar to thyroid hormone receptor interactor 13
MmugDNA.865.1.S1_at	PCNA	PCNA	3.09E-04	-1.05	2.15	1.38	1.31	proliferating cell nuclear antigen
MmuSTS.1779.1.S1_at	---	NEK2	3.42E-04	-1.05	3.69	2.60	1.58	nima (never in mitosis gene a)-related kinase 2
MmuSTS.236.1.S1_at	LOC703598	LOC703598	4.55E-07	-1.05	2.52	1.74	1.34	similar to high-mobility group box 3
MmugDNA.14204.1.S1_at	GZMB	GZMB	1.39E-03	-1.05	3.21	1.09	1.35	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
MmugDNA.32420.1.S1_at	LOC719817	LOC719817	6.50E-03	-1.05	-2.39	1.28	1.04	similar to sudD suppressor of bimD6 homolog isoform 1
MmuSTS.673.1.S1_at	LOC721861	LOC721861	6.87E-05	-1.06	2.44	1.23	1.22	similar to chromatin assembly factor 1, subunit A (p150)
MmugDNA.23764.1.S1_at	CCNA2	CCNA2	5.92E-06	-1.06	2.50	1.52	1.39	cyclin A
MmugDNA.14257.1.S1_at	CCNF	CCNF	3.17E-06	-1.06	2.16	1.41	1.12	cyclin F
MmugDNA.15585.1.S1_at	HSF4	KIF15	3.92E-07	-1.06	4.82	2.17	1.55	kinesin family member 15
MmuSTS.1332.1.S1_at	LOC695759	LOC695759	6.14E-03	-1.06	-4.55	1.15	-1.31	similar to ferrochelatase isoform a precursor
MmugDNA.36434.1.S1_at	---	GZMA	3.58E-06	-1.06	12.81	2.54	2.55	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)
MmugDNA.32729.1.S1_at	MKI67	MKI67	4.84E-06	-1.07	4.01	2.45	1.69	antigen identified by monoclonal antibody ki-67
MmuSTS.2244.1.S1_at	LOC710662	LOC710662	5.53E-03	-1.07	2.07	1.15	-1.05	similar to plasminogen activator, urokinase receptor isoform 1 precursor
MmugDNA.2694.1.S1_at	LOC702198	LOC702198	1.87E-05	-1.07	3.20	1.96	1.61	similar to ZW10 interactor (ZW10-interacting protein 1) (Zwint-1)
MmugDNA.34591.1.S1_s_at	IGKC	IGKC	1.33E-05	-1.07	2.18	1.28	1.15	Immunoglobulin kappa constant
MmugDNA.15250.1.S1_at	---	CENPA	1.31E-05	-1.07	4.38	2.49	1.61	centromere protein a, 17kda
MmuSTS.177.1.S1_at	SETBP1	SETBP1	5.48E-05	-1.07	-1.39	-1.22	2.12	SET binding protein 1
MmugDNA.9644.1.S1_at	LOC716378	LOC716378	2.56E-07	-1.07	-1.83	1.30	3.69	similar to activation-induced cytidine deaminase
MmuSTS.1531.1.S1_at	---	---	1.87E-05	-1.07	2.61	1.55	1.22	---
MmugDNA.30410.1.S1_s_at	LOC703488	LOC703488	2.55E-03	-1.08	2.19	1.32	1.15	hypothetical protein LOC703488
Mmu.12320.1.S1_at	LOC719606	LOC719606	1.14E-03	-1.08	2.03	1.04	1.11	similar to electron-transfer-flavoprotein, beta polypeptide isoform 1
MmugDNA.6268.1.S1_at	---	---	1.69E-06	-1.08	-2.17	-1.29	1.72	---
MmugDNA.11747.1.S1_at	LOC696925	LOC696925	4.66E-06	-1.08	3.82	2.09	1.45	similar to MLF1 interacting protein
MmuSTS.2700.1.S1_at	LOC694423	E2F7	7.83E-07	-1.08	3.30	1.71	1.32	e2f transcription factor 7
MmugDNA.12277.1.S1_at	TOP2A	TOP2A	8.39E-05	-1.08	2.92	1.81	1.43	DNA topoisomerase II, alpha isozyme
MmugDNA.41268.1.S1_at	CCNB1	CCNB1	2.48E-05	-1.09	3.10	1.77	1.51	cyclin B1
Mmu.15886.1.S1_s_at	LOC693464 /// LOC697705	LOC693464 /// LOC697705	4.41E-04	-1.09	2.32	1.07	1.21	similar to Nonhistone chromosomal protein HMG-17 (High-mobility group nucleosome
MmugDNA.22095.1.S1_at	LOC711012	LOC711012	2.64E-05	-1.09	-1.54	1.00	2.83	similar to protein phosphatase 1E
MmuSTS.2900.1.S1_at	LOC710216	LOC710216	2.72E-04	-1.09	-1.33	1.01	3.25	similar to testis zinc finger protein
MmugDNA.19256.1.S1_s_at	---	---	4.46E-04	-1.09	2.23	1.05	1.02	---
MmugDNA.17680.1.S1_at	---	---	7.60E-06	-1.09	2.77	1.56	1.28	---
MmugDNA.8226.1.S1_s_at	LOC706985	LOC706985	3.03E-03	-1.09	-2.58	1.11	-1.17	similar to alpha-synuclein isoform NACP140
MmuSTS.2629.1.S1_at	---	---	4.99E-05	-1.09	-1.62	-1.61	2.24	---
MmugDNA.21515.1.S1_at	---	PRC1	1.22E-06	-1.09	2.81	1.68	1.39	protein regulator of cytokinesis 1
MmugDNA.35654.1.S1_at	CAPZA2	CAPZA2	4.02E-06	-1.10	2.55	1.53	1.33	Capping protein (actin filament) muscle Z-line, alpha 2
MmugDNA.14075.1.S1_at	RSN	BUB1B	7.32E-04	-1.10	3.64	1.94	1.81	bub1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
MmugDNA.13584.1.S1_at	KIF23	KIF23	9.47E-06	-1.10	2.56	1.64	1.48	kinesin family member 23
MmugDNA.17329.1.S1_at	---	---	3.87E-08	-1.10	3.89	1.90	1.94	---
MmugDNA.42795.1.S1_s_at	---	---	1.82E-04	-1.11	2.35	1.01	1.11	---
MmugDNA.4575.1.S1_at	---	---	2.55E-05	-1.11	-1.30	-1.27	2.07	---
MmugDNA.20811.1.S1_at	---	---	2.68E-04	-1.11	-1.37	-1.26	2.50	---
MmuSTS.3501.1.S1_at	LOC722848	LOC722848	1.52E-03	-1.11	2.29	1.06	-1.34	similar to ADP-ribosyl cyclase 2 precursor (Cyclic ADP-ribose hydrolase 2) (cADP
MmugDNA.13565.1.S1_at	---	KIF11	1.05E-05	-1.12	4.25	2.02	1.97	kinesin family member 11
MmuSTS.61.1.S1_at	LOC701598	LOC701598	6.72E-04	-1.12	2.06	1.23	1.58	similar to helicase, lymphoid-specific
MmugDNA.31059.1.S1_at	PTTG1	PTTG1	6.32E-05	-1.13	2.24	1.30	1.26	pituitary tumor-transforming 1
MmuSTS.711.1.S1_at	---	---	3.50E-04	-1.13	-1.61	-1.16	2.52	---
MmunewRS.781.1.S1_s_at	LOC712849	LOC712849	6.67E-05	-1.13	2.12	-1.04	1.16	similar to High mobility group protein B1 (High mobility group protein 1) (HMG-1
MmugDNA.16319.1.S1_at	LOC697531	LOC697531	1.06E-03	-1.13	-3.62	1.05	-1.17	Similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (
MmugDNA.29822.1.S1_at	CA4	CA4	9.09E-05	-1.13	3.38	1.22	-1.45	carbonic anhydrase IV
MmuSTS.2959.1.S1_at	LOC706847	LOC706847	1.18E-04	-1.13	-16.68	-1.04	1.02	similar to acyl-CoA synthetase long-chain family member 6 isoform b
MmugDNA.18520.1.S1_at	LOC697160	LOC697160	4.11E-08	-1.14	-1.36	1.06	2.16	similar to ATP-binding cassette, sub-family C, member 4
MmuSTS.2615.1.S1_at	---	---	2.54E-03	-1.14	-2.02	1.03	-1.10	---
MmugDNA.701.1.S1_at	---	---	2.43E-03	-1.14	-7.16	-1.04	-1.29	---
MmuSTS.2130.1.S1_s_at	S100A9	S100A9	1.86E-04	-1.14	2.97	1.05	-1.04	S100 calcium binding protein A9
MmuSTS.8.1.S1_at	LOC696629	LOC696629	1.26E-05	-1.14	2.29	1.30	1.12	Similar to Histone H2A type 1-C
MmugDNA.25187.1.S1_at	---	---	4.92E-05	-1.15	3.01	1.31	1.44	---
MmunewRS.661.1.S1_at	LOC696253	LOC696253	1.83E-05	-1.15	3.07	2.57	1.70	similar to germinal histone H4 gene
Mmu.3274.1.S1_at	---	---	1.60E-03	-1.15	-6.00	1.00	-1.06	---
MmugDNA.14323.1.S1_at	SIGLEC6	SIGLEC6	5.37E-06	-1.16	-1.36	-1.19	2.42	sialic acid binding Ig-like lectin 6
MmugDNA.16529.1.S1_at	---	---	5.05E-04	-1.16	-1.08	1.17	2.46	---
MmugDNA.7428.1.S1_at	LOC712618	LOC712618	1.56E-05	-1.16	2.05	1.18	1.28	similar to Wolf-Hirschhorn syndrome candidate 1 protein isoform 1
MmugDNA.3623.1.S1_at	---	---	2.22E-03	-1.16	-2.22	1.04	1.02	---
MmugDNA.18123.1.S1_at	LOC708774	LOC708774	1.08E-04	-1.16	2.11	1.37	1.14	Hypothetical protein LOC708774
MmugDNA.18586.1.S1_at	SMC2	SMC2	9.53E-05	-1.17	2.98	1.72	1.54	structural maintenance of chromosomes 2
MmugDNA.11652.1.S1_at	LOC695759	LOC695759	6.39E-03	-1.17	-2.76	1.16	-1.03	similar to ferrochelatase isoform a precursor
MmuSTS.2672.1.S1_at	LOC709000	LOC709000	2.07E-05	-1.17	2.34	1.37	1.61	similar to centromere protein F (350/400kD)
MmugDNA.26023.1.S1_at	LOC704646	LOC704646	1.87E-06	-1.17	4.75	1.29	-1.12	similar to mast cell-expressed membrane protein 1
MmugDNA.30376.1.S1_at	IGKC	IGKC	1.07E-05	-1.17	2.75	1.30	1.13	Immunoglobulin kappa constant
MmugDNA.41835.1.S1_at	LOC702446	LOC702446	2.77E-06	-1.18	3.05	1.46	1.27	similar to Dihydrofolate reductase
MmugDNA.40649.1.S1_at	LOC704221	LOC704221	4.60E-03	-1.18	-4.02	1.04	-1.37	similar to spectrin domain with coiled-coils 1 NSP5a3a
MmugDNA.24595.1.S1_at	---	---	1.88E-03	-1.18	3.31	2.05	-1.65	---
Mmu.5569.1.S1_at	LOC710040	LOC710040	2.39E-04	-1.18	-1.54	-1.37	2.13	similar to B-cell scaffold protein with ankyrin repeats 1

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/DO	Gene Description
MmuSTS.1347.1.S1_at	LOC697057	LOC697057	7.26E-07	-1.18	2.41	1.30	1.22	similar to high-mobility group box 2
MmuSTS.4593.1.S1_at	LOC707336	LOC707336	4.76E-06	-1.19	-1.38	-1.23	2.03	similar to transducin-like enhancer protein 1
MmugDNA.11398.1.S1_s_at	DONSON	DONSON	5.27E-04	-1.19	2.05	1.08	1.33	downstream neighbor of SON
MmugDNA.11389.1.S1_at	LOC705913	LOC705913	2.85E-03	-1.19	2.07	1.11	-1.17	similar to cytidine deaminase
MmugDNA.17821.1.S1_at	---	---	1.87E-03	-1.19	-2.30	-1.07	1.02	---
MmuSTS.2866.1.S1_at	LOC714145	LOC714145	2.46E-06	-1.20	2.14	1.30	1.07	Hypothetical protein LOC714145
MmugDNA.32221.1.S1_at	LOC694209	LOC694209	4.02E-03	-1.20	-1.22	-1.01	2.14	similar to Protein FAM3C precursor (Protein GS3786)
MmugDNA.17376.1.S1_at	S100A8	S100A8	8.92E-04	-1.20	3.41	1.42	-1.01	s100 calcium binding protein a8 (calgranulin a)
MmugDNA.16198.1.S1_at	---	---	2.47E-06	-1.20	-1.30	-1.19	2.01	---
MmugDNA.24286.1.S1_at	F2RL1	F2RL1	8.14E-05	-1.20	-1.74	-1.44	2.87	coagulation factor II (thrombin) receptor-like 1
MmugDNA.6381.1.S1_at	LOC704850	LOC704850	4.97E-04	-1.20	2.26	1.01	1.21	similar to cystatin F
MmugDNA.19727.1.S1_at	LOC694428	LOC694428	1.72E-03	-1.21	-1.45	-1.34	2.39	similar to chemokine orphan receptor 1
MmugDNA.32264.1.S1_at	LOC706017	LOC706017	1.72E-03	-1.22	-5.54	1.39	1.02	similar to G protein-coupled receptor 126 alpha 2
MmugDNA.3247.1.S1_at	LOC704341	HIST2H4B	1.00E-04	-1.22	2.18	1.62	1.28	h4 histone, family 2
MmuSTS.3318.1.S1_at	CCNB1	CCNB1	1.97E-05	-1.22	2.25	1.29	1.19	cyclin B1
MmugDNA.22076.1.S1_at	LOC693572	MGC29506	6.07E-03	-1.23	2.15	2.28	1.67	proapoptotic caspase adaptor protein
MmugDNA.6706.1.S1_at	LOC693531	CKAP2	9.83E-06	-1.23	3.15	1.97	1.33	cytoskeleton associated protein 2
MmuSTS.4157.1.S1_at	LOC708574	MAD2L1	1.40E-05	-1.23	2.96	1.73	1.59	mad2 mitotic arrest deficient-like 1 (yeast)
MmugDNA.43394.1.S1_at	LOC698684	LOC698684	2.90E-08	-1.24	2.65	1.06	1.18	Similar to 60S ribosomal protein L26
MmugDNA.41790.1.S1_at	---	---	3.12E-04	-1.24	2.01	1.10	-1.08	---
MmugDNA.22516.1.S1_at	LOC718589	LOC718589	3.37E-06	-1.24	-1.40	-1.01	2.74	Similar to quiescin Q6 isoform a
MmugDNA.15415.1.S1_at	---	---	1.00E-04	-1.25	-1.22	-1.26	2.23	---
MmugDNA.17887.1.S1_s_at	NUCB2	NUCB2	2.27E-04	-1.25	2.01	-1.01	1.10	nucleobindin 2
MmugDNA.41593.1.S1_at	---	---	1.05E-05	-1.25	-2.36	-1.97	1.20	---
MmuSTS.2958.1.S1_at	LOC698034	LOC698034	8.81E-05	-1.26	-1.55	-1.31	3.32	Similar to Fructose-bisphosphate aldolase A (Muscle-type aldolase) (Lung cancer
MmugDNA.38781.1.S1_at	LOC698390	LOC698390	5.86E-03	-1.29	2.03	2.15	1.65	---
MmugDNA.10899.1.S1_s_at	ANKRD6	ANKRD6	6.23E-03	-1.30	-3.24	1.08	-1.27	ankyrin repeat domain 6
MmugDNA.303.1.S1_at	LOC699624	LOC699624	2.40E-05	-1.30	2.18	1.20	1.30	similar to coiled-coil domain containing 99
MmugDNA.24148.1.S1_at	---	---	2.19E-03	-1.31	-3.71	-1.00	-1.10	---
MmugDNA.21710.1.S1_at	LOC706506	LOC706506	4.39E-03	-1.32	-5.95	-1.03	-1.04	similar to leucine rich repeat containing 35
MmugDNA.10786.1.S1_at	LOC699208	LOC699208	1.43E-05	-1.32	2.03	-1.01	1.23	hypothetical protein LOC699208
MmugDNA.32373.1.S1_at	---	---	2.40E-04	-1.32	-1.87	-1.21	3.11	---
MmugDNA.34165.1.S1_at	---	---	1.58E-04	-1.34	3.00	1.15	-1.18	---
MmugDNA.40591.1.S1_s_at	CYP3A5	CYP3A5	1.02E-04	-1.35	2.14	1.17	1.07	cytochrome P450, family 3, subfamily A, polypeptide 5
MmugDNA.25319.1.S1_at	LOC707116	LOC707116	3.53E-05	-1.36	-1.68	-1.54	2.75	similar to SRY (sex determining region Y)-box 5 isoform a
MmugDNA.18443.1.S1_at	---	---	1.83E-04	-1.36	-2.01	-1.36	1.89	---
MmugDNA.18254.1.S1_at	---	---	3.15E-05	-1.36	-1.86	-1.47	2.15	---
MmugDNA.7878.1.S1_at	---	---	4.99E-07	-1.37	-1.84	-1.36	2.01	---
MmuSTS.1380.1.S1_at	---	---	6.42E-06	-1.37	-1.65	-1.22	2.72	---
MmugDNA.924.1.S1_at	---	---	4.64E-03	-1.40	-2.29	1.35	-1.29	---
MmugDNA.24307.1.S1_s_at	LOC718333	LOC718333	6.38E-05	-1.41	-1.18	1.15	2.87	Similar to Protein C11orf51
MmugDNA.14323.1.S1_s_at	SIGLEC6	SIGLEC6	9.65E-07	-1.42	-1.51	-1.30	2.16	sialic acid binding Ig-like lectin 6
MmugDNA.9521.1.S1_at	QPCT	QPCT	1.54E-03	-1.43	2.09	-1.16	1.00	glutaminyl-peptide cyclotransferase
Mmu.16454.1.S2_at	THY1	THY1	7.92E-04	-1.43	2.53	1.05	-1.21	Thy-1 cell surface antigen
MmugDNA.9989.1.S1_at	---	---	6.94E-07	-1.43	-1.19	1.02	2.65	---
MmugDNA.8010.1.S1_at	---	---	6.66E-03	-1.44	-1.19	-2.23	-1.71	---
MmugDNA.34165.1.S1_s_at	---	---	4.08E-04	-1.44	2.81	1.14	-1.23	---
MmuSTS.2780.1.S1_at	SLC27A2	SLC27A2	2.61E-04	-1.44	2.46	-1.07	-1.03	solute carrier family 27 (fatty acid transporter), member 2
MmugDNA.925.1.S1_at	---	---	1.97E-03	-1.44	-2.26	1.44	-1.27	---
MmugDNA.12754.1.S1_s_at	MS4A1	MS4A1	2.22E-04	-1.45	-2.34	-1.69	1.69	membrane-spanning 4-domains, subfamily A, member 1
MmugDNA.18367.1.S1_at	LOC708948	LOC708948	5.63E-04	-1.45	-2.24	-1.02	1.20	hypothetical protein LOC708948
MmugDNA.43107.1.S1_at	LOC718801	LOC718801	3.04E-04	-1.46	-1.58	-1.00	2.13	similar to Fc receptor-like 3 precursor
MmugDNA.580.1.S1_at	---	---	1.93E-03	-1.47	-2.78	-1.44	2.76	---
MmugDNA.11101.1.S1_at	---	---	1.21E-03	-1.48	-1.17	-2.15	-1.76	---
MmuSTS.1308.1.S1_at	---	---	2.19E-04	-1.48	-2.33	-1.32	2.65	---
MmugDNA.5951.1.S1_at	MS4A1	MS4A1	2.57E-05	-1.48	-2.07	-1.61	1.82	membrane-spanning 4-domains, subfamily A, member 1
MmugDNA.27586.1.S1_at	LOC701729	LOC701729	2.22E-05	-1.50	2.44	1.28	1.28	hypothetical protein LOC701729
MmugDNA.18304.1.S1_at	---	---	5.57E-03	-1.51	1.06	-1.55	-2.13	---
MmugDNA.20850.1.S1_s_at	---	---	2.95E-04	-1.51	2.67	1.10	-1.15	---
MmuSTS.529.1.S1_at	LOC698428	LOC698428	3.33E-03	-1.52	2.05	-1.19	-1.45	Similar to ornithine carbamoyltransferase precursor
MmugDNA.32887.1.S1_at	ANK3	ANK3	6.52E-04	-1.53	-1.59	-2.06	1.03	ankyrin 3
MmugDNA.23054.1.S1_at	LOC708634	LOC708634	3.06E-04	-1.56	1.08	-2.02	-1.96	similar to ion transporter protein
MmugDNA.38219.1.S1_at	LOC720578	LOC720578	2.90E-06	-1.57	-2.06	-1.30	1.43	similar to HLA class II histocompatibility antigen, DQ(1) beta chain precursor (
MmuSTS.1928.1.S1_at	LOC712321	LOC712321	4.86E-04	-1.59	2.37	1.09	-1.29	similar to myeloblastosis proto-oncogene product isoform 2
MmugDNA.32279.1.S1_at	---	---	1.61E-07	-1.59	-2.18	-1.40	1.52	---
MmugDNA.4335.1.S1_at	LOC706308	LOC706308	3.21E-03	-1.60	-1.30	-2.02	-1.15	similar to guanine nucleotide exchange factor p532
MmugDNA.10172.1.S1_at	---	---	6.99E-03	-1.61	-7.14	-1.05	-1.45	---
MmugDNA.14306.1.S1_at	CD1C	CD1C	7.88E-06	-1.62	-2.22	-1.39	1.64	CD1C antigen, c polypeptide
MmuSTS.2065.1.S1_s_at	PYGL	PYGL	4.24E-05	-1.63	2.50	-1.23	-1.14	phosphorylase, glycogen, liver
MmugDNA.40214.1.S1_at	LOC706847	LOC706847	5.23E-03	-1.64	-4.42	2.00	1.04	similar to acyl-CoA synthetase long-chain family member 6 isoform b
MmuSTS.2810.1.S1_at	ANK3	ANK3	3.51E-04	-1.71	-1.57	-2.02	1.12	ankyrin 3
MmugDNA.29333.1.S1_at	LOC703555	LOC703555	6.19E-05	-1.71	-2.12	-1.69	1.83	similar to oxysterol-binding protein-like protein 10
MmugDNA.38909.1.S1_at	---	---	5.23E-07	-1.74	-2.25	-1.71	1.39	---
MmugDNA.36201.1.S1_at	CYP3A5	CYP3A5	2.63E-05	-1.76	2.43	-1.04	1.07	cytochrome P450, family 3, subfamily A, polypeptide 5
MmugDNA.17530.1.S1_at	LOC715937	LOC715937	9.17E-04	-1.77	-2.11	-1.65	-1.03	similar to sulfatase 2 isoform a precursor
MmugDNA.40962.1.S1_at	---	---	6.31E-04	-1.77	-1.39	-2.16	-1.18	---
MmugDNA.16085.1.S1_at	---	---	2.21E-03	-1.82	-2.20	-1.35	-1.01	---
MmuSTS.4256.1.S1_at	LOC705300	LOC705300	1.90E-03	-1.86	1.03	-2.18	-1.90	similar to dynamin 3
MmugDNA.40060.1.S1_s_at	LOC694287	LOC694287	6.46E-04	-1.88	-1.43	-2.00	-1.06	similar to Fas apoptotic inhibitory molecule 3
MmugDNA.19209.1.S1_s_at	LOC697208	LOC697208	1.78E-04	-1.97	8.54	1.76	-3.79	similar to Neutrophil gelatinase-associated lipocalin precursor (NGAL) (p25) (25
MmugDNA.40456.1.S1_at	PNOC	PNOC	1.17E-04	-1.97	-2.01	-1.37	1.37	prepronociceptin
MmugDNA.40387.1.S1_at	---	---	3.79E-05	-2.00	-1.37	-1.50	1.31	---
MmugDNA.36545.1.S1_at	---	---	6.46E-03	-2.01	1.57	-1.24	-1.17	---
MmugDNA.10151.1.S1_at	---	---	2.59E-04	-2.01	-1.60	-1.34	1.05	---
MmugDNA.22591.1.S1_at	LOC712740	LOC712740	4.40E-05	-2.02	-1.20	-1.59	1.02	similar to nuclear receptor co-repressor/HDAC3 complex subunit
MmugDNA.749.1.S1_at	LOC705089	LOC705089	1.06E-04	-2.02	-1.26	-1.84	-1.03	similar to DRE1 protein
MmugDNA.38268.1.S1_at	LOC714408	LOC714408	1.48E-05	-2.02	-1.78	-1.89	1.41	similar to AF4/FMR2 family, member 3 isoform 2
MmugDNA.28371.1.S1_at	LOC696275	LOC696275	7.19E-03	-2.02	1.13	1.33	1.02	similar to neuregulin 1 isoform HRG-beta1
MmugDNA.12706.1.S1_at	---	---	1.31E-05	-2.03	-1.12	-1.56	-1.08	---
MmugDNA.7504.1.S1_at	LOC703597	LOC703597	2.69E-05	-2.04	-1.17	-1.64	-1.11	similar to Eukaryotic translation initiation factor 4B (eIF-4B)
MmugDNA.35245.1.S1_at	---	---	4.13E-04	-2.04	-1.14	-1.46	-1.33	---
MmugDNA.1637.1.S1_at	---	---	2.49E-04	-2.04	1.09	-1.44	-1.21	---
MmugDNA.31642.1.S1_at	---	---	1.32E-03	-2.04	-1.69	-2.00	1.03	---
MmugDNA.17480.1.S1_at	---	---	3.66E-05	-2.05	1.16	-1.19	-1.10	---
MmugDNA.12398.1.S1_at	LOC723437	LOC723437	3.10E-07	-2.06	1.09	-1.23	1.31	Similar to SH3 domain and tetratricopeptide repeats 1

Affymetrix Probeset ID	Affymetrix Gene Symbol	Corrected Gene Symbol	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	CHRONIC/DO	Gene Description
MmuSTS.1251.1.S1_at	LOC707560	LOC707560	2.28E-03	-2.06	1.16	-1.06	-1.30	similar to class-I MHC-restricted T cell associated molecule
MmuSTS.2592.1.S1_at	---	---	7.68E-06	-2.06	-1.12	-1.47	-1.02	---
MmugDNA.24527.1.S1_at	---	---	1.97E-03	-2.07	-1.50	-1.33	-1.05	---
MmugDNA.32882.1.S1_at	LOC718964	LOC718964	4.23E-04	-2.07	-1.85	-1.97	-1.20	Hypothetical protein LOC718964
MmugDNA.20716.1.S1_at	---	---	2.35E-03	-2.07	-1.36	-1.67	-1.28	---
MmugDNA.3847.1.S1_at	LOC717025	LOC717025	1.36E-03	-2.08	1.33	-1.74	-1.57	similar to TPR repeat-containing protein KIAA1043
MmugDNA.21074.1.S1_at	LOC698536	IRS2	7.08E-04	-2.09	-1.35	-1.30	-1.29	insulin receptor substrate 2
MmuSTS.535.1.S1_at	---	---	5.51E-03	-2.09	-1.29	-1.90	-1.39	---
MmugDNA.1596.1.S1_at	LOC713460	LOC713460	2.40E-04	-2.09	-1.14	-2.17	-1.81	similar to Profilin-2 (Profilin II)
MmugDNA.21123.1.S1_at	IGF1R	IGF1R	5.06E-03	-2.09	-1.34	-1.89	-1.80	insulin-like growth factor 1 receptor
MmugDNA.40920.1.S1_at	---	---	1.73E-03	-2.10	-1.20	-1.59	-1.11	---
MmugDNA.11294.1.S1_at	LOC713134	LOC713134	1.78E-06	-2.10	-1.00	-1.58	-1.14	similar to eukaryotic translation initiation factor 2C, 4
MmugDNA.31091.1.S1_at	LOC718266	LOC718266	7.76E-05	-2.11	-1.05	-1.67	1.13	Similar to Interleukin-18-binding protein precursor (IL-18BP) (Interferon gamma-
MmugDNA.22445.1.S1_at	---	---	1.02E-05	-2.11	-1.28	-1.89	-1.08	---
MmugDNA.24921.1.S1_at	---	---	5.15E-04	-2.11	-2.34	-2.11	1.08	---
MmuSTS.84.1.S1_at	LOC717702	LOC717702	1.26E-05	-2.11	-1.75	-1.70	1.19	similar to HLA class II histocompatibility antigen, DO beta chain precursor (MHC
MmugDNA.11989.1.S1_at	LOC701721	LOC701721	4.13E-04	-2.12	-2.01	-1.74	1.25	similar to X Kell blood group precursor-related, X-linked
MmugDNA.896.1.S1_at	LOC701925	LOC701925	7.23E-04	-2.12	-1.48	-1.63	-1.09	similar to solute carrier family 4, sodium bicarbonate cotransporter, member 7
MmugDNA.9983.1.S1_at	11-Sep	40067	2.57E-03	-2.12	1.02	-1.34	-1.08	septin 11
MmugDNA.13933.1.S1_at	LOC694219	LOC694219	4.50E-05	-2.14	-1.14	-1.59	1.07	similar to homeodomain-only protein
MmugDNA.15353.1.S1_at	LOC704513	LOC704513	3.93E-04	-2.16	-1.36	-2.38	-1.02	similar to ALEX3 protein
MmugDNA.28007.1.S1_at	LOC696781	LOC696781	2.57E-05	-2.17	-1.04	-1.78	-1.23	hypothetical protein LOC696781
MmugDNA.42700.1.S1_at	---	---	1.79E-03	-2.18	-1.54	-1.95	-1.16	---
MmugDNA.621.1.S1_at	---	RPL35	6.74E-05	-2.20	-1.34	-1.52	-1.14	ribosomal protein l35
MmugDNA.17084.1.S1_at	---	---	2.80E-07	-2.20	2.18	1.16	1.62	---
MmugDNA.7201.1.S1_at	LOC712407	LOC712407	2.22E-04	-2.21	-1.10	-1.77	-1.15	similar to carboxypeptidase D precursor
MmugDNA.34676.1.S1_at	LOC699035	LOC699035	3.58E-03	-2.21	1.17	-2.10	-2.04	Similar to chromosome 2 open reading frame 7
MmugDNA.41434.1.S1_at	LOC700747	LOC700747	3.03E-04	-2.21	1.07	-1.58	-1.27	similar to gamma-glutamyl hydrolase precursor
MmugDNA.42278.1.S1_s_at	---	---	6.20E-03	-2.21	-1.17	-1.15	-1.15	---
MmugDNA.8795.1.S1_at	---	---	4.69E-06	-2.23	-2.10	-1.89	1.46	---
MmugDNA.12780.1.S1_at	BMX	BMX	2.83E-05	-2.24	1.96	-1.27	-1.24	BMX non-receptor tyrosine kinase
MmugDNA.4445.1.S1_at	LOC713134	LOC713134	9.54E-06	-2.25	-1.22	-1.63	-1.13	similar to eukaryotic translation initiation factor 2C, 4
MmugDNA.34681.1.S1_at	LOC713011	LOC713011	3.71E-03	-2.26	-1.68	-1.97	-1.32	similar to sortilin-related receptor containing LDLR class A repeats preproprote
MmugDNA.37241.1.S1_at	LOC704834	LOC704834	6.13E-05	-2.29	-1.44	-1.88	-1.18	hypothetical protein LOC704834
MmuSTS.4018.1.S1_at	CXCR6	CXCR6	8.87E-05	-2.29	1.53	-1.45	-1.38	chemokine (C-X-C motif) receptor 6
MmugDNA.9129.1.S1_at	LOC713051	LOC713051	1.81E-03	-2.30	-1.09	-1.71	-1.37	Similar to 60S ribosomal protein L21
MmugDNA.39023.1.S1_at	---	---	4.11E-04	-2.31	1.01	-1.55	-1.25	---
MmugDNA.7501.1.S1_at	---	---	2.12E-03	-2.32	-1.66	-1.64	1.06	---
MmugDNA.7792.1.S1_at	LOC712407	LOC712407	1.30E-05	-2.34	-1.09	-1.66	-1.20	similar to carboxypeptidase D precursor
MmugDNA.10854.1.S1_at	---	---	1.50E-03	-2.34	-1.65	-1.87	-1.41	---
MmuSTS.1606.1.S1_at	LOC707343	LOC707343	4.24E-04	-2.34	-1.50	-1.79	-1.18	similar to kelch-like 14
MmugDNA.8916.1.S1_at	---	---	6.52E-08	-2.36	-1.16	-1.61	-1.06	---
Mmu.5879.1.S1_at	LOC701255	LOC701255	2.51E-04	-2.37	-1.32	-1.75	-1.11	similar to ribosomal protein L15
MmugDNA.7323.1.S1_at	---	---	1.96E-03	-2.38	-1.78	-1.99	-1.10	---
MmugDNA.437.1.S1_at	---	---	1.61E-04	-2.43	-1.76	-2.21	-1.29	---
MmugDNA.31648.1.S1_at	LOC713894	LOC713894	5.83E-03	-2.45	-1.66	-1.51	-1.16	similar to CG8312-PA, isoform A
MmugDNA.8131.1.S1_at	---	---	5.95E-07	-2.45	-1.37	-1.70	-1.06	---
MmugDNA.41979.1.S1_at	LOC696649	LOC696649	2.11E-04	-2.48	-1.83	-1.92	-1.31	Similar to Proenkephalin A precursor
MmugDNA.37748.1.S1_s_at	LOC722305	LOC722305	2.25E-03	-2.56	1.13	1.09	1.14	similar to cDNA sequence BC048546
MmugDNA.19071.1.S1_at	---	---	1.50E-03	-2.57	-1.73	-1.92	-1.29	---
MmugDNA.31051.1.S1_at	---	---	7.36E-05	-2.60	-1.05	-1.86	-1.18	---
MmugDNA.43512.1.S1_at	---	---	4.95E-05	-2.60	-1.06	-1.27	-1.11	---
MmuSTS.1982.1.S1_at	CD14	CD14	3.24E-04	-2.64	1.01	-1.61	-1.23	CD14 molecule
MmugDNA.7361.1.S1_at	LOC717617	LOC717617	2.72E-04	-2.66	1.23	-1.72	-2.16	similar to methionine sulfoxide reductase B3 isoform 2
MmuSTS.2215.1.S1_at	LOC713994	LOC713994	2.74E-04	-2.69	-1.74	-2.12	-1.05	similar to carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
MmugDNA.9503.1.S1_at	CLEC4E	CLEC4E	4.65E-03	-2.72	-1.35	-2.02	1.03	C-type lectin domain family 4, member E
MmugDNA.34736.1.S1_at	---	---	1.07E-06	-2.73	1.78	-1.40	-1.36	---
MmugDNA.15103.1.S1_at	---	---	3.58E-03	-2.74	-2.41	-2.96	-1.41	---
MmugDNA.37748.1.S1_at	LOC722305	LOC722305	1.52E-03	-2.74	1.33	1.07	1.15	similar to cDNA sequence BC048546
MmuSTS.4328.1.S1_x_at	SERPINE2	SERPINE2	2.52E-03	-2.80	-1.89	-2.74	-1.25	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type
MmugDNA.25139.1.S1_at	LOC712407	LOC712407	2.06E-05	-2.85	-1.25	-1.82	-1.19	similar to carboxypeptidase D precursor
MmugDNA.73.1.S1_s_at	---	---	3.32E-04	-2.90	-1.06	-2.09	-1.97	---
MmugDNA.22390.1.S1_at	SLC7A11	SLC7A11	3.61E-04	-2.93	-1.15	-1.82	1.07	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
MmuSTS.1883.1.S1_at	LOC712407	LOC712407	3.52E-06	-2.93	-1.34	-1.77	-1.26	similar to carboxypeptidase D precursor
MmugDNA.30433.1.S1_at	LOC716009	SHCBP1	1.25E-05	-2.93	1.14	-1.53	-1.11	shc sh2-domain binding protein 1
MmuAffx.23.8.S1_s_at	SERPINE2	SERPINE2	4.60E-03	-2.93	-2.06	-2.68	-1.25	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type
MmugDNA.26793.1.S1_at	---	---	1.45E-06	-3.01	1.68	-1.36	1.26	---
MmuSTS.4328.1.S1_at	SERPINE2	SERPINE2	7.93E-04	-3.07	-1.89	-3.23	-1.23	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type
MmugDNA.28513.1.S1_at	---	---	6.49E-06	-3.08	1.56	-1.70	-1.23	---
Mmu.11820.13.S1_a_at	SERPINE2	SERPINE2	3.91E-04	-3.09	-2.32	-2.71	-1.15	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type
MmugDNA.33453.1.S1_at	---	---	7.55E-06	-3.18	-1.86	-2.13	1.04	---
MmugDNA.42294.1.S1_at	---	---	2.19E-03	-3.25	1.08	-2.02	-1.13	---
MmugDNA.33472.1.S1_at	LOC708658	LOC708658	1.64E-04	-3.26	1.95	-1.65	-1.38	Similar to 60S ribosomal protein L7
MmugDNA.18548.1.S1_at	---	---	1.33E-04	-3.28	-3.39	-2.07	-1.31	---
MmugDNA.12660.1.S1_at	---	FAM101B	8.54E-06	-3.97	-1.39	-2.00	-1.70	family with sequence similarity 101, member b
MmuSTS.3721.1.S1_at	---	---	2.48E-04	-4.86	1.14	-2.15	1.11	---

Supplemental Table S6. 239 SIV-inducible probesets identified as differentially expressed between SMs and RMs defined by 2 way ANOVA. Gene symbols annotation is from Affymetrix Rhesus Genome Array and DAVID database. Ratios expressed in DX/D0 columns are the average gene expression (linear scale) between all animals in an infection relative to that group's pre-infection expression level (red >+2, green <-2).

		SM-SIVsmm								RM-SIVsmm							RM-SIVmac239			
Affymetrix Probeset ID	Corrected Gene Symbol	ANOVA p-value (Species/Time)	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	Chronic /D0
MmugDNA.3270.1.S1_at	YY1	5.42E-03	0.000315	1.21	-1.46	-2.00	-1.26	-1.02	1.08	8.31E-01	1.08	-1.08	-1.27	1.11	-1.01	-1.10	4.29E-05	-1.72	-1.40	-1.11	-1.02
MmugDNA.32611.1.S1_at	SLFN5	2.77E-04	0.00012	1.19	3.61	4.08	1.42	1.46	-1.06	2.57E-03	-1.17	2.37	2.86	2.01	1.86	-1.23	3.77E-03	3.45	1.75	1.44	1.14
MmugDNA.41044.1.S1_at	NBN	2.86E-17	0.001077	-1.06	1.74	2.42	1.47	-1.17	-1.38	7.51E-01	1.17	1.34	1.38	1.57	1.38	-1.23	1.89E-05	1.58	-3.11	1.10	1.01
MmuSTS.733.1.S1_at	AGRN	7.09E-04	0.000127	1.06	1.89	2.17	1.35	1.17	1.04	4.52E-03	-1.03	1.22	1.37	1.01	1.01	-1.02	8.08E-03	1.46	1.02	1.24	1.12
MmugDNA.27093.1.S1_at	A2M	2.58E-10	0.008363	1.13	1.81	2.04	1.21	1.27	1.10	1.12E-01	1.27	1.09	-1.22	-1.06	1.00	-1.14	2.35E-02	1.29	1.90	1.25	-1.07
MmugDNA.7313.1.S1_at	PAPD5	4.40E-06	5.66E-07	1.28	1.86	2.06	1.09	1.14	1.17	3.42E-01	1.09	1.26	1.43	1.18	-1.02	1.03	2.08E-04	1.60	1.16	-1.10	1.00
MmugDNA.17376.1.S1_at	S100A8	3.78E-03	0.000413	1.33	1.17	-1.28	1.81	1.13	-2.26	7.89E-01	-1.02	-1.33	-1.47	1.20	1.02	-1.42	8.92E-04	-1.20	3.41	1.42	-1.01
MmugDNA.38346.1.S1_at	PSAT1	1.27E-04	0.000182	1.01	-1.12	-1.16	2.33	1.29	1.11	1.09E-02	-1.07	-1.04	1.25	1.73	1.30	1.02	8.84E-03	1.28	2.26	1.83	1.24
MmugDNA.8521.1.S1_at	GOT2	3.08E-04	2.31E-09	1.01	6.35	7.79	2.64	1.84	-1.09	1.62E-03	1.05	3.39	4.57	2.68	3.11	1.49	1.49E-02	4.91	1.68	1.97	1.43
MmugDNA.494.1.S1_at	RAB8A	6.06E-06	0.002915	1.36	2.08	1.85	1.34	1.16	1.20	4.37E-01	1.05	1.53	1.35	1.35	1.37	1.03	8.07E-04	1.46	1.50	1.04	1.01
MmugDNA.37307.1.S1_at	LBA1	3.09E-03	8.27E-06	1.03	1.70	2.70	-1.01	1.15	1.03	3.92E-01	1.28	2.16	2.37	1.71	1.99	1.51	4.44E-04	2.18	1.06	1.04	1.07
MmugDNA.40394.1.S1_at	LY6E	4.12E-04	6.11E-05	1.17	1.93	2.40	1.25	1.32	1.54	3.44E-02	-1.26	1.41	2.12	1.53	1.33	-1.16	2.17E-04	2.97	1.59	1.50	1.49
MmugDNA.21136.1.S1_at	LTBP1	4.60E-24	0.038633	-1.13	-1.82	-2.59	-2.19	-1.57	-1.62	6.59E-01	1.34	1.04	-1.17	-1.04	-1.09	-1.03	8.98E-02	1.07	1.21	-1.12	-1.34
MmuSTS.4171.1.S1_at	MSRA	1.29E-04	5.93E-06	1.06	2.78	2.84	1.30	1.21	-1.12	7.89E-02	1.10	2.28	1.61	1.37	1.89	1.41	1.67E-03	2.18	1.52	1.27	-1.00
MmuSTS.1659.1.S1_at	RPL4	9.07E-06	0.000494	1.47	2.58	2.73	1.72	1.30	1.30	1.19E-01	-1.03	1.64	1.71	1.73	1.13	1.08	2.96E-04	2.35	1.80	1.39	1.40
MmuSTS.1580.1.S1_at	IFIT5	4.03E-06	0.000114	1.10	3.41	2.51	1.59	1.39	-1.00	5.30E-04	1.02	3.48	9.56	2.87	2.74	1.16	2.09E-03	7.71	2.17	2.71	1.81
MmugDNA.2075.1.S1_at	SMCHD1	1.07E-04	3.08E-05	1.23	2.84	2.35	1.50	1.12	-1.11	3.06E-01	-1.04	1.79	2.20	1.85	1.73	1.43	1.27E-03	1.79	-1.03	-1.04	1.09
MmuSTS.1185.1.S1_at	PLA1A	3.49E-03	1.93E-07	-1.11	1.32	2.01	1.05	-1.15	-1.03	2.70E-03	-1.03	-1.01	1.66	-1.18	-1.23	-1.15	3.58E-05	2.78	1.39	1.30	1.11
MmugDNA.21770.1.S1_at		8.35E-13	3.04E-08	1.06	-1.12	-2.64	-1.19	1.10	-1.06	7.27E-01	-1.04	1.01	-1.21	1.07	1.01	1.08	5.10E-05	-1.88	-1.09	-1.18	1.09
MmugDNA.4421.1.S1_at	MAFB	1.75E-04	0.000479	1.20	2.97	3.39	1.81	1.50	1.16	5.33E-03	-1.16	1.42	1.61	1.24	-1.02	-1.07	8.98E-03	2.52	1.71	1.63	1.08
MmugDNA.28010.1.S1_at	LGALS8	5.52E-05	4.79E-05	-1.02	2.17	1.76	1.06	1.03	-1.11	4.39E-03	1.05	2.36	3.43	1.53	1.37	-1.03	2.48E-03	3.35	1.25	1.68	1.15
MmugDNA.12946.1.S1_at	PML	1.27E-06	3.53E-08	1.02	2.22	2.97	1.36	1.25	-1.02	3.29E-03	-1.09	1.82	2.23	1.29	1.27	1.09	9.95E-04	3.14	1.49	1.55	1.45
MmunewRS.936.1.S1_at	GBP6	2.02E-14	9.87E-08	1.10	3.72	3.69	2.06	1.30	-1.17	3.97E-01	1.04	2.98	3.01	1.93	2.55	1.54	3.98E-02	3.27	1.56	1.38	1.56
MmugDNA.1519.1.S1_at	KIAA1618	6.22E-06	3.72E-07	1.13	1.79	2.20	-1.02	1.30	-1.03	3.51E-02	-1.23	1.59	1.63	1.19	1.38	-1.11	2.38E-01	1.99	1.13	1.21	1.52
MmugDNA.4894.1.S1_at	GSK3B	3.18E-04	0.000461	1.14	-1.53	-2.26	-1.25	-1.13	-1.03	9.23E-01	-1.01	-1.01	1.16	1.18	1.03	1.16	1.15E-05	-1.70	-1.25	-1.57	-1.18
MmugDNA.20819.1.S1_at	OAS3	1.78E-04	3.30E-10	1.31	15.14	13.24	3.41	2.20	1.24	9.40E-05	-1.17	7.47	6.48	3.50	5.01	1.22	1.07E-02	9.45	2.37	2.97	1.78
MmugDNA.36516.1.S1_at	IRF9	4.90E-05	4.15E-06	1.16	2.50	2.73	1.75	1.52	1.08	2.60E-01	1.12	1.65	1.46	1.40	1.49	1.19	1.45E-03	1.95	1.31	1.45	1.12
MmugDNA.21074.1.S1_at	IRS2	9.90E-04	0.000104	1.01	-2.02	-2.93	-1.46	-1.23	-1.35	4.25E-02	1.06	-1.04	-1.30	-1.07	1.25	1.41	7.08E-04	-2.09	-1.35	-1.30	-1.29
MmuSTS.1283.1.S1_at	DTL	9.86E-03	3.85E-06	1.23	1.50	1.25	3.09	1.57	1.11	7.78E-04	-1.01	1.11	3.33	4.48	1.64	1.24	2.43E-03	3.31	6.52	2.61	1.86
Mmu.11960.1.S1_x_at	GBP1	7.05E-12	3.66E-05	-1.05	2.68	4.06	1.33	1.05	1.06	5.39E-02	1.07	3.11	3.25	1.76	2.02	-1.30	7.51E-03	5.55	1.62	2.14	1.88
MmugDNA.41315.1.S1_at	GBP1	1.48E-14	1.02E-09	1.54	10.93	10.11	5.81	2.10	1.25	1.56E-01	-1.03	3.71	3.24	3.00	3.16	1.53	1.07E-01	4.34	1.86	2.27	2.07
MmugDNA.29625.1.S1_at	IRF7	1.49E-03	5.15E-09	1.14	5.10	8.04	2.41	1.84	1.07	5.85E-04	1.20	4.15	4.67	2.28	2.68	1.15	4.78E-03	6.96	2.34	2.55	1.71
MmugDNA.28886.1.S1_at	C6ORF150	7.30E-29	0.000461	-1.08	2.31	2.87	1.47	1.02	-1.18	1.37E-02	-1.13	2.11	2.37	1.47	1.74	-1.01	1.41E-03	3.29	1.53	1.30	1.47
MmugDNA.36196.1.S1_at	STAT2	1.03E-02	1.01E-07	1.19	3.22	4.16	1.59	1.36	1.06	2.29E-05	1.07	2.39	2.52	1.82	1.73	-1.02	4.17E-03	3.39	1.69	1.76	1.38
MmugDNA.39346.1.S1_at	SLC25A37	1.28E-03	0.016074	1.05	1.81	2.11	1.02	1.00	-1.61	5.36E-01	-1.26	1.69	1.09	1.35	1.71	1.03	6.41E-01	1.45	1.35	1.36	1.09
MmuSTS.1612.1.S1_at	OASL	5.20E-03	1.87E-10	1.44	27.76	35.26	6.49	3.10	1.09	2.30E-02	1.37	9.23	10.48	4.27	5.30	1.74	5.36E-03	14.06	2.76	3.78	2.27
MmugDNA.29151.1.S1_at	SPTLC2	1.53E-04	1.29E-05	1.17	1.95	2.41	1.29	1.18	-1.07	6.28E-01	-1.04	-1.02	1.03	-1.01	-1.26	-1.26	2.75E-02	1.60	1.39	1.08	1.11
MmugDNA.685.1.S1_at	ECGF1	1.74E-14	0.011705	-1.04	2.23	2.66	1.60	1.48	-1.09	2.24E-01	-1.28	1.98	1.64	1.15	1.93	1.34	1.11E-01	2.16	1.49	1.28	1.29
MmugDNA.29385.1.S1_at	MIRN21	1.06E-04	5.04E-05	1.28	2.01	2.47	2.04	1.32	-1.32	4.07E-01	-1.21	1.48	1.51	1.90	1.29	-1.10	6.97E-03	1.66	2.15	1.34	1.05
MmugDNA.29315.1.S1_at	DEPDC1	6.40E-07	5.18E-07	-1.03	-1.10	-1.19	3.18	1.57	-1.03	4.16E-04	-1.21	-1.09	1.06	2.25	1.42	-1.04	4.97E-05	1.10	2.89	2.12	1.28
MmugDNA.40745.1.S1_at	MLKL	1.46E-08	5.01E-11	1.14	3.22	2.95	1.44	1.16	-1.08	3.48E-01	1.22	1.46	1.76	1.20	1.31	1.37	5.82E-05	1.73	1.15	-1.01	1.33
MmugDNA.13458.1.S1_at	NAP1L1	4.41E-13	0.00113	-1.09	-1.52	-2.50	-1.13	-1.49	-1.49	2.90E-01	-1.11	-1.12	1.39	1.09	1.04	-1.07	7.25E-02	-1.32	1.08	-1.48	-1.10
MmugDNA.16608.1.S1_at	ELL2	2.93E-07	4.71E-05	1.36	-1.43	-2.03	1.46	1.06	-1.04	7.19E-01	1.38	1.19	1.70	1.54	1.47	1.25	7.30E-04	-1.52	1.07	1.11	-1.01
MmugDNA.12091.1.S1_at	BCL2L7P1	8.54E-06	1.61E-05	1.10	1.92	2.39	1.41	1.31	1.19	3.22E-02	-1.17	1.27	1.15	1.19	1.35	1.01	1.87E-03	1.77	1.39	1.29	1.30
MmugDNA.19523.1.S1_s_at	CD164	8.64E-06	3.83E-05	1.24	2.25	3.49	1.45	1.39	-1.14	6.28E-01	-1.21	1.54	1.28	1.30	1.53	-1.13	2.75E-05	2.36	1.47	1.23	1.21
MmugDNA.19588.1.S1_at	TIFA	6.06E-07	1.16E-07	1.32	2.00	3.88	1.94	-1.21	-1.49	6.52E-02	-1.22	1.41	1.82	3.21	2.47	1.22	8.96E-02	2.20	1.83	1.26	1.14
MmugDNA.15480.1.S1_at	ZC3HAV1	4.05E-15	5.80E-06	1.13	2.08	2.28	1.19	1.07	-1.05	5.18E-01	1.02	1.60	1.41	1.44	1.66	1.02	3.94E-04	1.80	-1.04	1.29	-1.09
MmugDNA.38781.1.S1_at	LOC698390	1.43E-09	0.000298	-1.13	-1.01	-1.03	7.79	2.09	-1.10	3.18E-01	-1.17	-1.10	-1.31	1.07	2.24	-1.31	5.86E-03	-1.29	2.03	2.15	1.65
MmugDNA.19278.1.S1_at	PHACTR2	1.57E-03	3.63E-07	1.21	3.82	3.82	1.77	1.55	1.11	5.45E-01	1.41	2.53	2.25	1.76	2.25	1.75	1.36E-02	2.55	1.53	1.31	1.22
MmugDNA.19523.1.S1_at	CD164	1.28E-06	0.000315	1.21	2.32	3.93	1.84	1.51	-1.01	4.65E-01	-1.20	1.75	1.55	1.28	1.69	1.15	2.08E-05	2.42	1.53	1.23	1.20
MmugDNA.11765.1.S1_at	ANKRD22	9.25E-14	5.46E-05	1.62	4.45	2.81	2.24	1.51	-1.04	5.68E-02	1.76	1.46	-1.33	1.23	1.17	1.10	5.43E-03	-1.28	1.93	-1.27	-1.74
MmugDNA.19992.1.S1_at	TRIM5	1.02E-06	1.04E-06	1.16	3.31	3.59	1.69	1.41	-1.07	3.41E-02	-1.17	1.93	1.69	1.60	1.86	1.25	4.19E-04	2.21	1.24	1.23	1.17
MmuSTS.4685.1.S1_at	TYMS	1.91E-06	1.58E-06	1.14	1.00	1.06	3.43	2.65	1.23	4.37E-06	-1.08	1.07	1.30	4.59	2.07	1.37	4.13E-05	1.53	7.85	3.29	1.90
MmugDNA.21336.1.S1_at	CMPK2	1.58E-03	1.58E-08	1.46	53.66	32.50	10.57	3.38	1.39	1.04E-02	1.12	6.04	13.46	8.17	7.78	-1.14	4.80E-02	17.36	2.81	6.74	2.63
MmugDNA.8251.1.S1_at	TMEM140	1.10E-06	3.58E-08	-1.01	2.45	3.41	1.26	1.03	-1.36	2.85E-01	1.09	2.40	2.34	1.52	2.16	1.54	4.47E-03	2.57	1.23	1.00	1.23
MmunewRS.254.1.S1_at	IFI27	5.72E-06	0.073948	1.31	4.27	2.43	2.94	1.62	1.35	1.33E-05	-1.03	6.07	16.33	28.94	6.38	1.26	3.67E-02	31.86	26.02	26.83	6.78
MmuSTS.4535.1.S1_at	ERAP2	7.01E-05	0.000105	1.23	2.00	2.45	1.21	1.12	1.14	4.62E-01	1.03	1.21	1.55	1.31	-1.10	-1.02	3.11E-07	2.41	1.47	1.04	1.03
MmugDNA.35809.1.S1_at	HIRA	1.72E-24	0.000412	1.16	1.86	2.31	1.05	1.08	1.05	2.03E-01	-1.25	1.11	1.18	1.03	1.30	-1.07	9.50E-04	1.56	1.06	1.19	1.01
MmugDNA.9703.1.S1_at	TREM1	1.51E-07	0.001879	1.22	1.92	2.47	1.16	1.34	-1.17	4.61E-01	-1.02	1.37	-1.00	1.18	1.90	1.17	2.61E-01	1.61	1.25	1.03	1.20
MmugDNA.17749.1.S1_at	XAF1	5.87E-09	0.000348	-1.11	2.69	2.75	1.73	1.11	-1.11	7.23E-02	1.14	3.43	2.67	2.88	3.54	1.29	9.89E-02	3.38	1.68	2.36	1.76
MmugDNA.26033.1.S1_at	CENPN	1.37E-13	0.000612	1.03	1.15	-1.12	2.06	1.56	1.22	1.54E-02	1.02	1.05	1.24	2.44	1.44	1.09	1.71E-04	1.13	2.56	1.70	1.28
MmugDNA.7052.1.S1_at	UBE2L6	4.33E-04	4.46E-06	1.29	3.21	3.52	1.90	1.37	1.24	9.12E-03	-1.03	2.10	2.20	1.66	1.60	1.17	7.14E-05	2.78	1.72	1.47	1.27
MmunewRS.902.1.S1_at	EMB	1.70E-04	0.00152	1.34	2.13	2.56	1.70	1.20	-1.07	2.32E-02	-1.01	1.46	1.60	2.41	2.10	1.31	5.50E-03	2.39	1.82	1.29	1.35
MmugDNA.1081.1.S1_at	TAP1	4.03E-03	0.000148	1.15	2.02	2.17	1.29	1.21	1.09	5.26E-01	1.03	1.72	1.55	1.52	1.52	1.23	7.30E-04	2.11	1.46	1.08	1.26
MmugDNA.1639.1.S1_at	ARG2	4.92E-06	0.000391	1.07	1.43	2.12	-1.09	-1.04	-1.52	4.61E-01	1.09	1.36	1.07	1.21	1.58	1.71	1.11E-01	1.27	1.53	-1.09	-1.04
MmugDNA.27480.1.S1_at	LGALS8	2.41E-06	0.003936	-1.02	2.54	2.29	1.27	1.27	1.11	3.09E-02	1.19	2.77	3.25	2.23	2.05	1.08	3.99E-05	3.83	1.46	1.96	1.33
MmuSTS.805.1.S1_at	ATP5G1	2.54E-05	0.007199	1.06	1.86	2.22	1.21	1.28	1.24	1.30E-01	-1.01	1.14	1.47	1.06	1.03	-1.28	2.95E-07	2.14	1.00	1.14	1.24
MmuSTS.3660.1.S1_at	POR	8.83E-03	0.000851	1.13	1.85	2.32	1.14	1.28	1.06	2.49E-03	-1.03	1.39	1.32	-1.09	1.11	1.04	3.14E-05	1.77	1.10	1.11	1.09
MmugDNA.11557.1.S1_at	NCAPG	8.01E-04	0.000129	1.18	1.10	-1.43	2.81	1.68	1.09	2.39E-03	-1.06	-1.10	1.17	3.23	1.37	-1.01	8.19E-06	1.08	4.49	2.43	1.85
MmuSTS.3349.1.S1_at	CCRL2	2.58E-07	1.33E-07	1.06	4.67	3.49	1.24	-1.11	-1.69	4.60E-02	1.18	2.57	2.74	1.73	2.19	1.28	4.33E-03	3.11	1.29	1.37	1.14
MmugDNA.3201.1.S1_at	BACH2	2.20E-12	0.102604	-1.34	-1.63	-1.61	-2.42	-1.41	-1.17	5.34E-02	1.46	1.46	-1.22	-1.34	1.15	1.73	3.21E-01	-2.69	-1.89	-2.50	-2.03
MmugDNA.14153.1.S1_at	LGALS8	8.10E-05	3.89E-07	1.24	3.31	2.70	1.62	1.27	-1.02	1.20E-01	1.04	1.52	1.62	1.35	1.19	1.02	8.83E-03	1.77	1.32	1.22	1.11
MmugDNA.35877.1.S1_s_at	ARMET	4.38E-06	0.004536	1.30	1.12	1.03	2.10	1.42	1.23	4.87E-01	-1.09	1.04	-1.06	1.42	1.16	-1.24	1.59E-02	1.01	1.63	1.37	1.14
MmugDNA.9650.1.S1_at	DTX3L	1.33E-08	1.03E-09	1.19	3.57	3.63	1.80	1.38	1.08	8.06E-03	1.00	2.20	2.26	1.58	1.58	1.19	5.72E-04	3.10	1.36	1.51	1.38
MmugDNA.3988.1.S1_at	ANKRD22	7.00E-25	1.12E-06	1.28	2.56	2.45	2.08	1.08	-1.03	4.42E-02	-1.08	-1.03	-1.60	-1.15	1.02	1.07	2.46E-02	-1.00	1.60	1.05	-1.19
Mmu.7639.1.S1_at	STAT1	1.66E-03	9.85E-08	1.54	4.54	3.68	2.14	1.35	1.26	3.99E-02	1.06	2.51	2.59	2.24	1.46	1.31	2.83E-04	2.71	1.41	1.38	1.38
MmugDNA.36105.1.S1_at	AMDHD2	1.63E-13	0.010583	1.29	1.74	2.40	1.45	1.47	1.24	7.48E-01	1.00	1.03	-1.08	1.08	1.07	-1.13	3.95E-01	1.39	1.36	1.31	1.20
MmugDNA.30129.1.S1_at	TNFSF10	3.98E-14	0.000542	-1.25	2.38	1.76	1.35	1.00	-1.85	4.10E-01	-1.34	1.38	1.72	1.31	1.42	-1.30	3.72E-06	2.52	1.30	1.06	-1.23
MmugDNA.27352.1.S1_at	ZNFX1	3.48E-05	2.20E-08	1.01	2.08	2.34	1.10	-1.05	-1.22	3.01E-01	1.24	1.75	1.55	1.15	1.32	1.45	3.11E-03	1.71	1.17	-1.02	1.06
MmuSTS.4655.1.S1_at	OAS1	3.55E-11	2.74E-14	1.25	18.11	23.84	5.52	2.29	1.35	2.43E-04	-1.15	3.37	6.61	2.79	1.49	-1.12	3.25E-07	16.88	4.37	3.50	1.59
MmuSTS.2164.1.S1_at	DDX10	3.64E-03	7.42E-06	-1.18	1.02	1.32	3.80	2.08	1.16	7.87E-04	-1.17	1.10	1.69	3.80	1.77	-1.10	1.92E-03	2.55	5.33	3.74	1.71
MmugDNA.40648.1.S1_at	JUP	2.94E-04	1.59E-08	-1.03	3.61	7.03	1.29	1.04	1.05	6.13E-01	1.11	1.05	1.03	-1.15	1.01	1.08	9.65E-03	1.76	-1.07	-1.03	-1.02
MmugDNA.14810.1.S1_at	TRAFD1	1.67E-06	3.04E-07	1.10	2.13	2.27	1.14	1.03	1.06	1.46E-01	1.10	2.18	2.13	1.39	1.70	1.51	1.81E-04	2.06	1.28	1.06	1.10
MmugDNA.8141.1.S1_at	UPP1	1.42E-10	0.003935	1.26	1.70	2.08	1.18	-1.08	-1.09	4.80E-01	1.24	1.27	-1.11	1.16	1.23	1.35	3.70E-03	1.09	1.72	-1.12	-1.13
MmuSTS.4660.1.S1_at	TNFAIP6	1.28E-06	9.21E-07	-1.05	4.08	7.06	1.89	1.04	-2.21	5.04E-02	-1.09	2.44	4.35	3.27	3.78	1.69	3.16E-03	5.94	3.66	2.28	1.54
MmugDNA.16432.1.S1_at	PRIC285	2.97E-05	3.07E-07	-1.00	2.68	3.69	1.39	1.20	1.10	5.30E-02	1.07	1.55	1.83	-1.01	1.27	1.04	2.95E-04	2.25	1.07	1.31	1.19
MmugDNA.19097.1.S1_at	SHROOM4	1.60E-05	5.14E-06	-1.06	1.82	2.62	1.24	1.04	1.08	6.77E-01	1.00	1.08	-1.07	1.02	-1.03	1.06	4.72E-04	1.32	1.00	1.26	1.02
MmugDNA.36433.1.S1_at	GBP2	7.96E-09	1.75E-09	1.32	12.46	14.37	2.76	1.96	1.11	4.31E-01	1.11	2.83	2.80	1.38	1.96	1.36	8.12E-03	4.85	2.37	1.67	1.65
MmugDNA.13052.1.S1_at	PIK3AP1	6.58E-05	0.000108	1.19	2.07	1.44	1.14	1.06	-1.03	1.98E-02	-1.22	1.84	2.05	1.36	1.55	1.46	1.25E-02	1.78	1.25	1.01	1.38
MmugDNA.3702.1.S1_at	EMB	2.32E-04	3.32E-05	1.27	2.31	2.25	1.83	1.09	-1.21	1.75E-02	-1.09	1.55	1.71	2.27	2.10	1.42	2.66E-02	1.74	1.97	1.10	1.25

Supplementary Table S6. part 1 of 3.

			SM-SIVsmm							RM-SIVsmm							RM-SIVmac239				
Affymetrix Probeset ID	Corrected Gene Symbol	ANOVA p-value (Species/Time)	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	Chronic /D0
MmugDNA.24620.1.S1_at	---	1.98E-19	0.001341	1.47	3.51	3.57	1.59	1.82	-1.08	4.48E-01	-1.13	1.39	2.04	1.90	1.22	-1.23	1.32E-04	2.30	1.61	1.41	-1.02
MmugDNA.22837.1.S1_at	WARS	1.12E-08	0.007483	1.49	2.36	2.66	1.61	1.19	1.42	5.41E-01	1.39	1.69	1.26	1.35	1.12	1.13	1.31E-01	1.60	1.29	1.15	1.12
MmugDNA.34026.1.S1_at	PLA2G4C	6.69E-08	9.94E-05	1.02	2.09	3.68	1.14	1.12	1.07	1.85E-03	1.10	3.67	12.30	1.96	1.92	1.06	5.39E-06	13.76	1.79	2.22	1.95
MmugDNA.31670.1.S1_at	FAM70A	3.65E-04	1.77E-08	1.14	13.45	7.26	2.75	1.39	1.30	6.49E-05	1.07	2.50	6.23	2.65	1.80	-1.09	1.33E-03	11.29	3.42	2.86	1.48
MmugDNA.23571.1.S1_at	EPSTI1	1.07E-11	2.95E-07	1.24	6.52	6.79	2.36	2.12	1.09	2.51E-02	1.27	4.78	5.03	2.98	3.98	1.64	4.83E-02	4.94	1.86	2.20	1.94
MmuSTS.1927.1.S1_at	MX2	1.24E-02	7.21E-08	1.32	9.07	7.55	3.62	2.18	1.21	1.40E-04	1.12	4.12	5.29	2.98	3.27	1.25	2.18E-02	5.79	2.10	2.82	1.89
MmugDNA.11115.1.S1_s_at	LOC707033	1.14E-03	6.19E-06	1.22	2.74	2.81	1.41	1.26	1.23	2.83E-03	-1.23	1.70	1.41	1.10	1.17	-1.21	1.55E-02	2.26	1.76	1.25	1.20
MmugDNA.25587.1.S1_at	PI4K2B	5.06E-03	2.00E-05	1.28	2.82	1.90	1.75	1.06	-1.00	2.01E-03	-1.39	1.70	3.91	2.03	1.48	-1.13	1.06E-05	3.54	1.50	1.58	1.35
MmugDNA.2972.1.S1_at	SP140	1.30E-03	0.000254	1.00	1.74	2.33	-1.10	1.16	1.05	2.77E-01	1.04	1.51	1.73	1.15	1.14	1.09	4.74E-05	2.39	-1.08	1.14	1.25
MmugDNA.28902.1.S1_at	GAB1	5.22E-08	1.88E-06	1.13	1.21	-1.16	2.12	1.06	-1.27	3.19E-01	-1.06	1.25	1.71	1.50	1.29	-1.09	2.81E-01	-1.03	-1.26	1.13	-1.13
MmugDNA.9235.1.S1_s_at	ADAR	6.34E-05	1.56E-06	1.15	2.64	2.39	1.28	1.22	-1.05	2.40E-01	1.29	2.19	1.76	1.63	1.88	1.59	5.99E-02	1.54	1.22	1.12	1.12
MmugDNA.2427.1.S1_at	TXNDC5	3.52E-04	8.28E-05	1.03	-1.20	-1.08	3.01	1.63	1.16	3.05E-01	1.00	1.16	1.01	1.66	1.70	1.18	1.51E-02	1.09	2.10	2.15	1.20
MmugDNA.15476.1.S1_at	EPSTI1	1.35E-21	2.94E-08	1.30	6.90	6.66	2.71	1.90	1.18	5.47E-03	1.23	5.93	5.63	3.90	4.69	1.44	9.04E-03	6.68	2.35	2.77	2.06
MmugDNA.25916.1.S1_at	PLSCR1	1.79E-08	1.10E-06	1.52	4.32	2.98	1.98	1.30	1.36	1.64E-01	-1.44	2.19	2.76	1.45	1.40	1.40	8.70E-02	4.31	2.91	2.01	1.67
MmugDNA.23425.1.S1_at	IL1RN	1.11E-06	3.26E-06	1.09	2.01	4.28	-1.08	-1.36	1.01	1.52E-03	1.33	4.52	6.57	1.74	2.12	1.95	2.20E-08	9.86	1.86	1.37	1.11
MmugDNA.621.1.S1_at	RPL35	4.66E-04	3.60E-05	1.35	-1.60	-2.05	-1.41	1.07	1.07	6.24E-03	1.38	1.08	-1.32	-1.03	1.05	1.20	6.74E-05	-2.20	-1.34	-1.52	-1.14
MmugDNA.10394.1.S1_at	RNASEL	1.63E-13	0.006118	1.49	2.08	1.45	1.30	1.28	1.02	2.62E-01	1.02	1.40	1.65	1.76	1.69	1.14	3.12E-02	1.43	1.18	-1.06	1.16
MmuSTS.1377.1.S1_at	BCL2L14	2.31E-03	9.65E-10	1.15	5.26	9.11	2.28	1.21	1.28	2.19E-04	1.05	1.27	3.19	1.53	-1.05	-1.12	6.80E-05	8.13	3.83	2.96	1.54
MmugDNA.22222.1.S1_at	NBN	4.68E-18	0.003032	-1.13	1.77	2.49	1.40	-1.09	-1.35	8.93E-01	-1.02	1.10	1.16	1.37	1.22	-1.41	3.51E-05	1.56	-3.92	1.18	1.03
MmugDNA.41250.1.S1_at	PAQR8	9.40E-16	0.000244	1.23	2.94	2.08	1.41	1.19	1.04	5.94E-02	1.00	1.32	1.44	1.14	1.08	-1.13	2.47E-03	1.70	1.21	1.27	1.19
MmunewRS.816.1.S1_s_at	IGJ	4.97E-10	8.83E-06	-1.20	-1.51	-1.47	4.07	1.72	-1.23	3.12E-01	-1.03	1.17	1.65	2.47	2.14	-1.31	9.73E-02	1.49	2.08	2.90	1.46
MmugDNA.12660.1.S1_at	FAM101B	1.06E-18	0.002111	1.16	-1.67	-2.58	-1.45	1.05	1.13	1.06E-03	1.10	1.02	-2.02	-1.27	1.16	1.59	8.54E-06	-3.97	-1.39	-2.00	-1.70
MmugDNA.30329.1.S1_at	PABPC4	1.04E-03	0.001448	1.28	-1.63	-2.37	-1.25	-1.10	1.18	9.57E-01	-1.06	1.02	-1.22	-1.11	-1.04	1.00	4.26E-03	-1.91	-1.07	-1.40	-1.06
MmugDNA.8486.1.S1_at	OAS2	4.80E-04	3.10E-09	1.34	15.72	11.01	3.32	1.84	1.26	1.26E-03	1.31	7.95	10.68	4.29	4.18	1.38	2.71E-03	11.10	2.17	3.33	2.01
MmugDNA.43121.1.S1_at	CLEC7A	2.01E-03	0.001144	1.70	2.41	2.21	1.76	1.39	1.17	1.25E-02	-1.31	1.51	1.54	1.92	1.34	1.02	3.05E-01	1.56	1.39	1.41	1.12
MmugDNA.18794.1.S1_at	CDC20	1.96E-05	3.23E-05	-1.02	1.10	1.08	2.61	1.82	1.29	1.69E-04	-1.01	1.03	-1.43	2.59	1.71	1.04	3.77E-05	1.07	5.16	2.57	1.64
Mmu.11960.1.S1_at	GBP1	1.47E-12	0.000185	1.00	3.01	4.91	1.55	1.39	1.01	4.47E-02	-1.10	3.23	4.05	1.68	2.08	-1.31	6.62E-03	5.75	1.76	2.18	1.96
MmuSTS.1789.1.S1_at	SCO2	2.26E-04	6.75E-07	1.14	3.09	3.65	1.64	1.33	-1.14	4.51E-02	1.04	1.60	1.85	1.66	1.26	-1.19	2.29E-02	2.36	1.44	1.52	1.15
MmuSTS.1081.1.S1_at	PDE6H	1.30E-15	2.60E-05	-1.06	-2.62	-3.03	-2.31	-1.52	-1.45	3.04E-02	1.01	-1.17	-1.62	-1.70	1.00	1.21	1.05E-02	-2.07	-1.64	-1.96	-1.21
MmugDNA.34302.1.S1_at	GBP1	1.04E-06	0.000764	1.13	1.80	2.28	1.07	1.16	1.15	1.50E-02	1.08	2.04	3.14	1.34	1.85	1.09	1.12E-02	3.60	1.04	1.73	1.74
MmugDNA.13092.1.S1_at	SHROOM4	5.25E-06	1.20E-05	1.06	4.19	5.26	1.99	1.24	1.00	9.36E-01	1.15	1.19	1.09	1.22	1.14	1.08	2.58E-04	1.79	1.82	1.73	1.06
Mmu.2142.1.S1_at	TRIM22	6.31E-12	4.55E-05	1.36	3.52	3.02	1.44	1.31	1.09	3.25E-01	1.03	2.24	1.57	1.71	1.63	1.48	2.49E-03	1.64	-1.05	1.05	1.12
MmugDNA.36872.1.S1_at	LYSMD2	6.55E-19	0.0005	1.10	2.74	2.65	1.54	1.15	1.19	1.76E-01	-1.37	1.13	1.57	1.31	1.19	-1.30	3.54E-06	2.41	1.19	1.14	1.31
MmugDNA.40942.1.S1_at	SAMD4A	1.75E-03	0.007158	1.15	2.38	2.24	1.42	-1.27	-1.01	3.93E-04	1.02	2.11	7.92	2.91	1.28	-1.07	3.72E-05	5.83	2.40	1.82	1.37
MmugDNA.30432.1.S1_at	MSRA	6.23E-03	0.000505	1.01	1.82	2.43	-1.02	1.14	1.11	5.57E-01	1.09	1.79	1.45	1.18	1.50	1.20	3.05E-03	1.94	1.43	1.01	-1.16
Mmu.13989.1.S1_at	LOC719212	7.11E-06	0.000232	1.24	1.86	2.34	1.44	1.32	1.11	7.51E-02	1.15	1.49	2.03	1.34	1.02	-1.09	6.63E-06	2.81	1.76	1.42	1.32
MmuSTS.1653.1.S1_at	TMPRSS3	6.02E-11	3.12E-05	1.28	-1.06	-1.24	2.15	1.56	1.16	5.63E-02	-1.23	1.01	1.17	2.82	1.73	-1.07	1.18E-05	-1.01	2.33	1.79	1.32
MmugDNA.27480.1.S1_s_at	LGALS8	2.72E-13	6.46E-06	1.04	5.80	5.01	1.76	1.38	-1.11	2.05E-03	1.06	2.95	3.64	2.02	2.07	1.15	3.84E-04	3.68	1.49	1.87	1.37
MmuSTS.3275.1.S1_at	RRM2	5.15E-08	8.50E-08	-1.33	-1.19	1.14	4.92	2.31	1.18	6.08E-06	-1.06	1.11	-1.10	4.12	2.12	1.32	7.87E-04	1.26	6.11	2.81	1.89
MmugDNA.29993.1.S1_s_at	FCGR2B	1.86E-17	8.84E-10	1.33	3.31	4.78	1.67	1.41	1.10	6.69E-01	1.01	1.64	1.31	1.34	1.69	1.39	1.78E-01	1.11	-1.03	-1.18	1.05
MmugDNA.18432.1.S1_at	INDO	1.73E-39	0.004659	1.19	3.31	3.20	2.06	1.41	1.40	3.09E-01	-1.10	1.81	1.11	1.37	1.68	1.52	3.78E-02	1.62	1.83	1.09	-1.01
MmuSTS.1497.1.S1_at	RSAD2	6.42E-09	5.34E-09	1.74	49.95	49.42	17.85	4.93	1.32	2.91E-03	1.52	11.20	21.24	10.33	14.18	1.57	4.32E-02	19.80	2.44	7.10	3.32
MmugDNA.16654.1.S1_at	GBP2	4.24E-22	2.47E-07	1.15	5.82	6.17	2.13	1.18	1.03	5.14E-01	1.17	1.13	1.15	1.05	1.26	1.02	4.17E-04	1.39	1.08	1.05	-1.08
MmugDNA.33437.1.S1_s_at	ZNF313	8.57E-06	8.80E-08	1.06	2.13	2.32	1.08	1.11	-1.16	7.32E-02	1.09	1.75	1.76	1.27	1.43	1.15	3.03E-05	2.00	1.17	1.02	1.11
MmugDNA.2077.1.S1_at	SMCHD1	6.04E-08	0.000442	1.29	2.90	2.03	1.64	1.07	-1.20	1.04E-02	-1.23	1.82	2.47	2.00	1.98	1.69	8.09E-03	1.73	1.10	1.01	1.23
MmugDNA.11097.1.S1_at	SRGAP2	8.66E-04	2.71E-06	1.09	2.04	1.91	1.01	1.16	1.20	1.54E-02	1.33	2.73	3.03	1.41	1.71	1.27	4.37E-04	2.81	1.15	1.30	1.61
MmugDNA.32941.1.S1_at	C16ORF75	1.30E-30	0.004566	-1.08	2.21	1.21	2.07	-1.14	-1.34	1.54E-02	1.30	1.11	1.19	2.44	1.62	1.01	1.82E-07	1.73	3.65	2.11	1.27
MmugDNA.36739.1.S1_at	CR1	8.22E-11	1.17E-05	1.12	-1.87	-2.82	-1.41	-1.25	-1.10	9.74E-01	1.14	1.12	-1.03	1.03	1.11	1.06	8.21E-02	-1.95	-1.66	-1.45	-1.34
MmugDNA.7056.1.S1_s_at	UCHL1	3.72E-09	6.51E-05	-1.01	1.11	1.04	2.82	1.56	1.16	1.16E-02	1.05	-1.10	-1.09	1.88	1.54	1.17	5.85E-02	1.43	3.25	2.78	1.70
MmugDNA.21377.1.S1_at	MOV10	1.37E-02	2.68E-05	1.08	2.83	3.32	1.32	1.23	1.09	2.36E-02	1.03	1.66	2.04	1.31	1.19	-1.16	9.14E-06	2.71	1.34	1.19	1.01
MmugDNA.38197.1.S1_at	LOC440836	1.18E-10	0.000104	1.38	3.51	2.68	1.85	1.80	1.01	3.57E-05	1.27	3.11	3.30	1.98	1.88	-1.16	9.42E-02	3.43	2.28	2.14	1.52
MmugDNA.27193.1.S1_at	FLJ20035	1.17E-02	2.00E-08	1.73	28.90	18.47	9.16	2.98	1.14	1.59E-05	-1.19	6.39	13.18	7.24	6.42	1.50	3.87E-02	11.13	3.12	4.40	2.77
MmugDNA.42826.1.S1_at	C21ORF91	3.52E-07	0.000109	-1.02	2.36	2.92	1.51	-1.03	-1.16	5.28E-02	-1.46	1.28	2.02	1.50	1.22	-1.09	7.26E-07	3.34	1.36	1.30	1.28
MmugDNA.29290.1.S1_at	PHACTR2	8.55E-18	4.37E-06	1.24	4.14	2.71	2.16	1.53	-1.03	1.06E-01	1.01	2.67	2.72	2.03	2.52	1.38	1.59E-02	2.61	1.66	1.34	1.29
MmugDNA.19.1.S1_at	SCIN	2.03E-09	0.00209	1.10	1.89	2.44	1.38	1.10	-1.02	4.42E-01	1.10	1.07	-1.01	1.00	1.04	1.10	4.21E-02	1.70	1.40	1.25	-1.01
MmugDNA.10692.1.S1_at	SCOTIN	6.72E-08	1.27E-05	1.14	2.33	2.29	1.31	1.23	1.16	4.78E-01	-1.07	1.37	1.42	1.47	1.35	1.12	4.84E-04	1.69	1.30	1.13	1.05
MmuSTS.2728.1.S1_at	GCN5L2	1.09E-03	7.17E-12	-1.14	2.72	3.01	-1.10	-1.08	-1.18	5.04E-03	1.08	2.60	3.66	1.31	1.22	1.06	1.43E-07	4.50	1.17	1.15	1.05
MmugDNA.36434.1.S1_at	GZMA	3.34E-11	9.48E-06	1.34	1.48	-1.75	6.15	1.70	1.00	1.99E-01	-1.84	-2.05	-1.02	2.29	-2.59	-2.22	3.58E-06	-1.06	12.81	2.54	2.55
MmugDNA.16397.1.S1_s_at	GRN	4.70E-04	0.000952	1.18	1.75	2.05	1.07	1.23	1.02	4.19E-01	-1.00	1.24	-1.03	1.00	-1.03	-1.09	4.27E-02	1.38	1.20	1.02	1.02
MmugDNA.30463.1.S1_at	NMI	8.88E-03	1.86E-07	1.25	3.04	2.69	1.81	1.28	-1.23	1.74E-01	1.01	1.85	1.93	1.74	1.94	1.39	2.92E-03	1.92	1.29	1.15	1.13
MmugDNA.5794.1.S1_at	MT2A	1.31E-08	0.000324	1.28	3.04	2.50	1.50	1.42	1.36	2.36E-01	-1.07	1.59	1.48	1.77	1.33	-1.07	5.03E-04	2.21	1.46	1.31	1.26
MmuSTS.2737.1.S1_at	ADAMDEC1	3.16E-06	2.11E-06	1.56	2.56	8.26	4.20	1.73	1.10	1.20E-01	-1.08	-1.04	-1.43	1.20	1.04	-1.02	1.51E-01	1.63	3.56	2.00	-1.00
MmugDNA.23544.1.S1_s_at	FCGR2C	7.85E-18	6.42E-11	1.26	3.29	5.35	1.53	1.40	-1.10	5.23E-01	-1.06	1.71	1.20	1.09	1.59	1.12	7.91E-02	1.22	-1.07	-1.23	1.18
MmugDNA.9213.1.S1_at	FLJ11286	8.97E-04	2.64E-06	-1.07	1.81	2.25	1.02	1.14	1.01	3.52E-03	-1.02	1.41	1.74	1.14	1.09	-1.12	1.09E-05	2.31	1.28	1.30	1.04
MmugDNA.27375.1.S1_at	PHACTR2	2.89E-03	3.44E-06	1.03	4.08	2.76	1.50	1.51	-1.03	5.02E-02	-1.19	2.23	2.21	1.05	1.74	-1.02	1.21E-02	2.52	1.51	1.18	1.13
MmuSTS.3006.1.S1_at	MX1	4.84E-05	8.61E-09	1.90	32.27	27.07	7.94	5.03	1.87	5.71E-04	1.17	8.31	7.84	5.59	5.67	1.62	8.90E-02	10.36	3.60	4.88	2.61
MmuSTS.4678.1.S1_at	TREX1	1.77E-03	7.39E-07	1.15	2.78	3.81	1.26	1.27	1.21	9.18E-02	-1.01	1.50	1.25	1.10	1.02	-1.20	3.70E-08	2.38	1.22	1.27	1.22
MmugDNA.6706.1.S1_at	CKAP2	1.17E-09	9.79E-06	1.22	1.13	-1.29	2.49	1.77	1.20	8.12E-04	-1.13	-1.01	-1.11	2.64	1.66	1.32	9.83E-06	-1.23	3.15	1.97	1.33
MmugDNA.36766.1.S1_at	TOR1B	5.59E-05	1.33E-05	1.33	2.77	2.44	1.42	1.19	1.03	3.60E-02	-1.10	1.71	2.35	1.66	1.34	1.08	2.64E-03	2.75	1.74	1.44	1.41
MmuSTS.4763.1.S1_at	FBXO6	2.82E-10	0.001061	1.13	1.75	2.09	1.32	1.10	1.04	2.55E-03	1.00	1.69	1.83	1.56	1.30	1.08	2.41E-04	2.97	2.24	1.57	1.28
MmugDNA.33861.1.S1_at	XAF1	3.70E-05	2.81E-07	1.13	7.59	6.70	3.24	1.97	1.08	4.42E-03	1.11	3.29	4.83	3.21	2.89	1.37	2.64E-02	5.13	2.40	2.84	1.89
MmuSTS.3639.1.S1_at	EXT1	3.21E-10	3.25E-05	1.22	2.01	2.85	1.39	1.30	1.17	3.23E-01	-1.00	1.11	1.17	1.04	-1.07	-1.17	5.32E-09	1.91	1.32	1.26	1.00
Mmu.11961.1.S1_x_at	GBP1	4.82E-13	0.000492	1.02	3.89	5.05	2.01	1.17	-1.29	1.26E-01	1.00	3.28	4.01	2.52	2.40	1.35	1.12E-02	4.74	1.58	2.05	1.74
MmugDNA.27150.1.S1_at	PATL1	1.26E-03	0.000442	-1.09	2.04	2.42	1.02	1.07	-1.04	3.86E-01	1.37	1.84	1.77	1.53	1.73	1.25	1.12E-04	2.18	1.26	1.21	1.09
MmugDNA.23750.1.S1_at	PARP11	9.22E-07	7.61E-06	1.32	2.42	2.12	1.52	1.16	1.19	1.96E-01	-1.07	1.61	2.43	1.78	1.52	1.17	3.23E-06	2.13	1.62	1.17	1.02
MmugDNA.31059.1.S1_at	PTTG1	5.14E-09	0.000101	1.22	1.05	1.09	2.82	1.95	1.43	2.06E-01	-1.16	-1.08	1.03	2.05	1.45	-1.05	6.32E-05	-1.13	2.24	1.30	1.26
MmuSTS.864.1.S1_at	LGALS8	3.68E-04	8.67E-08	-1.02	2.05	1.95	1.17	1.05	-1.04	4.07E-02	1.11	1.65	2.22	1.29	1.36	1.13	9.48E-04	2.56	1.26	1.55	1.25
MmugDNA.3485.1.S1_at	EPSTI1	1.21E-04	7.57E-07	1.27	4.30	3.26	2.06	1.61	1.18	9.35E-04	1.10	2.93	4.16	2.05	1.97	1.15	1.53E-04	4.32	1.67	1.83	1.42
MmugDNA.635.1.S1_at	TNFSF13B	2.16E-03	2.00E-07	1.35	3.42	2.44	1.98	1.31	-1.30	3.71E-03	-1.04	2.41	2.16	2.40	2.25	1.25	4.12E-02	1.94	1.41	1.34	1.24
MmugDNA.19768.1.S1_at	CENPM	2.46E-07	3.58E-05	-1.02	-1.30	-1.50	2.17	1.44	1.01	7.25E-02	1.09	1.10	-1.02	1.59	1.55	1.08	3.57E-04	-1.37	1.84	1.36	1.24
Mmu.11961.1.S1_at	GBP1	1.03E-04	0.000166	-1.15	1.86	2.71	1.01	-1.04	-1.03	4.11E-02	1.40	3.60	4.72	2.14	2.55	1.35	5.57E-04	4.94	1.33	1.96	1.73
MmugDNA.2761.1.S1_at	SP100	1.37E-02	3.15E-08	1.20	2.66	2.51	1.82	1.27	1.02	1.25E-02	1.05	1.89	2.24	1.84	1.85	1.20	8.00E-05	2.37	1.42	1.38	1.27
MmugDNA.22076.1.S1_at	MGC29506	9.81E-03	0.000237	-1.01	-1.05	1.01	5.43	2.50	1.00	3.44E-01	-1.20	-1.00	-1.23	1.09	1.65	-1.34	6.07E-03	-1.23	2.15	2.28	1.67
MmuSTS.1082.1.S1_at	PDE8B	2.63E-12	6.86E-07	1.33	4.02	4.00	2.52	1.78	1.22	1.95E-01	1.10	1.62	1.65	1.66	1.10	1.10	2.55E-02	2.09	1.33	1.65	1.21
MmugDNA.8112.1.S1_at	RNF213	4.90E-08	5.92E-07	1.37	5.13	4.99	2.29	1.68	1.14	1.81E-02	1.14	3.87	3.84	2.46	2.52	1.52	7.22E-02	3.76	1.82	2.05	1.67
MmugDNA.33090.1.S1_at	RNF213	3.40E-12	0.132418	1.10	1.61	2.57	1.22	1.29	1.12	4.84E-03	-1.16	2.59	2.57	1.42	1.92	-1.12	1.41E-01	2.11	1.37	1.26	1.27
MmugDNA.34622.1.S1_at	PARP9	1.39E-03	9.32E-09	1.41	5.39	4.16	2.30	1.74	1.16	3.35E-02	1.13	3.21	3.05	2.19	2.23	1.51	9.74E-03	3.15	1.60	1.60	1.56
Mmu.865.1.S1_at	OAS1	1.46E-12	5.58E-11	-1.05	4.98	7.91	1.80	1.34	1.04	4.21E-02	1.08	1.27	2.14	1.26	1.19	1.03	1.10E-09	5.10	1.60	1.80	1.15
MmugDNA.35036.1.S1_at	PHACTR2	1.89E-06	0.004201	1.07	3.66	1.79	1.50	1.33	-1.07	6.28E-01	-1.02	1.95	2.02	1.01	1.36	1.17	1.83E-02	2.48	1.73	1.27	1.24
MmugDNA.9803.1.S1_at	PML	1.12E-06	3.93E-06	1.33	4.21	3.67	1.80	1.47	1.21	8.52E-03	1.16	3.13	3.41	2.09	2.18	1.41	3.64E-04	3.44	1.40	1.59	1.36
MmugDNA.25634.1.S1_at	WARS	5.66E-17	0.000765	1.38	2.22	2.48	1.67	1.20	1.30	5.96E-01	1.24	1.46	1.08	1.21	1.12	1.17	4.02E-01	1.36	1.37	1.08	1.08
MmugDNA.41043.1.S1_at	NBN	1.74E-15	0.001005	-1.15	1.79	2.43	1.46	1.10	-1.87	8.14E-01	-1.19	1.29	1.46	1.47	1.49	-1.62	1.95E-05	2.11	-1.87	1.44	1.03
MmugDNA.6653.1.S1_at	TDRD7	1.38E-06	1.59E-06	1.25	2.67	2.21	1.46	1.26	1.15	1.13E-01	-1.05	1.72	1.69	1.43	1.35	1.01	4.33E-03	2.02	1.52	1.12	1.21

Supplementary Table S6. part 2 of 3.

		SM-SIVsmm								RM-SIVsmm							RM-SIVmac239				
Affymetrix Probeset ID	Corrected Gene Symbol	ANOVA p-value (Species/Time)	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	ANOVA (time) p-value	D3/D0	D7/D0	D10/D0	D14/D0	D30/D0	D180/D0	ANOVA (time) p-value	D10/D0	D14/D0	D30/D0	Chronic /D0
MmugDNA.22222.1.S1_s_at	NBN	2.18E-11	0.016709	-1.07	1.57	2.11	1.32	1.00	-1.41	7.41E-01	-1.24	1.12	1.23	1.30	1.29	-1.96	4.83E-06	1.89	-2.21	1.35	-1.00
MmugDNA.30433.1.S1_at	SHCBP1	1.43E-18	2.35E-07	1.00	-1.14	-1.05	5.10	1.82	1.08	4.52E-01	1.06	1.65	-1.18	-1.16	1.79	1.99	1.25E-05	-2.93	1.14	-1.53	-1.11
MmugDNA.39863.1.S1_at	C18ORF24	8.88E-03	0.007285	1.18	1.19	1.06	2.55	1.71	1.27	6.28E-03	-1.05	-1.19	1.04	2.21	1.36	-1.35	2.74E-03	1.27	3.73	2.48	1.75
Mmu.12633.1.S1_at	PARP14	2.41E-10	6.11E-08	1.38	5.86	5.36	2.52	1.56	1.04	1.25E-02	1.28	3.61	3.14	2.11	2.53	1.10	7.08E-03	3.37	1.23	1.56	1.60
MmugDNA.14075.1.S1_at	BUB1B	1.83E-03	3.01E-06	1.08	-1.00	-1.28	2.26	1.66	1.30	5.91E-03	1.04	-1.03	1.06	2.54	1.63	1.29	7.32E-04	-1.10	3.64	1.94	1.81
MmugDNA.1969.1.S1_at	MCM4	6.87E-05	0.011605	-1.03	-1.04	-1.24	2.01	1.44	1.00	1.22E-05	1.11	-1.07	1.06	2.64	1.36	1.15	7.37E-05	1.07	4.04	1.92	1.40
MmugDNA.28698.1.S1_at	SAMD9	1.16E-02	0.000162	1.19	2.26	2.01	1.73	1.12	-1.16	4.57E-02	-1.16	2.31	3.55	3.25	3.13	1.21	4.54E-03	3.28	1.52	1.80	1.32
MmugDNA.6512.1.S1_at	LOC26010	2.06E-08	9.66E-07	1.29	9.40	13.36	3.41	1.56	1.56	6.80E-03	-1.11	1.80	3.90	2.12	1.17	-1.10	2.36E-06	9.07	4.00	3.31	1.36
MmugDNA.32458.1.S1_at	NAGK	1.70E-14	0.000245	1.32	1.81	2.01	1.26	1.20	1.07	2.68E-02	1.13	2.06	1.93	1.39	1.54	1.25	4.57E-04	1.78	1.11	1.07	1.18
MmugDNA.28553.1.S1_at	PIK3AP1	7.02E-04	7.19E-06	1.02	2.26	2.40	-1.08	-1.01	-1.03	3.86E-01	-1.07	1.41	1.16	-1.10	1.13	1.01	1.92E-05	1.83	1.19	1.01	1.25
Mmu.10088.2.S1_at	MX2	1.22E-03	6.48E-07	1.32	11.46	9.28	2.83	2.10	1.24	5.73E-04	1.11	4.95	5.95	2.38	3.20	1.20	7.36E-03	7.94	1.98	2.98	2.18
MmugDNA.24210.1.S1_at	ATF6	1.01E-18	1.84E-05	1.22	2.61	2.58	1.30	1.16	-1.27	6.21E-01	1.02	1.44	1.17	1.25	1.40	1.46	1.52E-01	1.10	1.01	-1.18	-1.02
MmugDNA.22912.1.S1_s_at	GBP1	2.67E-18	4.24E-08	1.78	14.10	14.41	5.19	2.32	1.10	2.95E-01	1.06	4.51	2.96	2.63	3.61	1.31	1.22E-01	4.80	2.07	2.19	2.10
MmuSTS.1188.1.S1_at	PLSCR1	5.81E-12	1.30E-05	1.40	3.97	2.74	1.96	1.39	1.41	8.99E-02	-1.35	2.97	3.30	2.00	1.59	1.54	8.57E-02	4.71	2.95	2.04	1.76
Mmu.13018.2.S1_a_at	TRIM5	1.18E-04	3.36E-07	-1.04	2.65	4.98	1.25	1.25	-1.30	1.15E-01	1.12	2.36	1.85	1.65	2.13	1.18	1.79E-04	3.10	1.18	1.31	1.31
MmugDNA.27936.1.S1_s_at	CFLAR	6.22E-05	0.000138	-1.01	1.31	2.01	-1.04	1.04	-1.03	5.14E-01	-1.01	1.39	1.40	1.09	1.47	1.06	2.00E-02	1.77	1.42	1.20	1.08
MmugDNA.9266.1.S1_at	ECGF1	7.12E-11	0.000237	1.41	3.79	3.51	1.81	1.85	1.23	2.82E-03	1.14	2.19	1.99	1.96	1.45	-1.11	1.01E-02	3.16	2.45	2.11	1.36
MmugDNA.1987.1.S1_at	SLC2A5	5.66E-06	0.000246	1.13	1.89	2.36	1.71	1.22	1.09	1.84E-01	1.09	-1.00	-1.11	1.20	1.06	-1.10	6.61E-04	1.92	3.27	1.78	1.11
MmuSTS.4033.1.S1_at	TLR5	1.78E-09	0.00013	1.02	1.29	2.01	1.02	-1.11	-1.75	4.92E-01	-1.09	1.36	-1.10	1.06	1.23	1.20	1.05E-01	1.17	1.61	1.11	-1.05
MmugDNA.18451.1.S1_at	PRDX4	3.88E-16	0.000322	1.25	-1.09	-1.07	2.57	1.47	1.17	6.61E-01	-1.27	-1.30	1.01	1.14	-1.02	-1.41	1.34E-02	-1.09	1.44	1.30	1.27
Mmu.15443.1.S1_x_at	IGKV1-5	4.73E-08	0.040368	-1.31	1.02	-1.07	2.99	1.80	-1.17	2.63E-01	1.07	1.51	-1.21	1.41	1.92	1.15	3.29E-02	-1.07	1.74	1.60	2.03
MmuSTS.4666.1.S1_at	TNFSF10	2.15E-11	7.77E-07	1.17	4.21	3.92	1.50	-1.01	1.36	4.06E-01	-1.07	1.60	1.34	1.60	1.29	1.02	1.38E-05	2.55	1.28	1.06	-1.25
MmuSTS.2397.1.S1_s_at	GBP2	1.65E-03	2.63E-08	1.22	8.23	11.05	2.57	1.78	1.10	1.93E-01	1.22	2.59	3.22	1.62	2.20	1.45	6.32E-03	4.81	2.06	1.78	1.66
MmugDNA.2176.1.S1_at	ISG20	8.61E-06	8.12E-07	1.10	3.06	3.55	1.83	1.40	1.07	4.01E-02	-1.18	2.03	2.75	1.63	1.65	-1.05	1.70E-06	4.17	1.73	1.51	1.50
MmugDNA.13932.1.S1_at	RNF213	9.26E-08	1.54E-08	1.02	3.98	4.29	1.49	1.37	-1.11	9.91E-02	-1.00	1.56	1.55	1.27	1.34	1.03	1.13E-02	2.27	1.45	1.45	1.22
MmugDNA.22615.1.S1_s_at		5.19E-03	7.30E-08	1.08	2.08	2.40	-1.01	1.11	-1.05	1.41E-01	1.13	2.00	1.97	1.37	1.59	1.05	1.84E-04	2.38	1.01	1.18	1.19
MmugDNA.27612.1.S1_at	ANKMY2	2.41E-07	1.33E-05	1.17	2.14	1.69	1.52	1.05	-1.08	3.65E-01	-1.12	1.30	1.29	1.63	1.39	1.15	1.03E-02	1.39	1.28	1.02	1.14
MmugDNA.5879.1.S1_at	TNFRSF17	1.22E-02	3.09E-05	-1.20	-1.25	-1.48	3.81	1.76	-1.07	2.31E-01	1.04	1.02	1.38	1.72	1.95	-1.13	4.65E-02	1.04	2.02	2.61	1.42
MmugDNA.12648.1.S1_at	TRIM22	2.51E-19	1.39E-07	1.31	2.89	2.19	1.59	1.31	1.10	2.73E-01	1.02	1.88	1.75	1.74	1.74	1.48	4.55E-02	1.35	1.05	1.06	1.15
MmuSTS.1849.1.S1_at	DTX1	2.02E-05	2.41E-05	-1.00	1.79	2.33	2.95	1.37	1.20	2.36E-01	-1.11	1.09	1.41	1.67	1.46	-1.02	1.70E-01	2.23	2.16	1.83	1.44
MmugDNA.32729.1.S1_at	MKI67	8.08E-09	0.002639	1.38	1.25	-1.19	2.21	1.76	1.33	1.23E-04	1.14	1.01	-1.13	2.72	1.52	1.23	4.84E-06	-1.07	4.01	2.45	1.69
MmuSTS.4665.1.S1_s_at	FAS	6.75E-03	0.005132	1.34	2.17	1.51	1.60	1.11	1.07	6.05E-02	-1.30	1.53	1.96	1.67	1.86	1.21	1.21E-03	1.94	1.31	1.06	1.80
MmugDNA.25674.1.S1_at	KCTD14	5.05E-03	5.11E-09	1.22	5.12	10.29	2.53	1.40	1.34	2.66E-04	1.07	1.28	2.74	1.84	-1.13	-1.04	1.60E-04	6.83	5.45	2.19	1.20
MmugDNA.23497.1.S1_at	STAT1	5.54E-04	1.19E-06	1.39	3.49	4.02	2.05	1.64	1.20	9.64E-02	1.30	2.56	2.50	2.09	1.76	1.33	4.52E-02	2.84	1.65	1.58	1.41
MmugDNA.3158.1.S1_at	CCL8	2.12E-08	5.07E-06	-1.10	1.99	3.35	1.28	-1.10	-1.01	2.77E-05	1.08	1.19	2.17	1.00	1.07	1.05	2.36E-07	3.75	1.32	1.28	1.02
MmugDNA.13466.1.S1_at	ATF6	1.03E-15	0.000387	1.04	1.85	2.34	1.18	1.04	-1.24	3.26E-01	1.01	1.36	1.14	1.20	1.22	1.17	2.58E-03	1.53	1.12	1.09	1.05
MmugDNA.228.1.S1_at	C6ORF192	1.80E-04	4.70E-05	1.31	2.41	1.91	1.65	-1.00	-1.02	5.02E-02	-1.01	1.50	1.67	1.49	1.44	-1.06	5.23E-03	2.01	1.40	1.45	1.10
MmugDNA.12892.1.S1_at	IFI44	4.17E-05	1.93E-08	1.82	45.84	24.30	18.22	5.86	1.43	1.23E-02	1.27	11.45	14.61	13.25	11.49	2.22	2.97E-01	11.93	5.27	6.18	4.00
MmuSTS.1778.1.S1_at	SCIN	1.80E-04	1.70E-08	1.19	3.30	6.94	1.40	1.20	-1.12	4.20E-01	-1.02	1.21	1.05	-1.01	1.12	1.04	7.29E-03	4.02	4.29	1.67	1.04
MmugDNA.20995.1.S1_at	CCR1	5.65E-05	3.99E-05	1.14	2.36	2.29	1.32	-1.08	-1.31	3.55E-02	-1.01	2.47	1.85	1.95	1.72	1.47	6.61E-03	2.05	1.49	1.26	-1.09
MmugDNA.27315.1.S1_at	SAMD9	5.76E-04	1.88E-06	1.15	2.46	2.25	1.96	1.37	-1.33	1.17E-02	-1.04	2.52	4.17	2.86	3.08	1.40	4.65E-03	3.76	1.73	1.83	1.52
MmugDNA.21968.1.S1_at	LOC707687	6.57E-05	0.000235	1.12	2.10	2.22	1.55	1.33	1.03	9.43E-02	-1.22	1.32	1.55	1.17	1.19	-1.25	2.55E-03	2.35	1.49	1.34	1.18
MmugDNA.5663.1.S1_at	PLS3	1.17E-10	6.47E-06	1.26	-1.07	-1.06	3.90	-1.19	-1.18	9.56E-03	-1.12	-1.02	1.07	1.25	1.01	1.08	7.93E-05	-1.03	2.14	1.29	1.11
MmugDNA.42778.1.S1_at	PARP12	6.01E-03	2.84E-12	1.20	3.74	3.44	1.58	1.32	1.12	4.78E-04	1.08	2.65	3.53	1.69	1.86	1.41	1.27E-04	3.32	1.47	1.39	1.22
MmugDNA.22862.1.S1_at	PAQR8	2.50E-15	4.54E-07	1.03	2.05	1.55	1.07	1.02	1.04	4.17E-01	-1.04	1.01	1.06	-1.03	-1.09	-1.24	7.59E-03	1.28	-1.07	1.02	1.06
MmugDNA.13395.1.S1_at	IFI16	5.43E-10	0.00054	-1.32	2.75	3.33	1.75	1.44	-1.83	2.02E-01	-1.96	1.74	1.96	1.57	2.06	-1.65	2.30E-04	3.65	1.61	1.55	1.24
MmugDNA.15107.1.S1_at	ARG2	5.59E-03	0.002223	1.32	1.93	2.17	1.23	1.12	-1.57	2.76E-01	-1.02	1.24	-1.13	1.37	1.74	1.31	9.34E-02	1.27	1.77	-1.02	-1.03
MmugDNA.23281.1.S1_at	PELO	2.50E-03	0.002535	-1.10	-2.39	-2.72	-1.62	-1.70	-1.39	9.32E-01	-1.17	-1.08	1.01	1.14	-1.29	-1.16	1.17E-02	-2.40	-1.26	-2.36	-2.19
MmugDNA.6326.1.S1_at	SLFN5	1.72E-10	0.00041	-1.07	2.80	2.77	1.93	1.49	-1.61	2.17E-01	-1.53	1.63	1.96	1.39	1.07	-1.03	9.70E-05	2.40	1.78	1.25	1.08
MmugDNA.10888.1.S1_at	---	1.78E-03	0.00189	1.10	2.16	2.17	1.25	1.09	1.03	9.51E-01	1.04	1.07	1.03	1.05	-1.06	1.07	2.91E-02	1.18	1.00	1.32	-1.10
MmugDNA.22157.1.S1_at	PCGF5	4.12E-07	0.000394	-1.03	1.84	2.05	1.02	1.10	-1.11	4.26E-02	1.19	1.57	1.57	1.44	1.29	-1.10	9.87E-07	2.17	1.20	1.35	1.12
MmugDNA.24653.1.S1_at	HMMR	3.35E-03	4.11E-06	-1.07	-1.07	1.17	2.65	1.28	-1.05	1.84E-01	-1.12	-1.14	1.11	1.37	1.05	-1.00	3.17E-01	1.17	1.48	1.29	1.22
Mmu.10941.2.S1_at	LOC712466	6.73E-09	0.016853	1.54	2.15	1.86	1.47	1.13	1.07	6.06E-01	1.25	1.70	1.29	1.13	1.08	1.17	1.43E-01	1.34	1.28	-1.01	1.05
MmugDNA.36869.1.S1_at	DBF4B	6.91E-03	1.38E-06	1.02	2.87	2.09	1.35	1.04	1.01	8.47E-01	1.11	1.24	1.39	1.26	1.22	1.14	2.39E-01	1.40	1.38	-1.04	1.12
MmugDNA.43291.1.S1_at	OAS2	1.13E-02	9.79E-09	-1.03	2.62	3.90	1.22	-1.02	-1.05	2.10E-05	-1.00	3.07	6.54	1.79	1.81	1.22	2.74E-05	7.95	1.61	2.17	1.42
MmugDNA.41833.1.S1_at	BST2	3.29E-07	0.000273	1.18	3.21	3.50	2.22	1.43	-1.08	2.30E-01	-1.53	1.62	1.79	1.78	1.53	-1.19	4.17E-04	2.94	2.19	1.29	1.07

Supplementary Table S6. part 3 of 3.

Supplemental Table S7. Gene exrpression fold-changes in LNs at day 14 post-infection in SIVsmm-infected SMs and SIVmac239-infected RMs.

Fold changes at 14 dpi in SMs and RMs arranged by functional categories. Red indicates significantly increased expression, green significantly decreased expression, and black, not significantly altered in expression from base line by the criteria of ≥ 2-fold change or Wilcoxon signed-rank test, P < 0.05.

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Apoptosis	Anti-Apoptosis	2.5	2.1	BIRC5 (SURVIVIN)	Baculoviral IAP repeat-conta	MmuSTS.1955.1.S1_at
Apoptosis	Anti-Apoptosis	4.2	4.8	IFI-6-16	putative 6-16 protein	MmuSTS.4428.1.S1_at
Apoptosis	Anti-Apoptosis	3.6	4.1	PTTG1	Securin (Pituitary tumor-tran	MmugDNA.31059.1.S1_s_at
Apoptosis	Anti-Apoptosis	3.0	3.2	PTTG1	Securin (Pituitary tumor-tran	MmugDNA.31059.1.S1_at
Apoptosis	Anti-Apoptosis	2.3	3.3	**XAF1**	XIAP associated factor-1 iso	MmugDNA.33861.1.S1_at
Apoptosis	Anti-Apoptosis	1.3	2.1	**XAF1**	XIAP associated factor-1 iso	MmugDNA.32616.1.S1_at
Apoptosis	Anti-Apoptosis	1.1	2.4	CD5L	AIM (CD5L)	MmugDNA.36369.1.S1_at
Apoptosis	Anti-Apoptosis	-1.3	2.1	DDIT4		MmuSTS.813.1.S1_at
Apoptosis	Pro-apoptotic	1.1	6.8	H1d	Histone H1.2 (H1d)	MmugDNA.35559.1.S1_at
Apoptosis	Pro-apoptotic	2.1	2.8	ITGB3BP	NRIF3	MmugDNA.16765.1.S1_at
Apoptosis	Pro-apoptotic	1.3	2.3	LGALS3 (Galectin-3)	Galectin-3 (Galactose-speci	MmugDNA.32094.1.S1_at
Apoptosis	Pro-apoptotic	1.5	2.3	PERP	PERP, TP53 apoptosis effec	MmugDNA.13218.1.S1_at
Apoptosis	Pro-apoptotic	1.3	2.7	PERP	PERP, TP53 apoptosis effec	MmuSTS.1155.1.S1_at
Apoptosis	Pro-apoptotic	-1.1	2.2	PMAIP1	phorbol-12-myristate-13-ace	MmugDNA.28813.1.S1_at
Apoptosis	Pro-apoptotic	1.1	2.1	CRADD		MmuSTS.4151.1.S1_at
Apoptosis	Pro-apoptotic	2.3	2.0	CYCS	cytochrome c	MmugDNA.31771.1.S1_s_at
Apoptosis	Pro-apoptotic	2.4	2.4	CYCS	cytochrome c	Mmu.4398.1.S1_s_at
Apoptosis	Pro-apoptotic	2.3	2.3	CYCS	cytochrome c	MmugDNA.31771.1.S1_at
Apoptosis	Pro-apoptotic	2.3	1.4	BRI3BP	BRI3-binding protein	MmuSTS.560.1.S1_at
Apoptosis	Pro-apoptotic	2.0	1.9	IKIP	IKK interacting protein isofor	MmugDNA.13217.1.S1_at
Apoptosis	Pro-apoptotic	3.3	1.3	PACAP	Proapoptotic caspase adapt	MmugDNA.22076.1.S1_at
Apoptosis	Pro-apoptotic	2.9	1.4	PACAP	Proapoptotic caspase adapt	MmugDNA.12895.1.S1_s_at
Apoptosis	Pro-apoptotic	-3.6	-1.9	NR4A1	nuclear receptor subfamily 4	MmugDNA.18685.1.S1_at
Apoptosis	Pro-apoptotic	-2.2	-1.2	TIAM1	T-cell lymphoma invasion an	MmugDNA.20387.1.S1_at
Apoptosis	Pro-apoptotic	-2.2	-1.4	**TNFRSF25**	tumor necrosis factor recept	MmugDNA.10013.1.S1_s_at
Apoptosis	Pro-apoptotic	-2.1	-1.3	**TNFRSF25**	tumor necrosis factor recept	MmugDNA.5862.1.S1_s_at
B Cell Proliferation/Differentiation	Ig Related	4.5	-1.0	IGH chain complementarity	Ig heavy chain complementa	MmuAffx.225.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	2.6	1.4	LOC701504	Ig kappa chain V-III region H	MmugDNA.31268.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.3	1.7	LOC706650	Ig J chain	MmunewRS.816.1.S1_s_at
B Cell Proliferation/Differentiation	Ig Related	2.1	1.6	POU2AF1	---	MmugDNA.21562.1.S1_at
B Cell Proliferation/Differentiation		1.4	2.0	TNFSF13B	BAFF(TNFSF13B)	MmugDNA.31841.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.3	2.2	IGHV	Ig heavy chain V-III region V	Mmu.12915.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	4.1	-1.1	**Ig kappa chain V-II region**	Ig kappa chain V-II region R	Mmu.9614.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	5.4	1.7	**Ig kappa chain V-II region**	Ig kappa chain V-II region R	MmugDNA.3445.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	2.9	1.2	**Ig kappa chain V-II region**	Ig kappa chain V-II region R	MmugDNA.41808.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.8	1.5	IGHG1	Ig heavy chain V-I region HC	MmugDNA.15990.1.S1_s_at
B Cell Proliferation/Differentiation	Ig Related	3.8	1.3	IGKC	Ig rearranged light chain var	Mmu.2571.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	2.9	1.5	IGKC	Ig kappa chain V-I region W	MmugDNA.39296.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.3	-1.4	**IGKV**	---	MmugDNA.27721.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	2.6	1.1	**IGKV**	Immunoglobulin kappa light	MmugDNA.37783.1.S1_x_at
B Cell Proliferation/Differentiation	Ig Related	2.9	-1.1	IGKV1-5	Ig kappa chain V-I region HK	MmugDNA.27721.1.S1_x_at
B Cell Proliferation/Differentiation	Ig Related	2.2	1.1	IGKV1-5	Ig kappa chain V-I region HK	MmugDNA.16712.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	-2.4	2.3	**IGLC2**	Ig lambda chain V-I region B	MmugDNA.15988.1.S1_s_at
B Cell Proliferation/Differentiation	Ig Related	-1.0	3.8	**IGLC2**	Ig lambda chain V-I region B	MmugDNA.15791.1.S1_x_at
B Cell Proliferation/Differentiation	Ig Related	1.2	2.7	IGVL	Ig lambda chain V-III region	MmugDNA.29054.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	-1.0	2.6	IGHA1	IGHA1	MmugDNA.16283.1.S1_s_at
B Cell Proliferation/Differentiation	Ig Related	-1.5	-2.2	IGSF10	immunoglobulin superfamily	MmuSTS.91.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	1.3	-2.4	LOC390714		MmugDNA.16715.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	1.2	-2.5	LOC723533		Mmu.10484.2.S1_x_at
Chemokine Receptors and Ligands	SIV Coreceptor	1.4	3.7	**CCR5**	chemokine (C-C motif) recep	MmuSTS.1981.1.S1_at
Chemokine Receptors and Ligands	SIV Coreceptor	1.2	3.8	**CCR5**	chemokine (C-C motif) recep	Mmu.14249.1.S1_at
Chemokine Receptors and Ligands	SIV Coreceptor	1.9	2.7	CCR2	chemokine (C-C motif) recep	MmugDNA.36749.1.S1_at
Chemokine Receptors and Ligands	SIV Coreceptor	1.4	2.3	CX3CR1	chemokine (C-X3-C motif) re	MmugDNA.6875.1.S1_at
Chemokine Receptors and Ligands	SIV Coreceptor	1.1	2.2	CXCR6 (STRL33/Bonzo）	chemokine (C-X-C motif) rec	MmugDNA.34736.1.S1_at
Chemokine Receptors and Ligands	SIV Coreceptor	1.1	2.1	CXCR6 (STRL33/Bonzo）	chemokine (C-X-C motif) rec	MmuSTS.4018.1.S1_at
Chemokine Receptors and Ligands	SIV Coreceptor Ligand	1.2	5.8	**CCL3 (MIP-1-alpha)**	chemokine (C-C motif) ligan	Mmu.2053.1.S1_s_at
Chemokine Receptors and Ligands	SIV Coreceptor Ligand	1.1	3.1	**CCL3 (MIP-1-alpha)**	chemokine (C-C motif) ligan	MmuSTS.3571.1.S1_s_at
Chemokine Receptors and Ligands	SIV Coreceptor Ligand	1.4	3.5	CCL5 (RANTES)	chemokine (C-C motif) ligan	MmugDNA.43376.1.S1_s_at
Chemokine Receptors and Ligands	SIV Coreceptor Ligand	1.5	3.6	CCL5 (RANTES)	chemokine (C-C motif) ligan	Mmu.8608.1.S2_at
Chemokine Receptors and Ligands		1.5	2.5	CCL19 (MIP-3-beta）	CCL19	MmugDNA.8496.1.S1_at
Chemokine Receptors and Ligands		1.5	2.6	CCL25	Rab5ip	MmugDNA.33849.1.S1_at
Chemokine Receptors and Ligands		1.0	2.2	CCR9	CCR9	MmugDNA.17952.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Immune Defenses	IFN Related	1.7	3.3	OAS2	2-5-oligoadenylate syntheta	MmugDNA.43291.1.S1_at
Immune Defenses	IFN Related	2.4	2.5	OAS2	2-5-oligoadenylate syntheta	MmugDNA.8486.1.S1_at
Immune Defenses	IFN Related	3.9	4.3	MX1	myxovirus (influenza virus) r	MmuSTS.3006.1.S1_at
Immune Defenses	IFN Related	5.2	6.1	IFIT1 (IFI-56)	IFIT1	MmuSTS.1579.1.S1_at
Immune Defenses	IFN Related	2.5	4.2	**IFIT3 (IFI-60)**	interferon-induced protein w	MmugDNA.19594.1.S1_at
Immune Defenses	IFN Related	1.6	2.6	**IFIT3 (IFI-60)**	interferon-induced protein w	Mmu.3779.1.S1_at
Immune Defenses	IFN Related	2.6	3.5	IFIT4	interferon-induced protein w	MmugDNA.24962.1.S1_at
Immune Defenses	IFN Related	4.7	6.8	IFI-15K (ISG15)	interferon, alpha-inducible p	MmugDNA.17118.1.S1_at
Immune Defenses	IFN Related	2.0	3.9	IFI27	putative ISG12(c) protein	MmunewRS.254.1.S1_at
Immune Defenses	IFN Related	3.2	2.9	IFI44	interferon-induced, hepatitis	MmugDNA.12892.1.S1_at
Immune Defenses	IFN Related	3.1	2.8	IFI44	interferon-induced, hepatitis	MmuSTS.3682.1.S1_x_at
Immune Defenses	IFN Related	3.2	2.2	**GBP1**	guanylate binding protein 1,	MmugDNA.22912.1.S1_s_at
Immune Defenses	IFN Related	2.4	2.1	**GBP1**	guanylate binding protein 1,	Mmu.11961.1.S1_at
Immune Defenses	IFN Related	2.8	2.5	**GBP1**	guanylate binding protein 1,	MmugDNA.41315.1.S1_at
Immune Defenses	IFN Related	2.1	2.4	**GBP1**	guanylate binding protein 1,	Mmu.11960.1.S1_at
Immune Defenses	IFN Related	2.3	1.9	**GBP1**	guanylate binding protein 1,	Mmu.11961.1.S1_x_at
Immune Defenses	IFN Related	1.8	2.2	**GBP1**	guanylate binding protein 1,	Mmu.11960.1.S1_x_at
Immune Defenses	IFN Related	2.2	2.6	GBP2	guanylate binding protein 2,	MmuSTS.2397.1.S1_s_at
Immune Defenses	IFN Related	2.4	2.0	GBP2	guanylate binding protein 2,	MmugDNA.36433.1.S1_at
Immune Defenses	IFN Related	3.1	3.4	**RSAD2 (CIG5)**	radical S-adenosyl methioni	MmugDNA.41706.1.S1_at
Immune Defenses	IFN Related	2.1	5.3	**RSAD2 (CIG5)**	---	MmuSTS.1497.1.S1_at
Immune Defenses	IFN Related	1.8	3.6	IFIT2 (IFI-54)	interferon-induced protein w	MmugDNA.5747.1.S1_at
Immune Defenses	IFN Related	1.6	3.2	IFIT5	interferon-induced protein w	MmugDNA.7695.1.S1_at
Immune Defenses	IFN Related	1.1	3.7	IFIT5	interferon-induced protein w	MmuSTS.1580.1.S1_at
Immune Defenses	IFN Related	1.6	2.3	ISG20	ISG20	MmugDNA.2176.1.S1_at
Immune Defenses	IFN Related	1.6	2.6	MX2	myxovirus (influenza virus) r	MmuSTS.1927.1.S1_at
Immune Defenses	IFN Related	1.6	2.1	SP100	SP100	MmugDNA.2761.1.S1_at
Immune Defenses	Sentinel Molecules	1.5	4.2	**RIG-1 (DX58/RARRES3)**	retinoic acid receptor respor	MmugDNA.24353.1.S1_at
Immune Defenses	Sentinel Molecules	1.3	2.9	**RIG-1 (DX58/RARRES3)**	retinoic acid receptor respor	MmugDNA.22077.1.S1_at
Immune Defenses	Sentinel Molecules	1.5	2.3	**RIG-1 (DX58/RARRES3)**	retinoic acid receptor respor	MmugDNA.22278.1.S1_at
Immune Defenses	Sentinel Molecules	1.5	2.9	**RIG-1 (DX58/RARRES3)**	retinoic acid receptor respor	MmugDNA.11735.1.S1_at
Immune Defenses	Sentinel Molecules	1.1	2.7	**RIG-1 (DX58/RARRES3)**	TIG3	MmugDNA.8510.1.S1_s_at
Immune Defenses	Sentinel Molecules	1.8	2.3	MDA-5 (IFIHI)	MDA-5	MmugDNA.36297.1.S1_at
Immune Defenses	Sentinel Molecules	1.5	2.1	PKR (EIF2AK2)	PKR	MmugDNA.19136.1.S1_at
Immune Defenses	Sentinel Molecules	1.2	2.3	LY96	MD-2	MmugDNA.11614.1.S1_at
Immune Defenses	NK Cells	1.4	13.4	KLRC1 (NKG2A)	NKG2-B	Mmu.1906.10.S1_a_at
Immune Defenses	NK Cells	1.2	2.0	KLRC1 (NKG2A)		Mmu.1906.5.S1_s_at
Immune Defenses	NK Cells	2.4	-1.4	KLRC1 (NKG2A)	NKG2-A	MmuSTS.2945.1.S1_s_at
Immune Defenses	NK Cells	2.0	2.2	KLRC2 (NKG2-C)	killer cell lectin-like receptor	Mmu.1906.11.S1_a_at
Immune Defenses	NK Cells	1.7	2.3	**KLRD1(CD94)**	CD94	MmugDNA.32266.1.S1_at
Immune Defenses	NK Cells	1.5	3.2	**KLRD1(CD94)**	CD94	MmugDNA.9285.1.S1_at
Immune Defenses	NK Cells	1.5	2.3	**KLRD1(CD94)**	CD94	MmugDNA.17475.1.S1_s_at
Immune Defenses	NK Cells	1.4	2.1	KLRC3 (NKG2-E)		Mmu.1906.11.S1_x_at
Immune Defenses	NK Cells	1.6	2.8	KLRC3 (NKG2-E)		Mmu.1906.7.S1_at
Immune Defenses	NK Cells	-1.4	2.3	**HLA-E**	major histocompatibility com	MmunewRS.790.1.S1_x_at
Immune Defenses	NK Cells	-1.2	2.9	**HLA-E**	major histocompatibility com	MmunewRS.790.1.S1_at
Immune Defenses	Antiviral Proteins	2.1	2.0	TRIM25	Tripartite motif-containing 25	Mmu.8122.1.A1_at
Immune Defenses	Antiviral Proteins	2.2	1.2	PTX3	pentraxin-related gene, rapi	MmuSTS.3742.1.S1_at
Immune Defenses	Antiviral Proteins	1.2	3.1	APOBEC3G	apolipoprotein B mRNA edit	MmugDNA.33630.1.S1_at
Immune Defenses	Antiviral Proteins	1.4	2.1	APOBEC3H		MmunewRS.633.1.S1_s_at
Immune Defenses	Antiviral Proteins	1.5	2.4	ATG16L1	WDR30	MmugDNA.3016.1.S1_at
Immune Defenses	Antiviral Proteins	-1.4	-4.4	CLECSF14	C-type lectin, superfamily m	MmuSTS.1871.1.S1_at
Immune Defenses	C' and FcRs	3.0	2.4	FCGR3B (CD16b)	Fc fragment of IgG, low affir	MmugDNA.7038.1.S1_at
Immune Defenses	C' and FcRs	1.5	2.4	C3 precursor	No network object found	MmugDNA.18099.1.S1_at
Immune Defenses	C' and FcRs	1.3	2.5	CFB	C3bB *	MmugDNA.12153.1.S1_at
Immune Defenses	C' and FcRs	1.2	2.8	FCN1	ficolin (collagen fibrinogen d	MmugDNA.7797.1.S1_at
Immune Defenses	C' and FcRs	1.4	3.8	LOC698390	Ig lambda chain V-III region	MmugDNA.38781.1.S1_at
Immune Defenses	C' and FcRs	1.0	2.3	C4BPA	complement component 4 b	MmuSTS.3507.1.S1_at
Immune Defenses	C' and FcRs	3.6	1.7	LMAN1	lectin, mannose-binding, 1	Mmu.11962.1.S1_at
Immune Defenses	C' and FcRs	-1.4	-2.4	FCER1A	High affinity immunoglobulin	MmuSTS.4370.1.S1_at
Immune Defenses	C' and FcRs	-2.5	1.2	CFD	complement factor D prepro	Mmu.2136.1.S1_at
Immune Defenses	CD8 T cells, NK cells, and Cy	4.4	29.4	GZMA	Granzyme A precursor (Cyto	MmugDNA.36434.1.S1_at
Immune Defenses	CD8 T cells, NK cells, and Cy	2.3	5.7	GZMB	Granzyme B precursor (T-ce	MmugDNA.14204.1.S1_at
Immune Defenses	CD8 T cells, NK cells, and Cy	1.0	2.3	GZMK	Granzyme K	MmugDNA.17084.1.S1_at
Immune Defenses	CD8 T cells, NK cells, and Cy	1.9	3.1	GZMH	Granzyme H precursor (Cyto	MmugDNA.2086.1.S1_at
Immune Defenses	CD8 T cells, NK cells, and Cy	1.2	2.1	PRF1	perforin 1	MmugDNA.13673.1.S1_s_at
Immune Defenses	CD8 T cells, NK cells, and Cy	1.3	3.2	PRF1	perforin 1	MmugDNA.14985.1.S1_at
Immune Defenses	CD8 T cells, NK cells, and Cy	-1.1	2.1	PRG1	proteoglycan 1	MmugDNA.40727.1.S1_at
Immune Defenses	CD8 T cells, NK cells, and Cy	1.1	2.1	IBRDC3	IBR domain containing 3	MmugDNA.30847.1.S1_at
Immune Defenses	DCs and DC-SIGN Related	1.7	3.0	ADAMDEC1		MmuSTS.2737.1.S1_at
Immune Defenses	DCs and DC-SIGN Related	-1.6	-3.5	**CD209 (DC-SIGN/CLEC4L)**	CD209	MmuSTS.3353.1.S1_at
Immune Defenses	DCs and DC-SIGN Related	-1.5	-2.3	**CD209 (DC-SIGN/CLEC4L)**	CD209	MmugDNA.24821.1.S1_s_at
Immune Defenses	DCs and DC-SIGN Related	-1.8	-2.4	CD209L (CLEC4M)	DC-SIGNR	MmugDNA.36585.1.S1_at
Immune Defenses	DCs and DC-SIGN Related	-1.2	-2.3	CD209L2		Mmu.5240.1.S1_at
Immune Activation	Activation	2.8	3.4	CD38	CD38 antigen	MmuSTS.1849.1.S1_at
Immune Activation	Activation	2.6	2.1	**MKI67**	Antigen KI-67	MmugDNA.32726.1.S1_at
Immune Activation	Activation	2.1	3.7	**MKI67**	Antigen KI-67	MmugDNA.32729.1.S1_at
Immune Activation	Activation	2.6	2.9	PCNA	proliferating cell nuclear anti	MmugDNA.865.1.S1_at
Immune Activation	Activation	2.4	2.7	BAG2	BAG family molecular chap	MmuSTS.2142.1.S1_at
Immune Activation	Activation	2.8	2.7	CAF-1	Chromatin assembly factor 1	MmuSTS.673.1.S1_s_at
Immune Activation	Activation	2.1	2.4	FOXM1	forkhead box M1 isoform 3 (	MmugDNA.11364.1.S1_at
Immune Activation	Activation	3.1	4.3	HERC5	hect domain and RLD 5	MmugDNA.38910.1.S1_at
Immune Activation	Activation	4.6	3.5	PBK	T-LAK cell-originated protein	MmugDNA.33387.1.S1_at
Immune Activation	Activation	5.5	4.2	SHCBP1	SHC SH2-domain binding pr	MmugDNA.30433.1.S1_at
Immune Activation	Activation	2.3	2.1	TPX2	TPX2, microtubule-associate	MmuSTS.4420.1.S1_at
Immune Activation	Activation	2.0	2.3	TZFP	testis zinc finger protein	MmuSTS.2900.1.S1_at
Immune Activation	Activation	4.6	4.4	UHRF1	ubiquitin-like, containing PH	MmugDNA.19464.1.S1_at

Supplementary Table S7. part 2 of 13.

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Immune Activation	Activation	2.3	2.5	**RFC3**	replication factor C 3	MmugDNA.18123.1.S1_at
Immune Activation	Activation	2.2	2.0	**RFC3**	replication factor C 3	MmugDNA.24482.1.S1_at
Immune Activation	Activation	2.0	1.4	**SLC16A1 (MCT1)**	solute carrier family 16, mer	MmuSTS.3828.1.S1_at
Immune Activation	Activation	2.7	1.6	**SLC16A1 (MCT1)**	solute carrier family 16, mer	MmugDNA.21701.1.S1_at
Immune Activation	Activation	1.6	2.4	**HSPD1**	chaperonin /// 60 kDa heat s	MmugDNA.36856.1.S1_at
Immune Activation	Activation	2.1	2.0	**HSPD1**	heat shock 60kDa protein 1	MmugDNA.19456.1.S1_at
Immune Activation	Activation	3.0	3.4	HELLS	helicase, lymphoid-specific	MmuSTS.61.1.S1_at
Immune Activation	Activation	1.3	2.1	HELLS	HELLS (Lsh)	MmugDNA.25108.1.S1_at
Immune Activation	Activation	1.6	2.3	CALM3	Calmodulin *	MmugDNA.35002.1.S1_at
Immune Activation	Activation	1.4	3.3	GIG-1 (NKG7)	Protein NKG7 (Natural killer	MmugDNA.7157.1.S1_s_at
Immune Activation	Activation	1.2	2.1	TMEM189-UBE2V1	Kua-UEV	MmugDNA.9196.1.S1_at
Immune Activation	Activation	1.1	2.1	ADNP	ADNP	MmugDNA.42502.1.S1_at
Immune Activation	Activation	1.4	2.0	HRASLS2	HRAS-like suppressor 2	MmugDNA.30775.1.S1_at
Immune Activation	Activation	1.8	2.0	RAN	Ran	MmugDNA.3064.1.S1_at
Immune Activation	Activation	1.1	2.2	NR3C1	GCR-alpha	MmugDNA.1770.1.S1_at
Immune Activation	Activation	-1.2	-2.1	MAF	c-Maf	MmugDNA.38245.1.S1_at
Immune Activation	Activation	-1.7	-2.5	**TSPAN7**	tetraspanin 7	MmuSTS.4036.1.S1_at
Immune Activation	Activation	-2.1	-1.7	**TSPAN7**	tetraspanin 7	Mmu.11195.1.S1_at
Immune Activation	Activation	-2.2	-1.0	TCF7	transcription factor 7 (T-cell	MmugDNA.40627.1.S1_s_at
Immune Activation	Cell Cycle	1.9	3.0	**Anillin**	anillin, actin binding protein	MmugDNA.682.1.S1_at
Immune Activation	Cell Cycle	2.9	3.3	**Anillin**	anillin, actin binding protein	MmugDNA.2951.1.S1_at
Immune Activation	Cell Cycle	4.8	5.6	**Anillin**	anillin, actin binding protein	MmugDNA.2951.1.S1_s_at
Immune Activation	Cell Cycle	3.8	3.2	ASPM	asp (abnormal spindle)-like,	MmugDNA.5265.1.S1_at
Immune Activation	Cell cycle	3.2	4.6	ASPM	asp (abnormal spindle)-like,	MmugDNA.25197.1.S1_at
Immune Activation	Cell Cycle	3.5	3.3	**BUB1**	---	MmugDNA.14075.1.S1_at
Immune Activation	Cell Cycle	3.7	4.5	**BUB1**	BUB1 budding uninhibited b	MmugDNA.6277.1.S1_at
Immune Activation	Cell Cycle	5.7	5.8	**BUB1**	BUB1 budding uninhibited b	MmuSTS.2164.1.S1_at
Immune Activation	Cell Cycle	4.4	6.7	**BUB1**	BUB1 budding uninhibited b	MmuSTS.2164.1.S1_s_at
Immune Activation	Cell Cycle	2.5	3.4	CASC5	cancer susceptibility candida	MmugDNA.10186.1.S1_at
Immune Activation	Cell Cycle	4.5	5.7	**CDC2**	cell division cycle 2 protein	MmugDNA.14959.1.S1_at
Immune Activation	Cell Cycle	2.7	2.8	**CDC2**	cell division cycle 2 protein	MmugDNA.25206.1.S1_at
Immune Activation	Cell Cycle	3.9	5.3	**CDC2**	cell division cycle 2 protein	MmugDNA.42865.1.S1_at
Immune Activation	Cell Cycle	3.1	3.5	CDC20	cell division cycle 20	MmugDNA.18794.1.S1_at
Immune Activation	Cell Cycle	2.7	3.5	CDC25A	cell division cycle 25A isofor	MmugDNA.24430.1.S1_at
Immune Activation	Cell Cycle	2.5	2.4	CDC6	CDC6 homolog	MmuSTS.3380.1.S1_at
Immune Activation	Cell Cycle	3.6	1.8	CDC6	CDC6 homolog	MmugDNA.14956.1.S1_at
Immune Activation	Cell Cycle	3.6	4.6	CDCA1	cell division cycle associated	MmugDNA.2768.1.S1_at
Immune Activation	Cell Cycle	2.1	3.5	CDCA5	cell division cycle associated	MmugDNA.4124.1.S1_at
Immune Activation	Cell Cycle	2.7	2.9	CDCA7	cell division cycle associated	MmugDNA.17329.1.S1_at
Immune Activation	Cell Cycle	3.3	4.6	**CDKN3**	cyclin-dependent kinase inh	MmugDNA.10778.1.S1_at
Immune Activation	Cell Cycle	5.3	4.6	**CDKN3**	cytoskeleton associated pro	MmugDNA.6706.1.S1_at
Immune Activation	Cell Cycle	5.0	4.5	CENPA	centromere protein A	MmugDNA.15250.1.S1_at
Immune Activation	Cell Cycle	1.8	2.4	CENPA	Centromere protein A (CEN	MmugDNA.23496.1.S1_at
Immune Activation	Cell Cycle	2.4	3.1	CENPF	centromere protein F (350/4	MmuSTS.2672.1.S1_at
Immune Activation	Cell Cycle	4.3	5.5	CEP55	centrosomal protein 55kDa	MmugDNA.5873.1.S1_at
Immune Activation	Cell Cycle	2.7	3.4	CHEK1	CHK1 checkpoint homolog	MmugDNA.15754.1.S1_at
Immune Activation	Cell Cycle	2.2	2.4	CKS1B	Cyclin-dependent kinases re	MmugDNA.15861.1.S1_s_at
Immune Activation	Cell Cycle	4.3	4.6	CKS2	CDC28 protein kinase 2	MmugDNA.15862.1.S1_at
Immune Activation	Cell Cycle	4.2	3.8	**Cyclin A (CCNA2)**	cyclin A	MmuSTS.3576.1.S1_at
Immune Activation	Cell Cycle	2.2	2.9	**Cyclin A (CCNA2)**	cyclin A	MmugDNA.23764.1.S1_at
Immune Activation	Cell Cycle	3.5	3.6	Cyclin B1 (CCNB1)	cyclin B1	MmuSTS.3318.1.S1_at
Immune Activation	Cell Cycle	5.4	4.8	Cyclin B1 (CCNB1)	cyclin B1	MmugDNA.41268.1.S1_at
Immune Activation	Cell Cycle	4.0	5.6	Cyclin B2 (CCNB2)	cyclin B2	MmugDNA.40742.1.S1_at
Immune Activation	Cell Cycle	2.4	2.8	cyclin D2 (CCND2)	G1/S-specific cyclin-D2	MmugDNA.18851.1.S1_at
Immune Activation	Cell Cycle	2.8	2.6	Cyclin E1 (CCNE1)	cyclin E1 isoform 1	MmugDNA.4085.1.S1_at
Immune Activation	Cell Cycle	4.0	4.6	Cyclin E2 (CCNE2)	cyclin E2 isoform 1	MmuSTS.3320.1.S1_at
Immune Activation	Cell Cycle	3.1	3.2	**DTL**	RA-regulated nuclear matrix	MmuSTS.1283.1.S1_at
Immune Activation	Cell Cycle	1.9	2.0	**DTL**	DTL (hCdt2)	MmugDNA.29544.1.S1_at
Immune Activation	Cell Cycle	3.2	3.0	E2F7	E2F transcription factor 7	MmuSTS.2700.1.S1_at
Immune Activation	Cell Cycle	2.7	3.9	ECT2	epithelial cell transforming s	MmugDNA.5165.1.S1_at
Immune Activation	Cell Cycle	2.1	2.5	FBXO5	F-box only protein 5	MmugDNA.42135.1.S1_at
Immune Activation	Cell Cycle	2.1	2.5	FBXO5	F-box only protein 5	MmuSTS.4762.1.S1_at
Immune Activation	Cell Cycle	3.6	3.5	GMNN	geminin, DNA replication inh	MmuSTS.64.1.S1_at
Immune Activation	Cell Cycle	3.1	2.7	**GTSE1**	G-2 and S-phase expressed	MmugDNA.9770.1.S1_at
Immune Activation	Cell Cycle	3.0	3.3	**GTSE1**	G-2 and S-phase expressed	MmugDNA.33793.1.S1_at
Immune Activation	Cell Cycle	2.1	3.2	**GTSE1**	G-2 and S-phase expressed	MmugDNA.36210.1.S1_at
Immune Activation	Cell Cycle	1.9	2.1	**GTSE1**	GTSE1	MmugDNA.33793.1.S1_s_at
Immune Activation	Cell Cycle	3.9	2.5	HMMR (CD168)	hyaluronan-mediated motility	MmugDNA.24653.1.S1_at
Immune Activation	Cell Cycle	4.2	3.7	HMMR (CD168)	hyaluronan-mediated motility	MmugDNA.32449.1.S1_at
Immune Activation	Cell Cycle	2.1	2.0	HMMR (CD168)	hyaluronan-mediated motility	MmugDNA.32449.1.S1_s_at
Immune Activation	Cell Cycle	2.0	1.7	GSPT1	G1 to S phase transition 1	MmuSTS.225.1.S1_at
Immune Activation	Cell Cycle	2.2	1.8	INCENP	INCENP (Inner centromere	MmugDNA.39805.1.S1_at
Immune Activation	Cell Cycle	3.6	4.7	KIF11	kinesin family member 10	MmugDNA.13565.1.S1_at
Immune Activation	Cell Cycle	3.7	6.5	KIF14	kinesin family member 14	MmugDNA.35622.1.S1_at
Immune Activation	Cell Cycle	2.2	2.7	KIF18A	kinesin family member 18A	MmugDNA.32413.1.S1_at
Immune Activation	Cell Cycle	3.6	4.1	KIF23	kinesin family member 22	MmugDNA.13584.1.S1_at
Immune Activation	Cell Cycle	2.2	2.4	KIF2C	kinesin family member 2C	MmuSTS.1535.1.S1_at
Immune Activation	Cell Cycle	1.8	2.1	KIF4A	KIF4A	MmugDNA.21462.1.S1_at
Immune Activation	Cell Cycle	2.4	2.6	KIFC1	kinesin family member C1	MmugDNA.9497.1.S1_at
Immune Activation	Cell Cycle	2.6	4.7	KNSL7	kinesin family member 15	MmugDNA.15585.1.S1_at
Immune Activation	Cell Cycle	3.7	4.2	LOC696772	discs large homolog 7	MmuSTS.2303.1.S1_s_at
Immune Activation	Cell Cycle	3.2	4.8	MAD2A	Mitotic spindle assembly ch	MmuSTS.4157.1.S1_at
Immune Activation	Cell Cycle	2.6	3.7	MAD2L1	Mitotic spindle assembly che	MmugDNA.17868.1.S1_at
Immune Activation	Cell Cycle	2.3	2.3	MCM2	minichromosome maintenai	MmuSTS.144.1.S1_at
Immune Activation	Cell Cycle	2.4	3.5	MCM3	minichromosome maintenar	MmugDNA.25436.1.S1_at
Immune Activation	Cell Cycle	2.9	3.2	MCM6	minichromosome maintenar	MmugDNA.35654.1.S1_at
Immune Activation	Cell cycle	4.2	3.9	MELK	maternal embryonic leucine	MmuSTS.1558.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Immune Activation	Cell Cycle	3.0	3.7	MLF1IP	MLF1 interacting protein	MmugDNA.11747.1.S1_at
Immune Activation	Cell Cycle	2.5	1.6	MYBL2	MYB-related protein B	MmugDNA.41887.1.S1_at
Immune Activation	Cell Cycle	3.0	3.3	NDC80	kinetochore associated 2	MmugDNA.36470.1.S1_at
Immune Activation	Cell Cycle	4.2	4.2	NEK2	NIMA (never in mitosis gene	MmuSTS.1779.1.S1_at
Immune Activation	Cell Cycle	3.6	5.2	NUSAP1	nucleolar and spindle assoc	MmugDNA.38956.1.S1_at
Immune Activation	Cell cycle	3.6	6.9	OIP5	Opa-interacting protein 5	MmuSTS.3327.1.S1_at
Immune Activation	Cell Cycle	2.6	2.3	PLK1	polo-like kinase	MmuSTS.2029.1.S1_at
Immune Activation	Cell Cycle	2.7	2.1	RACGAP1	MmuSTS.2069.1.S1_at	MmuSTS.2069.1.S1_at
Immune Activation	Cell Cycle	2.7	5.4	**SGOL2**	shugoshin-like 2	MmugDNA.3428.1.S1_at
Immune Activation	Cell Cycle	2.8	5.3	**SGOL2**	shugoshin-like 2	MmugDNA.43348.1.S1_at
Immune Activation	Cell Cycle	2.5	3.1	SMC2L1	structural maintenance of ch	MmugDNA.18586.1.S1_at
Immune Activation	Cell Cycle	1.7	3.1	SMC2L1	structural maintenance of ch	MmugDNA.25187.1.S1_at
Immune Activation	Cell Cycle	2.1	1.9	**SMC4L1**	SMC4 structural maintenanc	MmugDNA.31959.1.S1_at
Immune Activation	Cell Cycle	2.0	2.0	**SMC4L1**	SMC4 structural maintenanc	MmugDNA.29900.1.S1_s_at
Immune Activation	Cell Cycle	2.4	3.0	SPAG5	sperm associated antigen 5	MmugDNA.19272.1.S1_s_at
Immune Activation	Cell Cycle	2.8	3.8	SPC25	spindle pole body componen	MmugDNA.20397.1.S1_at
Immune Activation	Cell Cycle	2.4	2.5	STIL	SCL/TAL1 interrupting locus	MmuSTS.220.1.S1_at
Immune Activation	Cell Cycle	2.1	2.9	TIPIN	timeless-interacting protein	MmugDNA.30164.1.S1_at
Immune Activation	Cell Cycle	3.9	5.2	UBE2C	Ubiquitin-conjugating enzym	MmugDNA.25384.1.S1_at
Immune Activation	Cell Cycle	2.0	2.6	WEE1	Wee1-like protein kinase (W	MmugDNA.3114.1.S1_at
Immune Activation	Cell Cycle	3.0	4.2	ZWINT	ZW10 interactor (ZW10-inte	MmugDNA.2694.1.S1_at
Immune Activation	Cell Cycle	2.4	3.6	**TFDP1 (DP1)**	transcription factor Dp-0	MmugDNA.14322.1.S1_at
Immune Activation	Cell Cycle	1.6	2.3	**TFDP1 (DP1)**	transcription factor Dp-1	MmuSTS.1343.1.S1_at
Immune Activation	Cell Cycle	2.1	2.4	MCM7	minichromosome maintenan	MmugDNA.30376.1.S1_at
Immune Activation	Cell Cycle	1.4	2.0	MCM7	MCM4/6/7 complex *	MmugDNA.34591.1.S1_s_at
Immune Activation	Cell Cycle	1.7	2.5	**STK6**	serine/threonine protein kina	MmugDNA.3562.1.S1_at
Immune Activation	Cell Cycle	1.8	3.1	**STK6**	serine/threonine protein kina	MmugDNA.3558.1.S1_at
Immune Activation	Cell Cycle	2.0	2.5	ZWILCH	Zwilch	MmugDNA.3020.1.S1_at
Immune Activation	Cell Cycle	1.5	2.0	SLBP	SLBP	MmugDNA.14893.1.S1_at
Immune Activation	Cell Cycle	1.8	2.1	MCTS1	MCT-1	MmugDNA.11610.1.S1_at
Immune Activation	Cell Cycle	-1.0	2.3	MAPK1	ERK1/2 *	MmugDNA.17107.1.S1_at
Immune Activation	Cell Cycle	1.8	3.0	**MCM10**	minichromosome maintenan	MmugDNA.8836.1.S1_at
Immune Activation	Cell Cycle	1.6	2.3	**MCM10**	MCM10	MmugDNA.7717.1.S1_at
Immune Activation	Cell Cycle	1.9	2.4	MCM4	MCM4	MmugDNA.26947.1.S1_at
Immune Activation	Cell Cycle	1.6	2.3	MCM5		MmuSTS.3146.1.S1_s_at
Immune Activation	Cell Cycle	1.5	2.6	PLK4	STK18	MmugDNA.38024.1.S1_at
Immune Activation	Cell Cycle	2.0	2.1	PRC1	PRC1	MmugDNA.21515.1.S1_at
Immune Activation	Cell Cycle	1.1	2.1	**RAD50**	MRN complex *	MmugDNA.2663.1.S1_at
Immune Activation	Cell Cycle	1.3	2.1	**RAD50**	MRN complex *	MmugDNA.21968.1.S1_at
Immune Activation	Cell Cycle	1.1	2.0	RBL1	p107	MmugDNA.19044.1.S1_s_at
Immune Activation	Cell Cycle	-1.1	2.1	S100A4	MTS1 (S100A4)	MmugDNA.17365.1.S1_at
Immune Activation	Cell Cycle	1.4	2.1	SASS6	SASS6	MmugDNA.1933.1.S1_at
Immune Activation	Cell Cycle	1.6	2.2	BCCIP	BCCIP	MmugDNA.5109.1.S1_at
Immune Activation	Cell Cycle	1.6	2.0	BRCA2	breast cancer 2, early onset	MmugDNA.41929.1.S1_at
Immune Activation	Cell Cycle	1.6	2.6	BRIP1	BRCA1 interacting protein C	MmugDNA.15158.1.S1_at
Immune Activation	Cell Cycle	2.0	2.1	**CDCA2**	CDCA2	MmugDNA.24523.1.S1_at
Immune Activation	Cell Cycle	2.0	2.1	**CDCA2**	CDCA2	MmugDNA.24523.1.S1_at
Immune Activation	Cell Cycle	1.8	2.3	CDCA3	Tome-1	MmugDNA.21403.1.S1_at
Immune Activation	Cell Cycle	1.8	2.3	CDCA3	Tome-1	MmugDNA.21403.1.S1_at
Immune Activation	Cell Cycle	2.1	3.3	**CDKN3**	cyclin-dependent kinase inh	MmugDNA.34975.1.S1_s_at
Immune Activation	Cell Cycle	1.1	2.5	CDT1	Cdt1	MmugDNA.7866.1.S1_at
Immune Activation	Cell Cycle	1.1	2.5	CDT1	Cdt1	MmugDNA.7866.1.S1_at
Immune Activation	Cell Cycle	1.9	2.1	**CENPJ**	CENPJ	MmugDNA.17253.1.S1_at
Immune Activation	Cell Cycle	1.9	2.1	**CENPJ**	CENPJ	MmugDNA.17253.1.S1_at
Immune Activation	Cell Cycle	2.0	2.5	CENPM	CENPM	MmugDNA.19768.1.S1_at
Immune Activation	Cell Cycle	2.0	2.5	CENPM	CENPM	MmugDNA.19768.1.S1_at
Immune Activation	Cell Cycle	1.7	2.4	**CENPQ**	Cenpq	MmugDNA.5876.1.S1_at
Immune Activation	Cell Cycle	1.7	2.4	**CENPQ**	Cenpq	MmugDNA.5876.1.S1_at
Immune Activation	Cell Cycle	1.1	2.1	CUL3	Cul3/KEAP1/Rbx1 E3 ligase	MmugDNA.23767.1.S1_at
Immune Activation	Cell Cycle	1.2	2.2	DCTN3	DCTN3	MmugDNA.14686.1.S1_s_at
Immune Activation	Cell Cycle	-1.4	2.0	DOCK11	DOCK11	MmugDNA.10303.1.S1_at
Immune Activation	Cell Cycle	1.4	2.1	ERH	ERH	MmugDNA.26837.1.S1_at
Immune Activation	Cell Cycle	1.5	2.6	ESCO2	establishment of cohesion 1	MmugDNA.10011.1.S1_at
Immune Activation	Cytokine and Cytokine Rece	2.2	2.4	TFEC	TFEC	MmugDNA.17449.1.S1_at
Immune Activation	Cytokine and Cytokine Rece	2.1	3.3	**HMGB3**	high-mobility group box 3	MmuSTS.236.1.S1_at
Immune Activation	Cytokine and Cytokine Rece	1.8	3.0	**HMGB3**	high-mobility group box 2	MmugDNA.12988.1.S1_s_at
Immune Activation	Cytokine and Cytokine Rece	-1.0	2.5	GREM1	Gremlin	MmugDNA.11761.1.S1_at
Immune Activation	Cytokine and Cytokine Rece	-1.0	4.0	GREM1	Gremlin	MmugDNA.42270.1.S1_at
Immune Activation	Cytokine and Cytokine Rece	-1.1	2.3	HNRNPM	hnRNP M	MmugDNA.15407.1.S1_at
Immune Activation	Cytokine and Cytokine Rece	1.3	2.2	NEDD4L	NEDD4L	MmugDNA.36137.1.S1_at
Immune Activation	Cytokine and Cytokine Rece	-2.0	-1.3	IL7R (CD127)	interleukin 7 receptor	MmugDNA.8010.1.S1_at
Immune Activation	Cytokine and Cytokine Rece	-1.4	-2.8	LIFR	Leukemia inhibitory factor re	MmugDNA.14420.1.S1_at
Immune Activation	TCR Signaling	1.5	2.0	NCBP2	CBP20	MmugDNA.32753.1.S1_s_at
Immune Activation	TCR Signaling	-1.1	2.5	NCK1	NCK1	MmugDNA.36871.1.S1_at
Immune Activation	TCR Signaling	-1.2	3.1	Beta-2-microglobulin	---	MmugDNA.26370.1.S1_at
Immune Activation	TCR Signaling	-2.5	4.4	Class I	Probe Set ID	MmugDNA.2178.1.S1_s_at
Immune Activation	TCR signaling	1.7	2.1	SHB	SHB	MmugDNA.11618.1.S1_at
Immune Activation	TCR signaling	-1.5	2.2	TCR beta chain CTL-L17 precursor		Mmu.4117.1.S1_at
Immune Activation	TCR Signaling	1.2	2.1	LY6E	TSA-1	MmugDNA.40394.1.S1_at
Immune Activation	TCR Signaling	-2.0	2.0	TCR beta chain C region	T-cell receptor beta chain C	Mmu.126.1.S1_a_at
Immune Activation	TCR Signaling	-2.1	1.5	TCR alpha chain C region	T-cell receptor alpha chain C	MmugDNA.19732.1.S1_s_at
Immune Activation	TCR Signaling	-2.4	1.2	TCR rearranged beta-chain V,D	T-cell receptor rearranged b	Mmu.11421.1.S1_a_at
Immune Activation	TCR Signaling	-2.2	1.1	**LEF1**	lymphoid enhancer binding f	Mmu.4923.1.S1_at
Immune Activation	TCR Signaling	-2.2	1.1	**LEF1**	lymphoid enhancer binding f	MmuSTS.1438.1.S1_at
Immune Activation	TCR Signaling	-2.2	-1.2	**LEF1**	lymphoid enhancer binding f	MmugDNA.32273.1.S1_at
Immune Activation	Transcriptinal Regulators	2.1	1.9	BARD1	BRCA1 associated RING dc	MmuSTS.549.1.S1_at
Immune Activation	Transcriptinal Regulators	1.0	2.4	ITCH	itchy homolog E3 ubiquitin p	MmugDNA.17916.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Immune Activation	Transcriptinal Regulators	1.9	2.5	E2F2	E2F transcription factor 2	MmugDNA.8851.1.S1_at
Immune Activation	Transcriptinal Regulators	1.8	2.6	TBX21	T-box 21	MmuSTS.4557.1.S1_at
Immune Activation	Transcriptinal Regulators	1.7	2.2	NMI	NMI	MmugDNA.30463.1.S1_at
Immune Activation	Transcriptinal Regulators	5.2	4.7	LOC715235	chromosome condensation	MmugDNA.11557.1.S1_at
Immune Activation	Transcriptinal Regulators	-1.6	-2.2	**DAB2**	disabled homolog 2	MmugDNA.16818.1.S1_at
Immune Activation	Transcriptinal Regulators	-1.3	-2.1	**DAB2**	disabled homolog 2	MmugDNA.36232.1.S1_at
Immune Activation	Transcriptinal Regulators	-1.1	-2.0	LITAF	LITAF	MmugDNA.5336.1.S1_at
Moderators of Activation & Inflammation		1.1	-2.1	SELE (CD62E)	E-selectin	MmugDNA.27403.1.S1_at
Suppressor of Immune Activation		-1.1	2.1	**CASP12**		Mmu.3474.1.S1_at
Suppressor of Immune Activation		1.0	2.2	**CASP12**	Caspase-12	MmugDNA.424.1.S1_at
Suppressor of Immune Activation		1.6	2.0	CREM	CREM (activators)	MmugDNA.9912.1.S1_at
Suppressor of Immune Activation		1.2	2.4	EHF	ESE3	MmugDNA.17230.1.S1_at
Suppressor of Immune Activation		1.9	2.6	IDO	indoleamine-pyrrole 2,3 diox	MmugDNA.18432.1.S1_at
Suppressor of Immune Activation		1.8	2.1	KYNU	KYNU	MmugDNA.22506.1.S1_s_at
Suppressor of Immune Activation		1.8	2.2	PRDM1	BLIMP1 (PRDI-BF1)	MmugDNA.39211.1.S1_at
Suppressor of Immune Activation		1.6	2.6	SAP	signaling lymphocyte activat	MmugDNA.13157.1.S1_s_at
Suppressor of Immune Activation		-1.1	2.1	TANK	TRAF family member-assoc	MmugDNA.6841.1.S1_at
Suppressor of Immune Activation		1.2	-2.8	CD33	CD33 antigen (gp67)	MmuSTS.1424.1.S1_at
Suppressor of Immune Activation		1.1	-2.1	SSX2	SSX2	MmugDNA.5682.1.S1_x_at
Suppressor of Immune Activation		1.1	-2.2	SSX4	SSX4 *	MmugDNA.7773.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		4.0	2.8	**TNFRSF17 (CD269)**	Tumor necrosis factor recep	MmugDNA.5879.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		4.0	2.8	**TNFRSF17 (CD269)**	Tumor necrosis factor recep	MmugDNA.5879.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		4.1	5.3	E2F8	E2F family member 7	MmugDNA.12490.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		2.5	3.2	PPIL5	peptidylprolyl isomerase (cy	MmugDNA.20073.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		1.9	2.1	KMO	KMO	MmugDNA.25657.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		1.6	2.3	**TMPO (LAP2)**	TMPOA	MmugDNA.3904.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		1.9	2.1	**TMPO (LAP2)**	TMPOA	MmugDNA.41740.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		3.0	1.5	TXNDC5	Thioredoxin domain-contain	MmugDNA.2427.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		-2.2	1.3	CD40LG (CD154)	CD40 ligand (TNF superfam	MmuSTS.4670.1.S1_s_at
Moderators of Activation & Inflammation (Antioxidants)		-2.3	1.5	CD40LG (CD154)	CD40 ligand (TNF superfam	Mmu.4194.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		-2.1	-3.1	TIMD4	T-cell immunoglobulin and m	MmugDNA.1353.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		-2.6	1.1	DGKA	diacylglycerol kinase, alpha	MmugDNA.1751.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		-2.1	1.2	TSC22	transforming growth factor b	MmuSTS.4615.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		-2.3	-1.9	**TXNIP**	thioredoxin interacting prote	MmugDNA.31894.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		-2.2	-1.1	**TXNIP**	thioredoxin interacting prote	Mmu.7507.2.S1_at
Moderators of Activation & Inflammation (Antioxidants)		-2.6	-1.3	**TXNIP**	thioredoxin interacting prote	MmugDNA.31894.1.S1_s_at
lymphatic vascular system		1.3	2.1	GCH1	GCH1	MmugDNA.41339.1.S1_at
lymphatic vascular system		-1.3	3.2	GUCY1A3	GUCY1A3	MmugDNA.10437.1.S1_at
lymphatic vascular system		1.9	2.0	HPSE	Heparanase 1	MmugDNA.14910.1.S1_at
lymphocyte homing		-1.2	2.3	ITGA4 (CD49D)	integrin, alpha 4 (antigen CD	MmugDNA.24387.1.S1_at
lymphocyte homing		-1.2	2.9	ITGA4 (CD49D)	integrin, alpha 4 (antigen CD	MmuSTS.717.1.S1_at
Metabolism	Cystein Proteinase	-1.1	2.4	CST6	Cystatin E/M	MmugDNA.35447.1.S1_at
Metabolism	Cystein Proteinase	1.2	2.1	CST7	Cystatin F	MmugDNA.6381.1.S1_at
Metabolism	Cystein Proteinase	1.2	2.2	CSTA	Cystatin A	MmugDNA.30019.1.S1_at
Metabolism	Cystein Proteinase	1.0	2.3	CTSL2		MmuSTS.4178.1.S1_at
Metabolism	Lipids & Glucose	2.0	2.1	FH	fumarate hydratase	MmuSTS.2656.1.S1_at
Metabolism	Lipids & Glucose	1.2	2.1	CMAS	cytidine monophosphate N-a	Mmu.5431.1.S1_at
Metabolism	Lipids & Glucose	1.7	2.0	PPP1R14B	PHI-1	MmugDNA.1433.1.S1_s_at
Metabolism	Lipids & Glucose	-1.0	2.3	GALNT3	GALNT3	MmugDNA.32216.1.S1_at
Metabolism	Lipids & Glucose	1.3	2.2	**GAPDH**		AFFX-Mmu-gapdh-5_at
Metabolism	Lipids & Glucose	1.4	2.1	**GAPDH**		AFFX-Mmu-gapdh-M_x_at
Metabolism	Lipids & Glucose	1.7	2.2	**GAPDH**	G3P1	MmugDNA.34587.1.S1_s_at
Metabolism	Lipids & Glucose	1.0	2.6	**PCK1**		MmunewRS.324.1.S1_at
Metabolism	Lipids & Glucose	-1.0	4.2	**PCK1**		MmuSTS.1126.1.S1_at
Metabolism	Lipids & Glucose	-1.1	2.0	UXS1	UXS1	MmugDNA.31644.1.S1_at
Metabolism	Lipids & Glucose	1.0	2.4	LOC706406	aldo-keto reductase family 1	Mmu.15276.1.S1_s_at
Metabolism	Lipids & Glucose	1.2	-2.1	ALDOB	ALDOB	MmugDNA.17915.1.S1_at
Metabolism	Lipids & Glucose	-1.1	-2.0	GAPDHL11	No network object found	MmugDNA.32304.1.S1_at
Metabolism	Lipids & Glucose	1.1	-2.2	FABP3	Fatty acid-binding protein *	MmugDNA.40769.1.S1_s_at
Metabolism	Lipids & Glucose	-1.5	-3.3	LEPR	Leptin receptor	MmugDNA.43193.1.S1_at
Metabolism	Lipids & Glucose	1.5	2.2	FABP5		MmunewRS.500.1.S1_at
Metabolism	Lipids & Glucose	-1.5	2.1	APOD	APOD	MmugDNA.10643.1.S1_s_at
Metabolism	Lipids & Glucose	1.1	3.9	ENPP6	ENPP6	MmugDNA.32991.1.S1_at
Metabolism	Lipids & Glucose	1.2	2.0	PMVK	PMVK	MmugDNA.15706.1.S1_at
Metabolism	Lipids & Glucose	1.0	3.3	PLA2G7	phospholipase A2, group VII	MmugDNA.17938.1.S1_at
Metabolism	Lipids & Glucose	1.6	2.0	MTHFD2L	MTHFD2L	MmugDNA.37.1.S1_at
Metabolism	Lipids & Glucose	1.3	5.7	ALDH1A3		MmuSTS.2795.1.S1_at
Metabolism	Lipids & Glucose	1.2	2.7	ADRP	Adipophilin (Adipose differer	Mmu.6559.1.S1_s_at
Metabolism	Lipids & Glucose	1.3	2.2	AGPS	ADAS	MmugDNA.35890.1.S1_at
Metabolism	Lipids & Glucose	2.9	1.6	**CYP1B1**	cytochrome P450, family 1,	MmuSTS.4020.1.S1_at
Metabolism	Lipids & Glucose	2.7	2.0	**CYP1B1**	cytochrome P450, family 1,	MmugDNA.36286.1.S1_at
Metabolism	Lipids & Glucose	2.3	1.6	**CYP1B1**	cytochrome P450, family 1,	MmugDNA.30721.1.S1_at
Metabolism	Lipids & Glucose	2.1	1.4	MANEA	mannosidase, endo-alpha	MmugDNA.11821.1.S1_at
Metabolism	Lipids & Glucose	2.1	1.4	STT3A	integral membrane protein 1	MmugDNA.21146.1.S1_at
Metabolism	Lipids & Glucose	-1.8	-2.8	**SCD**	---	MmugDNA.24505.1.S1_at
Metabolism	Lipids & Glucose	-2.0	1.1	**SCD**	stearoyl-CoA desaturase (de	MmugDNA.38238.1.S1_at
Metabolism	Lipids & Glucose	-2.3	-1.0	LGALS13	Galactoside-binding soluble	MmugDNA.43117.1.S1_at
Metabolism	Lipids & Glucose	-2.2	1.1	AMY2A	amylase, alpha 2A; pancrea	MmugDNA.4900.1.S1_s_at
Metabolism	Metals/Ions	2.2	2.6	PPA1	pyrophosphatase 1	Mmu.4786.2.S1_at
Metabolism	Metals/Ions	2.3	2.3	PPA1	pyrophosphatase 1	Mmu.4786.2.S1_s_at
Metabolism	Metals/Ions	2.4	2.1	PPA1	pyrophosphatase 1	MmugDNA.35236.1.S1_at
Metabolism	Metals/Ions	-1.1	2.1	SCN3A		MmuSTS.2368.1.S1_at
Metabolism	Metals/Ions	1.6	2.1	CISD2	CISD2	MmugDNA.2585.1.S1_at
Metabolism	Metals/Ions	2.3	2.0	KLHL23	KLHL23	MmugDNA.36416.1.S1_at
Metabolism	Metals/Ions	1.1	-2.2	SCNN1A	ENaC *	MmugDNA.31086.1.S1_at
Metabolism	Metals/Ions	-1.1	-2.7	TRPC6	TRPC6	MmugDNA.1894.1.S1_s_at
Metabolism	Mitochondrial Electron Trans	1.1	-2.0	CYB5A	Cytochrome B5	MmugDNA.32205.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Metabolism	Mitochondrial Electron Trans	1.0	2.2	CB310985	Mitochondrial integral memb	Mmu.6867.3.S1_s_at
Metabolism	Mitochondrial Electron Trans	1.8	3.9	CB549517	Mitochondria NADH dehydro	Mmu.3064.4.S1_s_at
Metabolism	Mitochondrial Electron Trans	-1.2	2.5	CB549588	Mitochondrial membrane ion	Mmu.3044.13.S1_x_at
Metabolism	Mitochondrial Electron Trans	-1.0	6.6	COX8C	---	MmugDNA.30366.1.S1_at
Metabolism	Mitochondrial Electron Trans	1.2	2.2	NDUFC2	NDUFC2	MmugDNA.29870.1.S1_at
Metabolism	Mitochondrial Electron Trans	1.3	2.2	**NDUFS8**	NDUFS8	MmugDNA.42544.1.S1_at
Metabolism	Mitochondrial Electron Trans	1.4	2.1	**NDUFS8**	NDUFS8	MmugDNA.42544.1.S1_s_at
Metabolism	Mitochondrial Electron Trans	1.3	2.1	UQCRH		Mmu.10533.2.S1_s_at
Metabolism	Mitochondrial Electron Trans	-1.0	4.6	COX1	---	Mmu.6867.1.A1_at
Metabolism	Mitochondrial Electron Trans	-1.8	2.9	Mitochondrion	mitochondrion, complete ge	MmuMitochon.4.1.S1_at
Metabolism	Nucleic Acids	6.3	6.0	RRM2	ribonucleotide reductase M2	MmugDNA.31369.1.S1_at
Metabolism	Nucleic Acids	2.8	2.8	DHFR	Dihydrofolate reductase	MmugDNA.10792.1.S1_at
Metabolism	Nucleic Acids	1.6	2.5	DHFR	DHFR	MmugDNA.41835.1.S1_at
Metabolism	Nucleic Acids	2.3	2.3	AHCY	S-adenosylhomocysteine hy	MmuSTS.44.1.S1_at
Metabolism	Nucleic Acids	6.0	6.7	LOC700582	Probable dimethyladenosin	MmuSTS.3275.1.S1_at
Metabolism	Nucleic Acids	2.9	4.3	TYMS	thymidylate synthetase	MmugDNA.30056.1.S1_at
Metabolism	Nucleic Acids	4.1	4.5	TYMS	thymidylate synthetase	MmuSTS.4685.1.S1_at
Metabolism	Nucleic Acids	2.4	2.0	FEN1	flap structure-specific endon	MmuSTS.2645.1.S1_at
Metabolism	Nucleic Acids	2.0	1.6	GART	phosphoribosylglycinamide f	MmugDNA.18615.1.S1_at
Metabolism	Nucleic Acids	2.4	1.8	LOC695725	uridine-cytidine kinase 2	MmugDNA.43419.1.S1_at
Metabolism	Nucleic Acids	2.5	2.0	NPM1	Nucleophosmin (NPM) (Nuc	MmugDNA.4269.1.S1_at
Metabolism	Nucleic Acids	2.1	1.9	SYNCRIP	NS1-associated protein 1 is	MmugDNA.20772.1.S1_s_at
Metabolism	Nucleic Acids	1.6	2.2	RAP1GDS1		MmuSTS.3103.1.S1_at
Metabolism	Nucleic Acids	2.0	2.5	RRM1	RRM1	MmugDNA.26585.1.S1_at
metabolism	Nucleic Acids	1.3	2.1	MSH2		MmuSTS.316.1.S1_at
Metabolism	Nucleic Acids	1.1	2.1	NAT1	NAT-1	MmugDNA.14909.1.S1_at
Metabolism	Nucleic Acids	1.2	2.3	ARHGDIB		MmuSTS.486.1.S1_at
Metabolism	Nucleic Acids	1.2	2.0	ARL5A	ARL5	MmugDNA.22459.1.S1_at
Metabolism	Nucleic Acids	1.7	2.6	DCK	---	MmugDNA.36254.1.S1_at
Metabolism	Nucleic Acids	1.1	2.5	BPNT1	3(2),5-bisphosphate nucleot	MmugDNA.35881.1.S1_at
Metabolism	Nucleic Acids	1.4	3.8	DNASE2B	deoxyribonuclease II beta	MmugDNA.36576.1.S1_at
Metabolism	Nucleic Acids	1.2	2.4	HNRNPA2B1	heterogeneous nuclear ribor	Mmu.7150.1.S1_at
Metabolism	Nucleic Acids	-1.0	2.1	HNRPH2	heterogeneous nuclear ribor	MmuSTS.2520.1.S1_at
Metabolism	Nucleic Acids	1.4	2.2	NEIL3	nei endonuclease VIII-like 3	MmugDNA.7448.1.S1_at
Metabolism	Nucleic Acids	1.2	2.4	DUT	dUTPase (DUT)	MmugDNA.20705.1.S1_at
Metabolism	Nucleic Acids	1.2	2.1	ENTPD1	ENP1	MmugDNA.14350.1.S1_at
Metabolism	Nucleic Acids	1.7	2.3	NT5C3	NT5C3	MmugDNA.12374.1.S1_at
Metabolism	Nucleic Acids	1.6	2.1	NUDT21	CPSF5	MmugDNA.6289.1.S1_at
Metabolism	Nucleic Acids	1.2	2.0	SF3B14	SF3B14a	MmugDNA.19706.1.S1_s_at
Metabolism	Nucleic Acids	1.0	2.1	SIP1	SIP1	MmugDNA.28962.1.S1_s_at
Metabolism	Nucleic Acids	1.8	2.0	SNRPD1	SNRPD1 (SMD1)	MmugDNA.25299.1.S1_at
Metabolism	Nucleic Acids	1.8	2.2	SNRPF	snRNP-F	MmugDNA.2701.1.S1_at
Metabolism	Nucleic Acids	1.6	2.0	TXNL4A	U5-15kD	MmugDNA.14759.1.S1_at
Metabolism	Proteins	2.2	2.1	SAR1B	SAR1a gene homolog 2	MmugDNA.38135.1.S1_at
Metabolism	Proteins	2.1	2.0	MRPL15	mitochondrial ribosomal prot	MmuSTS.954.1.S1_at
Metabolism	Proteins	2.1	2.0	MRPL19	mitochondrial ribosomal prot	MmuSTS.1524.1.S1_at
Metabolism	Proteins	2.1	1.7	DNAJB11	DnaJ (Hsp40) homolog, sub	MmuSTS.4249.1.S1_at
Metabolism	Proteins	2.2	1.5	ETF1	eukaryotic translation termin	MmugDNA.19076.1.S1_s_at
Metabolism	Proteins	2.0	1.3	**TRA1 (HSP90B1)**	tumor rejection antigen (gp9	MmugDNA.6621.1.S1_at
Metabolism	Proteins	2.0	1.5	**TRA1 (HSP90B1)**	tumor rejection antigen (gp9	Mmu.4005.1.S1_s_at
Metabolism	Proteins	2.3	1.8	SPCS3	signal peptidase complex su	MmugDNA.32060.1.S1_s_at
Metabolism	Proteins	3.3	1.7	PSAT1	phosphoserine aminotransf	MmugDNA.38346.1.S1_at
Metabolism	Proteins	2.1	1.5	PDIA4	protein disulfide isomerase-a	MmugDNA.9838.1.S1_at
Metabolism	Proteins	-1.3	2.2	MDN1	Midasin	MmugDNA.10175.1.S1_at
Metabolism	Proteins	1.9	2.8	HERC6	hect domain and RLD 6 isof	MmugDNA.30921.1.S1_at
Metabolism	Proteins	1.3	2.3	MRPL3	mitochondrial ribosomal prot	MmugDNA.6717.1.S1_at
Metabolism	Proteins	1.3	2.1	**PPIL1**	Peptidyl-prolyl cis-trans isom	Mmu.7805.1.S1_at
Metabolism	Proteins	-1.2	2.1	**PPIL1**	Peptidylprolyl isomerase A (	MmugDNA.8983.1.S1_at
Metabolism	Proteins	1.4	2.3	SLD5	SLD5	MmugDNA.33465.1.S1_s_at
Metabolism	Proteins	1.3	2.1	**DNAJA1**		Mmu.10506.1.S1_at
Metabolism	Proteins	1.5	2.2	**DNAJA1**		Mmu.10506.1.S1_s_at
Metabolism	Proteins	1.7	2.4	**DNAJA1**	Hdj-2	MmugDNA.19435.1.S1_s_at
Metabolism	Proteins	-1.0	2.8	ELAVL2	ELAVL2	MmugDNA.33494.1.S1_at
Metabolism	Proteins	1.2	2.2	FXR1	FXR1	MmugDNA.19474.1.S1_at
Metabolism	Proteins	1.8	2.1	MRPL12	Large 39S subunit *	MmugDNA.25924.1.S1_s_at
Metabolism	Proteins	1.5	2.6	PFDN4	PFD4	MmugDNA.5521.1.S1_at
Metabolism	Proteins	1.7	2.1	PI4K2B	PI4K2B	MmugDNA.25587.1.S1_at
Metabolism	Proteins	1.2	2.6	RPL12	Large 60S subunit *	MmugDNA.32762.1.S1_at
Metabolism	Proteins	-1.3	2.3	METTL7A	methyltransferase like 7A	MmugDNA.37173.1.S1_at
Metabolism	Proteins	-1.1	2.4	METTL7A	METTL7A	MmugDNA.38570.1.S1_s_at
Metabolism	Proteins	1.0	2.3	ENPP4	ENPP4	MmugDNA.10334.1.S1_at
Metabolism	Proteins	1.6	2.0	SULT1C2		MmuSTS.2999.1.S1_at
Metabolism	Proteins	1.1	2.2	TPH1	TPH1	MmugDNA.6193.1.S1_at
Metabolism	Proteins	-3.7	-1.0	LOC693289	ATP-binding cassette, sub-fa	MmuSTS.2655.1.S1_at
Metabolism	Proteins	-4.1	-1.6	LOC714206	ATP-binding cassette, sub-fa	MmunewRS.1009.1.S1_at
metabolism	Proteins	1.2	-2.1	PRSS2	Trypsin *	MmugDNA.22266.1.S1_at
Metabolism	Proteins	1.3	-2.8	SAT	Diamine acetyltransferase 1	MmugDNA.30414.1.S1_at
Metabolism	Proteins	1.1	-2.5	SULT2A1	SULT2A1	MmugDNA.4194.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.6	2.1	PSMA2	26S proteasome (20S core)	MmugDNA.22342.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.7	2.1	PSMA4	26S proteasome (20S core)	MmugDNA.22344.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.6	2.0	PSMA5	26S proteasome (20S core)	MmugDNA.22346.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.5	2.0	PSMA7	26S proteasome (20S core)	MmugDNA.22347.1.S1_s_at
Metabolism	Proteins: Proteasome/Ubiqui	1.4	2.2	PSMB8	Immunoproteasome (20S co	MmugDNA.36047.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.8	2.3	PSMD14	26S proteasome (19S regula	MmugDNA.13324.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.4	2.0	PSMG1	DSCR2	MmugDNA.40337.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.5	2.1	CACYBP	CacyBP(SIP)	MmugDNA.30673.1.S1_s_at
Metabolism	Proteins: Proteasome/Ubiqui	1.3	2.1	CACYBP	CacyBP(SIP)	Mmu.11667.1.S1_at

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Metabolism	Proteins: Proteasome/Ubiqui	1.0	2.1	SUMO1	SUMO-1	MmugDNA.31414.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.7	2.4	UBE2L6	UBCH8	MmugDNA.7052.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	1.7	2.2	UCHL3	UCHL3	MmugDNA.38706.1.S1_s_at
Metabolism	Proteins: Proteasome/Ubiqui	-1.0	2.0	ZYG11B	ZYG11B	MmugDNA.12338.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	2.0	2.3	PSMA3	Proteasome subunit alpha ty	MmugDNA.22343.1.S1_s_at
Metabolism	Proteins: Proteasome/Ubiqui	2.3	2.1	**UBE2S**	Ubiquitin-conjugating enzym	MmugDNA.15298.1.S1_x_at
Metabolism	Proteins: Proteasome/Ubiqui	2.5	2.2	**UBE2S**	Ubiquitin-conjugating enzym	MmugDNA.15298.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	2.2	2.0	UBE2T	Ubiquitin-conjugating enzym	MmugDNA.22787.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	2.2	2.1	UCHL5	ubiquitin C-terminal hydrolas	Mmu.1412.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	2.1	2.1	UCHL5	ubiquitin C-terminal hydrolas	MmugDNA.15179.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	2.1	2.3	UCHL5	ubiquitin C-terminal hydrolas	MmuSTS.4734.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	2.3	1.5	UBE2J1	ubiquitin-conjugating enzym	MmugDNA.42067.1.S1_at
Metabolism	Proteins: Proteasome/Ubiqui	-1.0	-2.1	LOC695064	promyelocytic leukemia zinc	MmuSTS.4766.1.S1_at
Metabolism	Proteins:eIF	1.5	2.5	**EIF1AX**	EIF1AX	MmugDNA.41569.1.S1_at
Metabolism	Proteins:eIF	1.4	2.3	**EIF1AX**	EIF1AX	MmugDNA.41569.1.S1_s_at
Metabolism	Proteins:eIF	1.3	2.9	**EIF4E**	eIF4E	MmugDNA.22671.1.S1_s_at
Metabolism	Proteins:eIF	1.5	2.0	**EIF4E**	eIF4E	MmugDNA.22673.1.S1_at
Metabolism	Proteins:eIF	1.9	5.5	EIF5A	eukaryotic translation initiati	MmugDNA.38446.1.S1_at
Metabolism	Proteins:eIF	1.1	-2.4	EIF3C	eIF3 *	MmugDNA.38182.1.S1_at
Metabolism	Water/ion transport	1.5	3.7	AQP3	aquaporin 3 (Gill blood grou	MmuSTS.1365.1.S1_s_at
Metabolism		2.1	1.2	NQO1	NAD(P)H dehydrogenase, q	MmuSTS.3015.1.S1_at
Metabolism		1.3	6.4	AQP4	aquaporin 4	MmugDNA.6205.1.S1_at
metabolism		1.5	2.0	STYX	STYX	MmugDNA.37636.1.S1_at
Others	Cytoskeleton Related	2.2	2.2	TUBA6	tubulin alpha 6	MmugDNA.32666.1.S1_s_at
Others	Cytoskeleton Related	2.5	3.1	**DIAPH3**	diaphanous homolog 3	MmugDNA.22775.1.S1_at
Others	Cytoskeleton Related	1.6	2.1	**DIAPH3**	mDIA2(DIAPH3)	MmugDNA.42203.1.S1_at
Others	DNA Replication/Repair	2.2	2.7	RAD51	RAD51 homolog protein isof	MmugDNA.23761.1.S1_at
Others	DNA Replication/Repair	2.2	3.1	HMGB2	high-mobility group box 2	MmuSTS.1347.1.S1_at
Others	DNA Replication/Repair	2.3	2.4	GINS2	GINS complex subunit 2 (Ps	MmuSTS.2066.1.S1_at
Others	DNA Replication/Repair	3.3	2.8	POLE2	DNA polymerase epsilon su	MmugDNA.2975.1.S1_at
Others	DNA Replication/Repair	2.5	3.7	RAD51AP1	RAD51-associated protein	MmuSTS.4250.1.S1_at
Others	DNA Replication/Repair	4.7	5.3	**TOP2A**	DNA topoisomerase II, alpha	MmugDNA.12273.1.S1_at
Others	DNA Replication/Repair	3.9	5.8	**TOP2A**	DNA topoisomerase II, alpha	MmugDNA.12277.1.S1_at
Others	Nucleosome structure and C	3.0	4.0	LMNB1	lamin B1	MmuSTS.1539.1.S1_at
Others	Nucleosome structure and C	2.0	2.3	HIST1H4J	histone cluster 1, H4j (germi	MmugDNA.3247.1.S1_at
Others	Nucleosome structure and C	2.0	2.6	HIST1H4J	Hist4h4 *	MmugDNA.3247.1.S1_s_at
Others	Nucleosome structure and C	2.4	3.2	LOC703073	Histone H2A.x (H2a/x)	MmuSTS.8.1.S1_at
Others	Transcriptinal Regulators	2.2	2.2	EAF2	ELL associated factor 2	MmugDNA.2321.1.S1_at
Others	Transcriptinal Regulators	3.0	3.3	EZH2	enhancer of zeste 2	MmuSTS.911.1.S1_at
Others	Transcriptinal Regulators	2.1	1.8	**ATAD2**	ATPase family, two AAA do	MmugDNA.12475.1.S1_s_at
Others	Transcriptinal Regulators	1.6	2.1	**ATAD2**	ATAD2	MmugDNA.31331.1.S1_at
Others	Transcriptinal Regulators	1.5	2.7	**ATAD2**	ATAD2	MmugDNA.5276.1.S1_at
Others		2.2	3.3	ANP32E	acidic (leucine-rich) nuclear	MmugDNA.22578.1.S1_at
Others		2.4	2.1	MTDH	LYRIC/3D3	MmugDNA.81.1.S1_s_at
Others		2.3	2.2	MTDH	LYRIC/3D3	MmugDNA.81.1.S1_at
Others		2.4	1.8	MTDH	LYRIC/3D3/ metadherin	Mmu.4898.1.S1_at
Others		2.6	2.7	NME1	non-metastatic cells 1, prote	MmugDNA.21289.1.S1_at
Others		3.6	3.1	TRIP13	thyroid hormone receptor int	MmuSTS.4722.1.S1_at
Others		5.0	5.4	NS5ATP9	---	MmugDNA.33823.1.S1_s_at
Others		2.7	4.3	TMPRSS3	Transmembrane protease, s	MmuSTS.1653.1.S1_at
Others		1.3	2.0	**MBNL1**	MBNL1	MmugDNA.11479.1.S1_at
Others		1.4	2.1	EPB41	EPB41	MmugDNA.19045.1.S1_at
Others		2.8	1.9	ARNTL2	aryl hydrocarbon receptor nu	MmugDNA.13595.1.S1_at
Others		2.6	1.4	**MOBKL1B**	Mol1b	MmugDNA.6802.1.S1_at
Others		2.1	1.1	**MOBKL1B**	Mob4B protein (Mps One Bi	MmugDNA.23022.1.S1_s_at
Others		-1.0	2.2	GFRA3	GFRalpha3	MmugDNA.29304.1.S1_at
Others		1.5	2.3	SUPT4H1	SPT4	MmugDNA.24909.1.S1_s_at
Others		-1.0	2.5	CHIT1		MmuSTS.3643.1.S1_at
Others		-1.0	2.3	ABI1	E3b1(ABI-1)	MmugDNA.25737.1.S1_at
Others		1.7	2.2	SUCNR1	GPR91	MmugDNA.3746.1.S1_at
Others		-1.1	2.3	GPNMB	GPNMB (Osteoactivin)	MmugDNA.43116.1.S1_at
Others		1.7	3.3	SAMD9L	sterile alpha motif domain co	MmugDNA.12043.1.S1_at
Others		1.2	2.8	SAMD9	Sterile alpha motif domain-c	MmugDNA.27315.1.S1_at
Others		1.3	2.0	ARPP-19	ARPP-19	MmugDNA.7517.1.S1_at
Others		-1.7	2.2	MALAT1	metastasis associated lung a	MmugDNA.13401.1.S1_s_at
Others		-1.2	3.0	SPINK2	serine protease inhibitor, Ka	MmugDNA.18486.1.S1_s_at
Others		1.9	2.2	DLEU2	deleted in lymphocytic leuke	MmugDNA.12590.1.S1_at
Others		1.3	2.1	DLEU2	DLEU2	MmugDNA.36289.1.S1_s_at
Others		-1.2	3.7	HOPX	homeodomain-only protein	MmugDNA.13933.1.S1_at
Others		-1.0	3.2	KIDINS220	---	MmugDNA.28052.1.S1_at
Others		1.9	2.8	LOC720683	sperm tail protein SHIPPO1	MmugDNA.38197.1.S1_at
Others		2.1	2.5	WDHD1	WD repeat and HMG-box D	MmugDNA.18618.1.S1_at
Others		-1.0	2.5	DSC2	DSC2	MmugDNA.18999.1.S1_at
Others		-1.0	2.0	FER1L3	Myoferlin	MmugDNA.28340.1.S1_at
Others		-1.0	2.2	GIMAP2	GIMAP2	MmugDNA.39974.1.S1_at
Others		1.0	2.1	KIAA1715	KIAA1715	MmugDNA.7879.1.S1_at
Others		1.6	2.1	MRPS18C	MRPS18 *	MmugDNA.10584.1.S1_s_at
Others		1.5	2.1	MRPS28	MRPS28	MmugDNA.32255.1.S1_at
Others		-1.2	2.1	OSBPL8	ORP-family *	MmugDNA.31287.1.S1_at
Others		1.3	2.4	PKM2		Mmu.10820.1.S1_at
Others		-1.1	2.6	TPR	Nuclear pore complex protei	MmugDNA.39372.1.S1_at
Others		1.4	2.3	WDHD1	WDHD1	MmugDNA.37680.1.S1_at
Others		2.0	2.0	WHSC1	WHSC1	MmugDNA.7428.1.S1_at
Others		1.2	-3.4	MYH11	CBFB/MYH11 fusion protein	MmugDNA.33340.1.S1_at
Others		-2.4	-1.3	MYH11	smooth muscle myosin heav	MmugDNA.15137.1.S1_at
Others		-2.2	-1.2	MYH11	smooth muscle myosin heav	MmugDNA.33337.1.S1_at
Others		-2.0	1.2	**MBNL1**	Muscleblind-like (Drosophila	MmugDNA.3546.1.S1_at

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Others		-2.2	1.5	EPB41	Erythrocyte membrane prote	MmugDNA.16997.1.S1_at
Others		-2.2	-1.2	TPM2	tropomyosin 2 (beta) isoforn	MmugDNA.6549.1.S1_at
Others		-2.3	-1.0	CNR1		MmugDNA.5294.1.S1_at
Others		-2.6	1.3	NOG	Noggin precursor	MmugDNA.19120.1.S1_at
Others		-3.2	-1.1	APBA2	amyloid beta (A4) precursor	MmugDNA.18477.1.S1_at
Others		-2.0	-1.1	FRZB	frizzled-related protein	MmugDNA.39998.1.S1_at
Others		-2.4	1.4	LIN7A	LIN-7 homolog A (LIN-7A) (	MmugDNA.33930.1.S1_at
Others		-2.0	-1.7	CIRBP	cold inducible RNA binding	MmugDNA.21025.1.S1_at
Others		-2.5	-1.3	**COCH**	coagulation factor C homolo	MmugDNA.12890.1.S1_at
Others		-2.3	-1.3	**COCH**	coagulation factor C homolo	MmuSTS.3519.1.S1_at
Others		-2.0	1.4	MAP7	microtubule-associated prot	MmugDNA.11043.1.S1_at
Others		-2.1	-1.3	NEFH	neurofilament, heavy polype	MmugDNA.18337.1.S1_at
Others		-2.1	-1.2	WIF1	Wnt inhibitory factor 1	MmuSTS.4753.1.S1_at
Others		-2.1	1.0	INADL	INADL	MmugDNA.26275.1.S1_at
Others		-1.9	-3.7	STAB1	hypothetical protein LOC69	MmugDNA.42885.1.S1_at
Others		-1.2	-2.9	**PCDHA9**	protocadherin alpha 9	MmuSTS.1120.1.S1_s_at
Others		-1.4	-2.7	**PCDHA9**	protocadherin alpha 9	MmugDNA.7782.1.S1_at
Others		-1.4	-2.8	**PCDHA9**	protocadherin alpha 9	MmuAffx.1252.1.A1_at
Others		-1.0	-2.7	Titin	titin isoform N2-A	MmugDNA.20569.1.S1_at
Others		-1.2	-5.5	beta globin	beta globin	MmugDNA.2571.1.S1_s_at
Others		-1.2	-6.5	beta globin	beta globin	MmugDNA.2571.1.S1_x_at
Others		-1.2	-6.7	beta globin	beta globin	MmugDNA.2571.1.S1_at
Others		-1.1	-5.2	beta globin	beta globin	MmugDNA.5184.1.S1_s_at
Others		-1.2	-6.7	beta globin	beta globin	MmuAffx.949.1.S1_x_at
Others		-1.4	-2.5	ADMR (GPR182)	---	MmugDNA.20969.1.S1_at
Others		-1.3	-2.5	ATRNL1	attractin-like 1	MmugDNA.33011.1.S1_at
Others		-1.1	-2.1	**DAB2**	DAB2	MmugDNA.41396.1.S1_at
Others		-1.5	-2.1	**DAB2**	---	MmugDNA.12457.1.S1_at
Others		1.1	-2.2	DOCK5	DOCK5	MmugDNA.4179.1.S1_at
Others		1.2	-2.7	GAGE1	GAGE-2	MmugDNA.40706.1.S1_s_at
Others		1.0	-3.0	HBA1	Adult hemoglobin *	MmugDNA.32562.1.S1_s_at
Others		1.1	-2.1	HOXD12	HOXD12	MmugDNA.36471.1.S1_at
Others		-1.1	-2.1	IRX1		MmunewRS.464.1.S1_at
Others		-1.3	-2.7	SHOX2	SHOX2	MmugDNA.3283.1.S1_at
Others		-2.0	-1.4	NTRK2	TrkB	MmugDNA.41948.1.S1_at
Others	DNA Replication/Repair	2.1	1.4	EXO1	exonuclease 1 isoform b	MmugDNA.17950.1.S1_s_at
Others	ER-Golgi Related	2.0	1.4	**ERGIC1**	endoplasmic reticulum-golgi	MmugDNA.42416.1.S1_s_at
Others	ER-Golgi Related	2.0	1.5	**ERGIC1**	endoplasmic reticulum-golgi	MmugDNA.42416.1.S1_at
Others	ER-Golgi Related	2.1	1.5	SSR1	Translocon-associated prote	MmugDNA.7350.1.S1_s_at
Others	ER-Golgi Related	-1.2	2.0	GOLGA1	Golgin-97	MmugDNA.12907.1.S1_at
Others	Insulin-like Growth Factor Bi	2.2	1.1	IMP-3	insulin-like growth factor 2 m	MmugDNA.31012.1.S1_at
Others	Insulin-like Growth Factor Bi	2.3	1.3	IMP-3	insulin-like growth factor 2 m	MmugDNA.15520.1.S1_s_at
Others	Insulin-like Growth Factor Bi	-1.7	2.2	AKT3	v-akt murine thymoma viral	MmugDNA.2158.1.S1_at
Others	Insulin-like Growth Factor Bi	-2.2	-1.8	**ILGFBP3**	insulin-like growth factor bin	Mmu.11638.2.S1_at
Others	Insulin-like Growth Factor Bi	-3.0	-1.6	**ILGFBP3**	insulin-like growth factor bin	MmuSTS.2537.1.S1_at
Others	Insulin-like Growth Factor Bi	-2.6	-1.5	**ILGFBP3**	insulin-like growth factor bin	MmugDNA.7729.1.S1_at
Others	Insulin-like Growth Factor Bi	-2.1	1.0	ILGFBP6	insulin-like growth factor bin	MmugDNA.23639.1.S1_at
Others	Insulin-like Growth Factor Bi	-2.2	-1.0	ILGFII	Insulin-like growth factor II p	Mmu.4374.2.S1_s_at
Others	Insulin-like Growth Factor Bi	1.1	-2.5	LOC714042	klotho isoform a	MmuSTS.1603.1.S1_at
Others	Post-Translational Modificati	2.1	1.8	SUV39H2	suppressor of variegation 3-	MmugDNA.12443.1.S1_at
Others	Solute Carrier Family	2.0	1.7	SLC31A1	High-affinity copper uptake	Mmu.7190.1.A1_at
Others	Solute Carrier Family	2.3	1.6	SLC7A5	solute carrier family 7 (catio	MmuSTS.3879.1.S1_at
Others	Transcriptional Regulators	2.5	1.5	ELL2	elongation factor, RNA poly	MmuSTS.4317.1.S1_at
Others	Transcriptional Regulators	-2.0	-1.0	ID4		MmuSTS.2533.1.S1_at
Others	Transcriptional Regulators	-2.1	1.0	---	---	MmugDNA.11023.1.S1_at
Others	Vesicle Trafficking	2.6	1.5	**SEC24A**	SEC24 related gene family,	MmugDNA.37864.1.S1_at
Others	Vesicle Trafficking	2.2	1.7	**SEC24A**	SEC24 related gene family,	MmugDNA.37865.1.S1_at
Others	Cell-Adhesion Related	1.6	2.5	SIGLEC8 (CD329)	sialic acid binding immunogl	MmugDNA.32892.1.S1_at
Others	Cell-Adhesion Related	-1.5	2.3	ITGB8	ITGB8	MmugDNA.42148.1.S1_at
Others	Cell-Adhesion Related	1.1	2.0	CEACAM5 (CD66e)	CEACAM5	MmugDNA.11426.1.S1_at
Others	Cell-Adhesion Related	1.2	10.8	**CEACAM6 (CD66c)**	---	MmugDNA.24595.1.S1_at
Others	Cell-Adhesion Related	1.0	4.1	**CEACAM6 (CD66c)**	carcinoembryonic antigen-re	MmugDNA.4023.1.S1_at
Others	Cell-Adhesion Related	-1.0	2.0	EMR2 (CD312)	EMR2	MmugDNA.34795.1.S1_at
Others	Cytoskeleton Related	-1.7	2.0	IQGAP1	IQGAP1	MmugDNA.19813.1.S1_at
Others	Cytoskeleton Related	1.2	2.0	MGC39900	No network object found	MmugDNA.40563.1.S1_at
Others	DNA Replication/Repair	1.6	2.2	RMI1	BLAP75	MmugDNA.33590.1.S1_at
Others	DNA Replication/Repair	1.4	2.3	RNASEH2B	RNaseh2b	MmugDNA.10980.1.S1_at
Others	DNA Replication/Repair	1.8	2.4	RPA3	RPA3	MmugDNA.13776.1.S1_s_at
Others	DNA Replication/Repair	1.0	2.1	XRCC4	XRCC4	MmugDNA.13749.1.S1_s_at
Others	DNA Replication/Repair	1.7	2.3	LIG1	DNA ligase I	MmugDNA.21105.1.S1_at
Others	DNA Replication/Repair	1.9	2.0	ORC6L	ORC6L	MmugDNA.18357.1.S1_at
Others	DNA Replication/Repair	1.6	2.1	SMC4	CAP-C	MmugDNA.20926.1.S1_at
Others	DNA Replication/Repair	1.5	2.0	ATIC	PUR9	MmugDNA.2533.1.S1_at
Others	DNA Replication/Repair	1.2	2.0	PRIM2	DNA polymerase alpha/prim	MmugDNA.21556.1.S1_at
Others	DNA Replication/Repair	1.5	2.1	FANCI	KIAA1794	MmugDNA.25448.1.S1_at
Others	Epithelial Cells	1.8	2.9	IQGAP3	IQGAP3	MmugDNA.36049.1.S1_at
Others	Epithelial Cells	1.1	5.9	CK 6A	Keratin, type II cytoskeletal	MmuSTS.4448.1.S1_at
Others	Epithelial Cells	1.0	3.0	SPRR3	Small proline-rich protein 3	MmuSTS.1819.1.S1_at
Others	Epithelial Cells	-1.1	3.4	KRT5	keratin 5	MmugDNA.21974.1.S1_at
Others	Epithelial Cells	1.1	2.2	KRT3		MmuSTS.2954.1.S1_at
Others	Epithelial Cells	1.1	2.1	KRTDAP	KRTDAP	MmugDNA.5366.1.S1_at
Others	Heat shock proteins	1.3	2.1	HSBP1	HSBP1	MmugDNA.20456.1.S1_at
Others	Heat shock proteins	1.6	2.2	HSP90AA1	HSP90 *	MmugDNA.854.1.S1_at
Others	Heat shock proteins	1.9	2.1	HSPE1	HSP10 (mitochondrial)	MmugDNA.19457.1.S1_s_at
Others	Heat shock proteins	1.9	2.1	HSPH1	HSP105	MmugDNA.14913.1.S1_at
Others	Heat shock proteins	1.7	2.1	HSPA4	HSP70 *	MmugDNA.4083.1.S1_s_at
Others	Nucleosome structure and C	1.1	2.0	NUP50	NUP50	MmugDNA.22310.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Others	Nucleosome structure and C	1.5	2.0	H2AFV	H2AFV	MmugDNA.16722.1.S1_at
Others	Nucleosome structure and C	1.7	2.1	H2AFX	Histone H2 *	MmugDNA.30974.1.S1_at
Others	Nucleosome structure and C	1.4	2.9	NHP2L1	NHP2 non-histone chromos	MmugDNA.3458.1.S1_at
Others	Post-Translational Modificati	1.6	2.1	SAE1		MmugDNA.35341.1.S1_at
Others	Post-Translational Modificati	1.6	2.4	CBX5	HP1 *	MmugDNA.34326.1.S1_at
Others	Protein Translocation	-1.3	2.0	VPS13B	COH1	MmugDNA.5302.1.S1_at
Others	Protein Translocation	1.9	2.4	TIMM17A	TIM23-PAM complex *	MmugDNA.10629.1.S1_at
Others	Protein Translocation	1.5	2.4	TIMM23	TIM23-PAM complex *	MmugDNA.40114.1.S1_at
Others	Signal Transduction	1.4	2.2	ITPR2	IP3 receptor *	MmugDNA.21230.1.S1_at
Others	Solute Carrier Family	1.9	2.6	SLC16A10	solute carrier family 16, men	MmugDNA.34150.1.S1_s_at
Others	Solute Carrier Family	1.6	2.1	SLC25A46	SLC25A46	MmugDNA.22043.1.S1_at
Others	Solute Carrier Family	1.5	2.0	SLC25A5	ANT *	MmugDNA.9969.1.S1_at
Others	Solute Carrier Family	1.0	-2.1	SLC13A4	SLC13A4	MmugDNA.16904.1.S1_at
Others	Solute Carrier Family	1.0	-2.0	SLC1A3	GLAST1/EAAT1	MmugDNA.20629.1.S1_at
Others	Transcriptinal Regulators	-1.2	-2.1	LOC709735	nuclear receptor subfamily 5	MmugDNA.9427.1.S1_at
Others	Transcriptinal Regulators	1.1	-2.0	ZNF44	ZNF44	MmugDNA.18822.1.S1_at
Others	Transcriptinal Regulators	1.2	2.1	**ENO1(MBP-1)**		Mmu.14495.1.S1_at
Others	Transcriptinal Regulators	1.3	2.0	**ENO1(MBP-1)**		Mmu.15249.2.S1_at
Others	Transcriptinal Regulators	1.0	2.1	HNRNPR	heterogeneous nuclear ribor	Mmu.4422.1.S1_s_at
Others	Transcriptinal Regulators	1.5	2.1	GTF3C6	GTF3C6	MmugDNA.899.1.S1_at
Others	Transcriptinal Regulators	1.0	2.0	ZNF254	ZNF254	MmugDNA.11625.1.S1_at
Others	Transcriptinal Regulators	1.4	2.0	POLR2G	POLR2G	MmugDNA.3015.1.S1_at
Others	Transcriptinal Regulators	1.5	2.3	POLR3K	POLR3K	MmugDNA.16215.1.S1_at
Others	Transcriptinal Regulators	1.4	2.1	TAF13	TAF13	MmugDNA.16488.1.S1_at
Others	Transcriptinal Regulators	1.6	3.1	TTF2	transcription termination fac	MmuSTS.2896.1.S1_s_at
Others	Transcriptinal Regulators	1.6	2.2	MED18	MED18	MmugDNA.27240.1.S1_at
Others	Transcriptinal Regulators	1.1	2.0	SSA2	Sjogren syndrome antigen A	MmugDNA.22925.1.S1_at
Others	Transcriptinal Regulators	1.1	2.4	JARID1A	RBB2	MmugDNA.42720.1.S1_at
Others	Transcriptinal Regulators	-1.2	2.1	YY1AP1	YAP (HCCA2)	MmugDNA.36917.1.S1_at
Others	Transcriptinal Regulators	-1.2	2.3	RQCD1	RCD1	MmugDNA.23157.1.S1_at
Others	Transcriptinal Regulators	1.1	2.8	ZNF33A	zinc finger protein 33a (KOX	MmugDNA.12643.1.S1_at
Others	Transcriptinal Regulators	1.1	2.1	EYA4	EYA4	MmugDNA.33614.1.S1_at
Others	Transcriptinal Regulators	1.5	2.9	NSBP1	NSBP1	MmugDNA.32637.1.S1_at
Others	Transcriptinal Regulators	-1.1	2.2	TCF21(Capsulin)	Transcription factor 21	MmugDNA.4384.1.S1_at
Others	Transcriptinal Regulators	1.2	2.4	ZNF326	ZNF326	MmugDNA.4607.1.S1_at
Others	Vesicle Trafficking	1.9	2.2	SEC24D	COPII *	MmugDNA.12530.1.S1_at
Others	Vesicle Trafficking	1.2	2.0	VPS29	VPS29	MmugDNA.39821.1.S1_at
Others	Vesicle Trafficking	-1.1	2.1	STX8	Syntaxin 8	MmugDNA.42140.1.S1_at
Others	Vesicle Trafficking	-1.3	2.1	SCFD1	SCFD1	MmugDNA.27824.1.S1_at
Others	Splicosome	1.6	2.4	**LSM5**	LSM5	MmugDNA.15339.1.S1_at
Others	Splicosome	1.4	2.1	**LSM5**	LSM5	MmugDNA.32606.1.S1_s_at
Others	Splicosome	1.5	2.9	MAGOHB	FLJ10292	MmugDNA.4402.1.S1_at
Others	Epithelial Cell Related	1.0	2.4	SPRR1B	Cornifin B	MmugDNA.2820.1.S1_at
Others	Epithelial Cell Related	1.0	2.3	RPTN	Rptn	MmugDNA.41659.1.S1_at
Others	p53-Related	1.2	2.0	RCHY1	PIRH2	MmugDNA.6164.1.S1_s_at
Others	p53-Related	1.3	2.0	**TPRKB**	CGI-121	MmugDNA.36086.1.S1_at
Others	p53-Related	1.5	2.1	**TPRKB**	CGI-121	MmugDNA.36086.1.S1_s_at
Tissue Repair, Remodeling		2.8	2.7	SCIN	scinderin	MmuSTS.1778.1.S1_at
Tissue Repair, Remodeling		-1.5	-2.4	FZD10		MmuSTS.3644.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	-2.0	-2.4	STAB2	stabilin 2	MmugDNA.15867.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	-2.1	1.3	**DCN**	decorin	MmugDNA.32965.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	-2.1	1.1	**DCN**	decorin	MmugDNA.14528.1.S1_s_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	-2.2	1.4	**DCN**	decorin	MmugDNA.22700.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	-2.2	-1.7	DPT	Dermatopontin precursor (T	MmugDNA.35051.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	-2.1	-1.1	SPOCK2	sparc/osteonectin, cwcv and	MmugDNA.7832.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	1.0	-2.2	TNC	Tenascin-C	MmugDNA.19512.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	1.0	-2.4	TNC	Tenascin-C	MmugDNA.39792.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	1.2	-2.7	COL5A3		MmugDNA.37545.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	-2.0	-2.2	Claudin 5	claudin 5	MmuSTS.3423.1.S1_at
Tissue Repair, Remodeling		1.0	-2.1	FGF10	FGF10	MmugDNA.6246.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	2.1	-1.2	**SDC1 (CD138)**	Syndecan-1 precursor (SYN	MmugDNA.27367.1.S1_x_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	2.2	-1.1	**SDC1 (CD138)**	Syndecan-1 precursor (SYN	MmugDNA.27367.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	2.1	1.7	ECGF1	endothelial cell growth facto	MmugDNA.9266.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	1.6	3.5	ERPINA3	alpha-1-antichymotrypsin	Mmu.10083.1.S1_s_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	1.7	2.2	TUBB	tubulin, beta, 4 /// tubulin, be	MmugDNA.20252.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	1.8	2.2	TUBB2C	Tubulin (in microtubules) *	MmugDNA.6145.1.S1_s_at
Tissue Repair, Remodeling	Extracellular Matrix Structura	1.1	4.9	MMP1		MmuSTS.921.1.S1_at
Tissue Repair, Remodeling	Oxidative-Stress Related	2.4	2.4	SOD2	superoxide dismutase 2, mit	MmugDNA.24030.1.S1_at
Tissue Repair, Remodeling	Oxidative-Stress Related	1.4	2.5	CLU (APO-J)		MmugDNA.25040.1.S1_at
Tissue Repair, Remodeling	Oxidative-Stress Related	-1.3	-2.1	CD163 (M160)	scavenger receptor cysteine	MmugDNA.27987.1.S1_at
Tissue Repair, Remodeling	Nerve Related Growth Facto	-1.1	-2.5	GRIA2	glutamate receptor, ionotrop	MmugDNA.37346.1.S1_at
Tissue Repair, Remodeling	Nerve Related Growth Facto	-1.5	-2.5	GRIA2	glutamate receptor, ionotrop	MmugDNA.27764.1.S1_at
Tissue Repair, Remodeling	Nerve Related Growth Facto	5.0	5.1	**UCH-L1 (PGP9.5)**	Ubiquitin carboxyl-terminal	MmugDNA.7056.1.S1_s_at
Tissue Repair, Remodeling	Nerve Related Growth Facto	5.0	5.0	**UCH-L1 (PGP9.5)**	Ubiquitin carboxyl-terminal	MmugDNA.7056.1.S1_at
Tissue Repair, Remodeling	Nerve Related Growth Facto	1.2	2.0	SERPINI1	Neuroserpin	MmugDNA.18538.1.S1_at
Tissue Repair, Remodeling	Nerve Related Growth Facto	1.1	2.0	KIF1B	kinesin family member 1B	MmugDNA.3072.1.S1_at
Hypothetical Protein		2.6	4.6	C28H8.3	C28H8.3	MmugDNA.27193.1.S1_at
Hypothetical Protein		2.3	2.4	CCDC58	coiled-coil domain containin	MmugDNA.24837.1.S1_s_at
Hypothetical Protein		2.5	2.2	CCDC99	coiled-coil domain containin	MmugDNA.303.1.S1_at
Hypothetical Protein		4.4	5.7	DEPDC1B (LOC709670)	DEP domain containing 1B	MmugDNA.28002.1.S1_at
Hypothetical Protein		4.1	4.4	LOC695836	hypothetical protein LOC695	MmugDNA.2512.1.S1_at
Hypothetical Protein		3.1	4.9	LOC708602	thymidylate kinase family LI	MmugDNA.21336.1.S1_at
Hypothetical Protein		2.8	3.4	LOC712570	hypothetical protein LOC712	MmugDNA.43588.1.S1_at
Hypothetical Protein		3.7	3.4	LOC714686	hypothetical protein LOC714	MmugDNA.1969.1.S1_at
Hypothetical Protein		2.8	2.7	LOC718812	hypothetical protein LOC718	MmugDNA.33404.1.S1_at
Hypothetical Protein		2.8	2.5	LOC718812	hypothetical protein LOC718	MmuSTS.340.1.S1_at
Hypothetical Protein		2.0	2.3	**LOC713624**	hypothetical protein LOC713	MmugDNA.26033.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Hypothetical Protein		2.7	1.8	FLJ40869	hypothetical protein FLJ408	MmugDNA.31368.1.S1_at
Hypothetical Protein		2.1	2.0	LOC711569	hypothetical protein LOC71	MmugDNA.32941.1.S1_at
Hypothetical Protein		2.0	1.2	LOC711872	hypothetical protein LOC71	MmuSTS.4350.1.S1_at
Hypothetical Protein		2.3	1.3	LOC696907	hypothetical protein LOC69	MmugDNA.30940.1.S1_at
Hypothetical Protein		2.2	1.6	LOC700659	hypothetical protein LOC70	MmugDNA.35877.1.S1_s_at
Hypothetical Protein		2.4	2.0	LOC714457	CG30497-PA, isoform A	MmugDNA.28074.1.S1_at
Hypothetical Protein		2.7	2.0	**LOC715967**	hypothetical protein LOC71	MmugDNA.23367.1.S1_s_at
Hypothetical Protein		2.6	1.9	**LOC715967**	hypothetical protein LOC71	MmugDNA.23367.1.S1_at
Hypothetical Protein		1.9	2.2	**LOC713624**	hypothetical protein LOC71	MmugDNA.2320.1.S1_at
Hypothetical Protein		1.0	3.2	---	---	MmugDNA.26764.1.S1_at
Hypothetical Protein		1.9	4.2	---	---	MmugDNA.17680.1.S1_at
Hypothetical Protein		1.1	2.0	LOC717665	hypothetical protein LOC71	MmugDNA.3828.1.S1_at
Hypothetical Protein		1.6	2.3	C11orf82	Noxin	MmugDNA.3959.1.S1_at
Hypothetical Protein		1.5	2.5	C12orf48	C12orf48	MmugDNA.33807.1.S1_at
Hypothetical Protein		1.1	2.2	C1orf174	C1orf174	MmugDNA.25707.1.S1_at
Hypothetical Protein		1.9	2.5	C1orf31	C1orf31	MmugDNA.26763.1.S1_at
Hypothetical Protein		-1.3	2.0	C20orf199	C20orf199	MmugDNA.23475.1.S1_s_at
Hypothetical Protein		1.2	2.0	C21orf45	FASP1	MmugDNA.35383.1.S1_at
Hypothetical Protein		1.3	2.1	C3orf38	C3orf38	MmugDNA.40301.1.S1_at
Hypothetical Protein		1.3	2.0	LOC283951	No network object found	MmugDNA.14392.1.S1_at
Hypothetical Protein		1.4	2.1	LOC695780	FAST kinase domain-contai	MmugDNA.19959.1.S1_at
Hypothetical Protein		1.4	7.5	LOC696059	hypothetical protein LOC69	MmugDNA.24630.1.S1_s_at
Hypothetical Protein		1.4	2.0	LOC701070	FAM111A	MmugDNA.35003.1.S1_at
Hypothetical Protein		1.3	2.6	LOC701729	hypothetical protein LOC70	MmugDNA.27586.1.S1_at
Hypothetical Protein		1.7	2.2	LOC704259	hypothetical protein LOC70	MmugDNA.35965.1.S1_at
Hypothetical Protein		2.0	2.2	LOC707481	Separase	MmugDNA.15260.1.S1_at
Hypothetical Protein		1.4	2.1	LOC714874	ETF complex *	MmugDNA.39133.1.S1_at
Hypothetical Protein		1.4	2.9	LOC717665	hypothetical protein LOC71	MmugDNA.28886.1.S1_at
Hypothetical Protein		1.9	2.4	MGC5370	No network object found	MmugDNA.37694.1.S1_at
Hypothetical Protein		1.8	2.4	MRPL35	Large 39S subunit *	MmugDNA.13781.1.S1_at
Hypothetical Protein		1.5	2.2	TOMM5	C9orf105	MmugDNA.31006.1.S1_at
Hypothetical Protein		1.5	2.0	TOMM5	C9orf105	MmugDNA.31006.1.S1_s_at
Hypothetical Protein		1.6	2.9	WDR76	WDR76	MmugDNA.9449.1.S1_at
Hypothetical Protein		-2.0	-1.0	---	Transcribed locus, strongly	MmuAffx.23.12.S1_x_at
Hypothetical Protein		-2.4	1.1	---	Transcribed locus, strongly	MmuAffx.23.21.S1_s_at
Hypothetical Protein		-2.0	1.5	---	---	MmugDNA.24683.1.S1_at
Hypothetical Protein		-2.5	-1.1	---	---	MmugDNA.20647.1.S1_at
Hypothetical Protein		-2.5	1.6	---	---	MmugDNA.12998.1.S1_at
Hypothetical Protein		-2.0	1.1	LOC100130976	No network object found	MmugDNA.36815.1.S1_at
Hypothetical Protein		-2.0	1.3	LOC711574	hypothetical protein LOC71	MmugDNA.13302.1.S1_at
Hypothetical Protein		-2.2	-1.6	MGC45871	hypothetical protein	MmugDNA.12660.1.S1_at
Hypothetical Protein		-2.5	1.2	LOC696781	hypothetical protein LOC69	MmugDNA.28007.1.S1_at
Hypothetical Protein		1.1	-2.0	DKFZP434P211	DKFZP434P211	MmugDNA.23655.1.S1_at
Hypothetical Protein		-1.1	-2.2	LOC285965	No network object found	MmugDNA.30474.1.S1_at
Hypothetical Protein		1.2	-2.3	LOC693403		MmugDNA.11146.1.S1_at
Hypothetical Protein		1.1	-2.7	LOC712553		Mmu.15902.2.S1_at
Hypothetical Protein		1.2	-2.5	LOC728904	No network object found	MmugDNA.20697.1.S1_at
Unknown	Gene Function Unknown	2.5	2.7	ZNF367	zinc finger protein 367	MmugDNA.40258.1.S1_at
Unknown	Gene Function Unknown	2.5	5.9	LOC574106	alpha-1-antichymotrypsin	MmuSTS.2150.1.S1_at
Unknown	Gene Function Unknown	2.5	3.2	LOC699255	c-Mpl binding protein isofor	MmugDNA.38020.1.S1_at
Unknown	Gene Function Unknown	2.7	2.9	FAM83D (LOC697925)	Protein C20orf129	MmugDNA.20671.1.S1_at
Unknown	Gene Function Unknown	2.9	2.7	**FAM54A (LOC705828)**	family with sequence similar	MmugDNA.28821.1.S1_at
Unknown	Gene Function Unknown	2.0	1.6	**FAM54A (LOC705828)**	family with sequence similar	MmugDNA.9831.1.S1_at
Unknown	Gene Function Unknown	3.0	3.7	ERCC6L	excision repair cross-comple	MmugDNA.27885.1.S1_at
Unknown	Gene Function Unknown	2.7	2.5	**ANKRD22**	ankyrin repeat domain 22	MmugDNA.11765.1.S1_at
Unknown	Gene Function Unknown	2.2	1.9	**ANKRD22**	ankyrin repeat domain 22	MmugDNA.3988.1.S1_at
Unknown	Gene Function Unknown	2.1	-1.1	---		Mmu.15443.1.S1_x_at
Unknown	Gene Function Unknown	2.6	1.4	FAM46C	family with sequence similar	MmugDNA.3623.1.S1_at
Unknown	Gene Function Unknown	1.6	2.2	C18orf54	C18orf54	MmugDNA.12151.1.S1_at
Unknown	Gene Function Unknown	1.2	2.3	CEP27	CEP27	MmugDNA.4248.1.S1_at
Unknown	Gene Function Unknown	1.2	2.3	CEP27	CEP27	MmugDNA.4248.1.S1_at
Unknown	Gene Function Unknown	1.0	2.0	COQ4	COQ4	MmugDNA.26236.1.S1_at
Unknown	Gene Function Unknown	1.4	2.4	COX4NB	NOC4	MmugDNA.37901.1.S1_at
Unknown	Gene Function Unknown	-1.0	2.9	CPEB4	cytoplasmic polyadenylation	MmugDNA.32209.1.S1_at
Unknown	Gene Function Unknown	-1.2	2.4	DBNDD2	DBNDD2	MmugDNA.629.1.S1_at
Unknown	Gene Function Unknown	1.5	2.4	FAM98B	FAM98B	MmugDNA.23710.1.S1_at
Unknown	Gene Function Unknown	1.4	2.4	GAS2L3	GAS2L3	MmugDNA.7107.1.S1_at
Unknown	Gene Function Unknown	1.4	2.2	GSTCD	GSTCD	MmugDNA.43572.1.S1_at
Unknown	Gene Function Unknown	1.1	2.1	GTPBP8	GTPBP8	MmugDNA.6122.1.S1_at
Unknown	Gene Function Unknown	1.4	2.1	HEBP2	HEBP2	MmugDNA.19999.1.S1_at
Unknown	Gene Function Unknown	1.4	2.2	KIAA1618	Protein ALO17	MmugDNA.1519.1.S1_at
Unknown	Gene Function Unknown	1.7	2.1	LOC699733		Mmu.4098.1.S1_at
Unknown	Gene Function Unknown	1.7	2.7	LOC700208	epithelial stromal interaction	MmugDNA.15476.1.S1_at
Unknown	Gene Function Unknown	1.5	2.2	LOC701865		Mmu.8286.1.S1_s_at
Unknown	Gene Function Unknown	1.2	2.0	LOC701891		MmugDNA.22406.1.S1_at
Unknown	Gene Function Unknown	1.6	2.3	LOC701917		Mmu.9683.1.S1_at
Unknown	Gene Function Unknown	1.6	2.9	LOC702520	defective in sister chromatid	MmugDNA.19989.1.S1_at
Unknown	Gene Function Unknown	1.4	2.2	LOC714930		Mmu.4737.1.S1_at
Unknown	Gene Function Unknown	1.1	2.3	LOC702789		MmuSTS.1193.1.S1_at
Unknown	Gene Function Unknown	1.5	3.0	LOC703327	mesoderm specific transcrip	MmugDNA.41111.1.S1_at
Unknown	Gene Function Unknown	-1.1	2.0	LOC710770	KIAA1913	MmugDNA.19520.1.S1_at
Unknown	Gene Function Unknown	-1.1	3.1	LOC713440	Normal mucosa of esophagu	MmugDNA.34136.1.S1_at
Unknown	Gene Function Unknown	1.6	2.1	PLAC8	PLAC8	MmugDNA.13757.1.S1_at
Unknown	Gene Function Unknown	1.3	2.2	PTPLAD2	Protein tyrosine phosphatas	MmugDNA.17986.1.S1_s_at
Unknown	Gene Function Unknown	1.3	2.0	RNF10	RNF10	MmugDNA.37275.1.S1_at
Unknown	Gene Function Unknown	-1.1	2.3	RORA	ROR-alpha	MmugDNA.789.1.S1_at
Unknown	Gene Function Unknown	1.2	2.1	RPL26L1	60S ribosomal protein L26-li	MmugDNA.38117.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Unknown	Gene Function Unknown	1.3	3.2	RPL39L	---	MmugDNA.27695.1.S1_at
Unknown	Gene Function Unknown	1.8	2.3	SCRN3	SCRN3	MmugDNA.895.1.S1_s_at
Unknown	Gene Function Unknown	1.8	2.0	SDF2L1	SDF2L1	MmugDNA.34901.1.S1_at
Unknown	Gene Function Unknown	-1.1	2.2	SMCHD1	Smchd1	MmugDNA.14214.1.S1_at
Unknown	Gene Function Unknown	1.4	2.3	SNHG1	No network object found	MmugDNA.6132.1.S1_at
Unknown	Gene Function Unknown	1.2	2.3	SNHG12	C1orf79	MmugDNA.33923.1.S1_at
Unknown	Gene Function Unknown	-1.4	2.0	SSBP2	SSBP2	MmugDNA.30899.1.S1_at
Unknown	Gene Function Unknown	-1.4	2.0	SVIP	SVIP	MmugDNA.26191.1.S1_at
Unknown	Gene Function Unknown	1.3	2.1	TACC3	TACC3	MmugDNA.37541.1.S1_at
Unknown	Gene Function Unknown	1.2	2.2	TMEM126B	TMEM126B	MmugDNA.2767.1.S1_at
Unknown	Gene Function Unknown	1.8	2.0	XRCC6BP1	XRCC6BP1	MmugDNA.12823.1.S1_at
Unknown	Gene Function Unknown	1.8	2.1	XTP3TPA	XTP3TPA	MmugDNA.19997.1.S1_s_at
Unknown	Gene Function Unknown	1.0	2.6	**ZCCHC2**	ZCCHC2	MmugDNA.28694.1.S1_at
Unknown	Gene Function Unknown	1.2	2.1	**ZCCHC2**	ZCCHC2	MmugDNA.28694.1.S1_s_at
Unknown	Gene Function Unknown	-2.3	-2.2	---	solute carrier family 26, men	MmuSTS.4436.1.S1_at
Unknown	Gene Function Unknown	-2.2	-1.1	LOC701902	---	Mmu.8061.1.S1_at
Unknown	Gene Function Unknown	1.1	-2.1	C14orf53	C14orf53	MmugDNA.31592.1.S1_at
Unknown	Gene Function Unknown	-1.1	-2.3	CAMK1G	CLICKIII	MmugDNA.22719.1.S1_s_at
Unknown	Gene Function Unknown	1.2	-2.6	CCDC108	CCDC108	MmugDNA.35731.1.S1_a_at
Unknown	Gene Function Unknown	1.2	-2.2	FHAD1	forkhead-associated (FHA)	MmugDNA.13222.1.S1_s_at
Unknown	Gene Function Unknown	1.1	-2.2	**LOC701581**		MmunewRS.301.1.S1_a_at
Unknown	Gene Function Unknown	1.2	-2.6	**LOC701581**		MmunewRS.301.1.S1_at
Unknown	Gene Function Unknown	1.1	-2.1	TACC1	TACC1	MmugDNA.40005.1.S1_at
Unknown		2.3	1.8	C14ORF106	chromosome 14 open readi	MmugDNA.5761.1.S1_at
Unknown		1.9	2.3	C14ORF106	M18BP1	MmugDNA.6067.1.S1_at
Unknown		4.0	3.7	---	---	MmuSTS.4748.1.S1_at
Unknown		3.7	6.1	---	---	MmuSTS.1531.1.S1_at
Unknown		3.1	2.9	---	---	MmuSTS.1534.1.S1_at
Unknown		3.5	7.2	C18ORF24	chromosome 18 open readi	MmugDNA.39863.1.S1_at
Unknown		2.5	3.6	CHAC2	ChaC, cation transport regul	MmugDNA.66.1.S1_at
Unknown		3.0	2.1	**DEPDC1 (LOC701888)**	DEP domain containing 1a	MmugDNA.29315.1.S1_at
Unknown		2.1	3.7	**DEPDC1 (LOC701888)**	DEP domain containing 1a	MmugDNA.40906.1.S1_at
Unknown		2.2	3.6	FLJ10292 (LOC717824)	mago-nashi homolog	MmugDNA.4402.1.S1_s_at
Unknown		2.1	2.1	LOC697934	Protein KIAA0152 precurso	MmugDNA.4669.1.S1_at
Unknown		2.2	2.8	LOC715676		Mmu.12263.1.S1_at
Unknown		2.2	1.8	---	???	MmugDNA.2759.1.S1_at
Unknown		2.2	1.7	---	???	Mmu.2276.1.S1_at
Unknown		3.5	1.3	---	---	Mmu.15507.1.S1_x_at
Unknown		2.1	1.5	LOC700859	CG11699-PA (chromosome	MmugDNA.31089.1.S1_s_at
Unknown		2.4	1.9	LOC704099	CG6597-PA, isoform A (def	MmugDNA.5478.1.S1_at
Unknown		1.9	2.5	---	???	MmugDNA.1253.1.S1_at
Unknown		-1.2	2.7	---	???	MmugDNA.43397.1.S1_at
Unknown		-1.1	2.2	---	Protein KIAA0143	Mmu.586.1.S1_at
Unknown		-1.0	4.3	---	Protein KIAA0143	Mmu.586.2.S1_at
Unknown		-1.3	2.5	---	???	MmuAffx.78.1.S1_s_at
Unknown		1.1	2.0	---		MmuSTS.1833.1.S1_at
Unknown		1.4	2.0	---		Mmu.6730.1.S1_at
Unknown		1.4	2.0	LOC708475		MmuSTS.961.1.S1_at
Unknown		1.0	2.0	**LOC712882**		MmugDNA.1074.1.S1_at
Unknown		1.8	2.1	**LOC712882**		MmuSTS.1683.1.S1_at
Unknown		1.1	2.0	LOC709637		MmugDNA.37112.1.S1_at
Unknown		1.1	2.0	---		MmugDNA.5668.1.S1_at
Unknown		1.4	2.0	---		MmunewRS.252.1.S1_at
Unknown		1.4	2.0	LOC698461		MmuSTS.3695.1.S1_at
Unknown		-1.0	2.0	LOC696653		MmuSTS.68.1.S1_at
Unknown		1.3	2.0	---		MmugDNA.10466.1.S1_at
Unknown		1.5	2.0	LOC715437		MmugDNA.5796.1.S1_s_at
Unknown		1.2	2.0	LOC719004		MmuSTS.958.1.S1_at
Unknown		-1.1	2.0	C8orf31	No network object found	MmugDNA.27925.1.S1_at
Unknown		1.9	2.0	C13orf3	C13orf3	MmugDNA.23023.1.S1_at
Unknown		1.4	2.0	LOC714828		MmuSTS.2341.1.S1_at
Unknown		1.5	2.0	---		MmugDNA.393.1.S1_at
Unknown		-1.2	2.0	---		MmugDNA.38123.1.S1_at
Unknown		1.4	2.0	---		MmugDNA.39220.1.S1_at
Unknown		1.6	2.1	LOC714844		Mmu.15592.2.S1_at
Unknown		1.8	2.1	---		MmuSTS.1595.1.S1_at
Unknown		-1.2	2.1	KIAA1310	FLJ10081	MmugDNA.34387.1.S1_at
Unknown		1.5	2.1	LOC719808		MmuSTS.4399.1.S1_at
Unknown		1.0	2.1	---		MmugDNA.17162.1.S1_at
Unknown		1.8	2.1	LOC697698		MmuSTS.713.1.S1_at
Unknown		1.1	2.1	---		MmugDNA.29255.1.S1_at
Unknown		1.6	2.1	---		Mmu.7716.1.S1_at
Unknown		2.0	2.1	LOC707321		MmuSTS.2151.1.S1_at
Unknown		1.3	2.1	---		MmugDNA.24318.1.S1_at
Unknown		1.7	2.1	LOC695971		MmuSTS.1377.1.S1_at
Unknown		1.0	2.1	---		MmugDNA.9710.1.S1_at
Unknown		-1.5	2.1	---		Mmu.8273.1.S1_at
Unknown		1.2	2.1	LOC710680		MmugDNA.20706.1.S1_at
Unknown		1.7	2.1	LOC698482		MmuSTS.2698.1.S1_x_at
Unknown		1.1	2.1	---		MmuMitochon.13.1.S1_at
Unknown		1.0	2.1	---		MmugDNA.9815.1.S1_at
Unknown		1.7	2.1	LOC709326		MmuSTS.54.1.S1_at
Unknown		1.7	2.2	LOC709326		MmuSTS.54.1.S1_s_at
Unknown		1.3	2.1	LOC714217		Mmu.3556.1.S1_s_at
Unknown		1.9	2.1	---		Mmu.11863.1.S1_at
Unknown		-1.2	2.1	---		Mmu.1819.1.S1_at
Unknown		1.2	2.1	LOC719260		Mmu.10556.1.S1_s_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Unknown		-1.7	2.1	LOC707432		MmuSTS.1462.1.S1_at
Unknown		1.0	2.2	---		MmugDNA.1781.1.S1_at
Unknown		1.9	2.2	LOC715866		MmuSTS.2830.1.S1_at
Unknown		-2.4	2.2	---		MmugDNA.23105.1.S1_at
Unknown		1.4	2.2	LOC711746		MmuSTS.2023.1.S1_at
Unknown		-1.0	2.2	---		MmugDNA.32814.1.S1_at
Unknown		1.0	2.2	---		MmugDNA.14777.1.S1_at
Unknown		1.8	2.2	LOC718376		MmuSTS.4765.1.S1_at
Unknown		-1.4	2.2	---		Mmu.3044.12.S1_s_at
Unknown		1.9	2.2	LOC713130		Mmu.11204.1.S1_s_at
Unknown		1.7	2.2	LOC719092		Mmu.11584.1.S1_at
Unknown		1.0	2.2	---		MmugDNA.7666.1.S1_at
Unknown		1.1	2.2	LOC713715		MmuSTS.3349.1.S1_at
Unknown		1.3	2.2	---		MmugDNA.20683.1.S1_at
Unknown		1.1	2.2	LOC714885		MmugDNA.43317.1.S1_at
Unknown		-1.3	2.2	LOC713696		MmuSTS.2193.1.S1_at
Unknown		-1.2	2.2	LOC712754		MmuSTS.3131.1.S1_at
Unknown		1.4	2.2	---		Mmu.10692.1.A1_at
Unknown		1.7	2.3	---		MmuSTS.4533.1.S1_at
Unknown		1.7	2.3	LILRAE		MmugDNA.20252.1.S1_x_at
Unknown		1.4	2.3	---		MmugDNA.9429.1.S1_at
Unknown		1.6	2.3	MRPL36	Large 39S subunit *	MmugDNA.33607.1.S1_at
Unknown		-1.0	2.3	LOC697232		MmuSTS.109.1.S1_at
Unknown		2.0	2.3	LYAR	LYAR	MmugDNA.22734.1.S1_at
Unknown		1.7	2.3	LOC705690		MmugDNA.7284.1.S1_at
Unknown		1.5	2.3	LOC709186		MmuSTS.597.1.S1_s_at
Unknown		-1.1	2.3	---		MmugDNA.39324.1.S1_at
Unknown		1.8	2.3	LOC696519		MmuSTS.2135.1.S1_at
Unknown		1.8	2.3	LOC697028		MmunewRS.881.1.S1_at
Unknown		1.9	2.3	**LOC695933**		MmuSTS.55.1.S1_at
Unknown		1.7	2.3	**LOC695933**		Mmu.7027.1.S1_at
Unknown		1.1	2.3	---		MmuSTS.3531.1.S1_at
Unknown		-1.1	2.3	Mmu.1314.2		Mmu.1314.2.S1_a_at
Unknown		1.4	2.3	LOC706022		MmugDNA.5960.1.S1_at
Unknown		1.4	2.3	---		MmuSTS.1253.1.S1_at
Unknown		1.1	2.3	LOC713563		MmuSTS.3453.1.S1_at
Unknown		1.2	2.3	---		MmugDNA.20633.1.S1_at
Unknown		1.4	2.4	---		MmuSTS.3999.1.S1_at
Unknown		1.8	2.4	---		MmuSTS.173.1.S1_at
Unknown		1.8	2.4	---		MmugDNA.43203.1.S1_at
Unknown		2.0	2.4	LOC716218		MmuSTS.3922.1.S1_at
Unknown		1.0	2.4	---		MmuSTS.874.1.S1_at
Unknown		1.3	2.5	LOC696142		Mmu.5234.1.S1_at
Unknown		1.2	2.5	LOC707233		Mmu.11739.1.S1_at
Unknown		1.0	2.5	LOC712288		MmuSTS.849.1.S1_at
Unknown		-1.6	2.5	---		Mmu.15402.1.A1_at
Unknown		-1.4	2.5	---		MmugDNA.31642.1.S1_at
Unknown		1.3	2.5	---		MmugDNA.31145.1.S1_at
Unknown		1.1	2.6	LOC706698		Mmu.5288.1.S1_at
Unknown		1.1	2.6	LOC715638		MmuSTS.602.1.S1_at
Unknown		1.2	2.7	LOC713150		Mmu.8081.1.S1_x_at
Unknown		1.0	2.7	LOC718942		MmunewRS.154.1.S1_s_at
Unknown		1.0	2.8	---		MmugDNA.12088.1.S1_at
Unknown		-1.3	2.8	---		MmugDNA.39778.1.S1_at
Unknown		-1.3	2.9	---		MmugDNA.15061.1.S1_at
Unknown		1.3	3.0	LOC696253		MmunewRS.661.1.S1_at
Unknown		2.0	3.1	---		MmugDNA.34912.1.S1_at
Unknown		1.5	3.1	---		MmuAffx.23.16.S1_s_at
Unknown		-1.1	3.1	---		Mmu.2120.1.A1_at
Unknown		1.3	3.4	---		MmugDNA.22699.1.S1_at
Unknown		1.4	3.9	---		Mmu.3117.1.S1_at
Unknown		-1.4	4.3	---		Mmu.12003.1.S1_s_at
Unknown		-1.1	4.9	---		MmuMitochon.6.1.S1_s_at
Unknown		-1.0	7.1	---		Mmu.10209.2.S1_at
Unknown		1.1	10.3	---		MmuMitochon.3.1.S1_s_at
Unknown		1.2	11.8	---		MmuMitochon.10.1.S1_s_at
Unknown		-2.3	1.0	---	---	MmugDNA.21478.1.S1_at
Unknown		-2.6	-1.1	---	---	MmugDNA.11704.1.S1_at
Unknown		-2.1	1.7	---	Transcribed locus	Mmu.12981.1.S1_s_at
Unknown		-2.1	-1.1	---	---	MmugDNA.2555.1.S1_at
Unknown		-2.3	-1.3	---	---	MmuSTS.4146.1.S1_at
Unknown		-2.3	1.1	---	---	MmugDNA.36051.1.S1_at
Unknown		-2.0	-1.2	LOC709116	Probable ATP-dependent he	MmugDNA.37035.1.S1_at
Unknown		-1.1	-24.6	---		Mmu.5392.1.S1_at
Unknown		-1.1	-5.5	LOC708902		MmuSTS.2297.1.S1_at
Unknown		1.1	-3.1	**LOC721825**		MmunewRS.138.1.S1_at
Unknown		1.1	-2.2	**LOC721825**		MmunewRS.138.1.S1_s_at
Unknown		1.1	-2.9	---		MmugDNA.31864.1.S1_at
Unknown		1.1	-2.9	---		Mmu.6835.1.S1_at
Unknown		1.1	-2.9	---		MmugDNA.31864.1.S1_x_at
Unknown		1.4	-2.5	LOC697303	Immunoglobulin omega chai	MmugDNA.23432.1.S1_at
Unknown		1.1	-2.5	---		MmugDNA.7727.1.S1_at
Unknown		-1.1	-2.4	---		MmugDNA.4213.1.S1_at
Unknown		1.1	-2.3	LOC715289		MmugDNA.29979.1.A1_at
Unknown		1.1	-2.3	---	---	MmugDNA.21052.1.S1_at
Unknown		1.2	-2.3	---		MmuSTS.1866.1.S1_at
Unknown		1.2	-2.3	---		MmuAffx.259.1.A1_at

Classification	Sub-Classification	SM Fold Changes 14dpi	RM Fold Canges 14dpi	Gene Symbol	Gene Title	Affymetrix ID
Unknown		-1.1	-2.3	---		Mmu.4119.3.S1_at
Unknown		1.1	-2.3	---		MmugDNA.15844.1.S1_at
Unknown		1.0	-2.2	---		MmunewRS.296.1.S1_at
Unknown		1.0	-2.2	---		MmugDNA.43046.1.S1_at
Unknown		1.1	-2.1	---		MmugDNA.20526.1.S1_at
Unknown		1.1	-2.1	---		MmugDNA.28701.1.S1_at
Unknown		-1.0	-2.1	---		MmugDNA.30494.1.S1_at
Unknown		1.3	-2.1	---		MmugDNA.26390.1.S1_x_at
Unknown		1.0	-2.1	LOC716322		MmugDNA.31119.1.S1_at
Unknown		1.1	-2.1	---		Mmu.1367.1.S1_at
Unknown		1.0	-2.1	FLJ42875	FLJ42875	MmugDNA.8763.1.S1_at
Unknown		-1.0	-2.1	---		MmugDNA.12100.1.S1_at
Unknown		-1.2	-2.1	---		MmuSTS.2916.1.S1_at
Unknown		1.0	-2.0	LOC697110		MmugDNA.24580.1.S1_at
Unknown		1.1	-2.0	---		MmugDNA.28093.1.S1_at
Unknown		1.1	-2.0	---		MmugDNA.34236.1.S1_at

Supplemental Table S8. Gene expression induced in SM LNs by SIVsmm infection.
Fold changes at 14 dpi and 30 dpi SMs arranged by functional categories. Red indicates significantly increased expression, green significantly decreased expression, and black, not significantly altered in expression from base line by the criteria of ≥ 2-fold change or Wilcoxon signed-rank test, P < 0.05.

Classification	Sub-Classification	SM Fold Changes 14 dpi	SM Fold Changes 30 dpi	Gene Symbol	Gene Name	Affymetrix ID
Apoptosis	Anti-Apoptosis	2.5	2.2	BIRC5 (SURVIVIN)	Baculoviral IAP repeat-co	MmuSTS.1955.1.S1_at
Apoptosis	Anti-Apoptosis	-1.0	2.3	PTTG1	Securin (Pituitary tumor-t	MmugDNA.11903.1.S1_at
Apoptosis	Anti-Apoptosis	3.6	3.5	PTTG1	Securin (Pituitary tumor-t	MmugDNA.31059.1.S1_s_at
Apoptosis	Anti-Apoptosis	3.0	3.7	PTTG1	Securin (Pituitary tumor-t	MmugDNA.31059.1.S1_at
Apoptosis	Anti-Apoptosis	4.2	1.8	IFI-6-16	putative 6-16 protein	MmuSTS.4428.1.S1_at
Apoptosis	Pro-apoptotic	2.3	1.8	BRI3BP	BRI3-binding protein	MmuSTS.560.1.S1_at
Apoptosis	Pro-apoptotic	2.3	1.5	CYCS	cytochrome c	MmugDNA.31771.1.S1_s_at
Apoptosis	Pro-apoptotic	2.4	1.6	CYCS	cytochrome c	Mmu.4398.1.S1_s_at
Apoptosis	Pro-apoptotic	2.3	1.6	CYCS	cytochrome c	MmugDNA.31771.1.S1_at
Apoptosis	Pro-apoptotic	2.0	1.5	IKIP	IKK interacting protein iso	MmugDNA.13217.1.S1_at
Apoptosis	Pro-apoptotic	3.3	1.2	PACAP	Proapoptotic caspase ada	MmugDNA.22076.1.S1_at
Apoptosis	Pro-apoptotic	2.9	1.3	PACAP	Proapoptotic caspase ada	MmugDNA.12895.1.S1_s_at
Apoptosis	Anti-Apoptosis	2.3	1.4	XAF1	XIAP associated factor-1	MmugDNA.33861.1.S1_at
Apoptosis	Pro-apoptotic	2.1	2.5	ITGB3BP	NRIF3	MmugDNA.16765.1.S1_at
Apoptosis	Pro-apoptotic	-1.3	-2.2	STK4	serine/threonine kinase 4	MmugDNA.25722.1.S1_at
Apoptosis	Pro-apoptotic	-1.3	-2.0	TNFSF10	tumor necrosis factor (liga	MmugDNA.30129.1.S1_at
Apoptosis	Pro-apoptotic	-3.6	-4.8	NR4A1	nuclear receptor subfamil	MmugDNA.18685.1.S1_at
Apoptosis	Pro-apoptotic	-2.2	-2.0	**TNFRSF25**	tumor necrosis factor rec	MmugDNA.10013.1.S1_s_at
Apoptosis	Pro-apoptotic	-2.1	-1.7	**TNFRSF25**	tumor necrosis factor rec	MmugDNA.5862.1.S1_s_at
Apoptosis	Pro-apoptotic	-2.2	-1.3	TIAM1	T-cell lymphoma invasion	MmugDNA.20387.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	4.5	2.8	IGH chain complementarity	Ig heavy chain compleme	MmuAffx.225.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.8	4.9	IGHG1	Ig heavy chain V-I region	MmugDNA.15990.1.S1_s_at
B Cell Proliferation/Differentiation	Ig Related	2.9	2.4	IGKV1-5	Ig kappa chain V-I region	MmugDNA.27721.1.S1_x_at
B Cell Proliferation/Differentiation	Ig Related	2.2	2.0	IGKV1-5	Ig kappa chain V-I region	MmugDNA.16712.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	2.4	2.2	IGKV1-5	Ig kappa chain V-I region	MmugDNA.41766.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	4.1	1.6	**Ig kappa chain V-II region**	Ig kappa chain V-II regior	Mmu.9614.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	5.4	2.4	**Ig kappa chain V-II region**	Ig kappa chain V-II regior	MmugDNA.3445.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	2.9	1.7	**Ig kappa chain V-II region**	Ig kappa chain V-II regior	MmugDNA.41808.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.3	1.1	IGHV	Ig heavy chain V-III regio	Mmu.12915.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.8	1.8	IGKC	Ig rearranged light chain	Mmu.2571.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	2.9	1.7	IGKC	Ig kappa chain V-I region	MmugDNA.39296.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.3	2.3	**IGKV**	Immunoglobulin kappa lig	MmugDNA.27721.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	2.6	2.2	**IGKV**	Immunoglobulin kappa lig	MmugDNA.37783.1.S1_x_at
B Cell Proliferation/Differentiation	Ig Related	2.6	1.7	LOC701504	Ig kappa chain V-III regio	MmugDNA.31268.1.S1_at
B Cell Proliferation/Differentiation	Ig Related	3.3	1.7	LOC706650	Ig J chain	MmunewRS.816.1.S1_s_at
B Cell Proliferation/Differentiation	Ig Related	-1.8	-2.5	IGLC2	Immunoglobulin lambda-	MmugDNA.11907.1.S1_s_at
B Cell Proliferation/Differentiation	Ig Related	-2.3	-2.7	IGLC2	Ig lambda chain V-I regi	MmugDNA.10412.1.S1_x_at
B Cell Proliferation/Differentiation	Ig Related	-2.3	-2.4	IGLC2	Ig lambda chain V-I regi	MmugDNA.10412.1.S1_at
B Cell Proliferation/Differentiation		2.1	2.1	POU2AF1	---	MmugDNA.21562.1.S1_at
B Cell Proliferation/Differentiation		2.7	7.2	AICDA	activation-induced cytidir	MmugDNA.40365.1.S1_at
B Cell Proliferation/Differentiation		1.9	2.2	BANK1	B-cell scaffold protein wi	MmuSTS.547.1.S1_at
B Cell Proliferation/Differentiation		1.5	2.6	LRMP	lymphoid-restricted memb	MmuSTS.4537.1.S1_at
Chemokine Receptors and Ligands		5.2	1.9	CXCL10 (IP-10)	chemokine (C-X-C motif)	Mmu.11363.1.S1_at
Chemokine Receptors and Ligands		6.6	2.4	CXCL10 (IP-10)	chemokine (C-X-C motif)	MmuSTS.1893.1.S1_s_at
Chemokine Receptors and Ligands		7.7	2.0	**CXCL11 (IP-9/I-TAC)**	chemokine (C-X-C motif)	MmugDNA.15618.1.S1_s_at
Chemokine Receptors and Ligands		7.2	1.8	**CXCL11 (IP-9/I-TAC)**	chemokine (C-X-C motif)	Mmu.11366.1.S1_at
Chemokine Receptors and Ligands		4.7	1.7	**CXCL11 (IP-9/I-TAC)**	chemokine (C-X-C motif)	MmugDNA.19126.1.S1_at
Chemokine Receptors and Ligands		3.9	1.8	**CCL20 (MIP3A)**	chemokine (C-C motif) lig	MmuSTS.1416.1.S1_at
Chemokine Receptors and Ligands		3.6	1.5	**CCL20 (MIP3A)**	chemokine (C-C motif) lig	Mmu.5186.1.S1_at
Chemokine Receptors and Ligands		3.5	1.0	**CXCL9 (MIG)**	chemokine (C-X-C motif)	Mmu.11358.1.S1_at
Chemokine Receptors and Ligands		4.9	1.7	**CXCL9 (MIG)**	chemokine (C-X-C motif)	MmuSTS.4003.1.S1_at
Chemokine Receptors and Ligands		2.4	1.4	XCL1	chemokine (C motif) ligar	MmugDNA.2039.1.S1_s_at
Chemokine Receptors and Ligands		-1.8	-2.3	CCL21	chemokine (C-C motif) lig	MmuSTS.3567.1.S1_at
Chemokine Receptors and Ligands		-2.9	-2.8	CXCL12 (SDF-1)	chemokine (C-X-C motif)	Mmu.6455.1.S1_at
Chemokine Receptors and Ligands		-2.1	-1.7	CCL22 (MDC)	chemokine (C-C motif) lig	MmuSTS.3569.1.S1_at
B Cell Proliferation/Differentiation		-3.7	-4.3	CD179b	Ig lambda chain V-II regi	MmugDNA.23105.1.S1_s_at
Immune Defenses	Antiviral Proteins	-1.0	2.6	alpha-defensin 3 precursor	alpha-defensin 3 precurs	Mmu.7520.1.S1_x_at
Immune Defenses	Antiviral Proteins	1.2	3.1	alpha-defensin 4 precursor	alpha-defensin 4 precurs	Mmu.9266.1.S1_x_at

Classification	Sub-Classification	SM Fold Changes 14 dpi	SM Fold Changes 30 dpi	Gene Symbol	Gene Name	Affymetrix ID
Immune Defenses	IFN Related	2.0	1.3	IFI27	putative ISG12(c) protein	MmunewRS.254.1.S1_at
Immune Defenses	IFN Related	5.2	1.9	IFIT1 (IFI-56)	IFIT1	MmuSTS.1579.1.S1_at
Immune Defenses	IFN Related	2.5	1.4	IFIT3 (IFI-60)	interferon-induced protein	MmugDNA.19594.1.S1_at
Immune Defenses	IFN Related	2.6	1.6	IFIT4	interferon-induced protein	MmugDNA.24962.1.S1_at
Immune Defenses	IFN Related	3.9	1.7	MX1	myxovirus (influenza virus	MmuSTS.3006.1.S1_at
Immune Defenses	IFN Related	2.3	1.2	**OAS1**	2',5'-oligoadenylate synth	MmuSTS.4655.1.S1_at
Immune Defenses	IFN Related	2.2	1.3	**OAS1**	2-5-oligoadenylate synthe	MmuSTS.1612.1.S1_at
Immune Defenses	IFN Related	2.4	1.1	OAS2	2-5-oligoadenylate synthe	MmugDNA.8486.1.S1_at
Immune Defenses	IFN Related	3.1	1.7	**RSAD2 (CIG5)**	radical S-adenosyl methio	MmugDNA.41706.1.S1_at
Immune Defenses	IFN Related	2.1	1.5	**RSAD2 (CIG5)**	---	MmuSTS.1497.1.S1_at
Immune Defenses	IFN Related	3.2	1.8	IFI44	interferon-induced, hepat	MmugDNA.12892.1.S1_at
Immune Defenses	IFN Related	3.1	2.4	IFI44	interferon-induced, hepat	MmuSTS.3682.1.S1_x_at
Immune Defenses	IFN Related	2.6	2.0	STAT1	signal transducer and act	MmugDNA.23497.1.S1_at
Immune Defenses	IFN Related	2.0	1.6	STAT1	signal transducer and act	MmuSTS.3917.1.S1_at
Immune Defenses	CD8 T cells, NK cells,	4.4	1.8	GZMA	Granzyme A precursor (C	MmugDNA.36434.1.S1_at
Immune Defenses	CD8 T cells, NK cells,	2.3	1.2	GZMB	Granzyme B precursor (T	MmugDNA.14204.1.S1_at
Immune Defenses	NK Cells	2.4	1.7	KLRC1 (NKG2A)	NKG2-A	MmuSTS.2945.1.S1_s_at
Immune Defenses	NK Cells	2.0	1.2	KLRC3/NKG2E	killer cell lectin-like recept	Mmu.1906.11.S1_a_at
Immune Activation	Activation	2.4	1.5	BAG2	BAG family molecular ch	MmuSTS.2142.1.S1_at
Immune Activation	Activation	2.1	1.8	FOXM1	forkhead box M1 isoform	MmugDNA.11364.1.S1_at
Immune Activation	Activation	2.1	1.4	HSPD1	heat shock 60kDa protein	MmugDNA.19456.1.S1_at
Immune Activation	Activation	2.3	1.7	TPX2	TPX2, microtubule-assoc	MmuSTS.4420.1.S1_at
Immune Activation	Activation	2.0	1.6	TZFP	testis zinc finger protein	MmuSTS.2900.1.S1_at
Immune Activation	Activation	2.7	2.0	**SLC16A1 (MCT1)**	solute carrier family 16, m	MmugDNA.21701.1.S1_at
Immune Activation	Activation	2.0	1.6	**SLC16A1 (MCT1)**	solute carrier family 16, m	MmuSTS.3828.1.S1_at
Immune Activation	Activation	2.8	1.4	CD38	CD38 antigen	MmuSTS.1849.1.S1_at
Immune Activation	Activation	2.6	1.9	**MKI67**	Antigen KI-67	MmugDNA.32726.1.S1_at
Immune Activation	Activation	2.1	2.2	**MKI67**	Antigen KI-67	MmugDNA.32729.1.S1_at
Immune Activation	Activation	2.6	2.5	PCNA	proliferating cell nuclear a	MmugDNA.865.1.S1_at
Immune Activation	Activation	2.8	2.3		Chromatin assembly facto	MmuSTS.673.1.S1_s_at
Immune Activation	Activation	4.6	5.8	UHRF1	ubiquitin-like, containing P	MmugDNA.19464.1.S1_at
Immune Activation	Activation	3.0	2.7	HELLS	helicase, lymphoid-specif	MmuSTS.61.1.S1_at
Immune Activation	Activation	3.1	2.0	HERC5	hect domain and RLD 5	MmugDNA.38910.1.S1_at
Immune Activation	Activation	4.6	5.5	PBK	T-LAK cell-originated prot	MmugDNA.33387.1.S1_at
Immune Activation	Activation	2.2	2.3	**RFC3**	replication factor C 3	MmugDNA.24482.1.S1_at
Immune Activation	Activation	2.3	2.8	**RFC3**	replication factor C 3	MmugDNA.18123.1.S1_at
Immune Activation	Activation	5.5	6.3	SHCBP1	SHC SH2-domain binding	MmugDNA.30433.1.S1_at
Immune activation	Activation	1.4	2.1	RBBP8	retinoblastoma binding pr	MmugDNA.24390.1.S1_at
Immune activation	Activation	1.4	2.6	LOC699158	T-cell activation kelch re	MmuSTS.3946.1.S1_at
Immune Activation	Activation	-2.2	-2.0	TCF7	transcription factor 7 (T-c	MmugDNA.40627.1.S1_s_at
Immune Activation	Activation	-2.1	-1.8	TSPAN7	tetraspanin 7	Mmu.11195.1.S1_at
Immune Activation	Activation	-1.9	-2.5	NFKB2	nuclear factor of kappa lig	MmugDNA.42566.1.S1_at
Immune Activation	Activation	-1.2	-2.4	SLC8A1	solute carrier family 8 (so	MmugDNA.19708.1.S1_at
Immune Activation	Activation	-1.1	-2.4	SLC8A1	solute carrier family 8 (so	MmugDNA.19708.1.S1_s_at
Immune Activation	Cell Cycle	-1.9	-2.1	SILV	Silver homolog	MmugDNA.27504.1.S1_at
Immune Activation	Cell Cycle	2.9	3.5	**Anillin**	anillin, actin binding prote	MmugDNA.2951.1.S1_at
Immune Activation	Cell Cycle	4.8	6.2	**Anillin**	anillin, actin binding prote	MmugDNA.2951.1.S1_s_at
Immune Activation	Cell Cycle	1.9	2.2	**Anillin**	anillin, actin binding prote	MmugDNA.682.1.S1_at
Immune Activation	Cell Cycle	3.8	3.7	ASPM	asp (abnormal spindle)-lik	MmugDNA.5265.1.S1_at
Immune Activation	Cell cycle	3.2	4.0	ASPM	asp (abnormal spindle)-lik	MmugDNA.25197.1.S1_at
Immune Activation	Cell Cycle	3.5	4.0	**BUB1**	---	MmugDNA.14075.1.S1_at
Immune Activation	Cell Cycle	3.7	5.2	**BUB1**	BUB1 budding uninhibited	MmugDNA.6277.1.S1_at
Immune Activation	Cell Cycle	5.7	8.5	**BUB1**	BUB1 budding uninhibited	MmuSTS.2164.1.S1_at
Immune Activation	Cell Cycle	4.4	7.7	**BUB1**	BUB1 budding uninhibited	MmuSTS.2164.1.S1_s_at
Immune Activation	Cell Cycle	2.5	3.0	CASC5	cancer susceptibility cand	MmugDNA.10186.1.S1_at
Immune Activation	Cell Cycle	4.5	4.7	**CDC2**	cell division cycle 2 protei	MmugDNA.14959.1.S1_at
Immune Activation	Cell Cycle	2.7	3.0	**CDC2**	cell division cycle 2 protei	MmugDNA.25206.1.S1_at
Immune Activation	Cell Cycle	3.9	5.2	**CDC2**	cell division cycle 2 protei	MmugDNA.42865.1.S1_at
Immune Activation	Cell Cycle	3.1	2.5	CDC20	cell division cycle 20	MmugDNA.18794.1.S1_at
Immune Activation	Cell Cycle	2.7	2.0	CDC25A	cell division cycle 25A iso	MmugDNA.24430.1.S1_at
Immune Activation	Cell Cycle	2.5	2.0	CDC6	CDC6 homolog	MmuSTS.3380.1.S1_at
Immune Activation	Cell Cycle	3.6	2.6	CDC6	CDC6 homolog	MmugDNA.14956.1.S1_at
Immune Activation	Cell Cycle	3.6	3.8	CDCA1	cell division cycle associa	MmugDNA.2768.1.S1_at
Immune Activation	Cell Cycle	2.1	2.1	CDCA5	cell division cycle associa	MmugDNA.4124.1.S1_at
Immune Activation	Cell Cycle	2.7	4.2	CDCA7	cell division cycle associa	MmugDNA.17329.1.S1_at
Immune Activation	Cell Cycle	3.3	3.4	**CDKN3**	cyclin-dependent kinase i	MmugDNA.10778.1.S1_at
Immune Activation	Cell Cycle	5.3	6.0	**CDKN3**	cytoskeleton associated p	MmugDNA.6706.1.S1_at
Immune Activation	Cell Cycle	2.1	2.2	**CDKN3**	cyclin-dependent kinase i	MmugDNA.34975.1.S1_s_at
Immune Activation	Cell Cycle	5.0	4.9	CENPA	centromere protein A	MmugDNA.15250.1.S1_at
Immune Activation	Cell Cycle	2.4	2.8	CENPF	centromere protein F (350	MmuSTS.2672.1.S1_at
Immune Activation	Cell Cycle	4.3	5.0	CEP55	centrosomal protein 55kD	MmugDNA.5873.1.S1_at
Immune Activation	Cell Cycle	2.7	2.6	CHEK1	CHK1 checkpoint homolo	MmugDNA.15754.1.S1_at
Immune Activation	Cell Cycle	2.2	1.8	CKS1B	Cyclin-dependent kinases	MmugDNA.15861.1.S1_s_at
Immune Activation	Cell Cycle	4.3	3.9	CKS2	CDC28 protein kinase 2	MmugDNA.15862.1.S1_at
Immune Activation	Cell Cycle	4.2	4.5	**Cyclin A (CCNA2)**	cyclin A	MmuSTS.3576.1.S1_at
Immune Activation	Cell Cycle	2.2	2.8	**Cyclin A (CCNA2)**	cyclin A	MmugDNA.23764.1.S1_at
Immune Activation	Cell Cycle	3.5	4.2	Cyclin B1 (CCNB1)	cyclin B1	MmuSTS.3318.1.S1_at
Immune Activation	Cell Cycle	5.4	7.0	Cyclin B1 (CCNB1)	cyclin B1	MmugDNA.41268.1.S1_at
Immune Activation	Cell Cycle	4.0	4.5	Cyclin B2 (CCNB2)	cyclin B2	MmugDNA.40742.1.S1_at
Immune Activation	Cell Cycle	4.0	5.1	Cyclin E2 (CCNE2)	cyclin E2 isoform 1	MmuSTS.3320.1.S1_at
Immune Activation	Cell Cycle	3.1	3.06071+L40639901997	**DTL**	RA-regulated nuclear ma	MmuSTS.1283.1.S1_at
Immune Activation	Cell Cycle	1.9	2.0	**DTL**	DTL (hCdt2)	MmugDNA.29544.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14 dpi	SM Fold Changes 30 dpi	Gene Symbol	Gene Name	Affymetrix ID
Immune Activation	Cell Cycle	3.2	3.1	E2F7	E2F transcription factor 7	MmuSTS.2700.1.S1_at
Immune Activation	Cell Cycle	2.7	4.0	ECT2	epithelial cell transformin	MmugDNA.5165.1.S1_at
Immune Activation	Cell Cycle	2.1	1.5	FBXO5	F-box only protein 5	MmugDNA.42135.1.S1_at
Immune Activation	Cell Cycle	2.1	2.2	FBXO5	F-box only protein 5	MmuSTS.4762.1.S1_at
Immune Activation	Cell Cycle	3.6	3.6	GMNN	geminin, DNA replication	MmuSTS.64.1.S1_at
Immune Activation	Cell Cycle	3.1	3.4	GTSE1	G-2 and S-phase express	MmugDNA.9770.1.S1_at
Immune Activation	Cell Cycle	3.9	4.0	HMMR (CD168)	hyaluronan-mediated mo	MmugDNA.24653.1.S1_at
Immune Activation	Cell Cycle	4.2	5.1	HMMR (CD168)	hyaluronan-mediated mo	MmugDNA.32449.1.S1_at
Immune Activation	Cell Cycle	2.1	2.0	HMMR (CD168)	hyaluronan-mediated mo	MmugDNA.32449.1.S1_s_at
Immune Activation	Cell Cycle	2.2	2.5	INCENP	INCENP (Inner	MmugDNA.39805.1.S1_at
Immune Activation	Cell Cycle	3.6	5.5	KIF11	kinesin family member 1	MmugDNA.13565.1.S1_at
Immune Activation	Cell Cycle	3.7	3.9	KIF14	kinesin family member 14	MmugDNA.35622.1.S1_at
Immune Activation	Cell Cycle	2.2	2.1	KIF18A	kinesin family member 18	MmugDNA.32413.1.S1_at
Immune Activation	Cell Cycle	3.6	4.4	KIF23	kinesin family member 22	MmugDNA.13584.1.S1_at
Immune Activation	Cell Cycle	2.2	2.0	KIF2C	kinesin family member 2	MmuSTS.1535.1.S1_at
Immune Activation	Cell Cycle	2.4	2.1	KIFC1	kinesin family member C	MmugDNA.9497.1.S1_at
Immune Activation	Cell Cycle	2.6	3.2	KNSL7	kinesin family member 1	MmugDNA.15585.1.S1_at
Immune Activation	Cell Cycle	3.7	3.8	LOC696772	discs large homolog 7	MmuSTS.2303.1.S1_s_at
Immune Activation	Cell Cycle	3.2	3.4	MAD2A	Mitotic spindle assembly	MmuSTS.4157.1.S1_at
Immune Activation	Cell Cycle	2.6	2.9	MAD2L1	Mitotic spindle assembly	MmugDNA.17868.1.S1_at
Immune Activation	Cell Cycle	2.3	2.1	MCM2	Minichromosome mainte	MmuSTS.144.1.S1_at
Immune Activation	Cell Cycle	2.4	2.7	MCM3	Minichromosome mainte	MmugDNA.25436.1.S1_at
Immune Activation	Cell Cycle	2.9	2.6	MCM6	minichromosome mainte	MmugDNA.35654.1.S1_at
Immune Activation	Cell Cycle	2.1	2.2	MCM7	minichromosome mainte	MmugDNA.30376.1.S1_at
Immune Activation	Cell cycle	4.2	4.4	MELK	maternal embryonic leuci	MmuSTS.1558.1.S1_at
Immune Activation	Cell Cycle	3.0	3.7	MLF1IP	MLF1 interacting protein	MmugDNA.11747.1.S1_at
Immune Activation	Cell Cycle	2.5	2.5	MYBL2	MYB-related protein B	MmugDNA.41887.1.S1_at
Immune Activation	Cell Cycle	3.0	3.4	NDC80	kinetochore associated 2	MmugDNA.36470.1.S1_at
Immune Activation	Cell Cycle	4.2	3.1	NEK2	NIMA (never in mitosis g	MmuSTS.1779.1.S1_at
Immune Activation	Cell Cycle	3.6	3.7	NUSAP1	nucleolar and spindle ass	MmugDNA.38956.1.S1_at
Immune Activation	Cell cycle	3.6	3.2	OIP5	Opa-interacting protein 5	MmuSTS.3327.1.S1_at
Immune Activation	Cell Cycle	2.6	2.3	PLK1	polo-like kinase	MmuSTS.2029.1.S1_at
Immune Activation	Cell Cycle	2.7	2.2	RACGAP1	MmuSTS.2069.1.S1_at	MmuSTS.2069.1.S1_at
Immune Activation	Cell Cycle	2.7	3.4	**SGOL2**	shugoshin-like 2	MmugDNA.3428.1.S1_at
Immune Activation	Cell Cycle	2.8	3.8	**SGOL2**	shugoshin-like 2	MmugDNA.43348.1.S1_at
Immune Activation	Cell Cycle	2.5	3.2	SMC2L1	structural maintenance of	MmugDNA.18586.1.S1_at
Immune Activation	Cell Cycle	1.7	2.8	SMC2L1	structural maintenance of	MmugDNA.25187.1.S1_at
Immune Activation	Cell Cycle	2.0	2.4	**SMC4L1**	SMC4 structural mainten	MmugDNA.29900.1.S1_s_at
Immune Activation	Cell Cycle	2.1	2.8	**SMC4L1**	SMC4 structural mainten	MmugDNA.31959.1.S1_at
Immune Activation	Cell Cycle	2.4	2.3	SPAG5	sperm associated antige	MmugDNA.19272.1.S1_s_at
Immune Activation	Cell Cycle	2.8	2.2	SPC25	spindle pole body compo	MmugDNA.20397.1.S1_at
Immune Activation	Cell Cycle	2.4	2.2	STIL	SCL/TAL1 interrupting lo	MmuSTS.220.1.S1_at
Immune Activation	Cell Cycle	2.4	2.0	TFDP1 (DP1)	transcription factor Dp-0	MmugDNA.14322.1.S1_at
Immune Activation	Cell Cycle	3.9	4.2	UBE2C	Ubiquitin-conjugating enz	MmugDNA.25384.1.S1_at
Immune Activation	Cell Cycle	2.0	2.7	WEE1	Wee1-like protein kinase	MmugDNA.3114.1.S1_at
Immune Activation	Cell Cycle	3.0	3.2	ZWINT	ZW10 interactor (ZW10-i	MmugDNA.2694.1.S1_at
Immune Activation	Cell Cycle	2.4	1.2	cyclin D2 (CCND2)	G1/S-specific cyclin-D2	MmugDNA.18851.1.S1_at
Immune Activation	Cell Cycle	2.8	1.7	Cyclin E1 (CCNE1)	cyclin E1 isoform 1	MmugDNA.4085.1.S1_at
Immune Activation	Cell Cycle	2.0	1.7	GSPT1	G1 to S phase transition	MmuSTS.225.1.S1_at
Immune Activation	Cell Cycle	2.1	1.8	TIPIN	timeless-interacting prote	MmugDNA.30164.1.S1_at
Immune Activation	Cell Cycle	1.6	2.2	BRIP1	BRCA1 interacting protei	MmugDNA.15158.1.S1_at
Immune Activation	Cell Cycle	2.0	2.0	CENPM	CENPM	MmugDNA.19768.1.S1_at
Immune Activation	pro-Inflammation	-1.0	3.5	S100A8	S100 calcium binding pro	MmugDNA.17376.1.S1_at
Immune Activation	pro-Inflammation	1.1	3.3	S100A9	S100 calcium binding pro	MmuSTS.2130.1.S1_s_at
Immune Activation	Signal Transduction	1.1	2.5	CRISP3	cysteine-rich secretory p	MmugDNA.38029.1.S1_at
Immune Activation	Signal Transduction	1.5	2.3	LNX1	ligand of numb-protein X	MmugDNA.43480.1.S1_at
Immune Activation	Signal Transduction	1.2	2.0	LOC699256	testis expressed sequen	MmugDNA.10238.1.S1_at
Immune Activation	Signal Transduction	1.6	2.1	LOC700839	G protein-coupled recep	MmugDNA.27652.1.S1_at
Immune Activation	Signal Transduction	1.5	2.4	LOC703987	Di-Ras2	MmugDNA.2925.1.S1_at
Immune Activation	Signal Transduction	1.1	2.3	LOC705748	SH2 domain binding pro	MmugDNA.10771.1.S1_at
Immune Activation	Signal Transduction	1.3	3.1	LOC707343	kelch-like 14	MmuSTS.1606.1.S1_at
Immune Activation	Signal Transduction	1.4	2.8	LOC711012	protein phosphatase 1E	MmugDNA.22095.1.S1_at
Immune Activation	Signal Transduction	-1.1	2.6	**LOC712688**	regulator of G-protein si	Mmu.1384.2.S1_at
Immune Activation	Signal Transduction	-1.4	6.5	**LOC712688**	regulator of G-protein si	MmuSTS.3764.1.S1_at
Immune Activation	Signal Transduction	1.5	2.2	LOC717165	Ral GEF with PH domai	MmugDNA.17171.1.S1_at
Immune Activation	Signal Transduction	1.3	2.5	LOC717165	Ral GEF with PH domai	MmugDNA.33772.1.S1_at
Immune Activation	Signal Transduction	1.6	2.1	PLCG2	phospholipase C, gamma	MmuSTS.2246.1.S1_at
Immune Activation	TCR Signaling	-2.1	-1.6	TCR alpha chain C region	T-cell receptor alpha cha	MmugDNA.19732.1.S1_s_at
Immune Activation	TCR Signaling	-2.0	-1.5	TCR beta chain C region	T-cell receptor beta chain	Mmu.126.1.S1_a_at
Immune Activation	TCR Signaling	-2.4	-1.7	TCR rearranged beta-chain V,	T-cell receptor rearrange	Mmu.11421.1.S1_a_at
Immune Activation	TCR Signaling	-2.2	-1.7	**LEF1**	lymphoid enhancer bindi	Mmu.4923.1.S1_at
Immune Activation	TCR Signaling	-2.2	-1.2	**LEF1**	lymphoid enhancer bindi	MmuSTS.1438.1.S1_at
Immune Activation	TCR Signaling	-2.2	-2.0	**LEF1**	lymphoid enhancer bindi	MmugDNA.32273.1.S1_at
Immune Activation	Transcriptinal Regulat	2.1	2.0	BARD1	BRCA1 associated RING	MmuSTS.549.1.S1_at
Immune Activation	Transcriptinal Regulat	5.2	4.7	LOC715235	chromosome condensat	MmugDNA.11557.1.S1_at
Immune Activation	Transcriptinal Regulat	1.3	2.0	LOC720557	methyl-CpG binding dom	MmugDNA.12549.1.S1_at
Immune Activation	Transcriptinal Regulat	-1.1	2.1	EP300	E1A binding protein p300	MmugDNA.17977.1.S1_at
Immune Activation	Transcriptinal Regulat	1.8	2.2	LOC703598	high-mobility group box	MmugDNA.36293.1.S1_at
Immune Activation	Transcriptinal Regulat	-1.2	2.1	BACH2		MmugDNA.3201.1.S1_at
Immune Activation	Transcriptinal Regulat	1.2	2.4	LOC702182	zinc finger protein 608	MmugDNA.30581.1.S1_at
Immune Activation	Transcriptinal Regulat	1.8	9.7	MYBL1	v-myb myeloblastosis vir	MmuSTS.3220.1.S1_at
Immune Activation	Transcriptinal Regulat	-1.6	-2.2	LOC708322	**vasculin**	Mmu.12457.1.S1_s_at

Supplemental Table S8. part 3 of 8.

Classification	Sub-Classification	SM Fold Changes 14 dpi	SM Fold Changes 30 dpi	Gene Symbol	Gene Name	Affymetrix ID
Immune Activation	Transcriptinal Regulat	-1.7	-2.2	LOC708322	**vasculin**	Mmu.12457.1.S1_at
Immune Activation	Cytokine and Cytokine	-1.7	-2.2	IL1B	interleukin 1, beta	MmuSTS.652.1.S1_at
Immune Activation	Cytokine and Cytokine	-2.0	-1.3	IL7R (CD127)	interleukin 7 receptor	MmugDNA.8010.1.S1_at
Immune Activation	Cytokine and Cytokine	2.2	1.8	TFEC	TFEC	MmugDNA.17449.1.S1_at
Immune Activation	Cytokine and Cytokine	2.1	2.2	HMGB3	high-mobility group box 3	MmuSTS.236.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	3.0	1.5	TXNDC5	Thioredoxin domain-conta	MmugDNA.2427.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	4.0	2.3	TNFRSF17 (CD269) (BCMA)	Tumor necrosis factor rec	MmugDNA.5879.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	1.8	2.1	AKR7A3	Aldo-keto reductase famil	MmugDNA.38789.1.S1_at
Moderators of Activation & Inflammation	Mediators	1.3	2.0	SLC4A7	solute carrier family 4, so	MmuSTS.4323.1.S1_at
Moderators of Activation & Inflammation	Mediators	1.0	2.0	SLC4A7	solute carrier family 4, so	MmugDNA.896.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	-2.2	-2.3	CD40LG (CD154)	CD40 ligand (TNF superf	MmuSTS.4670.1.S1_s_at
Moderators of Activation & Inflammation	Moderators of Activati	-2.3	-2.4	CD40LG (CD154)	CD40 ligand (TNF superf	Mmu.4194.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	-2.6	-2.6	DGKA	diacylglycerol kinase, alp	MmugDNA.1751.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	-1.9	-2.1	**TXNIP**	thioredoxin interacting pr	MmugDNA.31897.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	-2.3	-2.7	**TXNIP**	thioredoxin interacting pr	MmugDNA.31894.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	-2.2	-2.6	**TXNIP**	thioredoxin interacting pr	Mmu.7507.2.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	-2.6	-2.7	**TXNIP**	thioredoxin interacting pr	MmugDNA.31894.1.S1_s_at
Moderators of Activation & Inflammation	Moderators of Activati	-2.1	-1.2	TIMD4	T-cell immunoglobulin an	MmugDNA.1353.1.S1_at
Moderators of Activation & Inflammation	Moderators of Activati	-2.1	-1.7	TSC22	transforming growth facto	MmuSTS.4615.1.S1_at
Moderators of Activation & Inflammation	Negative regulation of	-1.8	-2.3	TGFB1	transforming growth facto	Mmu.6776.1.S1_at
Moderators of Activation & Inflammation	Negative regulation of	-1.9	-2.1	LOC702385	Ras association domain	Mmu.5207.1.S1_at
Moderators of Activation & Inflammation	Negative regulation of	-1.8	-2.0	IGFBP5	insulin-like growth factor	Mmu.5435.1.S1_at
Moderators of Activation & Inflammation	Negative regulation of	-1.6	-2.3	**DPT**	Dermatopontin precurso	MmugDNA.38796.1.S1_s_at
Moderators of Activation & Inflammation	Negative regulation of	-2.2	-2.8	**DPT**	Dermatopontin precursor	MmugDNA.35051.1.S1_at
Moderators of Activation & Inflammation	Negative regulation of	3.0	2.0	LOC714207	G-2 and S-phase expres	MmugDNA.33793.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		1.9	2.2	KMO	KMO	MmugDNA.25657.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		1.9	2.2	TMPO (LAP2)	TMPOA	MmugDNA.41740.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		4.1	5.5	E2F8	E2F family member 7	MmugDNA.12490.1.S1_at
Moderators of Activation & Inflammation (Antioxidants)		2.5	1.8	PPIL5	peptidylprolyl isomerase (	MmugDNA.20073.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	1.1	2.1	ELA2	elastase 2, neutrophil	MmugDNA.38450.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	1.1	2.1	LOC694095	echinoderm microtubule	MmugDNA.13576.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	-1.6	-2.3	FBLN1	fibulin 1	MmugDNA.38728.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	-1.9	-2.2	LOC700181	Dermatopontin precurso	MmugDNA.35052.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	-2.1	-2.5	**DCN**	decorin	MmugDNA.32965.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	-2.1	-2.4	**DCN**	decorin	MmugDNA.14528.1.S1_s_at
Tissue Repair, Remodeling	Extracellular Matrix St	-2.2	-2.4	**DCN**	decorin	MmugDNA.22700.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	-2.0	-2.1	LOC709521	microfibrillar-associated (	MmuSTS.159.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	-2.1	-1.5	SPOCK2	sparc/osteonectin, cwcv a	MmugDNA.7832.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	-2.0	-1.6	STAB2	stabilin 2	MmugDNA.15867.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	2.1	1.1	ECGF1	endothelial cell growth fa	MmugDNA.9266.1.S1_at
Tissue Repair, Remodeling	Extracellular Matrix St	2.1	-1.1	**SDC1 (CD138)**	Syndecan-1 precursor (S	MmugDNA.27367.1.S1_x_at
Tissue Repair, Remodeling	Extracellular Matrix St	2.2	-1.0	**SDC1 (CD138)**	Syndecan-1 precursor (S	MmugDNA.27367.1.S1_at
Tissue Repair, Remodeling	Nerver-related growth	2.0	2.1	LOC704085	M-phase phosphoprotein	MmuSTS.4168.1.S1_at
Tissue Repair, Remodeling	Nerve Related Growth	5.0	3.2	**UCH-L1 (PGP9.5)**	Ubiquitin carboxyl-termin	MmugDNA.7056.1.S1_s_at
Tissue Repair, Remodeling	Nerve Related Growth	5.0	4.0	**UCH-L1 (PGP9.5)**	Ubiquitin carboxyl-termin	MmugDNA.7056.1.S1_at
Tissue Repair, Remodeling	Nerver-related growth	1.6	2.2	LOC696717	otoferlin isoform a	MmugDNA.9131.1.S1_at
Tissue Repair, Remodeling	Nerver-related growth	1.2	2.1	LOC713673	neural precursor cell exp	MmugDNA.28623.1.S1_at
Tissue Repair, Remodeling	Nerver-related growth	1.2	2.0	MEGF9	multiple EGF-like-domain	MmugDNA.39298.1.S1_at
Tissue Repair, Remodeling	Oxidative-Stress Relat	2.4	1.3	SOD2	superoxide dismutase 2,	MmugDNA.24030.1.S1_at
Tissue Repair, Remodeling	Tissue Remodeling	-1.5	-2.1	TIMP3	TIMP metallopeptidase in	MmugDNA.33324.1.S1_at
Tissue Repair, Remodeling		2.8	1.8	SCIN	scinderin	MmuSTS.1778.1.S1_at
Metabolism	Lipids & Glucose	-1.8	-2.3	FABP4	fatty acid binding protein	MmugDNA.31873.1.S1_at
Metabolism	Lipids & Glucose	-1.6	-2.2	PFKFB3	6-phosphofructo-2-kinase	MmugDNA.2360.1.S1_at
Metabolism	Lipids & Glucose	1.6	2.0	SLC2A5	solute carrier family 2 (fa	MmugDNA.1987.1.S1_at
Metabolism	Lipids & Glucose	-2.2	-1.3	AMY2A	amylase, alpha 2A; panc	MmugDNA.4900.1.S1_s_at
Metabolism	Lipids & Glucose	-2.3	-1.5	LGALS13	Galactoside-binding solu	MmugDNA.43117.1.S1_at
Metabolism	Lipids & Glucose	-2.0	-1.2	SCD	stearoyl-CoA desaturase	MmugDNA.38238.1.S1_at
Metabolism	Lipids & Glucose	2.9	1.2	**CYP1B1**	cytochrome P450, family	MmuSTS.4020.1.S1_at
Metabolism	Lipids & Glucose	2.7	1.4	**CYP1B1**	cytochrome P450, family	MmugDNA.36286.1.S1_at
Metabolism	Lipids & Glucose	2.3	1.0	**CYP1B1**	cytochrome P450, family	MmugDNA.30721.1.S1_at
Metabolism	Lipids & Glucose	2.0	1.9	FH	fumarate hydratase	MmuSTS.2656.1.S1_at
Metabolism	Lipids & Glucose	2.1	1.8	MANEA	mannosidase, endo-alpha	MmugDNA.11821.1.S1_at
Metabolism	Lipids & Glucose	2.1	1.3	STT3A	integral membrane protei	MmugDNA.21146.1.S1_at
Metabolism	Metals/Ions	2.2	1.3	PPA1	pyrophosphatase 1	Mmu.4786.2.S1_at
Metabolism	Metals/Ions	2.3	1.4	PPA1	pyrophosphatase 2	Mmu.4786.2.S1_s_at
Metabolism	Metals/Ions	2.4	1.6	PPA1	pyrophosphatase 3	MmugDNA.35236.1.S1_at
Metabolism	Nucleic Acids	2.8	2.1	DHFR	Dihydrofolate reductase	MmugDNA.10792.1.S1_at
Metabolism	Metals/Ions	2.3	3.0	KLHL23	KLHL23	MmugDNA.36416.1.S1_at
Metabolism	Nucleic Acids	6.0	4.3	LOC700582	Probable dimethyladenos	MmuSTS.3275.1.S1_at
Metabolism	Nucleic Acids	2.5	2.0	NPM1	Nucleophosmin (NPM) (N	MmugDNA.4269.1.S1_at
Metabolism	Nucleic Acids	6.3	5.2	RRM2	ribonucleotide reductase	MmugDNA.31369.1.S1_at
Metabolism	Nucleic Acids	2.9	2.4	TYMS	thymidylate synthetase	MmugDNA.30056.1.S1_at
Metabolism	Nucleic Acids	4.1	3.9	TYMS	thymidylate synthetase	MmuSTS.4685.1.S1_at
Metabolism	Nucleic Acids	2.3	1.5	AHCY	S-adenosylhomocysteine	MmuSTS.44.1.S1_at
Metabolism	Nucleic Acids	2.4	1.8	FEN1	flap structure-specific end	MmuSTS.2645.1.S1_at
Metabolism	Nucleic Acids	2.0	1.4	GART	phosphoribosylglycinamid	MmugDNA.18615.1.S1_at
Metabolism	Nucleic Acids	2.4	1.8	LOC695725	uridine-cytidine kinase 2	MmugDNA.43419.1.S1_at
Metabolism	Nucleic Acids	2.1	1.6	SYNCRIP	NS1-associated protein 1	MmugDNA.20772.1.S1_s_at
Metabolism	Nucleic Acids	1.7	5.2	DCK	---	MmugDNA.36254.1.S1_at
Metabolism	Nucleic Acids	-1.0	2.1	LOC698070	NSE1	MmugDNA.21019.1.S1_at
Metabolism	Nucleic Acids	1.3	2.2	LOC707062	ribonucleotide reductase	Mmu.9802.1.S1_at
Metabolism	Nucleic Acids	1.2	2.4	LOC707062	ribonucleotide reductase	MmuSTS.2129.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14 dpi	SM Fold Changes 30 dpi	Gene Symbol	Gene Name	Affymetrix ID
Metabolism	Nucleic Acids	1.4	2.8	LOC711271	elongation factor RNA p	MmuSTS.4320.1.S1_at
metabolism	Nucleic Acids	1.3	2.1	MSH2		MmuSTS.316.1.S1_at
Metabolism	Nucleic Acids	2.0	2.2	RRM1	RRM1	MmugDNA.26585.1.S1_at
Metabolism	Nucleic Acids	2.1	2.1	TK1	thymidine kinase 1, solub	MmugDNA.24372.1.S1_at
Metabolism	Proteins	1.7	2.1	Function: E3 ubiquitin-	membrane-associated R	MmugDNA.31588.1.S1_s_at
Metabolism	Proteins	-1.0	2.2	B4GALT6	UDP-Gal:betaGlcNAc bet	MmugDNA.18724.1.S1_s_at
Metabolism	Proteins	-1.1	2.5	B4GALT6	UDP-Gal:betaGlcNAc bet	MmugDNA.38184.1.S1_at
Metabolism	Proteins	1.9	2.1	LOC696756	NS1-associated protein	MmugDNA.38526.1.S1_at
Metabolism	Proteins	1.7	2.2	LOC713533	selenophosphate synthe	MmugDNA.13390.1.S1_at
Metabolism	Proteins	-1.7	-2.2	LOC713999	tumor differentially expre	Mmu.9654.1.S1_at
Metabolism	Proteins	-1.3	-2.1	LOC717617	methionine sulfoxide red	MmugDNA.37672.1.S1_s_at
Metabolism	Proteins	1.0	-2.0	SRPR	signal recognition particle	MmugDNA.308.1.S1_at
Metabolism	Proteins	-1.1	-2.2	METTL7A	METTL7A	MmugDNA.38570.1.S1_s_at
Metabolism	Proteins	2.1	1.4	DNAJB11	DnaJ (Hsp40) homolog, s	MmuSTS.4249.1.S1_at
Metabolism	Proteins	2.2	1.7	ETF1	eukaryotic translation ter	MmugDNA.19076.1.S1_s_at
Metabolism	Proteins	2.1	1.6	MRPL15	mitochondrial ribosomal	MmuSTS.954.1.S1_at
Metabolism	Proteins	2.1	1.5	MRPL19	mitochondrial ribosomal	MmuSTS.1524.1.S1_at
Metabolism	Proteins	2.1	1.4	PDIA4	protein disulfide isomeras	MmugDNA.9838.1.S1_at
Metabolism	Proteins	2.2	1.6	SAR1B	SAR1 homolog B (S. cere	MmugDNA.38135.1.S1_at
Metabolism	Proteins	2.3	1.4	SPCS3	signal peptidase complex	MmugDNA.32060.1.S1_s_at
Metabolism	Proteins	2.0	-1.0	**TRA1 (HSP90B1)**	tumor rejection antigen (	MmugDNA.6621.1.S1_at
Metabolism	Proteins	2.0	1.2	**TRA1 (HSP90B1)**	tumor rejection antigen (	Mmu.4005.1.S1_s_at
Metabolism	Proteins	3.3	2.7	PSAT1	phosphoserine aminotra	MmugDNA.38346.1.S1_at
Metabolism	Proteins	-4.1	-2.6	LOC714206	ATP-binding cassette, su	MmunewRS.1009.1.S1_at
Metabolism	Proteins	-3.7	-1.8	LOC693289	ATP-binding cassette, su	MmuSTS.2655.1.S1_at
Metabolism	Proteins: Proteasome/	2.0	1.3	PSMA3	Proteasome subunit alph	MmugDNA.22343.1.S1_s_at
Metabolism	Proteins: Proteasome/	2.3	1.8	UBE2J1	ubiquitin-conjugating enz	MmugDNA.42067.1.S1_at
Metabolism	Proteins: Proteasome/	2.3	1.7	**UBE2S**	Ubiquitin-conjugating enz	MmugDNA.15298.1.S1_x_at
Metabolism	Proteins: Proteasome/	2.5	1.9	**UBE2S**	Ubiquitin-conjugating en	MmugDNA.15298.1.S1_at
Metabolism	Proteins: Proteasome/	2.2	1.4	UBE2T	Ubiquitin-conjugating enz	MmugDNA.22787.1.S1_at
Metabolism	Proteins: Proteasome/	2.2	1.6	UCHL5	ubiquitin C-terminal hydr	Mmu.1412.1.S1_at
Metabolism	Proteins: Proteasome/	2.1	1.6	UCHL5	ubiquitin C-terminal hydr	MmugDNA.15179.1.S1_at
Metabolism	Proteins: Proteasome/	2.1	1.9	UCHL5	ubiquitin C-terminal hydr	MmuSTS.4734.1.S1_at
Metabolism		2.1	1.3	NQO1	NAD(P)H dehydrogenase	MmuSTS.3015.1.S1_at
Metabolism		1.3	2.7	AQP4	aquaporin 4	MmugDNA.6205.1.S1_at
Others	Cell adhesion	-1.4	-2.4	PCDHA11	Protocadherin alpha 11	MmugDNA.37873.1.S1_at
Others	Cell Morphology	-1.3	-2.0	TAGLN	transgelin	MmugDNA.30842.1.S1_s_at
Others	Cytoskeleton Related	-1.7	-4.4	IQGAP1	IQGAP1	MmugDNA.19813.1.S1_at
Others	Cytoskeleton Related	2.5	2.5	DIAPH3	diaphanous homolog 3	MmugDNA.22775.1.S1_at
Others	Cytoskeleton Related	2.2	1.7	TUBA6	tubulin alpha 6	MmugDNA.32666.1.S1_s_at
Others	DNA Replication/Repa	2.2	1.7	RAD51	RAD51 homolog protein i	MmugDNA.23761.1.S1_at
Others	DNA Replication/Repa	2.3	1.8	GINS2	GINS complex subunit 2	MmuSTS.2066.1.S1_at
Others	DNA Replication/Repa	2.1	1.5	EXO1	exonuclease 1 isoform b	MmugDNA.17950.1.S1_s_at
Others	DNA Replication/Repa	2.2	2.8	HMGB2	high-mobility group box 2	MmuSTS.1347.1.S1_at
Others	DNA Replication/Repa	3.3	3.3	POLE2	DNA polymerase epsilon	MmugDNA.2975.1.S1_at
Others	DNA Replication/Repa	2.5	2.7	RAD51AP1	RAD51-associated prote	MmuSTS.4250.1.S1_at
Others	DNA Replication/Repa	4.7	4.6	**TOP2A**	DNA topoisomerase II, al	MmugDNA.12273.1.S1_at
Others	DNA Replication/Repa	3.9	4.3	**TOP2A**	DNA topoisomerase II, al	MmugDNA.12277.1.S1_at
Others	DNA Replication/Repa	1.6	2.1	SMC4	CAP-C	MmugDNA.20926.1.S1_at
Others	ER-Golgi Related	2.0	1.5	**ERGIC1**	endoplasmic reticulum-g	MmugDNA.42416.1.S1_s_at
Others	ER-Golgi Related	2.0	1.6	**ERGIC1**	endoplasmic reticulum-g	MmugDNA.42416.1.S1_at
Others	ER-Golgi Related	2.1	1.1	SSR1	Translocon-associated pr	MmugDNA.7350.1.S1_s_at
Others	Insulin-like Growth Fa	2.2	3.5	IMP-3	insulin-like growth factor	MmugDNA.31012.1.S1_at
Others	Insulin-like Growth Fa	2.3	3.7	IMP-3	insulin-like growth factor	MmugDNA.15520.1.S1_s_at
Others	Insulin-like Growth Fa	2.1	6.1	IMP-3	insulin-like growth factor	MmugDNA.15520.1.S1_at
Others	Insulin-like Growth Fa	-1.8	-2.2	IGFBP5	---	MmugDNA.42888.1.S1_at
Others	Insulin-like Growth Fa	-1.7	-2.0	IGFBP5	---	MmugDNA.42890.1.S1_at
Others	Insulin-like Growth Fa	-1.8	-2.3	LOC721120	Insulin-like growth factor	MmugDNA.23210.1.S1_x_at
Others	Insulin-like Growth Fa	-2.2	-1.9	**ILGFBP3**	insulin-like growth factor	Mmu.11638.2.S1_at
Others	Insulin-like Growth Fa	-3.0	-2.1	**ILGFBP3**	insulin-like growth factor	MmuSTS.2537.1.S1_at
Others	Insulin-like Growth Fa	-2.6	-1.5	**ILGFBP3**	insulin-like growth factor	MmugDNA.7729.1.S1_at
Others	Insulin-like Growth Fa	-2.1	-2.3	IGFBP6	insulin-like growth factor	MmugDNA.23639.1.S1_at
Others	Insulin-like Growth Fa	-2.2	-3.4	ILGFII	Insulin-like growth factor	Mmu.4374.2.S1_s_at
Others	Nucleosome structure	3.0	2.9	LMNB1	lamin B1	MmuSTS.1539.1.S1_at
Others	Nucleosome structure	2.4	2.2	LOC703073	Histone H2A.x (H2a/x)	MmuSTS.8.1.S1_at
Others	Nucleosome structure	2.0	1.8	HIST1H4J	histone cluster 1, H4j (ge	MmugDNA.3247.1.S1_at
Others	Other	-2.0	-2.4	GSN	gelsolin	MmugDNA.16424.1.S1_at
Others	Other	-2.0	-2.6	LOC713882	smooth muscle myosin h	MmugDNA.33337.1.S1_s_at
Others	Post-Translational Mo	2.1	1.7	SUV39H2	suppressor of variegation	MmugDNA.12443.1.S1_at
Others	Solute Carrier Family	2.3	1.4	SLC7A5	solute carrier family 7 (ca	MmuSTS.3879.1.S1_at
Others	Solute Carrier Family	2.0	2.0	SLC31A1	High-affinity copper uptak	Mmu.7190.1.A1_at
Others	Splicosome	1.6	2.4	LSM5	LSM5	MmugDNA.15339.1.S1_at
Others	Transcriptinal Regulat	-2.1	-1.3	---	---	MmugDNA.11023.1.S1_at
Others	Transcriptinal Regulat	-2.0	-1.6	ID4		MmuSTS.2533.1.S1_at
Others	Transcriptinal Regulat	2.5	1.6	ELL2	elongation factor, RNA p	MmuSTS.4317.1.S1_at
Others	Transcriptinal Regulat	2.2	2.8	EAF2	ELL associated factor 2	MmugDNA.2321.1.S1_at
Others	Transcriptinal Regulat	3.0	3.7	EZH2	enhancer of zeste 2	MmuSTS.911.1.S1_at
Others	Transcriptinal Regulat	2.1	2.3	**ATAD2**	ATPase family, two AAA	MmugDNA.12475.1.S1_s_at
Others	Transcriptinal Regulat	1.5	2.2	**ATAD2**	ATAD2	MmugDNA.5276.1.S1_at
Others	Transcriptinal Regulat	1.6	2.1	**ATAD2**	ATAD2	MmugDNA.31331.1.S1_at
Others	Transcriptinal Regulat	1.5	2.3	NSBP1	NSBP1	MmugDNA.32637.1.S1_at
Others	Transcriptinal Regulat	1.2	2.1	ZNF326	ZNF326	MmugDNA.4607.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14 dpi	SM Fold Changes 30 dpi	Gene Symbol	Gene Name	Affymetrix ID
Others	Vesicle Trafficking	2.6	1.7	SEC24A	SEC24 related gene fami	MmugDNA.37864.1.S1_at
Others	Vesicle Trafficking	2.2	2.1	SEC24A	SEC24 related gene fami	MmugDNA.37865.1.S1_at
Others	Vesicle Trafficking	-1.6	-2.1	EHBP1	EH domain binding prote	MmugDNA.41484.1.S1_at
Others	Vesicle Trafficking	-1.3	-2.8	SCFD1	SCFD1	MmugDNA.27824.1.S1_at
Others		2.2	2.0	ANP32E	acidic (leucine-rich) nucle	MmugDNA.22578.1.S1_at
Others		2.4	1.8	MTDH	LYRIC/3D3	MmugDNA.81.1.S1_s_at
Others		2.3	1.7	MTDH	LYRIC/3D3	MmugDNA.81.1.S1_at
Others		2.4	1.5	MTDH	LYRIC/3D3/ metadherin	Mmu.4898.1.S1_at
Others		2.6	1.8	NME1	non-metastatic cells 1, p	MmugDNA.21289.1.S1_at
Others		5.0	5.4	NS5ATP9	---	MmugDNA.33823.1.S1_s_at
Others		2.7	3.3	TMPRSS3	Transmembrane protease	MmuSTS.1653.1.S1_at
Others		3.6	2.9	TRIP13	thyroid hormone receptor	MmuSTS.4722.1.S1_at
Others		2.8	1.7	ARNTL2	aryl hydrocarbon recepto	MmugDNA.13595.1.S1_at
Others		2.6	1.9	**MOBKL1B**	Mol1b	MmugDNA.6802.1.S1_at
Others		2.1	1.8	**MOBKL1B**	Mob4B protein (Mps One	MmugDNA.23022.1.S1_s_at
Others		-3.2	-1.8	APBA2	amyloid beta (A4) precur	MmugDNA.18477.1.S1_at
Others		-2.0	-1.6	CIRBP	cold inducible RNA bindi	MmugDNA.21025.1.S1_at
Others		-2.3	-1.1	CNR1		MmugDNA.5294.1.S1_at
Others		-2.5	-1.4	**COCH**	coagulation factor C hom	MmugDNA.12890.1.S1_at
Others		-2.3	-1.2	**COCH**	coagulation factor C hom	MmuSTS.3519.1.S1_at
Others		-2.2	-1.4	EPB41	Erythrocyte membrane p	MmugDNA.16997.1.S1_at
Others		-2.0	-1.6	FRZB	frizzled-related protein	MmugDNA.39998.1.S1_at
Others		-2.1	-1.5	INADL	INADL	MmugDNA.26275.1.S1_at
Others		-2.4	-2.2	LIN7A	LIN-7 homolog A (LIN-7A	MmugDNA.33930.1.S1_at
Others		-2.0	-1.4	MAP7	microtubule-associated p	MmugDNA.11043.1.S1_at
Others		-2.0	1.2	MBNL1	Muscleblind-like (Drosop	MmugDNA.3546.1.S1_at
Others		-2.1	-1.5	NEFH	neurofilament, heavy pol	MmugDNA.18337.1.S1_at
Others		-2.6	-1.3	NOG	Noggin precursor	MmugDNA.19120.1.S1_at
Others		-2.1	-1.5	WIF1	Wnt inhibitory factor 1	MmuSTS.4753.1.S1_at
Others		-2.4	-3.4	MYH11	smooth muscle myosin h	MmugDNA.15137.1.S1_at
Others		-2.2	-3.2	MYH11	smooth muscle myosin h	MmugDNA.33337.1.S1_at
Others		-2.2	-2.5	TPM2	tropomyosin 2 (beta) isof	MmugDNA.6549.1.S1_at
Others		-1.2	2.1	beta globin	beta globin	MmugDNA.2571.1.S1_at
Others		-1.1	2.1	beta globin	beta globin	MmugDNA.5184.1.S1_s_at
Others		-1.2	2.8	beta globin	beta globin	MmuAffx.949.1.S1_x_at
Others		1.9	2.2	DLEU2	deleted in lymphocytic le	MmugDNA.12590.1.S1_at
Others		-1.2	4.1	SPINK2	serine protease inhibitor,	MmugDNA.18486.1.S1_s_at
Others		2.1	2.3	WDHD1	WD repeat and HMG-box	MmugDNA.18618.1.S1_at
Others		-1.7	-4.2	MALAT1	metastasis associated lu	MmugDNA.13401.1.S1_s_at
Others		-2.0	-1.5	NTRK2	TrkB	MmugDNA.41948.1.S1_at
Hypothetical Protein		1.1	2.2	---	---	MmugDNA.37488.1.S1_at
Hypothetical Protein		1.3	2.4	---	---	MmugDNA.18321.1.S1_at
Hypothetical Protein		1.6	2.6	---	---	MmugDNA.18007.1.S1_s_at
Hypothetical Protein		2.8	2.7	---	---	MmugDNA.26428.1.S1_at
Hypothetical Protein		1.6	3.3	---	---	MmugDNA.18007.1.S1_at
Hypothetical Protein		-1.0	2.0	LOC704002	hypothetical protein LOC	MmugDNA.32146.1.S1_at
Hypothetical Protein		1.6	2.2	WDR76	WDR76	MmugDNA.9449.1.S1_at
Hypothetical Protein		-1.7	-2.5	---	---	MmugDNA.28691.1.S1_at
Hypothetical Protein		-1.8	-2.3	---	---	MmugDNA.29568.1.S1_at
Hypothetical Protein		-1.6	-2.2	LOC703106 /// MAMU-I	hypothetical protein LOC	MmugDNA.13887.1.S1_s_at
Hypothetical Protein		-2.0	-1.7	---	Transcribed locus, strong	MmuAffx.23.12.S1_x_at
Hypothetical Protein		-2.4	-1.8	---	Transcribed locus, strong	MmuAffx.23.21.S1_s_at
Hypothetical Protein		-2.0	-1.5	---	---	MmugDNA.24683.1.S1_at
Hypothetical Protein		-2.5	-1.4	---	---	MmugDNA.20647.1.S1_at
Hypothetical Protein		-2.5	-1.4	---	---	MmugDNA.12998.1.S1_at
Hypothetical Protein		-2.0	-1.8	LOC100130976	No network object found	MmugDNA.36815.1.S1_at
Hypothetical Protein		-2.5	-1.3	LOC696781	hypothetical protein LOC	MmugDNA.28007.1.S1_at
Hypothetical Protein		-2.0	1.0	LOC711574	hypothetical protein LOC	MmugDNA.13302.1.S1_at
Hypothetical Protein		-2.2	-1.5	MGC45871	hypothetical protein	MmugDNA.12660.1.S1_at
Hypothetical Protein		2.3	1.9	LOC696907	hypothetical protein LOC	MmugDNA.30940.1.S1_at
Hypothetical Protein		2.2	1.1	LOC700659	hypothetical protein LOC	MmugDNA.35877.1.S1_s_at
Hypothetical Protein		3.1	1.8	LOC708602	thymidylate kinase family	MmugDNA.21336.1.S1_at
Hypothetical Protein		2.0	-1.2	LOC711872	hypothetical protein LOC	MmuSTS.4350.1.S1_at
Hypothetical Protein		2.4	1.3	LOC714457	CG30497-PA, isoform A	MmugDNA.28074.1.S1_at
Hypothetical Protein		2.7	1.3	**LOC715967**	hypothetical protein LOC	MmugDNA.23367.1.S1_s_at
Hypothetical Protein		2.6	1.3	**LOC715967**	hypothetical protein LOC	MmugDNA.23367.1.S1_at
Hypothetical Protein		2.6	2.3	C28H8.3	C28H8.3	MmugDNA.27193.1.S1_at
Hypothetical Protein		2.3	2.5	CCDC58	coiled-coil domain conta	MmugDNA.24837.1.S1_s_at
Hypothetical Protein		2.5	2.4	CCDC99	coiled-coil domain conta	MmugDNA.303.1.S1_at
Hypothetical Protein		4.4	7.6	DEPDC1B (LOC709670)	DEP domain containing	MmugDNA.28002.1.S1_at
Hypothetical Protein		2.7	4.1	FLJ40869	hypothetical protein FLJ	MmugDNA.31368.1.S1_at
Hypothetical Protein		4.1	4.4	LOC695836	hypothetical protein LOC	MmugDNA.2512.1.S1_at
Hypothetical Protein		2.1	2.6	LOC711569	hypothetical protein LOC	MmugDNA.32941.1.S1_at
Hypothetical Protein		2.8	2.6	LOC712570	hypothetical protein LOC	MmugDNA.43588.1.S1_at
Hypothetical Protein		2.0	2.0	LOC713624	hypothetical protein LOC	MmugDNA.26033.1.S1_at
Hypothetical Protein		3.7	3.4	LOC714686	hypothetical protein LOC	MmugDNA.1969.1.S1_at
Hypothetical Protein		2.8	2.1	LOC718812	hypothetical protein LOC	MmugDNA.33404.1.S1_at
Hypothetical Protein		2.8	2.4	LOC718812	hypothetical protein LOC	MmuSTS.340.1.S1_at
Unknown		-2.4	-3.7	---		MmugDNA.23105.1.S1_at
Unknown		-2.1	-5.9	---	---	MmugDNA.4718.1.S1_s_at
Unknown		-1.8	-4.6	---	---	Mmu.12981.1.S1_at
Unknown		1.4	-4.0	---	---	Mmu.15103.2.S1_at

Classification	Sub-Classification	SM Fold Changes 14 dpi	SM Fold Changes 30 dpi	Gene Symbol	Gene Name	Affymetrix ID
Unknown		1.4	-3.5	---	---	MmugDNA.41975.1.S1_at
Unknown		-1.9	-3.3	---	---	Mmu.3126.6.S1_x_at
Unknown		-1.9	-3.2	---	---	MmugDNA.10988.1.S1_at
Unknown		-2.9	-2.8	---	---	MmunewRS.711.1.S1_at
Unknown		-1.5	-2.6	---	---	MmugDNA.35103.1.S1_at
Unknown		-1.4	-2.5	---	---	MmugDNA.36139.1.S1_at
Unknown		1.1	-2.4	---	---	MmuAffx.10.1.A1_x_at
Unknown		-1.9	-2.3	---	---	Mmu.8637.1.S1_at
Unknown		-1.5	-2.3	---	---	MmugDNA.17953.1.S1_at
Unknown		-1.3	-2.3	---	---	MmugDNA.676.1.S1_at
Unknown		-1.8	-2.2	---	---	MmugDNA.480.1.S1_at
Unknown		-1.7	-2.2	---	---	MmugDNA.794.1.S1_s_at
Unknown		-1.2	-2.2	---	---	MmugDNA.13526.1.S1_at
Unknown		-2.9	-2.2	---	---	MmuSTS.3550.1.S1_s_at
Unknown		-1.6	-2.2	---	---	MmugDNA.39472.1.S1_at
Unknown		-1.5	-2.1	---	---	MmugDNA.1697.1.S1_at
Unknown		-1.4	-2.1	---	---	MmugDNA.11078.1.S1_s_at
Unknown		1.1	-2.1	---	---	MmunewRS.1070.1.S1_at
Unknown		-1.7	-2.1	---	---	MmugDNA.5369.1.S1_at
Unknown		-1.4	-2.0	---	---	MmugDNA.11513.1.S1_at
Unknown		-1.4	-2.0	---	---	MmugDNA.19260.1.S1_at
Unknown		-1.5	-2.0	EEF2 /// LOC699930	Eukaryotic translation elo	MmugDNA.39128.1.S1_at
Unknown		-1.4	-2.1	LOC699173	hypothetical protein LOC	MmugDNA.39398.1.S1_at
Unknown		-1.6	-2.2	LOC711742	kinesin family member 9	MmugDNA.21343.1.S1_at
Unknown		-1.5	-2.1	LOC722518	CTCL tumor antigen L14	MmugDNA.9437.1.S1_at
Unknown		-1.4	-2.1	MAGED2	melanoma antigen family	Mmu.15555.1.S1_at
Unknown		-1.3	2.0	---	---	MmugDNA.14181.1.S1_at
Unknown		1.6	2.2	---	---	MmugDNA.34770.1.S1_at
Unknown		1.5	2.3	---	---	Mmu.1262.1.A1_at
Unknown		1.1	2.1	---	---	MmugDNA.32373.1.S1_at
Unknown		-1.2	2.0	---	---	MmugDNA.42592.1.S1_at
Unknown		1.5	2.0	---	---	MmugDNA.31152.1.S1_at
Unknown		1.1	2.1	---	---	MmugDNA.42652.1.S1_at
Unknown		1.5	2.1	---	---	MmugDNA.38077.1.S1_at
Unknown		1.2	2.2	---	---	MmugDNA.16918.1.S1_at
Unknown		1.6	2.2	---	---	MmugDNA.1283.1.S1_at
Unknown		1.4	2.3	---	---	Mmu.16285.1.A1_at
Unknown		1.7	2.4	---	---	MmugDNA.35036.1.S1_at
Unknown		-1.1	2.4	---	---	MmugDNA.7842.1.S1_at
Unknown		1.9	2.7	---	---	MmugDNA.6095.1.S1_at
Unknown		1.3	3.0	---	---	MmugDNA.580.1.S1_at
Unknown		1.2	3.8	---	---	MmuAffx.949.1.A1_at
Unknown		1.4	2.1	---	---	MmuSTS.711.1.S1_at
Unknown		1.3	2.1	---	---	MmugDNA.27876.1.S1_at
Unknown		1.4	2.1	---		MmugDNA.39220.1.S1_at
Unknown		1.8	2.0	---		MmugDNA.43203.1.S1_at
Unknown		1.6	2.0	---	---	MmugDNA.36.1.S1_at
Unknown		1.4	2.0	---	---	MmugDNA.19588.1.S1_at
Unknown		1.6	2.0	---	---	MmugDNA.29178.1.S1_at
Unknown		1.9	2.1	C13orf3	C13orf3	MmugDNA.23023.1.S1_at
Unknown		1.5	2.2	LOC694209	Protein FAM3C precurso	MmugDNA.11181.1.S1_at
Unknown		1.9	2.1	LOC695933		MmuSTS.55.1.S1_at
Unknown		1.0	2.0	LOC696276	CG7220-PA, isoform A	MmugDNA.3104.1.S1_at
Unknown		2.0	2.3	LOC707321		MmuSTS.2151.1.S1_at
Unknown		2.0	3.3	LOC716218		MmuSTS.3922.1.S1_at
Unknown		4.0	1.7	---	---	MmuSTS.4748.1.S1_at
Unknown		2.2	1.4	---	???	MmugDNA.2759.1.S1_at
Unknown		2.2	1.6	---	???	Mmu.2276.1.S1_at
Unknown		2.5	1.8	CHAC2	ChaC, cation transport re	MmugDNA.66.1.S1_at
Unknown		2.1	1.2	LOC697934	Protein KIAA0152 precu	MmugDNA.4669.1.S1_at
Unknown		2.1	1.7	LOC700859	CG11699-PA (chromoso	MmugDNA.31089.1.S1_s_at
Unknown		2.4	1.9	LOC704099	CG6597-PA, isoform A (	MmugDNA.5478.1.S1_at
Unknown		2.2	1.8	LOC715676		Mmu.12263.1.S1_at
Unknown		3.7	3.0	---	---	MmuSTS.1531.1.S1_at
Unknown		3.1	2.7	---	---	MmuSTS.1534.1.S1_at
Unknown		3.5	2.1	---	---	Mmu.15507.1.S1_x_at
Unknown		1.9	2.4	C14ORF106	M18BP1	MmugDNA.6067.1.S1_at
Unknown		2.3	3.2	C14ORF106	chromosome 14 open rea	MmugDNA.5761.1.S1_at
Unknown		3.5	2.7	C18ORF24	chromosome 18 open rea	MmugDNA.39863.1.S1_at
Unknown		3.0	2.8	**DEPDC1 (LOC701888)**	DEP domain containing	MmugDNA.29315.1.S1_at
Unknown		2.1	2.9	**DEPDC1 (LOC701888)**	DEP domain containing	MmugDNA.40906.1.S1_at
Unknown		2.2	2.0	FLJ10292 (LOC717824)	mago-nashi homolog	MmugDNA.4402.1.S1_s_at
Unknown		-2.6	-2.2	---	---	MmugDNA.11704.1.S1_at
Unknown		-2.1	-4.6	---	Transcribed locus	Mmu.12981.1.S1_s_at
Unknown		-2.0	-2.2	LOC716001	steroid dehydrogenase h	MmugDNA.40447.1.S1_at
Unknown		-2.3	1.1	---	---	MmugDNA.21478.1.S1_at
Unknown		-2.1	-1.7	---	---	MmugDNA.2555.1.S1_at
Unknown		-2.3	-1.5	---	---	MmuSTS.4146.1.S1_at
Unknown		-2.3	-1.3	---	---	MmugDNA.36051.1.S1_at
Unknown		-2.0	-1.2	LOC709116	Probable ATP-dependent	MmugDNA.37035.1.S1_at
Unknown	Gene function unknow	3.0	2.0	ERCC6L	excision repair cross-com	MmugDNA.27885.1.S1_at
Unknown	Gene function unknow	2.0	1.6	**FAM54A (LOC705828)**	family with sequence sim	MmugDNA.9831.1.S1_at

Classification	Sub-Classification	SM Fold Changes 14 dpi	SM Fold Changes 30 dpi	Gene Symbol	Gene Name	Affymetrix ID
Unknown	Gene function unknow	2.9	3.3	**FAM54A (LOC705828)**	family with sequence sim	MmugDNA.28821.1.S1_at
Unknown	Gene function unknow	2.7	3.2	FAM83D (LOC697925)	Protein C20orf129	MmugDNA.20671.1.S1_at
Unknown	Gene function unknow	2.5	2.2	LOC574106	alpha-1-antichymotrypsin	MmuSTS.2150.1.S1_at
Unknown	Gene function unknow	2.5	2.4	LOC699255	c-Mpl binding protein iso	MmugDNA.38020.1.S1_at
Unknown	Gene function unknow	2.5	3.0	ZNF367	zinc finger protein 367	MmugDNA.40258.1.S1_at
Unknown	Gene function unknow	2.1	1.2	---		Mmu.15443.1.S1_x_at
Unknown	Gene function unknow	2.7	1.1	**ANKRD22**	ankyrin repeat domain 2	MmugDNA.11765.1.S1_at
Unknown	Gene function unknow	2.2	1.1	**ANKRD22**	ankyrin repeat domain 2	MmugDNA.3988.1.S1_at
Unknown	Gene function unknow	2.6	1.2	FAM46C	family with sequence sim	MmugDNA.3623.1.S1_at
Unknown	Gene function unknow	-2.3	-1.0	---	solute carrier family 26,	MmuSTS.4436.1.S1_at
Unknown	Gene function unknow	-2.2	-1.3	LOC701902	---	Mmu.8061.1.S1_at
Unknown	Gene function unknow	1.6	2.1	C18orf54	C18orf54	MmugDNA.12151.1.S1_at
Unknown	Gene function unknow	1.4	2.3	GAS2L3	GAS2L3	MmugDNA.7107.1.S1_at

Supplementary Table S9. Gene expression correlated with CD8+Ki-67+% cells in SIVmac239 infected rhesus macaques. P-value (species/time) indicates the significance in log10 intensity gene expression between SIVsmm infected SM, SIVsmm-infected RMs, and SIVmac239-infected RMs. P-value (time) indicates the significance of gene expression changes after SIV infection in RMs and SMs.

					RM-SIVmac239					SM-SIVsmm				
Affymetrix Probeset ID	Gene Symbol	r (log10 Int, CD8+Ki-67+)	p-value (correlation)	p-value (species/time)	p-value (time)	D10/D0	D14/D0	D30/D0	Chronic/D0	p-value (time)	D10/D0	D14/D0	D30/D0	D180/D0
MmugDNA.43348.1.S1_at	SGOL2	0.83	6.06E-08	9.94E-01	4.55E-05	1.60	3.01	2.68	1.40	3.11E-04	-1.31	1.85	1.55	1.00
MmuSTS.4399.1.S1_at	CDCA8	0.80	2.78E-07	3.25E-01	1.51E-05	1.01	2.16	1.36	1.21	1.18E-01	-0.95	-0.68	1.27	1.18
MmugDNA.33387.1.S1_at	HIP2	0.79	4.48E-07	6.92E-01	1.37E-03	1.14	2.41	1.72	1.29	3.20E-05	-1.18	1.55	1.22	1.09
MmugDNA.17219.1.S1_at	HIST1H3J	0.76	2.76E-06	1.82E-01	1.13E-09	1.34	3.97	1.76	1.11	1.65E-01	-1.04	1.12	1.02	0.86
MmuSTS.1955.1.S1_at	RTN4	0.76	3.12E-06	3.44E-04	7.90E-06	1.08	2.24	1.57	1.17	5.83E-07	1.01	2.00	1.52	1.15
MmuSTS.644.1.S1_at	SDHD	0.75	3.44E-06	4.80E-02	7.32E-06	0.99	2.61	1.63	1.23	1.93E-02	0.81	1.53	1.26	1.07
MmuSTS.1558.1.S1_at	MELK	0.75	4.85E-06	6.94E-02	2.59E-05	1.21	5.76	2.49	1.85	1.48E-03	-1.56	3.44	1.99	1.70
MmugDNA.2976.1.S1_at	HJURP	0.74	6.42E-06	2.64E-01	5.62E-07	1.12	2.18	1.48	1.10	1.11E-02	-1.07	1.49	1.20	1.10
MmugDNA.26033.1.S1_at	CENPN	0.74	6.46E-06	1.37E-13	1.71E-04	-0.89	2.56	1.70	1.28	6.12E-04	-1.12	2.06	-0.64	-0.82
MmugDNA.33823.1.S1_s_at	---	0.74	7.74E-06	5.42E-01	3.83E-05	1.29	6.44	3.89	2.12	4.16E-08	0.77	5.24	-0.38	-0.79
MmuSTS.1534.1.S1_at	KIF20A	0.74	7.91E-06	7.80E-01	3.25E-05	1.15	2.11	1.64	1.18	5.06E-02	1.09	1.37	1.14	1.09
MmugDNA.9770.1.S1_at	GTSE1	0.73	8.46E-06	1.49E-03	9.44E-05	1.19	3.43	2.03	1.38	8.22E-07	-1.16	1.88	1.44	1.22
MmuSTS.144.1.S1_at	MCM2	0.73	9.04E-06	9.08E-12	3.17E-04	1.33	2.28	1.85	1.33	2.87E-01	-0.83	1.46	1.31	1.16
MmuSTS.4250.1.S1_at	RAD51AP1	0.73	9.32E-06	1.06E-02	1.79E-05	1.08	2.87	1.75	1.59	9.29E-06	-1.34	1.81	1.35	1.13
MmugDNA.12490.1.S1_at	E2F8	0.73	1.15E-05	8.11E-01	2.11E-05	-0.93	4.53	2.14	1.55	5.89E-04	-1.37	2.20	1.28	1.15
MmugDNA.38956.1.S1_at	NUSAP1	0.73	1.16E-05	5.54E-01	9.61E-07	-0.95	3.81	2.34	1.60	5.92E-08	-1.31	3.08	1.73	1.06
MmugDNA.23761.1.S1_at	RAD51	0.73	1.19E-05	8.71E-01	6.13E-06	-0.77	4.71	2.68	1.48	3.09E-04	-1.31	1.83	1.38	1.07
MmugDNA.22775.1.S1_at	DIAPH3	0.73	1.23E-05	6.93E-01	2.66E-04	1.11	2.70	1.83	1.27	5.63E-04	0.74	1.55	1.09	1.03
MmuSTS.3320.1.S1_at	CCNE2	0.73	1.28E-05	5.82E-01	4.49E-05	1.07	3.88	1.83	1.52	3.04E-03	0.74	2.05	1.38	1.14
MmugDNA.28002.1.S1_at	DEPDC1B	0.72	1.32E-05	3.19E-01	2.66E-05	1.17	4.53	2.22	1.50	8.87E-04	-1.40	1.99	1.44	1.16
MmugDNA.10778.1.S1_at	CDKN3	0.72	1.33E-05	1.90E-02	1.96E-05	-0.86	4.34	2.34	1.59	6.78E-08	-1.10	4.35	1.73	1.09
MmugDNA.12988.1.S1_s_at	LOC703598	0.72	1.40E-05	5.65E-22	3.06E-04	1.09	2.52	1.78	1.44	2.26E-02	-2.43	0.95	1.05	1.05
MmugDNA.28020.1.S1_at	BIRC5	0.72	1.64E-05	2.60E-01	8.14E-05	1.09	2.69	2.07	1.27	2.07E-04	0.92	1.75	1.38	1.01
MmugDNA.4085.1.S1_at	CCNE1	0.71	1.99E-05	6.89E-02	4.89E-04	1.18	2.84	1.95	1.48	8.67E-04	-1.03	2.28	1.52	1.24
MmugDNA.41887.1.S1_at	MYBL2	0.71	2.01E-05	1.14E-04	3.00E-03	1.16	2.33	1.63	1.25	5.22E-05	-0.91	1.75	1.51	1.14
MmugDNA.4124.1.S1_at	CDCA5	0.71	2.43E-05	7.22E-01	1.32E-05	1.25	3.74	2.22	1.45	2.51E-05	-1.00	2.04	1.55	-0.88
MmuSTS.1535.1.S1_at	KIF2C	0.71	2.58E-05	4.93E-02	3.61E-08	-0.91	4.09	2.18	1.45	1.36E-04	-1.26	1.89	1.56	1.02
MmugDNA.5873.1.S1_at	CEP55	0.71	2.65E-05	5.42E-01	2.63E-05	1.11	5.24	2.57	1.81	8.08E-06	-1.36	2.47	1.63	1.18
MmuSTS.236.1.S1_at	HMGB3	0.70	3.35E-05	3.17E-14	4.55E-07	0.95	2.52	1.74	1.34	1.51E-03	0.21	1.28	0.67	0.87
MmugDNA.32941.1.S1_at	C16ORF75	0.70	3.38E-05	1.30E-30	1.82E-07	1.73	3.65	2.11	1.27	4.57E-03	-0.83	2.07	0.88	0.75
MmuSTS.2066.1.S1_at	GINS2	0.70	3.44E-05	3.17E-03	1.56E-04	1.13	2.74	1.76	1.30	6.77E-06	-0.92	1.96	1.43	1.14
MmugDNA.9497.1.S1_at	KIFC1	0.69	4.53E-05	5.18E-01	3.01E-06	-0.84	2.72	1.66	1.32	7.19E-02	-1.07	1.22	1.30	1.12
MmugDNA.43588.1.S1_at	C6ORF173	0.69	4.80E-05	3.39E-01	1.80E-07	-0.99	2.38	1.58	1.24	1.66E-02	-1.13	1.73	1.23	1.05
MmuSTS.673.1.S1_s_at	CHAF1A	0.69	4.83E-05	4.28E-01	5.97E-06	-0.89	3.75	1.94	1.40	3.06E-03	-1.45	1.59	1.36	1.20
MmuSTS.1653.1.S1_at	TMPRSS3	0.69	5.32E-05	6.02E-11	1.18E-05	0.99	2.33	1.79	1.32	3.12E-05	-1.24	2.15	1.56	1.16
MmugDNA.32729.1.S1_at	MKI67	0.69	5.70E-05	8.08E-09	4.84E-06	0.94	4.01	2.45	1.69	2.64E-03	-1.19	2.21	1.76	1.33
MmuSTS.4722.1.S1_at	TRIP13	0.69	5.77E-05	6.14E-02	1.53E-03	0.95	2.73	1.85	1.30	5.36E-05	-1.30	1.90	1.40	1.14
MmuSTS.4685.1.S1_at	TYMS	0.68	5.93E-05	1.91E-06	4.13E-05	1.53	7.85	3.29	1.90	1.58E-06	-0.95	3.43	2.65	1.23
MmuSTS.2164.1.S1_at	DDX10	0.68	6.03E-05	3.64E-03	1.92E-03	2.55	5.33	3.74	1.71	7.42E-06	-0.76	3.80	2.08	1.16
MmugDNA.21403.1.S1_at	CDCA3	0.68	6.20E-05	3.35E-01	1.58E-04	-0.93	3.03	2.06	1.28	3.32E-05	-1.24	2.11	1.26	1.09
MmugDNA.23764.1.S1_at	CCNA2	0.68	6.22E-05	2.80E-06	5.92E-06	-1.06	2.50	1.52	1.39	1.34E-02	-1.22	2.57	1.63	-0.81
MmugDNA.15754.1.S1_at	CHEK1	0.68	6.26E-05	1.38E-01	7.27E-05	1.13	3.51	1.76	1.25	2.89E-05	0.80	1.98	1.33	1.08
MmuSTS.4420.1.S1_at	TPX2	0.68	7.21E-05	3.32E-03	1.15E-04	1.18	2.13	1.61	1.29	2.96E-01	-0.96	1.31	1.29	-0.85
MmuSTS.3327.1.S1_at	OIP5	0.68	7.63E-05	6.27E-01	3.85E-04	-0.84	3.70	2.25	1.53	1.10E-03	-1.05	2.17	1.57	1.23
MmugDNA.14322.1.S1_at	TFDP1	0.68	8.08E-05	2.58E-01	2.22E-03	-0.93	2.35	1.76	1.39	9.46E-06	-1.33	2.50	1.64	1.37
MmuSTS.64.1.S1_at	GMNN	0.67	8.99E-05	9.43E-01	5.65E-04	-0.91	2.39	1.61	1.60	1.00E-04	-1.49	2.91	1.46	0.93
MmuSTS.4762.1.S1_at	FBXO5	0.67	9.53E-05	2.20E-01	2.71E-04	0.96	2.14	1.39	1.31	2.60E-03	-1.70	1.89	1.16	1.16
MmugDNA.1969.1.S1_at	MCM4	0.67	9.95E-05	6.87E-05	7.37E-05	-0.93	4.04	1.92	1.40	1.16E-02	-1.24	2.01	1.44	1.00
MmugDNA.30746.1.S1_at	LAG3	0.67	1.01E-04	9.80E-02	2.68E-04	1.32	3.07	1.69	1.31	9.33E-01	-0.75	1.59	1.30	1.33
MmugDNA.19989.1.S1_at	DCC1	0.67	1.02E-04	1.10E-01	5.87E-03	1.03	3.07	1.63	1.35	2.19E-03	-1.36	1.42	1.24	1.08
MmugDNA.19464.1.S1_at	UHRF1	0.67	1.03E-04	1.99E-01	1.86E-06	1.09	4.94	2.13	1.42	9.65E-05	-1.65	1.85	1.43	1.06
MmugDNA.15585.1.S1_at	KIF15	0.67	1.10E-04	1.78E-01	3.92E-07	0.94	4.82	2.17	1.55	5.06E-03	-1.64	2.09	1.37	1.04
MmugDNA.15250.1.S1_at	CENPA	0.67	1.10E-04	6.23E-02	1.31E-05	0.93	4.38	2.49	1.61	1.46E-06	-1.22	3.01	1.80	1.21
MmuSTS.2645.1.S1_at	FEN1	0.66	1.15E-04	5.85E-01	2.77E-06	-1.04	2.51	1.47	1.28	6.20E-03	-1.26	1.55	1.30	1.08
MmuSTS.2070.1.S1_s_at	MICB	0.66	1.18E-04	2.68E-01	6.41E-05	1.03	2.66	1.61	1.22	4.29E-01	0.91	1.06	1.20	1.08
MmugDNA.21462.1.S1_at	KIF4A	0.66	1.23E-04	9.76E-02	3.67E-05	-0.85	2.41	1.46	1.13	2.37E-02	-1.03	1.34	1.17	1.20
MmugDNA.11364.1.S1_at	FOXM1	0.66	1.27E-04	1.34E-01	2.73E-04	1.14	2.87	2.01	1.44	6.20E-03	-1.06	1.89	1.48	1.20
MmuSTS.2303.1.S1_s_at	DLG7	0.66	1.29E-04	3.26E-01	5.49E-05	-0.99	2.59	1.34	1.23	2.54E-02	-1.07	1.50	1.41	1.08
MmugDNA.40742.1.S1_at	CCNB2	0.66	1.32E-04	9.29E-01	4.76E-06	1.08	5.88	2.74	1.66	3.91E-09	0.96	4.79	2.43	1.37
MmuSTS.1779.1.S1_at	NEK2	0.66	1.35E-04	1.31E-01	3.42E-04	-1.05	3.69	2.60	1.58	4.23E-05	0.79	2.59	1.82	1.15
MmunewRS.661.1.S1_at	HIST1H4C	0.66	1.36E-04	4.83E-13	1.83E-05	-1.15	3.07	2.57	1.70	3.53E-02	-1.76	5.36	1.98	0.84
MmugDNA.18794.1.S1_at	CDC20	0.66	1.36E-04	1.96E-05	3.77E-05	1.07	5.16	2.57	1.64	3.23E-05	-0.92	2.61	1.82	1.29
MmugDNA.29315.1.S1_at	DEPDC1	0.66	1.43E-04	6.40E-07	4.97E-05	-0.91	2.89	2.12	1.28	5.18E-07	-1.19	3.18	1.57	0.97
MmugDNA.11747.1.S1_at	MLF1IP	0.66	1.43E-04	3.85E-03	4.66E-06	0.92	3.82	2.09	1.45	5.81E-07	-1.77	1.68	1.25	1.06
MmugDNA.14257.1.S1_at	CCNF	0.66	1.50E-04	1.77E-02	3.17E-06	-1.06	2.16	1.41	1.12	2.30E-02	-1.22	1.34	1.20	-0.87
MmugDNA.41835.1.S1_at	DHFR	0.66	1.55E-04	8.99E-01	2.77E-06	0.85	3.05	1.46	1.27	3.57E-03	-1.33	1.34	1.45	-0.91
MmugDNA.31369.1.S1_at	RRM2	0.65	1.58E-04	1.62E-01	2.58E-04	1.27	8.14	3.57	2.20	2.30E-07	-1.24	7.31	3.50	1.54
MmugDNA.2694.1.S1_at	ZWINT	0.65	1.67E-04	2.51E-01	1.87E-05	0.94	3.20	1.96	1.61	5.92E-04	-1.26	2.50	1.76	1.30
MmuSTS.220.1.S1_at	SIL	0.65	1.68E-04	3.03E-01	2.09E-04	1.01	2.26	1.50	1.43	4.81E-03	-1.29	1.31	1.31	1.13
MmugDNA.30056.1.S1_at	TYMS	0.65	1.69E-04	1.61E-06	1.29E-05	1.32	4.35	2.31	1.51	4.83E-04	0.90	1.90	1.72	1.11
MmugDNA.2768.1.S1_at	NUF2	0.65	1.75E-04	6.55E-01	7.28E-05	-0.86	3.25	1.51	1.35	2.59E-02	-1.17	1.50	1.19	1.08
MmugDNA.14959.1.S1_at	CDC2	0.65	1.76E-04	2.21E-01	2.89E-04	1.06	2.11	1.40	1.30	3.54E-03	-1.07	1.36	1.23	1.02
MmugDNA.31059.1.S1_s_at	PTTG1	0.65	1.98E-04	1.19E-09	1.92E-04	-0.98	2.45	1.46	1.23	1.55E-03	-1.11	2.27	1.66	1.21
MmugDNA.17329.1.S1_at	CDCA7	0.64	2.12E-04	3.85E-04	3.87E-08	0.91	3.89	1.90	1.94	5.52E-05	0.63	2.17	1.73	1.33
MmugDNA.25384.1.S1_at	UBE2C	0.64	2.15E-04	3.17E-01	4.85E-06	-0.84	4.65	2.68	1.46	1.65E-07	-0.96	2.99	1.95	1.28
MmuSTS.2700.1.S1_at	E2F7	0.64	2.16E-04	1.34E-01	7.83E-07	-1.08	3.30	1.71	1.32	2.15E-06	-1.27	2.58	1.57	1.26
MmugDNA.8836.1.S1_at	MCM10	0.64	2.23E-04	1.88E-07	2.38E-04	1.18	4.24	2.35	1.57	1.23E-04	-1.33	1.61	1.37	1.11
MmugDNA.6706.1.S1_at	CKAP2	0.64	2.23E-04	1.17E-09	9.83E-06	-1.23	3.15	1.97	1.33	9.79E-06	-1.29	2.49	1.77	1.20
MmuSTS.3146.1.S1_s_at	MCM5	0.64	2.36E-04	7.77E-06	6.36E-05	1.00	2.94	1.56	1.49	2.63E-02	-0.85	1.78	1.57	1.34
Mmu.11047.2.S1_s_at	LOC711303	0.64	2.49E-04	6.24E-02	1.17E-03	1.00	2.03	1.83	1.96	9.96E-03	1.41	4.40	2.44	1.03
MmugDNA.12277.1.S1_at	TOP2A	0.64	2.51E-04	7.08E-01	8.39E-05	-1.08	2.92	1.81	1.43	1.05E-05	-1.12	1.96	1.38	1.15
MmugDNA.12273.1.S1_at	TOP2A	0.64	2.56E-04	6.33E-01	2.10E-06	1.06	3.77	2.32	1.56	3.25E-06	-1.17	2.80	2.42	1.19
MmugDNA.14075.1.S1_at	BUB1B	0.64	2.60E-04	1.83E-03	7.32E-04	-1.10	3.64	1.94	1.81	3.01E-06	-1.28	2.26	1.66	-0.77
MmugDNA.25436.1.S1_at	MCM3	0.64	2.61E-04	1.56E-03	2.05E-04	-0.96	3.18	1.64	1.42	1.79E-01	-1.06	1.74	1.70	1.29

Supplementary Table S9. part 1 of 3.

					RM-SIVmac239					SM-SIVsmm				
Affymetrix Probeset ID	Gene Symbol	r (log10 Int, CD8+Ki-67+)	p-value (correlation)	p-value (species/time)	p-value (time)	D10/D0	D14/D0	D30/D0	Chronic/D0	p-value (time)	D10/D0	D14/D0	D30/D0	D180/D0
MmugDNA.38781.1.S1_a	LOC698390	0.64	2.62E-04	1.43E-09	5.86E-03	-1.29	2.03	2.15	1.65	2.98E-04	-1.03	7.79	2.09	0.91
MmugDNA.2512.1.S1_a	RP5-998N21.9	0.64	2.67E-04	9.11E-01	4.66E-04	1.27	2.01	1.52	1.26	1.87E-04	-1.10	1.45	1.19	-1.01
MmugDNA.24430.1.S1_a	CDC25A	0.63	3.19E-04	2.18E-11	1.30E-04	-0.97	3.16	1.99	1.54	2.61E-01	-1.23	1.46	1.44	1.18
MmugDNA.25197.1.S1_a	ASPM	0.63	3.21E-04	6.87E-02	1.06E-04	-0.98	2.44	1.78	1.22	1.74E-04	0.79	2.11	1.50	1.03
MmuSTS.3576.1.S1_a	CCNA2	0.63	3.25E-04	2.91E-02	2.51E-04	1.06	3.45	1.94	1.57	2.01E-04	-1.07	2.96	1.80	1.26
MmuSTS.2164.1.S1_s_a	DDX10	0.63	3.51E-04	5.14E-01	4.38E-04	2.10	6.45	2.91	1.73	9.45E-04	-0.85	2.41	1.83	-0.78
MmugDNA.35622.1.S1_a	KIF14	0.63	3.53E-04	8.12E-01	2.20E-04	0.99	2.39	1.56	-0.85	2.79E-02	-1.17	1.41	1.25	1.10
MmuSTS.2071.1.S1_a	RAD54L	0.63	3.55E-04	9.10E-01	2.94E-05	1.01	2.17	1.44	1.09	2.67E-04	-1.07	1.50	1.30	-0.82
MmuSTS.1531.1.S1_a	KIF14	0.63	3.64E-04	5.28E-02	1.87E-05	-1.07	2.61	1.55	1.22	1.59E-02	-1.26	1.34	1.23	1.13
MmugDNA.36470.1.S1_a	NDC80	0.63	3.67E-04	3.09E-03	1.28E-03	1.69	3.35	1.90	1.56	1.97E-01	1.13	1.85	1.40	1.11
MmuSTS.2866.1.S1_a	STMN1	0.62	3.82E-04	2.42E-01	2.46E-06	-1.20	2.14	1.30	1.07	5.65E-06	-1.42	1.53	1.24	1.24
MmuSTS.4157.1.S1_a	MAD2L1	0.62	3.93E-04	9.90E-01	1.40E-05	-1.23	2.96	1.73	1.59	6.23E-05	-1.69	3.71	1.57	1.13
MmugDNA.23023.1.S1_a	C13ORF3	0.62	4.10E-04	7.24E-01	2.09E-05	-0.94	2.45	1.54	1.21	3.40E-02	-1.14	1.40	-0.86	-0.92
MmugDNA.17680.1.S1_a	PRR11	0.62	4.33E-04	3.33E-01	7.60E-06	0.92	2.77	1.56	1.28	2.04E-04	0.81	1.05	1.41	1.15
MmugDNA.35559.1.S1_a	HIST1H1D	0.62	4.84E-04	1.26E-01	1.83E-05	-0.88	3.91	2.22	1.33	3.50E-03	-1.23	1.40	1.33	1.23
MmuSTS.3275.1.S1_a	RRM2	0.62	4.87E-04	5.15E-08	7.87E-04	-0.79	6.11	2.81	1.89	8.50E-08	-0.88	4.92	2.31	1.18
MmugDNA.35654.1.S1_a	CAPZA2	0.61	5.23E-04	2.01E-02	4.02E-06	-1.10	2.55	1.53	1.33	1.74E-04	-1.41	1.65	1.32	1.21
MmugDNA.11557.1.S1_a	NCAPG	0.61	5.67E-04	8.01E-04	8.19E-06	1.08	4.49	2.43	1.85	1.29E-04	-1.43	2.81	1.68	-0.92
MmugDNA.21515.1.S1_a	PRC1	0.61	5.69E-04	1.51E-01	1.22E-06	0.91	2.81	1.68	1.39	1.31E-06	0.70	2.05	1.49	0.97
MmugDNA.2975.1.S1_a	POLE2	0.61	5.71E-04	3.41E-02	8.84E-06	0.99	2.50	1.64	1.46	9.22E-08	0.84	2.35	1.56	1.12
MmugDNA.41268.1.S1_a	CCNB1	0.61	5.95E-04	2.83E-09	2.48E-05	0.92	3.10	1.77	1.51	3.63E-04	-1.28	3.07	1.93	1.12
MmuSTS.2698.1.S1_a	HIST1H2BH	0.61	6.01E-04	2.37E-01	3.39E-04	1.02	2.07	1.68	1.17	3.54E-03	0.90	1.73	1.09	0.95
MmugDNA.13565.1.S1_a	KIF11	0.61	6.03E-04	2.91E-01	1.05E-05	0.90	4.25	2.02	1.97	2.20E-05	-1.51	2.31	1.57	-0.85
MmuSTS.4348.1.S1_a	IGHG1	0.61	6.11E-04	6.26E-02	7.27E-04	1.00	3.04	2.37	2.74	3.14E-04	1.26	5.77	2.81	1.06
MmugDNA.3558.1.S1_a	AURKA	0.61	6.16E-04	1.74E-20	1.42E-06	1.02	2.17	1.60	1.15	1.47E-01	0.94	1.21	1.35	1.04
MmugDNA.24523.1.S1_a	CDCA2	0.61	6.21E-04	2.26E-01	3.43E-04	1.20	2.62	1.61	1.37	2.52E-02	0.88	1.38	1.02	0.99
MmuSTS.3714.1.S1_a	FHL2	0.61	6.44E-04	2.65E-15	5.26E-06	-0.91	2.09	1.33	0.95	5.53E-02	-1.36	1.13	1.05	1.14
MmugDNA.3020.1.S1_a	ZWILCH	0.60	6.56E-04	6.62E-04	3.55E-04	1.11	2.12	1.45	1.31	3.51E-01	0.71	1.51	1.29	0.98
MmuSTS.2672.1.S1_a	CENPF	0.60	6.63E-04	9.41E-08	2.07E-05	0.85	2.34	1.37	1.61	1.47E-03	-1.43	1.64	1.31	1.08
MmugDNA.6277.1.S1_a	BUB1	0.60	6.80E-04	2.89E-01	2.78E-04	1.89	5.88	2.47	1.69	4.13E-05	1.11	2.29	1.96	1.36
MmuSTS.3318.1.S1_a	CCNB1	0.60	7.09E-04	9.28E-01	1.97E-05	0.82	2.25	1.29	1.19	5.39E-02	0.66	1.56	1.06	1.08
MmugDNA.18123.1.S1_a	RFC3	0.60	7.28E-04	9.69E-01	1.08E-04	-1.16	2.11	1.37	1.14	1.24E-03	0.57	2.28	1.28	1.11
MmugDNA.5663.1.S1_a	PLS3	0.59	8.52E-04	1.17E-10	7.93E-05	0.97	2.14	1.29	1.11	6.47E-06	0.95	3.90	0.84	0.85
MmugDNA.7866.1.S1_a	CDT1	0.59	9.92E-04	5.42E-01	1.46E-03	1.13	2.23	1.45	1.24	3.24E-03	-0.95	1.22	-0.69	1.14
MmugDNA.36434.1.S1_a	GZMA	0.59	1.02E-03	3.34E-11	3.58E-06	0.94	12.81	2.54	2.55	9.48E-06	-1.75	6.15	1.70	1.00
MmugDNA.31030.1.S1_a	LOC91431	0.59	1.02E-03	8.12E-06	3.07E-05	-1.01	2.13	1.21	1.13	1.94E-01	-1.30	1.22	1.16	1.01
MmugDNA.13584.1.S1_a	KIF23	0.58	1.09E-03	4.42E-02	9.47E-06	0.91	2.56	1.64	1.48	6.61E-04	-1.42	1.37	1.22	-0.98
MmugDNA.2951.1.S1_a	ANLN	0.58	1.09E-03	5.33E-01	8.26E-06	-0.97	2.31	1.51	1.15	6.77E-05	-1.30	1.53	1.15	0.96
MmugDNA.39863.1.S1_a	C18ORF24	0.58	1.12E-03	8.88E-03	2.74E-03	-0.79	3.73	2.48	1.75	7.29E-03	-0.94	2.55	1.71	1.27
MmugDNA.34150.1.S1_s_a	MGC4677	0.58	1.12E-03	1.80E-04	3.79E-03	-0.57	1.95	2.40	1.46	2.86E-01	1.28	1.68	1.30	1.07
MmugDNA.30164.1.S1_a	TIPIN	0.58	1.17E-03	7.72E-01	4.29E-04	-0.89	2.71	1.48	1.31	1.46E-02	-1.24	1.63	1.39	1.06
MmugDNA.3247.1.S1_s_a	HIST2H4B	0.58	1.33E-03	5.71E-01	2.54E-03	-1.00	2.07	1.53	1.23	1.23E-04	-0.79	2.23	1.62	1.26
MmugDNA.42135.1.S1_a	FBXO5	0.58	1.36E-03	8.12E-01	4.22E-04	-0.93	2.01	1.32	1.27	2.61E-02	-1.40	1.45	1.33	0.96
MmugDNA.34901.1.S1_a	SDF2L1	0.57	1.46E-03	1.23E-01	1.59E-03	1.00	2.05	1.30	1.30	3.14E-01	1.18	2.07	1.64	1.35
MmugDNA.39221.1.S1_a	HAVCR2	0.57	1.49E-03	1.04E-03	2.34E-06	-0.73	3.32	1.34	1.22	7.85E-02	-0.94	1.41	1.37	1.16
MmuSTS.1283.1.S1_a	DTL	0.57	1.64E-03	9.86E-03	2.43E-03	3.31	6.52	2.61	1.86	3.85E-06	-0.80	3.09	-0.64	-0.90
MmuSTS.673.1.S1_a	CHAF1A	0.57	1.73E-03	4.64E-01	6.87E-05	-1.06	2.44	1.23	1.22	2.05E-02	-1.07	1.38	1.32	-0.82
MmugDNA.16154.1.S1_a	MSRB2	0.56	1.74E-03	8.95E-21	6.19E-05	-0.82	2.05	1.44	1.13	9.84E-01	-0.77	1.39	1.23	1.32
MmugDNA.19272.1.S1_s_a	SPAG5	0.56	2.09E-03	6.10E-01	3.43E-04	-0.94	3.37	1.72	1.37	1.35E-01	0.98	1.44	1.47	1.13
MmuSTS.911.1.S1_a	ALDH9A1	0.55	2.22E-03	6.03E-02	2.10E-04	1.08	2.62	1.59	-0.58	4.04E-03	1.11	2.37	1.43	1.07
MmuSTS.1343.1.S1_a	TFDP1	0.55	2.23E-03	3.85E-02	1.20E-03	1.44	3.81	1.67	-0.80	6.69E-01	-0.77	-0.59	-0.75	-0.81
MmugDNA.31059.1.S1_a	PTTG1	0.55	2.35E-03	5.14E-09	6.32E-05	-1.13	2.24	1.30	1.26	1.01E-04	-0.92	2.82	1.95	1.43
MmuSTS.2509.1.S1_a	H2AFJ	0.55	2.35E-03	2.18E-03	1.12E-04	-0.96	2.04	1.34	1.13	4.74E-01	-0.68	2.17	1.64	1.11
MmugDNA.8456.1.S1_a	KDELR3	0.55	2.44E-03	6.77E-01	3.15E-04	1.16	2.26	1.49	1.18	8.81E-03	-1.24	1.37	0.89	1.01
MmugDNA.14956.1.S1_a	CDC6	0.55	2.56E-03	7.38E-05	1.70E-06	1.01	2.28	1.47	1.22	4.71E-03	-1.10	1.63	1.29	1.08
MmugDNA.34591.1.S1_s_a	IGKC	0.55	2.57E-03	2.16E-01	1.33E-05	-1.07	2.18	1.28	1.15	1.61E-01	0.90	1.50	1.31	1.21
MmugDNA.20669.1.S1_a	FAM111B	0.55	2.58E-03	1.84E-01	8.15E-05	-0.86	2.87	1.24	1.17	3.72E-03	-1.26	1.15	1.08	0.94
MmugDNA.865.1.S1_a	PCNA	0.54	2.84E-03	3.62E-02	3.09E-04	-1.05	2.15	1.38	1.31	3.29E-04	-1.29	1.99	1.49	1.12
MmugDNA.18586.1.S1_a	SMC2	0.54	3.10E-03	2.18E-03	9.53E-05	-1.17	2.98	1.72	-0.65	4.33E-03	-1.71	3.02	-0.63	-0.76
MmugDNA.22076.1.S1_a	MGC29506	0.54	3.28E-03	9.81E-03	6.07E-03	-1.23	2.15	-0.44	1.67	2.37E-04	-0.99	5.43	2.50	1.00
MmuSTS.1347.1.S1_a	HMGB2	0.53	3.39E-03	1.03E-01	7.26E-07	0.84	2.41	1.30	-0.82	1.90E-03	-1.47	1.99	1.51	1.25
MmugDNA.43394.1.S1_a	RNF157	0.53	3.40E-03	9.10E-01	2.90E-08	0.81	2.65	1.06	1.18	1.13E-02	0.86	1.29	-0.67	-0.78
MmugDNA.7428.1.S1_a	WHSC1	0.53	3.52E-03	3.87E-02	1.56E-05	-1.16	2.05	1.18	1.28	6.83E-04	-1.22	1.57	1.23	1.21
Mmu.6559.1.S1_s_a	LOC701387	0.53	3.62E-03	2.48E-04	8.24E-04	1.22	3.45	1.46	1.09	4.42E-01	1.57	2.07	2.09	1.07
MmugDNA.8750.1.S1_a	PHF19	0.53	3.98E-03	6.25E-01	6.71E-04	0.99	2.86	1.34	-0.83	4.90E-04	-1.08	-0.57	1.47	-0.89
Mmu.14249.1.S1_a	CCR5	0.53	4.01E-03	4.70E-02	1.46E-03	1.08	2.84	1.51	-0.64	9.37E-01	-1.07	-1.00	-1.05	-1.02
MmuSTS.61.1.S1_a	HELLS	0.52	4.35E-03	3.38E-03	6.72E-04	0.89	2.06	1.23	1.58	1.89E-04	-2.00	1.82	1.21	0.98
MmugDNA.30376.1.S1_a	IGKC	0.52	4.39E-03	2.55E-02	1.07E-05	0.85	2.75	1.30	1.13	1.72E-02	-1.27	1.79	-0.70	1.23
MmuSTS.8.1.S1_a	H2AFX	0.52	4.61E-03	2.02E-03	1.26E-05	0.88	2.29	1.30	1.12	1.41E-02	-0.91	1.88	1.62	1.25
MmuSTS.4740.1.S1_a	F13A1	0.51	5.19E-03	4.61E-17	8.79E-04	1.45	2.28	1.30	0.96	3.25E-01	1.15	1.16	1.04	1.30
MmugDNA.37873.1.S1_a	MYLK	0.51	5.68E-03	5.01E-01	2.64E-04	-0.77	2.89	1.13	0.85	6.54E-01	-1.21	0.84	0.74	0.79
MmugDNA.27586.1.S1_a	OCC-1	0.51	5.87E-03	1.54E-06	2.22E-05	-1.50	2.44	-0.78	1.28	1.81E-05	-2.18	1.79	1.47	-0.79
MmugDNA.2951.1.S1_s_a	ANLN	0.51	5.93E-03	2.90E-01	2.95E-05	-1.01	4.27	2.07	1.30	1.27E-04	-1.49	1.46	1.37	-0.89
Mmu.7460.4.S1_a_a	KIR2DL4	0.50	6.32E-03	4.04E-03	8.70E-04	1.02	3.20	1.31	1.05	2.31E-01	0.76	1.01	1.57	1.45
MmugDNA.10186.1.S1_a	CASC5	0.50	6.33E-03	7.52E-01	6.54E-04	1.03	2.36	1.60	1.83	4.42E-07	0.72	2.24	1.55	1.33
MmugDNA.3247.1.S1_a	HIST2H4B	0.50	6.88E-03	2.84E-01	1.00E-04	-1.22	2.18	1.62	-0.78	9.20E-04	-0.78	3.22	1.96	1.52
MmugDNA.303.1.S1_a	CCDC99	0.50	7.09E-03	4.17E-06	2.40E-05	0.77	2.18	1.20	1.30	4.05E-04	-1.45	2.16	1.25	1.29
MmugDNA.6381.1.S1_a	CST7	0.50	7.25E-03	2.21E-01	4.97E-04	0.83	2.26	1.01	-0.83	1.21E-01	-1.13	1.15	-0.69	-0.81
MmugDNA.26023.1.S1_a	C19ORF59	0.49	7.74E-03	2.98E-04	1.87E-06	0.85	4.75	1.29	0.89	3.48E-01	0.85	1.24	0.95	-1.41
MmugDNA.41979.1.S1_a	C11ORF32	-0.48	9.43E-03	9.86E-01	2.11E-04	-2.48	-1.83	-1.92	-1.31	8.42E-03	-1.47	-1.15	-0.99	-1.05
MmuSTS.4328.1.S1_a	SERPINE2	-0.48	9.21E-03	1.58E-14	7.93E-04	-3.07	-1.89	-3.23	-1.23	3.66E-01	-1.68	-1.39	-1.53	-1.70
MmuSTS.4328.1.S1_x_a	SERPINE2	-0.49	8.24E-03	3.88E-14	2.52E-03	-2.80	-1.89	-2.74	-1.25	6.37E-01	-1.42	-1.37	-1.37	-1.54
MmugDNA.11101.1.S1_a	---	-0.49	7.86E-03	9.24E-18	1.21E-03	-1.48	-1.17	-2.15	-1.76	8.05E-01	-1.08	-1.16	-1.13	-1.02
MmugDNA.15103.1.S1_a	FNBP1L	-0.50	7.37E-03	1.91E-13	3.58E-03	-2.74	-2.41	-2.96	-1.41	8.87E-01	-1.18	-1.12	-1.04	-1.14
MmuAffx.23.8.S1_s_a	SERPINE2	-0.50	7.12E-03	7.06E-11	4.60E-03	-2.93	-2.06	-2.68	-1.25	7.11E-01	-1.50	-1.28	-1.33	-1.52
MmugDNA.437.1.S1_a	SLC25A16	-0.50	6.82E-03	3.53E-04	1.61E-04	-2.43	-1.76	-2.21	-1.29	2.17E-03	-2.29	-1.77	-1.39	-1.41
MmugDNA.24921.1.S1_a	AFF3	-0.53	3.37E-03	6.39E-29	5.15E-04	-2.11	-2.34	-2.11	-0.93	1.59E-01	-1.12	-1.74	-0.89	-1.03

Supplementary Table S9. part 2 of 3.

					RM-SIVmac239					SM-SIVsmm				
Affymetrix Probeset ID	**Gene Symbol**	**r (log10 Int, CD8+Ki-67+)**	**p-value (correlation)**	**p-value (species/time)**	**p-value (time)**	**D10/D0**	**D14/D0**	**D30/D0**	**Chronic/D0**	**p-value (time)**	**D10/D0**	**D14/D0**	**D30/D0**	**D180/D0**
MmugDNA.17530.1.S1_at	SULF2	-0.54	3.21E-03	3.45E-01	9.17E-04	-1.77	-2.11	-1.65	-1.03	1.36E-01	-0.65	-0.95	-0.86	-1.05
MmugDNA.8010.1.S1_at	IL7R	-0.54	3.08E-03	1.86E-01	6.66E-03	-1.44	-1.19	-2.23	-1.71	2.43E-01	-1.32	-1.13	-1.15	-1.06
MmugDNA.34681.1.S1_at	SORL1	-0.54	2.74E-03	2.34E-08	3.71E-03	-2.26	-1.68	-1.97	-1.32	8.79E-02	-0.96	-1.41	-0.99	-1.17
MmugDNA.32882.1.S1_at	LOC718964	-0.55	2.34E-03	1.56E-02	4.23E-04	-2.07	-1.85	-1.97	-1.20	1.55E-01	-1.47	-1.20	-1.09	-1.51
MmugDNA.4335.1.S1_at	HERC1	-0.59	1.05E-03	2.04E-19	3.21E-03	-1.60	-1.30	-2.02	-1.15	8.86E-03	-0.86	-1.48	-0.93	-1.64
MmugDNA.41593.1.S1_at	C20ORF32	-0.63	3.07E-04	5.99E-08	1.05E-05	-1.25	-2.36	-1.97	-0.83	4.77E-01	-1.03	-1.44	-0.98	-1.32

Supplementary Table S9. part 3 of 3.

Supplementary Table S10. Oligonucleotide Primer Sequences used for Real-Time PCR.

cDNA	Forward (5'-3')	Reverse (5'-3')
SYBR		
GAPDH	GAAGGTGAAGGTCGGAGTC	CAAGCTTCCCGTTCTCAGCC
G1P2	TCCTGGTGAGGAATAACAAGGG	GTCAGCCAGAACAGGTCGTC
G1P3	GGTCTGCGATCCTGAATGGG	TCACTATCGAGATACTTGTGGGT
OAS1	GGAAAGGGCTCCAGTGTTATC	GGATCAAGAGTCCCACCTGAAAA
OAS2	CAGTCCTGGTGAGTTTGCAGT	GCCAGTGCTTTATCAAGAGGAT
GBP1	TTCTGAACAAAGAGACGATAGCC	AGGAGTTCCTTCAAAGATGTGGA
GBP2	TTTTTCCAGCATTTGTGTGGACT	CTTTAGCGAAAGCTCCAAGTAGT
IFIT3	TCAGAAGTCTAGTCACTTGGGG	ACACCTTCGCCCTTTCATTTC
MX1	AGGAGTTGCCCTTCCCAGA	TCGTTCACAAGTTTCTTCAGTTTCA
MX2	CAGAGGCAGCGGAATCGTAA	CTGAAGCTCTAGCTCGGTGT
BST2	GAG TGT CGC AAT GTC ACC CAT	GGA AGC CAT TAG GGC CAT CAC
ZC3HAV1	AGG CTA CTG TAA CCC CGG AAT	CCA TAC TGA ATC CAT GTG CCA G
TRIM22	CTG TCC TGT GTG TCA GAC CAG	TGG GCT CAT CTT GAC CTC TTT
TaqMan	**Material #.**	
GAPDH	AB# Rh02621745_g1	
INDO	AB# Rh02841203_m1	
CXCL10	AB# Rh02788358_m1	