

SUPPLEMENTAL MATERIAL

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I. Supplemental Methods

Animal experiments

Male C3H/HeN mice (4-week-old) were purchased from Taconic Farms (Hudson, NY). Mice were maintained on 12/12-hour light/dark cycles in standard animal cages with filter tops under specific pathogen-free conditions in the animal care facility at Louisiana State University Health Sciences Center (LSUHSC)-Shreveport. Mice were given standard laboratory rodent chow and water ad libitum. All experimental procedures involving the use of animals were reviewed and approved by the Institutional Animal Care and Use Committee of LSUHSC and performed according to the criteria outlined by the National Institutes of Health.

We infected 5-week-old mice with 2×10^7 plaque forming units (PFUs) of the DA strain of TMEV intraperitoneally. We used age-matched uninfected mice as controls. Mice were monitored and weighed daily for up to 2 months. On 0, 4, 7, 14, 30, and 60 days post infection (dpi), we conducted echocardiography using the Vevo 770 High-Resolution *In Vivo* Micro-Imaging System (VisualSonics, Toronto, Ontario, Canada). We used B- and M-modes of echocardiography to monitor longitudinal morphological and functional changes, without killing mice. On 4, 7, and 60 dpi, we anesthetized five mice per group, using IsoSolTM (isoflurane, USP, Vedco, Saint Joseph, MO), and harvested the hearts.

Enzyme-linked immunosorbent assay (ELISA) of serum troponin I

Blood samples were collected from five infected mice by submandibular bleeding⁶¹ on 4, 7, 14, and 30 dpi and the sera were separated by centrifugation. The levels of cardiac troponin I in the sera were measured by ELISA using the Ultra Sensitive Mouse Cardiac Troponin-I ELISA Kit (Life Diagnostics, West Chester, PA), according to the manufacturer's instructions.

RNA preparation

The hearts were homogenized in TRI Reagent[®] (Molecular Research Center, Cincinnati, OH), using the Kinematica PolytronTM homogenizer (Kinematica, Bohemia, NY). Total RNA was extracted

from the homogenate, using the RNeasy Mini Kit (Qiagen, Valencia, CA), according to the manufacturer's instructions.⁶² DNase treatment was performed during RNA isolation using the RNase-Free DNase Set (Qiagen). All samples were purified to an absorbance ratio (A260/A280) between 1.9 and 2.1. Samples were collected from five infected animals and five age-matched controls at each time point (4, 7, and 60 dpi).

Microarray analysis

We reverse-transcribed 100 ng of total RNA to first-stranded cDNA, using the Poly-A RNA Control (Affymetrix, Santa Clara, CA) and Ambion[®] WT Expression Kit (Life Technologies Corporation, Carlsbad, CA).⁶² The double-stranded cDNA was generated from single-stranded cDNA and transcribed *in vitro* into cRNA. The resulting cRNA was purified and 10 µg of purified cRNA was reverse-transcribed into 2nd-cycle cDNA. Second-cycle cDNA was fragmented and labeled with terminal deoxynucleotidyl transferase using the Affymetrix proprietary DNA Labeling Reagent (Affymetrix). Labeled cDNA was hybridized to the GeneChip[®] Mouse 1.0ST Array (Affymetrix) that includes 28,853 transcripts. Mouse Gene 1.0ST array contains 50-60 microRNA probe sequences, although it is not designed for microRNA study. Hybridized arrays were washed and stained using the GeneChip[®] Hybridization Wash and Stain Kit (Affymetrix) and Fluidics station 450 (Affymetrix), and scanned using the GeneChip[®] Scanner 3000 (Affymetrix). The data was visualized and quantified by the Affymetrix GeneChip[®] Command Console (AGCC), and normalized by Robust Multi-array Average (RMA), using Expression Console[™] (Affymetrix). Fold changes were calculated as ratios of signal value, compared with the age-matched controls. Log ratios were calculated by the logarithm of fold changes to base 2. Microarray results were filtered by 2-fold cutoff and *P* value threshold.⁶³ Only transcripts that pass this filter (fold change > 2 and *P* < 0.05) are considered statistically significant. The microarray results were analyzed using the Ingenuity Pathway Analysis[®] (IPA, Ingenuity Systems, www.ingenuity.com), NetAffx database (Affymetrix, www.affymetrix.com/index.affx), and Mouse Genome Informatics (Jackson Laboratory, Bar Harbor, ME, www.informatics.jax.org/). The data have been deposited into the Gene

Expression Omnibus (GEO) repository in National Center for Biotechnology Information (NCBI) (Accession number: GSE53607). We analyzed samples from five infected animals and five age-matched controls at each time point (4, 7, and 60 dpi) (total 15 infected and 15 control samples).

Real-time polymerase chain reaction (PCR)

We reverse-transcribed 1 μ g of total RNA into cDNA, using the ImProm-IITM Reverse Transcription System (Promega, Madison, WI). Using 50 ng of cDNA, real-time PCR was conducted by the MyiQTM2 Real Time PCR Detection System (Bio-Rad, Hercules, CA). Primer sets of *Cxcl9*, *Tlr3*, *Gzmb*, *Cd3g*, *Mmp12*, *Gpnmb*, and *Gapd* were purchased from RealTimePrimers.com (Elkins Park, PA). VP2 capsid protein of TMEV was used to detect the viral RNA in heart tissue samples. The primer sequences of VP2 are as follows: forward; 5'-TGGTCGACTCTGTGGTTACG-3' and reverse; 5'-GCCGGTCTTGCAAAGATAGT-3'.⁶⁴ The results were normalized using a housekeeping gene *Gapd*. The expression of housekeeping gene *Gapd* did not change with the stages of viral infection (data not shown). Fold changes were calculated by the $\Delta\Delta$ Ct method. We analyzed samples from five infected animals and five age-matched controls at each time point (4, 7, and 60 dpi) (total 15 infected and 15 control samples).

Bioinformatics and statistics analyses

Volcano plot. We drew a volcano plot, using the OriginPro 8.1 (OriginLab Corporation, Northampton, MA), to assess significance together with log ratio of transcriptome data.⁶⁵⁻⁶⁷ In the volcano plot, log ratios of gene expression in the heart of TMEV-infected mice compared with control mice were used as the x-axis and the logarithms of *P* values to base 10 were used as the y-axis.

Heat map. Heat maps were drawn to determine the expression patterns of top 20 up- or downregulated genes at each time point and compare the expression levels with the other time points, using R version 2.15.1 and the R packages 'gplots' and 'genefilter'.⁶⁸

K-means clustering. To find the differences of gene expression profiles between the time points, we conducted *k*-means clustering using an R package ‘cclust’. We used Davies-Bouldin index⁶⁹ to determine the optimum number of clusters and obtained the lowest score (0.51) when microarray data were separated into 20 clusters (Online Figure 2). Graphs were drawn using 240 genes (top 80, middle 80, and bottom 80 genes) in each cluster. Radar chart was drawn using the expression patterns of cluster center genes.

IPA. To classify the genes functionally, we used IPA where we entered the genes whose fold changes were more than 2-fold and *P* values were less than 0.05. IPA shows possible networks involved in microarray profiles by the IPA Network Generation Algorithm.⁷⁰ Genes were clustered and classified by the IPA Network Generation algorithm and the networks were ranked by the network score. The network score was calculated based on the right-tailed Fisher’s Exact Test that takes into account: 1) the number of Network Eligible molecules in the network, 2) size of the network, 3) the total number of Network Eligible molecules in the given dataset, and 4) the number of molecules in the IPA database that could potentially be included in the networks.^{71,72} In the networks, solid and dashed lines indicated direct and indirect interactions, respectively. Direct interactions require the two molecules make direct physical contact with each other; there is no intermediate step. Indirect interactions do not require that there is physical contact between the two molecules, such as a signaling cascade instead of the two molecules making physical contact with each other.

PCA. PCA can reduce the dimensionality of a data set (e.g. microarray data) consisting of a large number of interrelated variables, while retaining as much as possible of the variation present in the data set.⁷³ PCA was conducted as an “unsupervised” analysis to clarify the variance among microarray data from heart samples using R. To clarify the variances among samples, microarray data were calculated using a Q-mode PCA package ‘prcomp’ of R. The proportion of variance and factor loading were also calculated.

Statistics. The data were showed as mean + standard error of the mean (SEM). Statistical comparisons were conducted using Student *t* test or analysis of variance (ANOVA) in the OriginPro 8.1.

$P < 0.05$ was considered as significant difference. Correlation analysis was conducted using the Microsoft Excel (Microsoft Corporation, Redmond, WA).

II. Supplemental Results

Two-way supervised analyses of gene expression profiles in TMEV infection

Among the downregulated genes in the volcano plots (Figure 4), we were able to identify 16 genes on 4 dpi, 7 genes on 7 dpi, and 4 genes on 60 dpi. The expression levels of these downregulated genes together with top 20 upregulated genes at each phase were visualized using heat maps: Online Figure 1A, 20 upregulated and 16 downregulated genes on 4 dpi; Online Figure 1B, 20 upregulated and 7 downregulated genes on 7 dpi; Online Figure 1C, 20 upregulated and 4 downregulated genes on 60 dpi. These gene expression patterns in each time point were compared with those at the other two time points.

On 4 dpi, interferon (IFN)-induced genes, such as IFN regulatory factor 7 (*Irf7*), IFN-induced protein with tetratricopeptide repeats (*Ifit1* and *Ifit3*), and IFN- γ induced GTPase (*Igtp*), were upregulated significantly (Online Figure 1A). In contrast, myosin, light polypeptide 7, regulatory (*Myl7*), myosin binding protein H-like (*Mybphl*), and microRNA 690 (*Mir690*) were downregulated.

On 7 dpi, similar to 4 dpi, IFN-induced genes, including chemokine (C-X-C motif) ligand 9 (*Cxcl9*) and *Igtp*, were upregulated. In addition, granzyme B (*Gzmb*), natural killer cell group 7 sequence (*Nkg7*), and CD274 antigen (*Cd274*) were also upregulated significantly (Online Figure 1B). All top 20 upregulated genes on 4 dpi, which were associated with innate immune responses, were also upregulated on 7 dpi. On the other hand, angiopoietin-like 7 (*Angptl7*), Ras association (RalGDS/AF-6) domain family (N-terminal) member 9 (*Rassf9*), and methyltransferase like 21E (*Mettl21e*) were downregulated on 7 dpi.

On 60 dpi, we found significant upregulation of genes associated with cardiac remodeling and fibrosis, such as matrix metalloproteinase 12 (*Mmp12*), glycoprotein (transmembrane) nmb (*Gpnmb*, osteoactivin), and secreted phosphoprotein 1 (*Spp1*, osteopontin) (Online Figure 1C). Although this suggested that cardiac remodeling was active on 60 dpi, these genes were also upregulated on 7 dpi. We also found upregulation of immunoglobulins (*Igkv10-96*, *Igkv1-43*, and *Igj*), complement component (C1s), CD74 antigen (*Cd74*), and MHC class II-related antigens (*H2-Ea-ps* and *H2-Aa*). Although this indicated that acquired immune responses associated with B cells were present on 60 dpi, most of the

genes were also upregulated on 7 dpi, thus their expression on the heat map did not distinguish between 7 and 60 dpi. On the other hand, downregulations of nuclear receptor subfamily 4, group A, member 3 (*Nr4a3*), leucine rich repeat containing 52 (*Lrrc52*), and a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9 (*Adamts9*) were shown in the hearts of infected mice.

Thus, although the heat maps of significantly expressed genes between 4 and 60 dpi showed distinct patterns, the heat maps did not show different patterns between 4 and 7 dpi as well as 7 and 60 dpi. This could be due to the upregulation of many genes associated with innate immunity, acquired immunity, and cardiac remodeling on 7 dpi.

The lists of differentially expressed genes for each time point

Up- or downregulated genes in the hearts of TMEV-infected mice at each time point were listed in Online Tables 8 to 10. Red background indicates upregulation and blue indicates downregulation at each time point.

Categorization of up- or down-regulated genes in the hearts of TMEV-infected mice

To categorize genes that were up- or down-regulated in the hearts of TMEV-infected mice by function, we uploaded the microarray results into the IPA that shows possible networks involved in microarray profiles by IPA Network Generation Algorithm (Online Table 11). On 4 dpi, the top network was associated with ‘Infectious Disease’, ‘Antimicrobial Response’, and ‘Inflammatory Response’. This network was composed of IFN- α/β -related genes (Online Figure 7). On 7 dpi, the top network was associated with ‘Infectious Disease’, ‘Cellular Function and Maintenance’, and ‘Antimicrobial Response’. This network was composed of pattern recognition receptors and interleukin 6- and 12-associated genes (Online Figure 8). On 60 dpi, the top networks were ‘Cellular Function and Maintenance’, ‘Inflammatory Response’, and ‘Cellular Movement’, composed of remodeling- and immune response-related genes (Online Figure 9). Remodeling-related genes [*Mmp12*, *Spp1*, and cytochrome b-245, beta polypeptide

(*Cybb*)] were included in the network. The network associated with ‘Antimicrobial Responses’ was listed on both 4 and 7 dpi, but not on 60 dpi. The network associated with ‘Cellular Function and Maintenance’ was listed on both 7 and 60 dpi. These networks shown in Online Figures 7-9 included both direct (solid lines) and indirect interactions (dashed lines). Thus, we conducted IPA using only direct interactions. Significant networks identified allowing only for direct connections were as follows: the top network on 4 dpi was associated with ‘Endocrine System Disorders’, ‘Gastrointestinal Disease’, and ‘Immunological Disease’; the top network on 7 dpi was associated with ‘Hematological System Development and Function’, ‘Tissue Morphology’, and ‘Cellular Movement’; the top network on 60 dpi was not connected well among up- or down-regulated genes. While IPA using only direct interaction is supposed to be stringent, identified networks contained pathways irrelevant to our myocarditis models, including ‘Endocrine System Disorders’, ‘Gastrointestinal Disease’ and ‘Hematological System Development and Function’.

Using IPA, we also ranked the top five canonical pathways involved in each time point (Online Figure 10). Among the pathways, the top two highly induced pathways in each phase were as follows: on 4 dpi, the pathways associated with ‘Activation of IFN Regulatory Factor by Cytosolic Pattern Recognition Receptors’ and ‘IFN Signaling’; on 7 dpi, the ‘Antigen Presenting Pathway’ and a pathway associated with ‘Communication Between Innate and Adaptive Immune Cells’; and on 60 dpi, the ‘B Cell Development Pathway’ and ‘Antigen Presenting Pathway’.

IPA also showed upregulated genes that could be associated with cardiotoxicity (Online Table 12). Cardiac inflammation was listed as the top toxicity function on both 4 and 7 dpi, where chemokines (*Ccl13*, *Ccl2*, and *Ccl311*), toll-like receptor (*Tlr3*), and IFN- γ (*Ifng*) were upregulated. Cardiac necrosis, dysfunction, and dilation were listed on 7 and 60 dpi because of upregulation of *Cybb* and *Spp1*. These results suggested the presence of inflammation in the heart on both 4 and 7 dpi and cardiac dysfunction and dilation on 7 and 60 dpi. Thus, the categorization of the genes based on supervised analyses showed involvement of different pathways in each phase to some extent. However, this approach did not identify molecules that can be used to distinguish between the different phases.

III. Supplemental References

61. Golde WT, Gollobin P, Rodriguez LL. A rapid, simple, and humane method for submandibular bleeding of mice using a lancet. *Lab Anim (NY)*. 2005;34:39-43.
62. Omura S, Koike E, Kobayashi T. Microarray analysis of gene expression in rat alveolar epithelial cells exposed to fractionated organic extracts of diesel exhaust particles. *Toxicology*. 2009;262:65-72.
63. Vacha SJ. Pitfall 7: Paying more attention to the magnitude of the log ratio than significance of the log ratio. *Ten Pitfalls of Microarray Analysis. Agilent in Life Sciences*.
64. Deb C, Lafrance-Corey RG, Zoecklein L, Papke L, Rodriguez M, Howe CL. Demyelinated axons and motor function are protected by genetic deletion of perforin in a mouse model of multiple sclerosis. *J Neuropathol Exp Neurol*. 2009;68:1037-1048.
65. Li WT. Volcano Plots in Analyzing Differential Expressions with Mrna Microarrays. *Journal of Bioinformatics and Computational Biology*. 2012;10.
66. Chen JJ, Wang SJ, Tsai CA, Lin CJ. Selection of differentially expressed genes in microarray data analysis. *Pharmacogenomics J*. 2007;7:212-220.
67. Oberg AL, Mahoney DW, Eckel-Passow JE, Malone CJ, Wolfinger RD, Hill EG, et al. Statistical analysis of relative labeled mass spectrometry data from complex samples using ANOVA. *J Proteome Res*. 2008;7:225-233.
68. R Core Team (2012) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL <http://www.R-project.org/>.
69. Davies DL, Bouldin DW. A cluster separation measure. *IEEE Trans Pattern Anal Mach Intell*. 1979;1:224-227.
70. Savli H, Szendroi A, Romics I, Nagy B. Gene network and canonical pathway analysis in prostate cancer: a microarray study. *Exp Mol Med*. 2008;40:176-185.

71. Naito Y, Kuroda M, Mizushima K, Takagi T, Handa O, Kokura S, et al. Transcriptome Analysis for Cytoprotective Actions of Rebamipide against Indomethacin-Induced Gastric Mucosal Injury in Rats. *J Clin Biochem Nutr.* 2007;41:202-210.
72. Kaveh F, Edvardsen H, Borresen-Dale AL, V NK, Solvang HK. Allele-specific disparity in breast cancer. *BMC Med Genomics.* 2011;4:85.
73. Jolliffe IT. Principal Component Analysis, Second Edition. New York: Springer. *Briefings in bioinformatics.* 2011;12:714-722.

IV. Online Tables

Online Table 1. Gene abbreviations

Gene symbol	Gene name
<i>Adamts8</i>	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8
<i>Adamts9</i>	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9
<i>Angptl7</i>	angiopoietin-like 7
<i>Atp6v0d2</i>	ATPase, H ⁺ transporting, lysosomal V0 subunit D2
<i>Bmp10</i>	bone morphogenetic protein 10 (TGF β family)
<i>C1s</i>	complement component 1, s subcomponent
<i>Car3</i>	carbonic anhydrase 3
<i>Casp1</i>	caspace 1
<i>Ccl2</i>	chemokine (C-C motif) ligand 2
<i>Ccl3</i>	chemokine (C-C motif) ligand 3
<i>Ccl5</i>	chemokine (C-C motif) ligand 5
<i>Ccl8</i>	chemokine (C-C motif) ligand 8
<i>Ccna2</i>	cyclin A2
<i>Ccr5</i>	chemokine (C-C motif) receptor 5
<i>Cd274</i>	CD274 antigen (B7-H1, PD-L1)
<i>Cd3d</i>	CD3 antigen, δ polypeptide
<i>Cd3e</i>	CD3 antigen, ϵ polypeptide
<i>Cd3g</i>	CD3 antigen, γ polypeptide
<i>Cd74</i>	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)
<i>Cfd</i>	complement factor D (adipsin)
<i>Clec7a</i>	C-type lectin domain family 7, member a
<i>Ctsk</i>	cathepsin K
<i>Cxcl9</i>	chemokine (C-X-C motif) ligand 9 (Mig)
<i>Cybb</i>	cytochrome b-245, beta polypeptide (Nox2)
<i>Cyp2e1</i>	cytochrome P450, family 2, subfamily e, polypeptide 1
<i>Ddx58</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 (RIG-I)
<i>Dhx58</i>	DEXH (Asp-Glu-X-His) box polypeptide 58 (LGP2)
<i>Dkk3</i>	dickkopf homolog 3 (<i>Xenopus laevis</i>)
<i>Elovl3</i>	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3
<i>Fam107a</i>	family with sequence similarity 107, member A
<i>Fasn</i>	fatty acid synthase
<i>Fcer1g</i>	Fc receptor, IgE, high affinity I, γ polypeptide
<i>Fgf12</i>	fibroblast growth factor 12
<i>Gapd</i>	glyceraldehyde-3-phosphate dehydrogenase
<i>Gbp11</i>	guanylate binding protein 11
<i>Gbp2b</i>	guanylate binding protein 2b
<i>Gbp3</i>	guanylate binding protein 3
<i>Glipr1</i>	GLI pathogenesis-related 1 (glioma)
<i>GpnmB</i>	glycoprotein (transmembrane) nmb (osteoactivin)
<i>Gzmb</i>	granzyme B
<i>H2-Aa</i>	major histocompatibility 2, class II antigen A, α
<i>H2-Ab1</i>	major histocompatibility 2, class II antigen A, β 1
<i>H2-Ea-ps</i>	major histocompatibility 2, class II antigen E α , pseudogene
<i>Hamp</i>	hepcidin antimicrobial peptide
<i>Hp</i>	haptoglobin
<i>Ifi44</i>	interferon-induced protein 44
<i>Ifi44l</i>	interferon-induced protein 44 like
<i>Ifih1</i>	interferon induced with helicase C domain 1 (MDA5)
<i>Ifit1</i>	interferon-induced protein with tetratricopeptide repeats 1
<i>Ifit2</i>	interferon-induced protein with tetratricopeptide repeats 2
<i>Ifit3</i>	interferon-induced protein with tetratricopeptide repeats 3
<i>Ighv1-43</i>	immunoglobulin heavy variable V1-43
<i>Ighv1-61</i>	immunoglobulin heavy variable 1-61
<i>Igj</i>	immunoglobulin joining chain
<i>Igkv10-96</i>	immunoglobulin κ variable 10-96

<i>Igkv6-32</i>	immunoglobulin κ variable 6-32
<i>Igtp</i>	interferon γ induced GTPase
<i>ligp1</i>	interferon inducible GTPase 1
<i>Il1b</i>	interleukin 1 β
<i>Il1rn</i>	interleukin 1 receptor antagonist
<i>Il6</i>	interleukin 6
<i>Inmt</i>	indolethylamine N-methyltransferase
<i>Irf7</i>	interferon regulatory factor 7
<i>Irgm1</i>	immunity-related GTPase family M member 1
<i>Itgal</i>	integrin α L
<i>Itgam</i>	integrin α M
<i>Itgax</i>	integrin α X
<i>Itgb2</i>	integrin β 2
<i>Lck</i>	lymphocyte protein tyrosine kinase
<i>Lcn2</i>	lipocalin 2
<i>Lgals3</i>	lectin, galactose binding, soluble 3
<i>Lgi1</i>	leucine-rich repeat LGI family, member 1
<i>Lrrc52</i>	leucine rich repeat containing 52
<i>Mavs</i>	mitochondrial antiviral signaling protein
<i>Mettl21e</i>	methyltransferase like 21E
<i>Mir690</i>	microRNA 690
<i>Mmp12</i>	matrix metalloproteinase 12
<i>Ms4a4c</i>	membrane-spanning 4-domains, subfamily A, member 4C
<i>Mybphl</i>	myosin binding protein H-like
<i>My17</i>	myosin, light polypeptide 7, regulatory
<i>Nkg7</i>	natural killer cell group 7 sequence
<i>Nr4a3</i>	nuclear receptor subfamily 4, group A, member 3
<i>Pah</i>	phenylalanine hydroxylase
<i>Penk</i>	preproenkephalin
<i>Pfkfb1</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1
<i>Phf11d</i>	PHD finger protein 11D
<i>Pkhd11l</i>	polycystic kidney and hepatic disease 1-like 1
<i>Plac8</i>	placenta-specific 8
<i>Plau</i>	plasminogen activator, urokinase
<i>Ppargc1a</i>	peroxisome proliferative activated receptor γ , coactivator 1 α
<i>Prfl</i>	perforin 1 (pore forming protein)
<i>Pyhin1</i>	pyrin and HIN domain family, member 1
<i>Rassf9</i>	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
<i>Retla</i>	resistin like α
<i>Rsad2</i>	radical S-adenosyl methionine domain containing 2
<i>Sln</i>	sarcolipin
<i>Sox7</i>	SRY-box containing gene 7
<i>Spp1</i>	secreted phosphoprotein 1 (osteopontin)
<i>Sprr1a</i>	small proline-rich protein 1A
<i>Stap1</i>	signal transducing adaptor family member 1
<i>Stard10</i>	START domain containing 10
<i>Stat1</i>	signal transducer and activator of transcription 1
<i>Stat4</i>	signal transducer and activator of transcription 4
<i>Tgtp1</i>	T cell specific GTPase 1
<i>Timpl</i>	tissue inhibitor of metalloproteinase 1
<i>Tlr3</i>	toll-like receptor 3
<i>Tlr7</i>	toll-like receptor 7
<i>Tnfaip3</i>	tumor necrosis factor, α -induced protein 3
<i>Tnfsf10</i>	tumor necrosis factor (ligand) superfamily, member 10
<i>Usp18</i>	ubiquitin specific peptidase 18

Online Table 2. Gene list of cluster 2

Cluster	Probe Set ID	Day 4	Day 7	Day 60	Symbol	Entrez Gene Name
2	10583056	-0.0392816	0.241738	3.4960326	MMP12	matrix metalloproteinase 12 (macrophage elastase)
2	10538187	-0.066586	1.2876936	3.1650604	GPNMB	glycoprotein (transmembrane) nmb
2	10511779	0.2294848	0.3602788	2.9750388	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2
2	10545237	-0.1361568	-0.067529	2.0623402		
2	10545175	-0.052077	0.9486478	1.7071394	Igk-J1	immunoglobulin kappa joining 1
2	10547740	1.4358614	0.2003274	1.6863684	C1S	complement component 1, s subcomponent
2	10545173	-0.095812	0.6494674	1.5954512	Igk	immunoglobulin kappa chain complex
2	10494262	-0.3787916	0.1369422	1.5008528	CTSK	cathepsin K
2	10538882	-0.1900148	-0.006567	1.4665974		
2	10403021	0.1299884	0.3088364	1.3770836		
2	10531126	-0.2783984	0.5021218	1.3460858	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
2	10338640	0.9966784	-0.32691	1.3380414		
2	10557895	0.0705552	1.280888	1.3302184	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)
2	10403038	-0.1089806	0.4155	1.1938834		
2	10548375	-0.011575	1.052778	1.1820744	CLEC7A	C-type lectin domain family 7, member A
2	10403069	-0.2337452	0.1563804	1.1816562	IGHM	immunoglobulin heavy constant mu
2	10338365	0.1495842	0.4229512	1.1044422		
2	10545247	0.2576838	0.3979584	1.0589932	Igkv6-15	immunoglobulin kappa variable 6-14
2	10545198	-0.2593444	0.0025162	1.0287108		
2	10341488	-0.085396	0.3632384	0.98846		
2	10523128	-0.2019334	0.4205996	0.9853106	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)
2	10339525	0.0073388	0.1754834	0.9570168		
2	10545215	0.0340812	0.0750176	0.8951984	Igk-V28	immunoglobulin kappa chain variable 28 (V28)
2	10403018	-0.1739206	0.2330356	0.8843548	AI324046	expressed sequence AI324046
2	10339025	-0.1649434	0.0354696	0.8558128		
2	10523359	-0.7706774	0.0794764	0.851305	CXCL13	chemokine (C-X-C motif) ligand 13
2	10339941	-0.1160354	0.0745046	0.8334982		
2	10538921	-0.1330676	0.4694028	0.828054		
2	10343595	0.0891906	-0.2639426	0.8266714		
2	10341654	-0.7300586	0.475328	0.821276		
2	10339870	0.0483848	0.2322026	0.8127254		
2	10545190	0.300976	0.1443338	0.8058268		
2	10538903	-0.1147284	0.3407664	0.8052908	Igkv8-30	immunoglobulin kappa chain variable 28 (V28)
2	10403028	-0.1004406	0.4395714	0.7976784		
2	10343187	0.5628796	0.665346	0.794683		
2	10358421	-0.1254366	0.6664756	0.789772	RGS18	regulator of G-protein signaling 18
2	10545184	-0.0250938	0.0930944	0.7864136		
2	10545862	-0.2290526	-0.1370138	0.7836834	Cml3/Gm4477	camello-like 3
2	10403015	0.1046814	0.1404718	0.7698862	AI324046	expressed sequence AI324046
2	10419934	0.0568668	0.3467786	0.7662178	MYH7	myosin, heavy chain 7, cardiac muscle, beta
2	10591739	-0.2079734	0.6678674	0.7590626	ACP5	acid phosphatase 5, tartrate resistant
2	10350473	-0.0225758	0.0532318	0.750761	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2
2	10492798	-0.2841524	0.0995462	0.7417692	SFRP2	secreted frizzled-related protein 2
2	10341453	0.610481	0.349168	0.7381912		
2	10545869	-0.2882584	-0.0452272	0.7361532	Cml3/Gm4477	camello-like 3
2	10341089	-0.0412908	0.1667672	0.7333504		
2	10338976	0.191292	0.138382	0.7246336		
2	10338165	-0.3136412	-0.1215916	0.7232488		
2	10564818	-0.323219	0.3850666	0.7192478	ANPEP	alanyl (membrane) aminopeptidase
2	10341001	-0.2865824	0.1558054	0.7161202		
2	10340173	-0.4694412	-0.095255	0.7027516		
2	10545865	-0.1828148	-0.1209574	0.6947052	Cml3/Gm4477	camello-like 3
2	10545196	-0.205896	0.0505448	0.693595		
2	10339305	-0.0885026	0.077951	0.6852978		
2	10343889	-0.1562914	0.5248406	0.6834124		
2	10462442	0.111467	0.6132776	0.6746374	IL33	interleukin 33
2	10341243	-0.3177444	0.0417542	0.6704908		
2	10340884	-0.227121	-0.1288554	0.6631158		
2	10445781	-0.0277506	0.1798908	0.661405	TREM2	triggering receptor expressed on myeloid cells 2
2	10339171	-0.425703	0.6999032	0.6598412		
2	10340594	-0.283164	-0.0585778	0.656075		
2	10342563	-0.0007634	-0.001319	0.655842		
2	10395273	0.0007438	0.5410032	0.645488	Gdap10	ganglioside-induced differentiation-associated-protein 10
2	10343700	-0.171202	0.246582	0.6445726		
2	10435043	0.0218306	0.4911668	0.6433614	TM4SF19	transmembrane 4 L six family member 19
2	10403048	-0.056381	0.3094678	0.6390022		
2	10504127	0.292127	0.3561266	0.6327726	CCL21	chemokine (C-C motif) ligand 21
2	10504154	0.292127	0.3561266	0.6327726	CCL21	chemokine (C-C motif) ligand 21
2	10504183	0.292127	0.3561266	0.6327726	CCL21	chemokine (C-C motif) ligand 21
2	10512377	0.292127	0.3561266	0.6327726	CCL21	chemokine (C-C motif) ligand 21
2	10338332	-0.1862604	0.0724472	0.626833		
2	10545205	-0.0629944	0.3353452	0.6266194	Gm1418	immunoglobulin kappa variable 4-57-1
2	10339626	0.2172436	0.3965274	0.6230718		
2	10545187	-0.064152	0.093604	0.61922	Gm1502	predicted gene 1502
2	10340840	0.1259392	-0.0043936	0.612312		
2	10341148	-0.4386734	0.264262	0.61065		
2	10340070	0.2296546	0.5199256	0.6095988		
2	10419568	-0.1874534	0.0152962	0.6027982	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)
2	10370000	-0.1777124	0.1178444	0.5985182	GSTT1	glutathione S-transferase theta 1
2	10339622	-0.4800984	0.3703308	0.5949622		
2	10343323	-0.150792	-0.0271844	0.5918356		

2	10342102	0.269756	0.183977	0.591503		
2	10538880	-0.0375536	0.205469	0.5838978		
2	10338872	-0.254688	0.0788602	0.5835852		
2	10519998	-0.4282306	0.0257682	0.5796416	LRRC17	leucine rich repeat containing 17
2	10338676	-0.2461476	0.4030146	0.5773306		
2	10547752	0.5518134	0.3649818	0.5760028	C1S	complement component 1, s subcomponent
2	10342867	0.0706604	0.2041016	0.5743686		
2	10342275	-0.0165772	0.3326464	0.5719828		
2	10450369	0.2145322	0.2540182	0.5716578	HSPA1A/HSPA1B	heat shock 70kDa protein 1A
2	10557175	-0.2737868	0.0926244	0.571169		
2	10403060	-0.0087198	0.2787722	0.5635208		
2	10343820	-0.2387554	0.0591568	0.5547106		
2	10341259	-0.4340426	0.2240006	0.5542188		
2	10339130	0.0752054	0.0929756	0.54716		
2	10358597	-0.2788662	0.0270332	0.5450396	Hmcn1	hemicentin 1
2	10340963	-0.0122214	0.0185678	0.5443816		
2	10339636	-0.1617256	0.0688568	0.5440882		
2	10341138	-0.0730652	0.0999904	0.5347006		
2	10403054	0.0251384	0.1963096	0.5334576	LOC435333	similar to monoclonal antibody heavy chain
2	10342411	-0.1360698	0.094731	0.5318112		
2	10514275	-0.3487288	0.4313314	0.5248414	PTPLAD2	protein tyrosine phosphatase-like A domain containing 2
2	10438405	-0.0999018	0.1139124	0.5232862	IgI-V1	immunoglobulin lambda variable 1
2	10339701	-0.1907344	0.255432	0.5207038		
2	10343852	-0.2831682	0.2589402	0.5181406		
2	10341176	-0.1827082	0.0170758	0.516327		
2	10407803	-0.4183238	0.3232694	0.5154	GPR137B	G protein-coupled receptor 137B
2	10428376	-0.1964356	0.1281504	0.5150654	ANGPT1	angiotensinogen 1
2	10525365	-0.0844586	0.4382686	0.513776	HVCN1	hydrogen voltage-gated channel 1
2	10344498	-0.098598	0.019697	0.5125674		
2	10340641	-0.1823064	0.3971678	0.5103816		
2	10341856	0.0394748	0.6117738	0.5099288		
2	10341404	0.4446882	0.3058046	0.5086178		
2	10341424	-0.0363316	0.605655	0.507274		
2	10593499	0.1906922	0.2947926	0.5027192	C11orf87	chromosome 11 open reading frame 87
2	10554599	-0.0138944	0.045797	0.5023502	ADAMTSL3	ADAMTS-like 3
2	10342825	0.0919492	0.12097	0.5006594		
2	10514185	-0.1280094	0.121993	0.4984276		
2	10343375	-0.2763744	0.5417344	0.4982356		
2	10387821	-0.2005068	0.1055504	0.4945546	ALOX12	arachidonate 12-lipoxygenase
2	10341902	-0.189241	0.12061	0.4942444		
2	10411373	-0.112559	0.2547298	0.4907994	HEXB	hexosaminidase B (beta polypeptide)
2	10372648	0.073996	0.508846	0.49076	Lyz1/Lyz2	lysozyme 2
2	10339368	-0.188901	0.1598632	0.4904694		
2	10341472	-0.0834932	0.0515348	0.484064		
2	10581151	0.149494	0.2003284	0.4825694	RRAD	Ras-related associated with diabetes
2	10538871	-0.081158	0.054819	0.4748436		
2	10340944	-0.1083164	0.122037	0.474302		
2	10538868	-0.0319804	0.0941336	0.471769		
2	10342258	-0.0886528	0.2759672	0.4612006		
2	10342615	-0.2178104	0.2196296	0.4513272		

Online Table 3. Gene list of cluster 8

Cluster	Probe Set ID	Day 4	Day 7	Day 60	Symbol	Entrez Gene Name
8	10343814	0.057474	-0.260061	-1.044283		
8	10343210	-0.006554	0.29227	-0.906136		
8	10343359	0.0335406	-0.114459	-0.898168		
8	10340089	-0.069631	-0.447173	-0.842473		
8	10340454	-0.176305	-0.150989	-0.813968		
8	10342440	-0.165801	-0.459581	-0.810953		
8	10342239	-0.22637	-0.365949	-0.807563		
8	10340111	-0.691877	0.2855862	-0.800236		
8	10339482	-0.19713	0.125478	-0.797052		
8	10344438	-0.609841	-0.075026	-0.794139		
8	10584870	-0.061601	0.3343204	-0.783085	TMPRSS13	transmembrane protease, serine 13
8	10546450	-0.186072	0.2033814	-0.7797	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9
8	10546454	-0.173559	0.2577978	-0.762913	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9
8	10339483	0.086864	-0.05119	-0.742528		
8	10339551	-0.413509	-0.546079	-0.736669		
8	10409876	0.0430542	0.150188	-0.73402	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha
8	10339687	-0.155523	0.046138	-0.734003		
8	10343997	-0.057852	0.0413066	-0.728557		
8	10341429	0.0724998	-0.040937	-0.726538		
8	10343609	-0.134781	-0.052952	-0.718581		
8	10374558	-0.123948	-0.17435	-0.710369		
8	10338694	-0.149355	0.3857772	-0.685437		
8	10341953	-0.029092	0.3241066	-0.663133		
8	10338444	-0.576996	-0.573967	-0.657339		
8	10339112	-0.070495	0.170341	-0.652994		
8	10342899	-0.060883	0.0534208	-0.652899		
8	10344097	-0.030691	-0.108291	-0.644524		
8	10338454	-0.610685	-0.490796	-0.643212		
8	10342346	0.0911672	-0.152515	-0.638822		
8	10582658	-0.159881	-0.299674	-0.634761	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
8	10343687	-0.873226	-0.119928	-0.632122		
8	10343669	-0.098684	0.0694318	-0.626682		
8	10342759	-0.112837	0.1364118	-0.624105		
8	10342055	-0.232442	-0.121436	-0.618854		
8	10339575	-0.503908	-0.169805	-0.614889		
8	10343523	-0.265503	0.2772682	-0.611669		
8	10343668	-0.171751	0.2788828	-0.61049		
8	10338735	-0.247834	-0.153316	-0.600365		
8	10341481	-0.222642	0.054183	-0.592426		
8	10344406	-0.117725	0.1935422	-0.591294		
8	10339466	0.0199036	0.038895	-0.583974		
8	10340328	-0.133862	0.0259804	-0.575554		
8	10342225	-0.089146	-0.036936	-0.568064		
8	10340891	-0.47981	-0.134343	-0.561921		
8	10344349	-0.017971	-0.046669	-0.560743		
8	10342818	-0.161457	-0.152445	-0.558365		
8	10343751	-0.237626	0.2536828	-0.55621		
8	10342379	0.048178	-0.1463	-0.555147		
8	10379840	-0.044166	0.0759032	-0.553581	MYO19	myosin XIX
8	10341924	-0.406748	0.3219298	-0.537201		
8	10343789	-0.15811	-0.06754	-0.536874		
8	10339730	-0.041331	0.047343	-0.533815		
8	10339258	-0.037248	-0.143286	-0.532816		
8	10342679	-0.250192	-0.137234	-0.532184		
8	10343243	-0.245494	-0.405605	-0.530705		
8	10582896	-0.317428	0.1010356	-0.529798		
8	10342033	-0.222276	-0.247679	-0.52553		
8	10343890	-0.081156	0.0355814	-0.524317		
8	10341708	-0.208428	-0.418306	-0.523708		
8	10342564	-0.069737	-0.21409	-0.522057		
8	10339927	-0.128385	-0.299444	-0.516851		
8	10546452	-0.221495	-0.007042	-0.512991	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9
8	10339543	-0.181043	-0.196952	-0.51234		
8	10582888	-0.33681	-0.006591	-0.509682		
8	10338511	0.002489	-0.12981	-0.507331		
8	10344560	-0.147628	-0.12679	-0.499866		
8	10342541	-0.32466	-0.230056	-0.499548		
8	10343527	-0.300646	0.1084552	-0.499098		
8	10339085	-0.116887	-0.225779	-0.496338		
8	10375313	0.0136774	-0.202263	-0.493559	CCN1L	cyclin J-like
8	10342207	-0.245279	-0.236198	-0.492659		
8	10338941	-0.31031	-0.144122	-0.489919		
8	10342075	-0.12968	-0.131082	-0.48744		
8	10417235	-0.236034	0.0386916	-0.485718	Gm16440 (includes others)	predicted gene 16440
8	10417315	-0.236034	0.0386916	-0.485718	Gm16440 (includes others)	predicted gene 16440
8	10341415	-0.153661	-0.040949	-0.485596		
8	10338115	-0.213307	0.413667	-0.483695		
8	10417226	-0.288499	-0.038072	-0.481924	Gm16440 (includes others)	predicted gene 16440
8	10342500	-0.208908	-0.094152	-0.48061		
8	10341394	-0.249291	0.1178438	-0.480173		
8	10340451	-0.308496	-0.026275	-0.479864		

8	10342849	-0.172329	-0.263163	-0.479368		
8	10344129	-0.290719	-0.216272	-0.479095		
8	10343349	-0.340894	-0.313825	-0.478528		
8	10341292	-0.592945	0.0272726	-0.478418		
8	10406334	-0.132724	0.386618	-0.474837	MCTP1	multiple C2 domains, transmembrane 1
8	10343656	-0.334096	-0.101618	-0.471975		
8	10344514	-0.516229	0.1883406	-0.471427		
8	10340714	-0.255807	-0.043323	-0.470382		
8	10343952	0.016714	-0.208138	-0.469359		
8	10485840	-0.458445	-0.192511	-0.467961	RYR3	ryanodine receptor 3
8	10340397	-0.551116	0.1849844	-0.466994		
8	10338304	-0.089312	0.3853574	-0.466588		
8	10341972	-0.238572	-0.092749	-0.460335		
8	10343689	-0.233525	-0.18641	-0.459112		
8	10342626	-0.062494	0.024749	-0.458706		
8	10340400	-0.452172	-0.313471	-0.4577		
8	10338336	-0.260591	0.284172	-0.457535		
8	10340346	-0.138686	0.193348	-0.456546		
8	10412517	-0.221063	0.106317	-0.456167		
8	10340896	-0.289683	0.1137688	-0.454815		
8	10338740	-0.035458	-0.054936	-0.45337		
8	10338775	-0.321407	-0.270201	-0.451961		
8	10338183	-0.491491	-0.087994	-0.451764		
8	10338467	-0.16067	-0.351098	-0.449783		
8	10417408	-0.300479	-0.246387	-0.448749	Gm16440 (includes others)	predicted gene 16440
8	10342231	-0.278965	0.0384412	-0.446843		
8	10342097	-0.37157	-0.352113	-0.443872		
8	10342311	-0.048637	-0.212998	-0.443197		
8	10343765	-0.055235	-0.006336	-0.442502		
8	10338445	-0.033066	0.0142492	-0.44242		
8	10339992	-0.118933	0.0115622	-0.440094		
8	10341887	-0.366725	-0.067226	-0.440001		
8	10343309	-0.299251	0.0887494	-0.439257		
8	10417258	-0.297422	-0.104262	-0.439031	Gm16440 (includes others)	predicted gene 16440
8	10417371	-0.294654	0.0717922	-0.438682	Gm2897	predicted gene 2897
8	10479047	-0.599109	-0.38376	-0.438358	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)
8	10417302	-0.315854	-0.093141	-0.438228	Gm16440 (includes others)	predicted gene 16440
8	10343655	-0.189866	0.1208892	-0.437892		
8	10417446	-0.286566	-0.07533	-0.436575	Gm16440 (includes others)	predicted gene 16440
8	10417452	-0.286566	-0.07533	-0.436575	Gm16440 (includes others)	predicted gene 16440
8	10343193	-0.265318	-0.147605	-0.434836		
8	10344077	-0.346702	0.1751756	-0.432688		
8	10582882	-0.279818	-0.059763	-0.430957		
8	10417319	-0.304108	-0.225864	-0.429823	Gm16440 (includes others)	predicted gene 16440
8	10343171	-0.106573	0.0688612	-0.429037		
8	10343256	-0.172659	-0.106678	-0.428571		
8	10342340	-0.394726	-0.140377	-0.426665		
8	10338859	-0.168585	-0.166341	-0.425653		
8	10344255	-0.359483	0.2479562	-0.424418		
8	10342695	-0.238759	-0.202227	-0.423707		
8	10339552	-0.002391	-0.184565	-0.42336		
8	10339700	-0.32304	-0.247053	-0.422909		
8	10560719	-0.156289	-0.018259	-0.422552	LOC147710	hypothetical protein LOC147710
8	10541644	-0.223554	-0.144275	-0.420935	CD163	CD163 molecule
8	10417421	-0.303026	-0.032895	-0.418581	Gm16440 (includes others)	predicted gene 16440
8	10569870	-0.578125	-0.095982	-0.417666	RETN	resistin
8	10412549	-0.319118	-0.271854	-0.417528	Gm16440 (includes others)	predicted gene 16440
8	10412491	-0.348178	0.0461062	-0.416952		
8	10417458	-0.366682	-0.136461	-0.416151	Gm16440 (includes others)	predicted gene 16440
8	10343485	-0.303343	-0.068276	-0.412863		
8	10344138	-0.390965	-0.176965	-0.412505		
8	10566205	-0.599107	-0.221109	-0.412316	USP17L2 (includes others)	ubiquitin specific peptidase 17-like 2
8	10343044	-0.229195	0.2471892	-0.411114		
8	10341330	-0.117604	-0.224287	-0.410309		
8	10525831	-0.101296	-0.062671	-0.409452		
8	10342602	-0.263089	-0.101726	-0.402354		
8	10341042	-0.310178	0.1062262	-0.402248		
8	10342132	-0.218116	-0.367014	-0.401276		
8	10472514	-0.157265	0.1591126	-0.400952	NOSTRIN	nitric oxide synthase trafficker
8	10417286	-0.2538	-0.065725	-0.399924		
8	10516910	-0.071214	-0.21553	-0.39839	PHACTR4	phosphatase and actin regulator 4
8	10417269	-0.259373	0.0708936	-0.396012		
8	10417239	-0.291879	-0.156488	-0.394771	Gm16440 (includes others)	predicted gene 16440
8	10412537	-0.273151	-0.049177	-0.394336	Gm16440 (includes others)	predicted gene 16440
8	10571860	-0.146354	0.0049078	-0.394139	HAND2	heart and neural crest derivatives expressed 2
8	10343964	-0.23063	-0.286814	-0.392593		

8	10592044	-0.470623	-0.291752	-0.392409	TMEM45B	transmembrane protein 45B
8	10556297	-0.02382	-0.128412	-0.39186	ADM	adrenomedullin
8	10417366	-0.300055	-0.133695	-0.389423	Gm16440 (includes others)	predicted gene 16440
8	10485117	-0.177666	0.1404688	-0.388722	CREB3L1	cAMP responsive element binding protein 3-like 1
8	10339204	-0.227876	-0.08941	-0.386793		
8	10412520	-0.230829	-0.080682	-0.386179	Gm16440 (includes others)	predicted gene 16440
8	10343321	-0.42069	0.2130392	-0.381301		
8	10341310	-0.125914	-0.024266	-0.381157		
8	10417373	-0.260023	-0.048878	-0.380417	Gm16440 (includes others)	predicted gene 16440
8	10344103	-0.121463	0.1500182	-0.380258		
8	10340011	-0.355634	-0.264917	-0.380123		
8	10338990	-0.237975	-0.331808	-0.380043		
8	10340500	-0.15484	0.0716388	-0.379108		
8	10338606	-0.055807	-0.194168	-0.378679		
8	10339445	-0.113983	-0.0665	-0.378632		
8	10343231	-0.134982	-0.044001	-0.378569		
8	10344296	-0.088777	0.0959224	-0.377986		
8	10344222	-0.435427	0.2020756	-0.376073		
8	10343450	-0.568889	0.1000554	-0.374765		
8	10417461	-0.273723	-0.052921	-0.374539	Gm16440 (includes others)	predicted gene 16440
8	10340868	-0.172004	0.0062092	-0.374411		
8	10340348	-0.095527	-0.253397	-0.373329		
8	10417264	-0.289424	-0.026723	-0.372672	Gm16440 (includes others)	predicted gene 16440
8	10421730	-0.140118	-0.172687	-0.371971	C13orf30	chromosome 13 open reading frame 30
8	10364702	-0.08798	-0.009696	-0.371656	MIDN	midnolin
8	10341514	-0.189421	-0.047354	-0.371555		
8	10341689	-0.163101	-0.130894	-0.371229		
8	10340196	-0.238356	-0.042083	-0.370474		
8	10608100	-0.056955	-0.103744	-0.370319	Zfy1/Zfy2	zinc finger protein 1, Y linked
8	10340264	-0.23117	0.0832176	-0.370211		
8	10417245	-0.295934	-0.253074	-0.370194	Gm16440 (includes others)	predicted gene 16440
8	10369290	-0.037997	-0.186712	-0.370011	DDIT4	DNA-damage-inducible transcript 4
8	10417411	-0.328547	-0.194052	-0.367151	HN1L	hematological and neurological expressed 1-like
8	10344065	-0.121017	-0.143936	-0.367079		
8	10344295	-0.482019	0.2227288	-0.367053		
8	10409866	-0.10078	0.0492606	-0.364796	Ctla2b	cytotoxic T lymphocyte-associated protein 2 beta
8	10338378	-0.367165	-0.284667	-0.36229		
8	10341207	-0.2916	-0.14443	-0.357818		
8	10343681	-0.170371	-0.151064	-0.35779		
8	10342223	-0.256812	-0.124895	-0.356855		
8	10343209	-0.201601	-0.035445	-0.356663		
8	10340459	-0.175355	-0.268712	-0.354854		
8	10362628	-0.074213	0.0396628	-0.353916		
8	10342751	-0.277966	-0.212993	-0.352302		
8	10341130	-0.074885	-0.264668	-0.350977		
8	10338685	-0.243043	0.0613576	-0.349644		
8	10342384	-0.298297	-0.235433	-0.349317		
8	10344199	-0.09449	0.0420494	-0.349027		
8	10417326	-0.242191	-0.024587	-0.348913	Gm16440 (includes others)	predicted gene 16440
8	10341152	-0.318506	0.101641	-0.348157		
8	10339531	-0.180499	-0.037833	-0.347827		
8	10343645	-0.173245	0.2145328	-0.346607		
8	10341666	-0.051049	-0.063908	-0.343754		
8	10344499	-0.310503	0.000494	-0.343519		
8	10497323	-0.142723	-0.089847	-0.343112	Gm10745	predicted gene 10745
8	10339800	-0.106697	-0.0159	-0.342907		
8	10342038	-0.140026	0.1191986	-0.342625		
8	10344398	-0.312625	-0.009168	-0.342559		
8	10342941	-0.162702	-0.113457	-0.342449		
8	10342767	-0.052148	-0.08102	-0.340488		
8	10340771	-0.104352	0.1323156	-0.339692		
8	10344537	-0.218055	-0.086577	-0.339665		
8	10471018	-0.136093	-0.167839	-0.339611	FAM73B	family with sequence similarity 73, member B
8	10340696	-0.449799	-0.314795	-0.338799		
8	10338620	-0.393238	0.1009024	-0.337971		
8	10417769	-0.179688	0.0953506	-0.33757	Gm2897	predicted gene 2897
8	10344342	-0.25722	0.1943124	-0.337142		
8	10340160	-0.1109	0.0775744	-0.337112		
8	10608693	-0.275379	-0.28359	-0.335815		
8	10342670	-0.461336	0.1803992	-0.335271		
8	10340859	-0.181561	-0.308287	-0.333946		
8	10338742	-0.248499	-0.182399	-0.333668		
8	10403248	-0.079034	0.0098688	-0.333619	Speer6-ps1	spermatogenesis associated glutamate (E)-rich protein 6, pseudogene 1
8	10339105	-0.159482	0.0787314	-0.332771		
8	10342845	-0.238552	-0.062155	-0.33151		
8	10340552	-0.196721	0.1220386	-0.331385		
8	10504986	-0.158237	-0.310626	-0.331338		
8	10344381	-0.242594	-0.00442	-0.331263		
8	10342585	-0.336986	0.2043106	-0.331244		
8	10338438	-0.100256	0.0943342	-0.330074		

8	10398362	-0.554912	0.0890954	-0.329338	AF357355	snoRNA AF357355
8	10343513	-0.43054	-0.07914	-0.328909		
8	10341676	-0.130463	-0.025333	-0.32889		
8	10339082	-0.399683	-0.200451	-0.328882		
8	10341248	-0.214827	0.1217572	-0.328337		
8	10362937	-0.136109	-0.24487	-0.327643		
8	10344283	-0.228082	0.0533264	-0.32753		
8	10342159	-0.175223	-0.197507	-0.326965		
8	10412495	-0.327985	0.0251292	-0.326112		
8	10417359	-0.316844	-0.083124	-0.32568	Gm16440 (includes others)	predicted gene 16440
8	10488804	-0.081785	-0.191367	-0.325504		
8	10339119	-0.316348	0.0557388	-0.323799		
8	10509947	-0.184982	0.1048454	-0.323165	ARHGEF19	Rho guanine nucleotide exchange factor (GEF) 19
8	10602038	-0.078705	-0.216869	-0.322588	CXorf41	chromosome X open reading frame 41
8	10339346	-0.232927	-0.171761	-0.322413		
8	10342691	-0.125132	-0.087516	-0.322204		
8	10343429	-0.329688	0.0106798	-0.322012		
8	10339063	-0.139756	0.012978	-0.321805		
8	10392221	-0.12925	-0.145632	-0.320681	PECAM1	platelet/endothelial cell adhesion molecule
8	10563943	-0.137742	-0.231032	-0.319765		
8	10338314	-0.143217	-0.113702	-0.319326		
8	10342471	-0.204236	0.053316	-0.318421		
8	10417504	-0.245995	-0.16544	-0.316812	Gm16440 (includes others)	predicted gene 16440
8	10340093	-0.067578	-0.071574	-0.31665		
8	10342731	-0.401167	0.0184874	-0.314487		
8	10448131	-0.070439	-0.062383	-0.31382	EG224552 (includes others)	vomeronal 2, receptor 107
8	10605633	-0.074906	-0.114926	-0.313755	Pet2	plasmacytoma expressed transcript 2
8	10341578	-0.21565	-0.122194	-0.313207		
8	10344396	-0.065553	-0.080023	-0.313019		
8	10340664	-0.230705	-0.159785	-0.311764		
8	10525837	-0.1362	0.128989	-0.311179	DNAH10	dynein, axonemal, heavy chain 10
8	10479740	-0.150688	-0.146352	-0.310289		
8	10342414	-0.186483	-0.08339	-0.309966		
8	10343892	-0.17809	-0.288905	-0.308562		
8	10343174	-0.266691	-0.192188	-0.308538		
8	10340239	-0.327378	-0.333815	-0.307884		
8	10342305	-0.078939	-0.229537	-0.307066		
8	10498568	-0.338753	0.0581608	-0.306609	SHOX2	short stature homeobox 2
8	10564795	-0.396624	-0.252961	-0.305425	PLIN1	perilipin 1
8	10347291	-0.240868	0.213194	-0.305303	CXCR2	chemokine (C-X-C motif) receptor 2
8	10339089	-0.538814	-0.249183	-0.303939		
8	10341060	-0.327688	0.2547564	-0.303341		
8	10338238	-0.135645	-0.124075	-0.302628		
8	10510604	-0.103529	0.058184	-0.301402	DNAJC11	DnaJ (Hsp40) homolog, subfamily C, member 11
8	10340839	-0.299516	-0.205938	-0.300026		
8	10338499	-0.482279	-0.354847	-0.298715		
8	10364030	-0.084806	-0.020635	-0.29857	ADORA2A	adenosine A2a receptor
8	10358991	-0.100347	0.026636	-0.29652	KIAA1614	KIAA1614
8	10338617	-0.153139	-0.107193	-0.296359		
8	10413416	-0.25307	-0.178073	-0.296208	IL17RD	interleukin 17 receptor D
8	10340159	-0.22935	-0.06575	-0.295973		
8	10343224	-0.228365	-0.113099	-0.295951		
8	10345527	-0.211699	0.0507954	-0.293646		
8	10340817	-0.347658	-0.147173	-0.29318		
8	10340350	-0.403138	-0.04769	-0.292836		
8	10489451	-0.090254	-0.223507	-0.292627	Svs2	seminal vesicle secretory protein 2
8	10606654	-0.224125	0.2120846	-0.292399	XKRX	XK, Kell blood group complex subunit-related, X-linked
8	10344303	-0.22335	0.0436574	-0.292107		
8	10340463	-0.231815	-0.278607	-0.291566		
8	10338901	-0.175605	0.2313366	-0.29147		
8	10341347	-0.328009	-0.203693	-0.291083		
8	10343411	-0.091389	-0.003119	-0.290966		
8	10590383	-0.168881	-0.302088	-0.290547	SS18L2	synovial sarcoma translocation gene on chromosome 18-like 2
8	10339837	-0.190296	0.13286	-0.290389		
8	10354598	-0.130874	-0.214024	-0.290258	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2
8	10340142	-0.084988	-0.036424	-0.290198		
8	10417253	-0.191799	-0.23945	-0.289662	Gm16440 (includes others)	predicted gene 16440
8	10417281	-0.191799	-0.23945	-0.289662	Gm16440 (includes others)	predicted gene 16440
8	10343507	-0.375351	0.1357864	-0.289082		
8	10340323	-0.370184	-0.226815	-0.288734		
8	10466359	-0.244784	0.0306732	-0.288587	Olf1472/Olf1475	olfactory receptor 1475
8	10529091	-0.344295	-0.154936	-0.288149		
8	10340762	-0.427294	0.0084886	-0.288007		
8	10338143	-0.099759	-0.20656	-0.287093		
8	10513186	-0.140472	-0.070741	-0.287081	Gm12538	predicted gene 12538
8	10400803	-0.179707	-0.107481	-0.286171		
8	10344536	-0.087497	-0.164715	-0.285821		
8	10340390	-0.521609	-0.070476	-0.284241		
8	10338564	-0.121147	-0.016374	-0.282849		
8	10564165	-0.54	-0.161959	-0.282184	PWCR1	small nucleolar RNA, C/D box 116 cluster
8	10338721	-0.317571	-0.187175	-0.281839		

8	10343912	-0.161742	0.0691242	-0.280797		
8	10338259	-0.24496	-0.241193	-0.280442		
8	10343416	-0.104425	0.0285892	-0.280424		
8	10417485	-0.214332	-0.061144	-0.280214	Gm16440 (includes others)	predicted gene 16440
8	10417415	-0.213421	-0.160285	-0.28001	Gm16440 (includes others)	predicted gene 16440
8	10602765	-0.159422	-0.08274	-0.279595	KLHL34	kelch-like 34 (Drosophila)
8	10343571	-0.221499	-0.127319	-0.27945		
8	10341092	-0.134834	0.1378524	-0.279135		
8	10340253	-0.379277	-0.19059	-0.279064		
8	10370608	-0.122034	-0.274074	-0.27878		
8	10412503	-0.25631	-0.138371	-0.278527		
8	10341841	-0.225648	-0.097406	-0.278339		
8	10341284	-0.201288	0.165742	-0.276275		
8	10343930	-0.182379	-0.094684	-0.274768		
8	10343029	-0.193953	-0.195918	-0.274278		
8	10342979	-0.154913	-0.114845	-0.274273		
8	10342351	-0.0845	-0.113184	-0.273433		
8	10342536	-0.228884	-0.188389	-0.273344		
8	10340166	-0.453666	-0.238127	-0.271686		
8	10487886	-0.170372	0.132912	-0.270108	ADRA1D	adrenergic, alpha-1D-, receptor
8	10338451	-0.232567	0.0708276	-0.269438		
8	10338776	-0.499155	0.1465858	-0.268269		
8	10343038	-0.382079	-0.266792	-0.267469		
8	10569331	-0.077391	-0.161265	-0.267065	Gm14492	predicted gene 14492
8	10344504	-0.191272	-0.181418	-0.265858		
8	10344183	-0.086172	-0.061285	-0.265204		
8	10343101	-0.1983	0.1356988	-0.26508		
8	10340699	-0.429548	-0.262122	-0.264489		
8	10339561	-0.107321	-0.252356	-0.263955		
8	10507152	-0.454368	0.1462166	-0.263722	CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 22
8	10364856	-0.174531	0.015259	-0.263603	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)
8	10343391	-0.192866	0.0787776	-0.262558		
8	10343583	-0.480697	0.2306948	-0.262514		
8	10340455	-0.192013	0.0149976	-0.262296		
8	10419465	-0.130481	0.0055718	-0.261528	CCNB1IP1	cyclin B1 interacting protein 1, E3 ubiquitin protein ligase
8	10341618	-0.174316	-0.082875	-0.261521		
8	10338323	-0.426284	0.1887564	-0.261503		
8	10344416	-0.218606	-0.274815	-0.259829		
8	10412699	-0.287593	-0.213032	-0.259721		
8	10405781	-0.183862	0.0738744	-0.259682	mir-27	microRNA 27a
8	10341674	-0.203367	0.0863468	-0.2594		
8	10539080	-0.161582	-0.205782	-0.259055	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5
8	10343830	-0.26963	0.0625298	-0.258379		
8	10344542	-0.136382	-0.091236	-0.258145		
8	10341215	-0.119385	-0.048098	-0.25727		
8	10341046	-0.363697	-0.057822	-0.256688		
8	10344156	-0.12518	0.0612728	-0.255548		
8	10342144	-0.136323	-0.210652	-0.2554		
8	10451932	-0.178182	-0.30303	-0.255367	PLIN4	perilipin 4
8	10340233	-0.130731	-0.20432	-0.255123		
8	10341281	-0.200267	-0.204992	-0.253598		
8	10344357	-0.373728	0.0172438	-0.253512		
8	10341296	-0.197382	0.147644	-0.253087		
8	10343925	-0.11782	-0.132958	-0.252939	HES1	hairy and enhancer of split 1, (Drosophila)
8	10503234	-0.126173	0.0224428	-0.252311	CLVS1	clavesin 1
8	10342902	-0.518509	-0.096973	-0.252185		
8	10338805	-0.116028	-0.067146	-0.252087		
8	10339309	-0.090574	-0.192989	-0.251997		
8	10343946	-0.148025	0.0592572	-0.251738		
8	10340250	-0.274245	-0.02747	-0.250759		
8	10339235	-0.280985	-0.093618	-0.250516		
8	10342079	-0.155027	-0.131186	-0.250317		
8	10492452	-0.158713	-0.059334	-0.24946		
8	10343650	-0.244602	0.1486712	-0.249115		
8	10342766	-0.160843	-0.03879	-0.248731		
8	10478772	-0.11989	-0.120563	-0.248365	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)
8	10344428	-0.094425	-0.202283	-0.247805		
8	10499560	-0.128266	-0.194768	-0.246831	ADAM15	ADAM metallopeptidase domain 15
8	10412543	-0.183427	-0.19228	-0.246685	Gm16440 (includes others)	predicted gene 16440
8	10341270	-0.22742	-0.021506	-0.246573		
8	10338534	-0.282875	-0.225242	-0.246484		
8	10341640	-0.20449	-0.136875	-0.245892		
8	10439080	-0.290188	-0.118461	-0.24557	OSTalpha	organic solute transporter alpha
8	10570068	-0.215152	-0.034761	-0.245366	COL4A2	collagen, type IV, alpha 2
8	10453939	-0.143641	-0.139409	-0.244483	LAMA3	laminin, alpha 3
8	10367828	-0.226996	0.0016966	-0.242654	GRM1	glutamate receptor, metabotropic 1
8	10372805	-0.165543	0.0728342	-0.242168	Gm10743	predicted gene 10743
8	10339451	-0.239928	0.1307144	-0.241588		
8	10380549	-0.380253	0.0664244	-0.24087		
8	10375062	-0.121461	0.0349228	-0.240826	HBQ1	hemoglobin, theta 1
8	10398420	-0.249869	-0.093797	-0.240758	mir-154	microRNA 656
8	10598087	-0.346756	0.0505858	-0.240497		
8	10341848	-0.270125	0.03774	-0.24011		

8	10564169	-0.421228	-0.1985	-0.239041	PWCR1	small nucleolar RNA, C/D box 116 cluster
8	10603252	-0.17863	-0.102166	-0.238612	LARP4	La ribonucleoprotein domain family, member 4
8	10417773	-0.256633	-0.162403	-0.237971	Gm16440 (includes others)	predicted gene 16440
8	10343759	-0.151292	-0.283123	-0.237319		
8	10339428	-0.300562	0.0704936	-0.236979		
8	10339484	-0.303885	-0.124769	-0.236865		
8	10342284	-0.185752	0.0533684	-0.236204		
8	10343093	-0.128842	-0.186408	-0.236134		
8	10460194	-0.153186	-0.268086	-0.236128		
8	10567739	-0.168187	-0.162766	-0.234747	4933440M02Rik	RIKEN cDNA 4933440M02 gene
8	10339783	-0.109908	-0.143389	-0.23405		
8	10371844	-0.209545	-0.039877	-0.23397		
8	10576835	-0.32464	-0.001306	-0.233753	Cd209f/Cd209g	CD209g antigen
8	10420171	-0.141882	-0.112938	-0.232734	ADCY4	adenylate cyclase 4
8	10341994	-0.293669	0.0187494	-0.232671		
8	10341135	-0.232101	0.045258	-0.232361		
8	10344022	-0.214864	-0.232948	-0.232291		
8	10532592	-0.251064	-0.127217	-0.231579	MYO18B	myosin XVIIIIB
8	10543870	-0.111617	-0.086006	-0.231556	Npn2	neoplastic progression 2
8	10454235	-0.264465	-0.118204	-0.231452	ASXL3	additional sex combs like 3 (Drosophila)
8	10407416	-0.096805	-0.08297	-0.230378	CALML3	calmodulin-like 3
8	10338717	-0.196079	-0.169528	-0.230183		
8	10343087	-0.383043	-0.255052	-0.229685		
8	10497077	-0.246855	-0.117059	-0.229463	mir-186	microRNA 186
8	10576680	-0.172341	-0.216136	-0.228931	ZNF821	zinc finger protein 821
8	10341506	-0.121456	0.0402508	-0.22892		
8	10468415	-0.110675	-0.180605	-0.228686	WDR96	WD repeat domain 96
8	10410235	-0.177822	-0.044917	-0.227669		
8	10340085	-0.421906	-0.094255	-0.227081		
8	10402997	-0.158691	-0.225727	-0.22696	LOC630837	ig heavy chain V region 5-84-like
8	10508788	-0.122615	-0.062374	-0.22647	AHDC1	AT hook, DNA binding motif, containing 1
8	10342048	-0.104357	-0.157793	-0.225663		
8	10422164	-0.23054	-0.19178	-0.225622	EDNRB	endothelin receptor type B
8	10343451	-0.502599	-0.080583	-0.225084		
8	10343752	-0.231035	-0.016829	-0.224774		
8	10584309	-0.175753	-0.023137	-0.223771	C11orf61	chromosome 11 open reading frame 61
8	10605355	-0.130288	-0.205801	-0.223591		
8	10339058	-0.162668	-0.017862	-0.223552		
8	10341313	-0.14936	0.0626136	-0.222563		
8	10412513	-0.227094	-0.252989	-0.222423	Gm16440 (includes others)	predicted gene 16440
8	10510908	-0.091757	-0.135669	-0.222413		
8	10570972	-0.094254	-0.141394	-0.222328	A730045E13Rik	RIKEN cDNA A730045E13 gene
8	10549265	-0.115275	-0.096711	-0.221914	IFLTD1	intermediate filament tail domain containing 1
8	10395849	-0.134856	-0.019873	-0.221616	PAX9	paired box 9
8	10344496	-0.443335	0.1398238	-0.220675		
8	10471550	-0.16645	0.0576694	-0.220449	RpH2	ribosomal protein L12
8	10515974	-0.144439	-0.142086	-0.220267	NFYC	nuclear transcription factor Y, gamma
8	10340396	-0.544263	0.1212022	-0.220031		
8	10367471	-0.161757	0.0440228	-0.219606	Olfir763/Olfr9	olfactory receptor 9
8	10427879	-0.263447	0.0958018	-0.217993		
8	10341500	-0.490407	-0.084223	-0.217945		
8	10427659	-0.151985	-0.19669	-0.217386		
8	10448350	-0.117633	-0.116959	-0.217224	PAQR4	progesterin and adipoQ receptor family member IV
8	10490845	-0.165375	-0.198912	-0.217102	CHMP4C	chromatin modifying protein 4C
8	10563931	-0.14396	-0.191815	-0.217073		
8	10338301	-0.517518	-0.079925	-0.21705		
8	10493307	-0.298185	-0.197765	-0.216896		
8	10552288	-0.130438	-0.115579	-0.216438	VSTM2B	V-set and transmembrane domain containing 2B
8	10517067	-0.134084	-0.092445	-0.215499	SFN	stratifin
8	10473363	-0.345935	0.1896584	-0.215355	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)
8	10340869	-0.385066	-0.112162	-0.215222		
8	10398354	-0.435925	0.078274	-0.214984		
8	10470392	-0.352137	-0.210214	-0.214704	ADAMTSL2	ADAMTS-like 2
8	10551421	-0.284097	0.0742338	-0.214049	Zfp60 (includes others)	zinc finger protein 60
8	10531675	-0.155424	0.028196	-0.21378	SEC31A	SEC31 homolog A (S. cerevisiae)
8	10339935	-0.221859	-0.179159	-0.213566		
8	10338469	-0.279198	-0.225112	-0.213272		
8	10342175	-0.170098	-0.183305	-0.213103		
8	10354370	-0.166035	-0.204998	-0.212821		
8	10341598	-0.222546	-0.144559	-0.211102		
8	10338823	-0.227717	-0.220252	-0.211031		
8	10340445	-0.462918	-0.124705	-0.210592		
8	10339496	-0.20754	-0.233672	-0.210258		
8	10581266	-0.17067	-0.13141	-0.209591	TPPP3	tubulin polymerization-promoting protein family member 3
8	10341158	-0.182291	-0.047074	-0.209235		
8	10354003	-0.165563	-0.134562	-0.208936	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A
8	10447079	-0.30529	-0.292102	-0.207367	LOC100502965	hypothetical protein LOC100502965
8	10342614	-0.24877	-0.107097	-0.207199		
8	10595848	-0.294923	0.1457502	-0.207077	SPSB4	splA/ryanodine receptor domain and SOCS box containing 4
8	10343486	-0.140262	-0.163923	-0.206499		
8	10339433	-0.487406	0.0857854	-0.206482		
8	10339200	-0.126697	-0.138939	-0.205829		
8	10489357	-0.155555	-0.136334	-0.205367	JPH2	junctophilin 2

8	10563764	-0.15293	-0.148619	-0.204904	Mrgprb3 (includes EG:292928)	MAS-related GPR, member B3
8	10480379	-0.145376	-0.116415	-0.204663	MRP5	mitochondrial ribosomal protein S5
8	10489355	-0.328134	-0.122406	-0.204465	JPH2	junctional protein 2
8	10341821	-0.356074	-0.109092	-0.204462		
8	10366163	-0.144536	-0.180706	-0.204377	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15
8	10342114	-0.417156	-0.229549	-0.204246		
8	10601768	-0.221899	-0.2589	-0.204067	ARMCX4	armadillo repeat containing, X-linked 4
8	10339747	-0.201718	0.0117166	-0.204054		
8	10392464	-0.166157	0.025509	-0.203737	FAM20A	family with sequence similarity 20, member A
8	10563989	-0.311615	-0.12134	-0.203678		
8	10460879	-0.147927	-0.09504	-0.203535	MEN1	multiple endocrine neoplasia 1
8	10581643	-0.140322	-0.112104	-0.203372		
8	10594301	-0.22898	-0.240603	-0.202219	CORO2B	coronin, actin binding protein, 2B
8	10420437	-0.320742	-0.046138	-0.201935	ZDHHC20	zinc finger, DHHC-type containing 20
8	10559790	-0.234197	-0.200671	-0.201166	Zim1	zinc finger, imprinted 1
8	10582890	-0.294369	-0.041459	-0.200622		
8	10340938	-0.212447	-0.132549	-0.200114		
8	10491858	-0.284056	-0.112619	-0.200097		
8	10442254	-0.289371	-0.154774	-0.199925		
8	10430127	-0.134596	-0.082904	-0.199388	ZNF251	zinc finger protein 251
8	10394798	-0.192683	-0.081493	-0.198928		
8	10404336	-0.248431	-0.066713	-0.197722		
8	10338631	-0.234799	-0.221083	-0.197322		
8	10602271	-0.268202	-0.162147	-0.197085		
8	10576495	-0.163572	-0.161988	-0.196948	TRIM67	tripartite motif containing 67
8	10340974	-0.183563	-0.21089	-0.196549		
8	10417501	-0.334936	-0.198439	-0.196023	Gm16440 (includes others)	predicted gene 16440
8	10576218	-0.186349	-0.219848	-0.195902	CPNE7	copine VII
8	10566800	-0.181325	-0.153887	-0.195742	ASCL3	achaete-scute complex homolog 3 (Drosophila)
8	10338289	-0.16204	-0.144913	-0.195665		
8	10523277	-0.222296	-0.173408	-0.194927	ANKRD56	ankyrin repeat domain 56
8	10461100	-0.15006	0.0087234	-0.194109	HRASLS5	HRAS-like suppressor family, member 5
8	10596135	-0.174444	-0.042668	-0.192841		
8	10440647	-0.159573	0.0266334	-0.192374	CLDN8	claudin 8
8	10343180	-0.312017	-0.056468	-0.192032		
8	10344544	-0.461764	-0.221578	-0.191844		
8	10592856	-0.162201	-0.078854	-0.191816	RPS25	ribosomal protein S25
8	10341675	-0.299296	-0.06617	-0.191368		
8	10339723	-0.307543	0.0746594	-0.191056		
8	10491773	-0.221109	0.0983504	-0.190942	SLC25A31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31
8	10361250	-0.205227	0.0794396	-0.190784	CAMK1G	calcium/calmodulin-dependent protein kinase IG
8	10484886	-0.197231	-0.180662	-0.190705	Olf1272/Olf1273-ps	olfactory receptor 1272
8	10339720	-0.393693	-0.026985	-0.190477		
8	10340508	-0.368699	0.018861	-0.190211		
8	10473261	-0.180748	0.0053478	-0.190109	FSIP2	fibrous sheath interacting protein 2
8	10343265	-0.168164	-0.066676	-0.189427		
8	10341737	-0.492329	0.010091	-0.188461		
8	10578413	-0.157728	-0.038237	-0.188384	Adam34 (includes others)	a disintegrin and metallopeptidase domain 34
8	10591668	-0.158496	-0.134116	-0.187883	RGL3	ral guanine nucleotide dissociation stimulator-like 3
8	10572755	-0.284376	0.1300696	-0.187734		
8	10339539	-0.260429	-0.160332	-0.186763		
8	10387257	-0.328299	-0.180602	-0.18663	ALOX15B	arachidonate 15-lipoxygenase, type B
8	10339467	-0.349107	-0.193788	-0.186523		
8	10342133	-0.23931	-0.10236	-0.185616		
8	10444717	-0.22616	-0.064759	-0.185553	C6orf47	chromosome 6 open reading frame 47
8	10344355	-0.383942	0.0436264	-0.185403		
8	10484555	-0.14987	-0.128719	-0.184832	Olf1037	olfactory receptor 1037
8	10344411	-0.257262	-0.239261	-0.184731		
8	10563527	-0.302414	-0.074121	-0.184034	USH1C	Usher syndrome 1C (autosomal recessive, severe)
8	10342167	-0.337313	0.0503388	-0.183927		
8	10343372	-0.155085	0.0066144	-0.183607		
8	10345167	-0.18296	0.0371888	-0.183606		
8	10342985	-0.322365	-0.034603	-0.183369		
8	10448916	-0.282699	-0.069342	-0.183281	Tpsab1	tryptase alpha/beta 1
8	10476512	-0.4292	0.0093482	-0.183256	SNAP25	synaptosomal-associated protein, 25kDa
8	10583291	-0.202073	-0.215991	-0.182962	C11orf90	chromosome 11 open reading frame 90
8	10344408	-0.256562	-0.074193	-0.182925		
8	10367513	-0.125158	-0.094086	-0.182559	Olf1777/Olf1800	olfactory receptor 777
8	10519028	-0.180272	0.04633	-0.182325	PRDM16	PR domain containing 16
8	10376938	-0.268292	-0.261037	-0.182252	CDRT4	CMT1A duplicated region transcript 4
8	10488382	-0.347352	-0.039446	-0.18143	CD93	CD93 molecule
8	10407704	-0.222314	0.073607	-0.181115		
8	10390022	-0.17594	0.0336058	-0.179354	RSAD1	radical S-adenosyl methionine domain containing 1
8	10412488	-0.144104	-0.057546	-0.179021		
8	10340120	-0.421564	-0.048129	-0.178712		
8	10338897	-0.294011	-0.207964	-0.178505		
8	10559516	-0.148333	-0.069309	-0.178239	RDH13	retinol dehydrogenase 13 (all-trans/9-cis)
8	10493498	-0.188188	-0.131864	-0.178039	DCST1	DC-STAMP domain containing 1
8	10590031	-0.217657	0.0174478	-0.177453	ITGA9	integrin, alpha 9
8	10478109	-0.305947	-0.201601	-0.177187	ADIG	adipogenin
8	10343489	-0.376028	-0.057386	-0.177129		
8	10343262	-0.357342	-0.171605	-0.177036		

8	10342765	-0.21631	0.0053532	-0.176265		
8	10413615	-0.223517	-0.034536	-0.176001	ITIH4	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)
8	10530393	-0.154607	-0.012829	-0.175865	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1
8	10343690	-0.27588	0.0026398	-0.175794		
8	10339243	-0.263969	-0.256079	-0.175694		
8	10344467	-0.240654	-0.185711	-0.175603		
8	10399581	-0.200002	-0.10393	-0.175084	3110053B16Rik	RIKEN cDNA 3110053B16 gene
8	10497012	-0.268173	-0.083684	-0.174075	C1orf173	chromosome 1 open reading frame 173
8	10338203	-0.430777	0.026665	-0.173771		
8	10410317	-0.233575	-0.008979	-0.173725	Zfp459	zinc finger protein 459
8	10607366	-0.129326	-0.049113	-0.173286	SHROOM2	shroom family member 2
8	10522661	-0.314947	-0.209268	-0.172975	KIAA1211	KIAA1211
8	10339160	-0.201851	0.0312372	-0.172916		
8	10582899	-0.383528	0.001306	-0.172889		
8	10339486	-0.152183	-0.077126	-0.172828		
8	10338811	-0.257351	0.0711324	-0.172715		
8	10342906	-0.218907	-0.156758	-0.172609		
8	10537406	-0.211062	-0.191172	-0.172445	CLEC2L	C-type lectin domain family 2, member L
8	10340030	-0.292248	0.052939	-0.171789		
8	10338827	-0.298392	-0.245593	-0.17147		
8	10411274	-0.137321	-0.074024	-0.17138	SV2C	synaptic vesicle glycoprotein 2C
8	10513002	-0.172843	-0.118107	-0.17069	Gm12471	predicted gene 12471
8	10463138	-0.162647	-0.053301	-0.170526	DPPA2	developmental pluripotency associated 2
8	10408900	-0.174968	-0.022994	-0.170362		
8	10341897	-0.300439	-0.055409	-0.169861		
8	10588509	-0.141228	-0.065886	-0.169558	PCBP4	poly(rC) binding protein 4
8	10508800	-0.185139	-0.081353	-0.168798	Gm3579	predicted gene 3579
8	10573865	-0.185139	-0.081353	-0.168798	Gm3579	predicted gene 3579
8	10340225	-0.365348	0.1520552	-0.168649		
8	10577782	-0.28276	-0.031168	-0.167588	HTRA4	HtrA serine peptidase 4
8	10341685	-0.242699	-0.173371	-0.166765		
8	10383358	-0.185822	-0.079687	-0.166718		
8	10398130	-0.24767	-0.02524	-0.166558	AK7	adenylate kinase 7
8	10427075	-0.187904	-0.010871	-0.166062	KRT18	keratin 18
8	10524345	-0.210537	-0.116297	-0.165863	TPST2	tyrosylprotein sulfotransferase 2
8	10383785	-0.172846	-0.027582	-0.165801	C5orf52	chromosome 5 open reading frame 52
8	10571198	-0.269069	-0.069969	-0.165631	Gm1698	predicted gene 1698
8	10492341	-0.285352	-0.09126	-0.165624	ARHGEP26	Rho guanine nucleotide exchange factor (GEF) 26
8	10502519	-0.146047	-0.076811	-0.164697		
8	10342483	-0.227912	-0.176177	-0.164492		
8	10528036	-0.255168	-0.161103	-0.164432		
8	10550931	-0.203071	-0.11142	-0.163846	IRGQ	immunity-related GTPase family, Q
8	10345911	-0.273466	-0.032046	-0.163707	Gm8211	predicted gene 8211
8	10481577	-0.242149	-0.123986	-0.163406	UCK1	uridine-cytidine kinase 1
8	10543065	-0.245721	-0.235828	-0.163051		
8	10339797	-0.2244	-0.203748	-0.162904		
8	10344554	-0.311818	0.1049666	-0.162463		
8	10343554	-0.433781	0.0105858	-0.162382		
8	10338198	-0.4248	-0.267158	-0.162032		
8	10341103	-0.154253	-0.057558	-0.161785		
8	10576189	-0.203769	-0.169596	-0.161097		
8	10342262	-0.376449	0.0304478	-0.160764		
8	10344140	-0.407843	0.0600582	-0.16052		
8	10424075	-0.168292	-0.014246	-0.160354		
8	10338440	-0.146351	-0.055625	-0.159812		
8	10341170	-0.236377	0.021074	-0.159123		
8	10474073	-0.345967	-0.091855	-0.158401		
8	10340671	-0.191805	-0.021583	-0.158397		
8	10493889	-0.300356	-0.031934	-0.156074	LCE1B	late cornified envelope 1B
8	10341740	-0.388692	-0.126514	-0.155849		
8	10480849	-0.163965	-0.049947	-0.155386	Fcna	ficolin A
8	10447880	-0.236248	-0.190782	-0.155268	MRPL18	mitochondrial ribosomal protein L18
8	10600703	-0.398885	-0.154836	-0.155195	1700072E05Rik	RIKEN cDNA 1700072E05 gene
8	10343305	-0.335202	-0.092936	-0.154703		
8	10603425	-0.147247	-0.05162	-0.154038	GLOD5	glyoxalase domain containing 5
8	10341457	-0.302657	-0.209247	-0.153842		
8	10441899	-0.267229	-0.222618	-0.153839	4930488N24Rik (includes others)	RIKEN cDNA 4930488N24 gene
8	10340386	-0.367564	-0.098845	-0.153178		
8	10522944	-0.248409	-0.190602	-0.153164		
8	10506254	-0.306372	-0.052062	-0.153034	RAVER2	ribonucleoprotein, PTB-binding 2
8	10340737	-0.278937	-0.080999	-0.152706		
8	10604761	-0.186136	-0.095378	-0.152052	mir-504	microRNA 504
8	10339049	-0.419972	-0.189499	-0.152003		
8	10433795	-0.193204	-0.098259	-0.15182		
8	10349828	-0.182657	-0.000242	-0.151488	LRRN2	leucine rich repeat neuronal 2
8	10413338	-0.171944	-0.024522	-0.150788		
8	10468419	-0.253399	-0.167824	-0.150452	WDR96	WD repeat domain 96
8	10378649	-0.174968	-0.046198	-0.150384	SLC43A2	solute carrier family 43, member 2
8	10567456	-0.22443	-0.166277	-0.150268	DNAH3	dynein, axonemal, heavy chain 3
8	10339027	-0.191095	-0.046054	-0.148907		
8	10339079	-0.372364	0.0248342	-0.148849		
8	10477715	-0.258223	-0.001525	-0.148393	mir-499	microRNA 499
8	10338106	-0.32429	0.0217172	-0.148381		
8	10526541	-0.185353	-0.04728	-0.148146		
8	10343784	-0.392612	-0.030413	-0.148078		

8	10339969	-0.304955	0.0306362	-0.147554		
8	10342313	-0.16177	-0.033094	-0.147033		
8	10477167	-0.27789	-0.018603	-0.146826	Mets2	malignant T cell amplified sequence 2
8	10342300	-0.341892	0.1283944	-0.146637		
8	10342790	-0.235858	0.0269998	-0.146375		
8	10465185	-0.252837	-0.07708	-0.14592	EHBPI1L1	EH domain binding protein 1-like 1
8	10380303	-0.194526	-0.085784	-0.14539	CA10	carbonic anhydrase X
8	10466351	-0.233963	0.0433786	-0.144967	Olf1459	olfactory receptor 1459
8	10364888	-0.27757	0.0034734	-0.144852	DOT1L	DOT1-like, histone H3 methyltransferase (S. cerevisiae)
8	10599461	-0.171033	-0.056966	-0.144181	Calml (includes others)	calmodulin 1
8	10506736	-0.261029	0.0544352	-0.144111	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)
8	10385542	-0.29288	-0.124045	-0.143665	BTNL9	butyrophilin-like 9
8	10343797	-0.23986	0.0586098	-0.143563		
8	10343012	-0.216731	-0.087678	-0.14337		
8	10365926	-0.239767	-0.076363	-0.142717	4732465J04Rik	RIKEN cDNA 4732465J04 gene
8	10344184	-0.384985	-0.003214	-0.141137		
8	10585703	-0.254061	-0.111891	-0.141077	RPP25	ribonuclease P/MRP 25kDa subunit
8	10341498	-0.323174	-0.187013	-0.140955		
8	10404012	-0.307003	0.0397752	-0.139844	Vmn1r188 (includes others)	vomeroneasal 1 receptor 194
8	10586433	-0.212314	-0.092251	-0.138931	RBPM52	RNA binding protein with multiple splicing 2
8	10342309	-0.224615	-0.134538	-0.138389		
8	10371006	-0.230448	-0.054346	-0.138056	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)
8	10513504	-0.276707	-0.179967	-0.137775	Mup1 (includes others)	major urinary protein 1
8	10356876	-0.237916	-0.024498	-0.137402		
8	10344045	-0.248426	0.0239014	-0.136621		
8	10341871	-0.295595	-0.240091	-0.136617		
8	10404898	-0.258799	-0.194043	-0.136225	FLJ23152	hypothetical protein LOC401236
8	10559916	-0.215014	-0.023751	-0.136157		
8	10357239	-0.251248	-0.177358	-0.135299	TMEM37	transmembrane protein 37
8	10522784	-0.266081	0.0576836	-0.135224		
8	10346150	-0.25995	-0.122171	-0.135017	TMEFF2	transmembrane protein with EGF-like and two follistatin-like domains 2
8	10407072	-0.266328	0.026732	-0.134443	ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast)
8	10343547	-0.418964	0.0683108	-0.134127		
8	10340052	-0.342951	-0.238559	-0.133378		
8	10353794	-0.19715	-0.016017	-0.13266	FAM168B	family with sequence similarity 168, member B
8	10532630	-0.262021	0.0596818	-0.132499	ADRBK2	adrenergic, beta, receptor kinase 2
8	10339010	-0.355882	-0.012739	-0.132498		
8	10340034	-0.213512	0.007784	-0.131717		
8	10394534	-0.211602	-0.058781	-0.131656	OSR1	odd-skipped related 1 (Drosophila)
8	10340115	-0.250358	0.0365924	-0.131313		
8	10601648	-0.219175	-0.063152	-0.130661	TNMD	tenomodulin
8	10497319	-0.394797	0.0009582	-0.130639		
8	10522494	-0.229195	-0.081864	-0.130513		
8	10344229	-0.371902	0.0248098	-0.13045		
8	10413598	-0.265887	-0.001654	-0.129054	TMEM110	transmembrane protein 110
8	10383819	-0.217943	-0.06955	-0.126522	SEC14L2	SEC14-like 2 (S. cerevisiae)
8	10405779	-0.352316	0.0777996	-0.126475	mir-23	microRNA 23a
8	10515277	-0.198482	-0.062722	-0.126198	C1orf190	chromosome 1 open reading frame 190
8	10342319	-0.399642	-0.007539	-0.123178		
8	10344815	-0.258324	-0.085949	-0.122875	CSPP1	centrosome and spindle pole associated protein 1
8	10593776	-0.365291	-0.162203	-0.122784	NRG4	neuregulin 4
8	10522388	-0.272278	-0.069377	-0.121957	SLC10A4	solute carrier family 10 (sodium/bile acid cotransporter family), member 4
8	10503008	-0.312501	-0.0419	-0.121788		
8	10581388	-0.315231	0.0853754	-0.120772	LCAT	lecithin-cholesterol acyltransferase
8	10569335	-0.233889	0.0081914	-0.118936	H19	H19, imprinted maternally expressed transcript (non-protein coding)
8	10341512	-0.334161	-0.246212	-0.118648		
8	10435543	-0.214131	-0.066368	-0.117498	GOLGB1	golgin B1
8	10562181	-0.218691	-0.062964	-0.116952	LSR	lipolysis stimulated lipoprotein receptor
8	10513467	-0.316349	-0.156031	-0.113816	Mup1 (includes others)	major urinary protein 1
8	10512332	-0.289104	-0.049	-0.113407	4930466F19Rik	RIKEN cDNA 4930466F19 gene
8	10512354	-0.289104	-0.049	-0.113407	4930466F19Rik	RIKEN cDNA 4930466F19 gene
8	10507143	-0.293161	-0.159971	-0.111485	CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 22
8	10475314	-0.439013	0.052199	-0.110167	MAP1A	microtubule-associated protein 1A
8	10499160	-0.380511	-0.213707	-0.104239	CD1D	CD1d molecule
8	10545014	-0.356304	-0.041719	-0.104052	VOPP1	vesicular, overexpressed in cancer, pro-survival protein 1
8	10465701	-0.29889	-0.103965	-0.103983	LGALS12	lectin, galactoside-binding, soluble, 12
8	10340564	-0.386181	-0.063664	-0.103704		
8	10479185	-0.324799	-0.06893	-0.101131		
8	10490248	-0.324799	-0.06893	-0.101131		
8	10343334	-0.309086	-0.119324	-0.097288		
8	10339150	-0.373083	-0.112068	-0.093319		

Online Table 4. Gene list of cluster 9

Cluster	Probe Set ID	Day 4	Day 7	Day 60	Symbol	Entrez Gene Name
9	10455970	6.5951544	6.8408488	2.7550844	LOC667597	cDNA sequence BC023105
9	10608681	5.0975162	6.3055612	1.4049014		
9	10569102	4.1126826	4.610839	0.0802472	IRF7	interferon regulatory factor 7
9	10462621	4.0853566	4.1545878	0.735528	IFIT3	interferon-induced protein with tetratricopeptide repeats 3
9	10459066	3.8964194	6.333378	0.9808462	Gm4841	predicted gene 4841
9	10376324	3.7566458	5.4298996	1.0434714	Gm12250	predicted gene 12250
9	10462623	3.6725474	3.830307	0.4157976	IFIT1	interferon-induced protein with tetratricopeptide repeats 1B
9	10462618	3.6540016	4.0203848	0.6145778	IFIT3	interferon-induced protein with tetratricopeptide repeats 3
9	10502791	3.3811272	3.7192634	0.5582916	IFI44	interferon-induced protein 44
9	10376326	3.3571768	4.8523036	0.6859844	Igtp	interferon gamma induced GTPase
9	10455961	3.3253228	4.2918706	1.1203902	ligp1/ligp1b	interferon inducible GTPase 1
9	10541307	3.1859268	3.4566536	0.234833	USP18	ubiquitin specific peptidase 18
9	10462613	3.1582036	3.6723572	0.3264784	IFIT2	interferon-induced protein with tetratricopeptide repeats 2
9	10399710	2.9592028	2.9425508	0.3071108	RSAD2	radical S-adenosyl methionine domain containing 2
9	10531407	2.8710192	4.9151102	1.0306794	CXCL9	chemokine (C-X-C motif) ligand 9
9	10455954	2.8416838	3.9194812	0.573159	Gm4951	predicted gene 4951
9	10461594	2.7655198	4.0269044	0.0122602	Ms4a4c (includes others)	membrane-spanning 4-domains, subfamily A, member 4C
9	10420308	2.6737512	5.0710288	0.0711108	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
9	10385500	2.6184044	4.318854	0.441812	IRGM	immunity-related GTPase family, M
9	10385507	2.5200064	5.2899154	0.346628	993011J21Rik1 (includes others)	RIKEN cDNA 993011J21 gene 1
9	10462390	2.4727748	4.1343234	0.4389764	CD274	CD274 molecule
9	10608646	2.4056752	3.4126048	0.840732		
9	10385533	2.3628012	3.9464244	0.5936638	Tgtp1	T-cell specific GTPase 1
9	10496580	2.3356844	3.5278056	0.3420088	GBP4	guanylate binding protein 4
9	10385518	2.3049124	3.7979412	0.6501804	Tgtp1	T-cell specific GTPase 1
9	10420488	2.293081	2.7739404	0.1588924	D14Erd668e	DNA segment, Chr 14, ERATO Doi 668, expressed
9	10502801	2.2841482	2.9312582	0.261261	IFI44L	interferon-induced protein 44-like
9	10531724	2.2815106	3.822894	0.6683916	PLAC8	placenta-specific 8
9	10351873	2.2629668	3.185545	0.2148632	BC094916/Pyhin1	pyrin and HIN domain family, member 1
9	10531415	2.1851942	3.4002956	0.3333844	CXCL10	chemokine (C-X-C motif) ligand 10
9	10420483	2.1796906	3.1472144	0.2032514	Gm4902/Phf11	PHD finger protein 11
9	10437224	2.1391056	2.200803	0.1448582	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
9	10351880	2.0908962	2.4197626	0.2390196	Pydc3	pyrin domain containing 3
9	10455957	2.0768002	3.296937	0.498244		
9	10389207	2.0050012	3.523642	0.2292062	CCL5	chemokine (C-C motif) ligand 5
9	10531994	1.9820206	3.1900306	0.178119	GBP6	guanylate binding protein family, member 6
9	10434778	1.976805	2.6322212	0.1693046	RTP4	receptor (chemosensory) transporter protein 4
9	10574145	1.9392818	3.3258394	0.4290558	Nlr5	NLR family, CARD domain containing 5
9	10524621	1.9303814	2.56658	0.1803046	Oas2	2'-5' oligoadenylate synthetase-like 2
9	10441233	1.8923404	2.2067206	0.1452954	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
9	10496569	1.877639	2.983852	0.5104528	GBP7	guanylate binding protein 7
9	10379518	1.8525756	3.2992484	-0.0624348	CCL7	chemokine (C-C motif) ligand 7
9	10379636	1.8405584	2.9966644	-0.0240438	SLFN12	schlafen family member 12
9	10496555	1.8366324	3.697625	0.4470678	GBP5	guanylate binding protein 5
9	10379511	1.8287706	3.346293	-0.0876922	CCL13	chemokine (C-C motif) ligand 13
9	10571984	1.8221954	2.3671382	0.3725068	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
9	10574149	1.7968578	3.0695354	0.4724992	Nlr5	NLR family, CARD domain containing 5
9	10532019	1.7941714	3.5220264	0.1689848	GBP6	guanylate binding protein family, member 6
9	10531987	1.790064	3.1560436	0.391632	Gbp4	guanylate binding protein 4
9	10496592	1.7553108	3.2674944	0.4885906	GBP2	guanylate binding protein 2, interferon-inducible
9	10393573	1.7477276	2.354204	0.1808506	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein
9	10346191	1.7256992	2.9799744	0.420577	STAT1	signal transducer and activator of transcription 1, 91kDa
9	10378068	1.7227144	2.3397758	0.2228566	XAF1	XIAP associated factor 1
9	10566366	1.7179298	2.3147196	-0.0518948	Trim30a/Trim30d	tripartite motif-containing 30A
9	10533246	1.7111238	2.4574944	0.2578654	OAS1	2'-5' oligoadenylate synthetase 1, 40/46kDa
9	10490150	1.706555	3.1057082	0.1551604	ZBP1	Z-DNA binding protein 1
9	10538590	1.7048226	2.7449572	0.3294514	HERC6	hect domain and RLD 6
9	10574098	1.6705832	2.7335696	0.4907736	Nlr5	NLR family, CARD domain containing 5
9	10450075	1.659463	2.7334578	0.673535	HLA-C	major histocompatibility complex, class I, C
9	10450325	1.6577664	3.2779914	0.734277	CFB	complement factor B
9	10444814	1.6493638	2.7096858	0.7286634	H2-Gs10	MHC class I like protein GS10
9	10563597	1.592759	2.6958494	-0.2240294	SAA1	serum amyloid A1
9	10496539	1.5636138	2.6202612	0.526842	GBP5	guanylate binding protein 5
9	10398075	1.5247712	2.3072352	0.862975	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 3
9	10375515	1.511729	2.9587816	0.2477772	Olfir56	olfactory receptor 56
9	10574102	1.4913794	2.3381306	0.4186204	Nlr5	NLR family, CARD domain containing 5
9	10439249	1.4881932	2.5694386	0.268583	PARP14	poly (ADP-ribose) polymerase family, member 14
9	10512470	1.4672758	2.713331	0.8777808	CD72	CD72 molecule

9	10531980	1.3998878	2.8079486	0.4323052	GBP6	guanylate binding protein family, member 6
9	10444244	1.3898032	2.82886	0.3361584	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
9	10531420	1.373296	2.7521388	0.1020954	CXCL11	chemokine (C-X-C motif) ligand 11
9	10574135	1.3660986	2.7838982	0.3928514	Nlrc5	NLR family, CARD domain containing 5
9	10379633	1.3600938	2.6242244	-0.0063712	Slfn1	schlafen 1
9	10574104	1.3326482	2.4592106	0.43494	Nlrc5	NLR family, CARD domain containing 5
9	10552406	1.3129002	3.9631866	0.2317442	NKG7	natural killer cell group 7 sequence
9	10412211	1.3109074	2.7028486	0.043377	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
9	10574139	1.266601	2.5442016	0.4044042	Nlrc5	NLR family, CARD domain containing 5
9	10389231	1.241656	2.6696048	0.5231642	CCL3L1/CCL3L3	chemokine (C-C motif) ligand 3-like 1
9	10444258	1.2360028	3.1446588	0.310859	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
9	10351509	1.1382366	3.2340278	0.5539904	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)
9	10398039	1.1319066	3.09938	0.2524934	Serpina3g (includes others)	serine (or cysteine) peptidase inhibitor, clade A, member 3G
9	10590635	1.1121718	3.1067198	0.4734302	CCR5	chemokine (C-C motif) receptor 5
9	10598013	1.1121718	3.1067198	0.4734302	CCR5	chemokine (C-C motif) receptor 5
9	10598976	1.1008642	3.34966	0.202005	TIMP1	TIMP metalloproteinase inhibitor 1
9	10360173	1.0780114	2.6692734	0.5169692	SLAMF7	SLAM family member 7
9	10517165	1.0225362	3.0034194	1.0157522	CD52	CD52 molecule
9	10406928	0.9670856	2.8278394	0.9209294	CD180	CD180 molecule
9	10379535	0.8391164	3.4532374	0.8826676	CCL8	chemokine (C-C motif) ligand 8
9	10461605	0.8125756	2.924889	0.2364798	Ms444c (includes others)	membrane-spanning 4-domains, subfamily A, member 4C

Online Table 5. Gene list of cluster 15

Cluster	Probe Set ID	Day 4	Day 7	Day 60	Symbol	Entrez Gene Name
15	10465840	-2.2956392	0.5069734	-0.1592758	SCGB1A1	secretoglobin, family 1A, member 1 (uteroglobin)
15	10477475	-1.9624504	0.6485402	0.0085248	PLUNC	palate, lung and nasal epithelium associated
15	10559698	-1.5803518	-0.5150376	0.2130634		
15	10384044	-1.5290928	-1.0592308	-0.2904826	MYL7	myosin, light chain 7, regulatory
15	10551293	-1.5033586	0.132909	-0.1104016	CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1
15	10495306	-1.4696242	-0.8238158	-0.2067764	MYBPHL	myosin binding protein H-like
15	10438813	-1.461875	-0.3215578	-0.2862966	Mir690	microRNA 690
15	10343452	-1.3793982	0.4214158	0.477727		
15	10438801	-1.272881	-0.7286604	-0.2572798	FGF12	fibroblast growth factor 12
15	10545569	-1.2333692	0.0831254	-0.055882	REG3A	regenerating islet-derived 3 alpha
15	10341006	-1.2295416	0.5526588	0.7657264		
15	10551226	-1.092523	0.1502732	0.080991	CYP2A6 (includes others)	cytochrome P450, family 2, subfamily A, polypeptide 6
15	10340401	-1.056792	-0.2263494	0.1509078		
15	10581605	-1.043173	0.0246328	0.0310348	HP	haptoglobin
15	10490913	-1.0196648	-0.4262078	-0.6297108	CA3	carbonic anhydrase III, muscle specific
15	10558673	-1.0071206	-0.5332772	-0.0576994	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1
15	10463551	-1.0064976	-0.8150412	-0.4083922	ELOVL3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3
15	10467979	-1.0015662	-0.7415896	-0.7367598	SCD	stearoyl-CoA desaturase (delta-9-desaturase)
15	10585390	-0.998934	-0.2365078	-0.233866	SLN	sarcolipin
15	10344101	-0.9953794	0.0645112	-0.2127962		
15	10340043	-0.9779604	-0.3457098	0.0430692		
15	10584047	-0.9581856	-0.5313074	-0.3420212	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif, 8
15	10339357	-0.941271	-0.3391036	-0.1856724		
15	10339283	-0.9412686	0.040212	-0.0093682		
15	10364542	-0.9295686	-0.0475666	-0.2764278	CFD	complement factor D (adipsin)
15	10342781	-0.891894	0.0451544	-0.0015708		
15	10393970	-0.88474	-0.3832922	-0.165098	FASN	fatty acid synthase
15	10340912	-0.8830934	0.1461882	-0.14105		
15	10567010	-0.8826092	-0.5083008	0.2189958	DKK3	dickkopf homolog 3 (Xenopus laevis)
15	10455015	-0.8822134	0.1051976	-0.0270132	Vaultrc5	vault RNA component 5
15	10555460	-0.8815882	-0.4265174	-0.0482752	STARD10	StAR-related lipid transfer (START) domain containing 10
15	10423971	-0.8711336	-0.0461542	0.2713584	PKHD1L1	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1
15	10544932	-0.865147	-0.5935824	0.7039278	INMT	indolethylamine N-methyltransferase
15	10581011	-0.8552584	-0.6304278	-0.2204044		
15	10342619	-0.8527634	0.0910836	-0.2701002		
15	10341442	-0.8461204	-0.161685	0.049025		
15	10359593	-0.846087	-0.6952236	-0.0108932	FMO3	flavin containing monooxygenase 3
15	10342202	-0.8341682	-0.1359126	0.0720194		
15	10341620	-0.8332534	-0.326992	-0.2424374		
15	10338149	-0.8285372	0.0771772	-0.2625344		
15	10338338	-0.8070274	-0.0816116	-0.0397952		
15	10339294	-0.805873	-0.2382392	0.109409		
15	10339847	-0.8023556	-0.2012496	0.488191		
15	10546929	-0.8010954	-0.3809128	-0.3583322	CIDEA	cell death-inducing DFFA-like effector c
15	10479852	-0.8002542	0.2082754	0.1551466	CAMK1D	calcium/calmodulin-dependent protein kinase ID
15	10341005	-0.7999998	-0.2713018	-0.0929068		
15	10342355	-0.7973892	-0.2810516	-0.377012		
15	10559694	-0.7907846	-0.243225	0.1487572	SBK2	SH3-binding domain kinase family, member 2
15	10564203	-0.7901094	-0.219156	-0.2525038		
15	10338296	-0.7811626	0.0092496	-0.1007944		
15	10476321	-0.775281	-0.2188836	0.2742436	PRND	prion protein 2 (duplet)
15	10344243	-0.7749226	0.099985	-0.1589342		
15	10375261	-0.7743786	-0.2073936	0.4387006	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2
15	10498852	-0.7713674	-0.240725	-0.0728406	RXFP1	relaxin/insulin-like family peptide receptor 1
15	10542983	-0.7679158	-0.3579208	-0.1578324	PON1	paraoxonase 1
15	10399407	-0.766469	-0.5161166	-0.0276582	VSNL1	visinin-like 1
15	10341860	-0.766002	-0.0136452	0.099293		
15	10342070	-0.765101	0.077392	-0.3484024		
15	10339977	-0.7620848	0.2181792	0.4023774		
15	10512499	-0.759286	-0.354252	-0.0057074	TPM2	tropomyosin 2 (beta)
15	10339214	-0.7504284	-0.040816	-0.162133		
15	10341691	-0.7487936	-0.0073434	-0.4036284		
15	10483131	-0.7446606	-0.233467	0.1928198	KCNH7	potassium voltage-gated channel, subfamily H (eag-related), member 7
15	10357371	-0.7415082	-0.2376742	0.0072202	TMEM163	transmembrane protein 163
15	10559796	-0.7391714	-0.2200308	0.0916782	PEG3	paternally expressed 3
15	10339028	-0.7383398	-0.097584	0.1155432		
15	10342469	-0.7342964	-0.1719774	0.2388244		
15	10340743	-0.7324662	0.1324836	0.0606104		
15	10349947	-0.7294244	-0.586905	0.14617	FMOD	fibromodulin
15	10342257	-0.728917	-0.3162386	0.3090518		
15	10526441	-0.7285922	-0.2112744	0.0366402	UPK3B	uroplakin 3B
15	10343426	-0.725131	-0.171054	0.260365		
15	10371740	-0.7243954	0.0534942	0.1366136	ANO4	anoctamin 4
15	10545180	-0.717027	0.117737	0.283135		
15	10514939	-0.713054	-0.1509262	0.2566822	PODN	podocan
15	10439500	-0.7055502	0.0297604	0.0167674	UPK1B	uroplakin 1B

15	10344523	-0.7003158	-0.2100398	-0.2264324		
15	10339818	-0.6978396	0.0627052	0.1002826		
15	10344365	-0.6927648	-0.363878	0.1490812		
15	10434747	-0.6911724	-0.4027102	-0.44772	ADIPOQ	adiponectin, C1Q and collagen domain containing
15	10338826	-0.6868322	0.2527106	0.0771428		
15	10578986	-0.6849572	-0.3329448	0.1572596	PSD3	pleckstrin and Sec7 domain containing 3
15	10462435	-0.6832826	-0.2263314	0.1227912	MLANA	melan-A
15	10549877	-0.6816468	-0.2826532	0.0500024		
15	10339284	-0.6814454	-0.1330862	0.1275216		
15	10375259	-0.6777006	-0.2298238	0.706073	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2
15	10463355	-0.6751864	0.007469	0.1176028	Scd2	stearoyl-Coenzyme A desaturase 2
15	10361186	-0.6731044	-0.2319286	0.1385664	SERTAD4	SERTA domain containing 4
15	10341583	-0.672145	-0.15081	-0.005701		
15	10454807	-0.6718818	-0.154624	0.0892842	SNORA74A	small nucleolar RNA, H/ACA box 74A
15	10604576	-0.6672268	-0.4279352	-0.0103998	GPC3	glypican 3
15	10342753	-0.661519	-0.0742532	-0.0553512		
15	10342029	-0.6597642	0.1923698	-0.046069		
15	10343059	-0.6576826	-0.0770446	0.0266754		
15	10476353	-0.6566752	-0.1671524	0.3916594		
15	10476401	-0.656306	-0.0500812	0.3150764	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)
15	10341599	-0.6544618	0.0154676	0.299438		
15	10341210	-0.6528634	-0.1732748	-0.0039846		
15	10531100	-0.6492672	0.0680276	-0.0307268	Sult1d1	sulfotransferase family 1D, member 1
15	10341772	-0.6475636	-0.0756704	0.0323998		
15	10341621	-0.6474788	-0.409102	-0.1624958		
15	10338312	-0.6452806	-0.1888264	0.507192		
15	10339263	-0.6447964	-0.1647512	-0.0662924		
15	10343106	-0.6415206	0.15405	0.504682		
15	10358531	-0.6365948	-0.2055716	0.4162144	Hmnl	hemocentin 1
15	10343336	-0.635782	0.166135	0.151082		
15	10341318	-0.6351848	-0.1335428	0.238071		
15	10341438	-0.6329922	-0.0391888	-0.1007348		
15	10343900	-0.6305448	-0.0680562	-0.0452292		
15	10342433	-0.6302448	-0.4435564	0.2766938		
15	10339979	-0.6263072	-0.0941376	-0.1343062		
15	10523376	-0.6255668	0.0264256	0.1390666	FRAS1	Fraser syndrome 1
15	10342203	-0.6251876	-0.1605242	0.0237994		
15	10344223	-0.6150312	-0.064594	-0.0061608		
15	10340398	-0.6141948	-0.085211	0.0088488		
15	10339644	-0.613872	-0.0354892	-0.039445		
15	10341350	-0.6121466	-0.2180362	0.0148188		
15	10341610	-0.6098502	0.0402924	0.0109952		
15	10344569	-0.6075752	0.0306298	0.2473168		
15	10340504	-0.6052114	0.115599	0.0431448		
15	10338153	-0.6043226	-0.2610942	-0.2737684		
15	10339554	-0.6038936	-0.0582088	-0.0771268		
15	10338362	-0.6032732	-0.4120548	-0.0040402		
15	10564183	-0.6026968	-0.1842118	-0.2242214	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10343835	-0.602062	-0.0751876	0.1600992		
15	10571815	-0.6020494	-0.1630078	0.5179504	GPM6A	glycoprotein M6A
15	10564161	-0.6018794	-0.241563	-0.2066542	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10344161	-0.60183	-0.036852	0.124944		
15	10502805	-0.5995024	-0.2544794	0.1432198	PTGFR	prostaglandin F receptor (FP)
15	10399908	-0.5991376	-0.4501954	-0.1050954	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta
15	10427796	-0.5984588	-0.2948742	0.25344	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
15	10564177	-0.5981568	-0.2496334	-0.245196	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10460253	-0.5981044	-0.2727442	0.12765	Aldh3b2	aldehyde dehydrogenase 3 family, member B2
15	10342681	-0.595462	0.206372	-0.017176		
15	10599530	-0.5952852	-0.3725764	-0.208679	RAB33A	RAB33A, member RAS oncogene family
15	10537062	-0.5947484	-0.1443504	0.1652448	MEST	mesoderm specific transcript homolog (mouse)
15	10340697	-0.5936514	-0.480459	0.4308308		
15	10352916	-0.5936212	-0.0993702	0.0840374	A330023F24Rik	RIKEN cDNA A330023F24 gene
15	10564163	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564167	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564171	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564173	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564175	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564179	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564181	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564185	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564187	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564189	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564191	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564193	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564195	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564197	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564199	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564201	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564205	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10564207	-0.593094	-0.2315066	-0.2668876	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10339683	-0.5927726	-0.0019282	0.417323		
15	10340830	-0.5918724	0.1879816	-0.1568012		
15	10342181	-0.589525	0.182476	-0.178547		
15	10338929	-0.589183	0.0181158	0.1578098		

15	10564159	-0.5878142	-0.193827	-0.2370974	PWCR1	small nucleolar RNA, C/D box 116 cluster
15	10341619	-0.5862432	-0.4147102	0.064426		
15	10343114	-0.5846328	-0.243109	-0.1247486		
15	10342316	-0.583578	-0.2806516	0.0934592		
15	10387797	-0.5802202	0.1830602	-0.1532592	BCL6B	B-cell CLL/lymphoma 6, member B
15	10376778	-0.5797336	-0.2714492	0.0990338	MFAP4	microfibrillar-associated protein 4
15	10338854	-0.5783688	-0.0129544	0.1750374		
15	10343102	-0.5776454	-0.0534068	0.0021764		
15	10339897	-0.5752488	0.1842976	-0.1179972		
15	10341190	-0.5709786	0.0624272	0.108368		
15	10356154	-0.5709158	-0.0836988	0.0999184	SPHKAP	SPHK1 interactor, AKAP domain containing
15	10341781	-0.57091	-0.2926012	0.1445288		
15	10338538	-0.5689276	-0.1551536	-0.2185734		
15	10343772	-0.5687894	0.012318	0.3778168		
15	10525076	-0.5685774	-0.2203972	0.4024862	SDS	serine dehydratase
15	10343484	-0.5674898	-0.0904158	-0.0072704		
15	10445078	-0.5632046	-0.2880596	-0.2215066	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1
15	10343055	-0.5578384	-0.3197886	0.223676		
15	10340900	-0.5536864	-0.068072	0.0694474		
15	10502770	-0.5529858	-0.0842992	0.2460052	LPHN2	latrophilin 2
15	10338389	-0.5524678	-0.2582182	0.2454212		
15	10593123	-0.5520694	-0.4458724	-0.0102698	TAGLN	transgelin
15	10578989	-0.5514234	-0.1628992	0.0860516	PSD3	pleckstrin and Sec7 domain containing 3
15	10340392	-0.550297	-0.3547862	0.0755544		
15	10572070	-0.5492288	-0.3876624	0.40219	NPY1R	neuropeptide Y receptor Y1
15	10374929	-0.5488596	-0.287085	0.2545858	LOC100289085	protein fem-1 homolog A-like
15	10524308	-0.5487498	-0.295248	0.0570668	Mir701	microRNA 701
15	10342934	-0.5486424	-0.2061196	0.2065986		
15	10341540	-0.5482438	0.1488496	0.4171384		
15	10428302	-0.54528	-0.2563392	0.1533626	KLF10	Kruppel-like factor 10
15	10344018	-0.5439694	-0.3235654	0.122912		
15	10355500	-0.5436762	-0.1624658	-0.01942	IGFBP5	insulin-like growth factor binding protein 5
15	10341157	-0.5417404	-0.227787	-0.1421526		
15	10397835	-0.5391888	-0.0739312	0.1564226	SLC24A4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4
15	10486403	-0.5368332	0.006502	0.1314696	PLA2G4E	phospholipase A2, group IVE
15	10342772	-0.5356348	-0.290951	0.1621438		
15	10358577	-0.5341718	-0.0636786	0.3990358	Hmcn1	hemimentin 1
15	10572378	-0.5341268	-0.4250414	0.538208	COMP	cartilage oligomeric matrix protein
15	10505438	-0.5338752	-0.3108636	-0.1614116	ORM1/ORM2	orosomucoid 1
15	10342773	-0.5316084	0.0171828	-0.0059806		
15	10395103	-0.5313978	0.1330212	0.1052046	PXDN	peroxidasin homolog (Drosophila)
15	10343370	-0.5312452	0.0412164	-0.179915		
15	10411519	-0.5288676	0.0688928	0.160208	MAP1B	microtubule-associated protein 1B
15	10341246	-0.528814	-0.0157192	0.3693832		
15	10478525	-0.5275228	-0.074484	-0.1244834	WFDC2	WAP four-disulfide core domain 2
15	10340739	-0.526661	0.0681462	0.0203622		
15	10474064	-0.524422	-0.039046	0.0113192	TP53I1	tumor protein p53 inducible protein 11
15	10338437	-0.5228256	0.1444666	0.0568242		
15	10586718	-0.5224748	-0.2101674	0.2898426	9530091C08Rik	RIKEN cDNA 9530091C08 gene
15	10338450	-0.5221092	-0.3192872	0.189177		
15	10601519	-0.5218808	0.0107242	0.2787996	KLHL4	kelch-like 4 (Drosophila)
15	10343949	-0.5216276	0.1507026	-0.1197944		
15	10342816	-0.5214536	-0.3104336	-0.202339		
15	10358529	-0.5187262	-0.1621222	0.354732	Hmcn1	hemimentin 1
15	10551282	-0.5160582	0.0444344	0.0168864	CYP2A6 (includes others)	cytochrome P450, family 2, subfamily A, polypeptide 6
15	10344216	-0.514146	-0.2708818	0.015782		
15	10427125	-0.5135312	-0.2942712	0.0409294	IGFBP6	insulin-like growth factor binding protein 6
15	10343834	-0.512598	-0.1688934	0.2423448		
15	10341468	-0.511433	-0.288258	0.1785044		
15	10343498	-0.510802	-0.3197762	0.4931538		
15	10342547	-0.5107824	-0.0970698	0.161848		
15	10344274	-0.5105182	0.0316052	0.21227		
15	10369702	-0.5105026	-0.0687848	0.1223294	TET1	tet oncogene 1
15	10339013	-0.5087892	0.1287268	-0.0409896		
15	10596148	-0.5073158	-0.4017566	0.1319624	TF	transferrin
15	10339943	-0.5064012	0.0808442	0.0287998		
15	10472398	-0.5047618	-0.0299858	0.0886018	SCN2A	sodium channel, voltage-gated, type II, alpha subunit
15	10374202	-0.5043794	-0.0724094	-0.1038296	ADCY1	adenylate cyclase 1 (brain)
15	10339646	-0.5036946	0.009057	-0.0375272		
15	10459905	-0.5018498	0.1307	0.0904772	SETBP1	SET binding protein 1
15	10513420	-0.5012336	-0.1280988	-0.060874	Mup1 (includes others)	major urinary protein 1
15	10477069	-0.5012002	-0.1828464	0.0365854	TCF15	transcription factor 15 (basic helix-loop-helix)
15	10358515	-0.5009404	0.152703	0.3434002	Hmcn1	hemimentin 1
15	10358621	-0.5004512	-0.1075242	0.229847	Hmcn1	hemimentin 1
15	10355403	-0.4995658	0.060508	0.4579366	FNI	fibronectin 1
15	10340037	-0.496505	-6.32E-05	0.1552282		
15	10358527	-0.4963606	-0.2105526	0.3798042	Hmcn1	hemimentin 1
15	10341272	-0.4955972	-0.2600412	0.0591286		
15	10547404	-0.4955278	-0.0343426	0.2015428	ERC1	ELKS/RAB6-interacting/CAST family member 1
15	10495206	-0.495076	-0.054637	0.3853118	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter 5)
15	10341830	-0.4935744	0.0813578	0.1701708		
15	10340889	-0.49345	-0.2209052	-0.0115394		
15	10552857	-0.4916616	-0.320385	-0.1318964	SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7

15	10504137	-0.4914844	-0.1705168	0.239486	ENSMUSG00000073868	predicted gene 10590
15	10504201	-0.4914844	-0.1705168	0.239486	ENSMUSG00000073868	predicted gene 10590
15	10512350	-0.4914844	-0.1705168	0.239486	4933409K07Rik	RIKEN cDNA 4933409K07 gene
15	10512352	-0.4914844	-0.1705168	0.239486	ENSMUSG00000073868	predicted gene 10590
15	10522024	-0.4906026	0.0099836	0.022899	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1
15	10537296	-0.4899162	0.0020456	0.0055712	mir-490	microRNA 490
15	10569618	-0.4898964	-0.2219676	0.1293174	ANO1	anoctamin 1, calcium activated chloride channel
15	10342519	-0.4898032	-0.1330716	0.364536		
15	10339493	-0.4895916	-0.0902304	-0.1528628		
15	10458764	-0.4892398	-0.0333594	-0.0272702		
15	10418506	-0.488914	-0.0430702	0.1473962	STAB1	stabilin 1
15	10340336	-0.4884332	0.0572964	-0.1072362		
15	10343470	-0.4881638	-0.3156976	0.2381994		
15	10360418	-0.4860076	-0.2445636	0.1174414	RGS7	regulator of G-protein signaling 7
15	10495285	-0.4856428	-0.207142	0.0373982	SORT1	sortilin 1
15	10344573	-0.4846726	-0.0528472	0.3985652		
15	10339861	-0.484644	-0.0013196	0.3051692		
15	10339231	-0.4844578	0.1155618	0.0432108		
15	10559702	-0.4835648	0.110475	0.092486	ZNF579	zinc finger protein 579
15	10339179	-0.48352	0.021374	0.2813186		
15	10338736	-0.4821186	0.0492548	0.3745982		
15	10342333	-0.4807066	-0.2527356	-0.0572074		
15	10391036	-0.480433	-0.0646436	0.0127948	Krt19	keratin 19
15	10340309	-0.479189	-0.1065724	0.1240324		
15	10358533	-0.477346	-0.1884918	0.3563526	Hmcn1	hemicentin 1
15	10339087	-0.4755778	-0.4057834	0.2801968		
15	10518781	-0.475147	-0.0898828	0.4661848	PER3	period homolog 3 (Drosophila)
15	10339896	-0.474165	-0.2111804	0.0431722		
15	10338981	-0.4736194	-0.174735	-0.078084		
15	10472757	-0.4733682	-0.1782552	0.1310222	CYBRD1	cytochrome b reductase 1
15	10348299	-0.4724384	-0.1052132	-0.0111792	5830472F04Rik	RIKEN cDNA 5830472F04 gene
15	10578207	-0.4717056	0.0121318	0.2870122	LONRF1	LON peptidase N-terminal domain and ring finger 1
15	10343317	-0.4715052	-0.0218298	-0.003351		
15	10343606	-0.4714186	0.0238078	0.0478108		
15	10340802	-0.46941	-0.1244284	0.2781372		
15	10338255	-0.468918	-0.1379084	0.1576414		
15	10343998	-0.4688786	-0.164483	0.0509916		
15	10341625	-0.4686234	-0.1121662	-0.0317636		
15	10339395	-0.4681412	-0.0390346	0.248171		
15	10338494	-0.467775	0.0919058	-0.0441702		
15	10341688	-0.4672728	0.1101452	0.3750346		
15	10340942	-0.4666964	0.109623	0.1451346		
15	10338822	-0.4662164	-0.2424192	0.0056498		
15	10494548	-0.4661592	0.116879	0.0687426	GJA5	gap junction protein, alpha 5, 40kDa
15	10339988	-0.465986	-0.0423416	0.038215		
15	10425799	-0.4634066	-0.1795578	-0.1422542	RNU12	RNA, U12 small nuclear
15	10441813	-0.4625452	-0.0585852	0.003301	Snora20	small nuclear RNA, H/ACA box 20
15	10502783	-0.4624324	-0.06917	0.1346768	Gm9912	predicted gene 9912
15	10588592	-0.4624258	-0.3715388	0.0141932	CACNA2D2	calcium channel, voltage-dependent, alpha 2/delta subunit 2
15	10585982	-0.4621548	0.0223794	0.1571454	MYO9A	myosin IXA
15	10538408	-0.4619636	-0.4376616	0.2377674	C7orf41	chromosome 7 open reading frame 41
15	10343388	-0.4617446	-0.2157948	0.0719972		
15	10395201	-0.4603808	-0.1306144	-0.1119378	SLC26A3	solute carrier family 26, member 3
15	10338226	-0.4594242	-0.1082558	0.1570382		
15	10383731	-0.4593718	-0.229204	0.0137558	SMTN	smoothenin
15	10513472	-0.4593682	-0.1272044	-0.049519	Mup1 (includes others)	major urinary protein 1
15	10340569	-0.459244	-0.088217	0.0491702		
15	10339019	-0.4579408	-0.3504302	0.3355804		
15	10339544	-0.4574282	0.035807	0.316243		
15	10358517	-0.4554662	-0.0100392	0.3110802	Hmcn1	hemicentin 1
15	10599696	-0.4553666	0.0640964	0.1841906	DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B
15	10471721	-0.454629	-0.3796134	0.2281408	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
15	10338169	-0.453847	-0.0703328	-0.119985		
15	10358549	-0.4529196	-0.0819464	0.450674	Hmcn1	hemicentin 1
15	10586722	-0.4526796	-0.106645	0.2476708	F830001A07Rik	RIKEN cDNA F830001A07 gene
15	10358575	-0.4526128	-0.1450598	0.3928966	Hmcn1	hemicentin 1
15	10358656	-0.4517864	0.0203552	0.4445454	Hmcn1	hemicentin 1
15	10396606	-0.4514894	-0.0493434	0.1335	SYNE2	spectrin repeat containing, nuclear envelope 2
15	10344166	-0.4511974	-0.342465	0.097029		
15	10343190	-0.4509566	-0.1833448	-0.0824146		
15	10396936	-0.450783	-0.3529578	0.020492	SMOC1	SPARC related modular calcium binding 1
15	10343438	-0.4503734	-0.0436154	-0.0694042		
15	10525030	-0.4483902	-0.1710602	-0.0287152	TBX5	T-box 5
15	10341287	-0.447455	-0.2913028	0.1028708		
15	10467319	-0.4466646	-0.2159646	-0.1304528	RBP4	retinol binding protein 4, plasma
15	10590267	-0.4438492	-0.1258352	0.0301786	SNORA62	small nuclear RNA, H/ACA box 62
15	10519527	-0.4434186	-0.1263726	0.240507	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1
15	10494413	-0.4421264	-0.0946072	0.0411978	Rnu1b2	U1b2 small nuclear RNA
15	10494421	-0.4421264	-0.0946072	0.0411978	Rnu1b2	U1b2 small nuclear RNA
15	10500343	-0.4421264	-0.0946072	0.0411978	Rnu1b2	U1b2 small nuclear RNA
15	10500358	-0.4421264	-0.0946072	0.0411978	Rnu1b2	U1b2 small nuclear RNA
15	10512937	-0.4421264	-0.0946072	0.0411978	Rnu1b2	U1b2 small nuclear RNA

15	10340257	-0.4420148	-0.0619408	0.0714312		
15	10379344	-0.4400408	-0.195761	-0.0065278	Gm10387	predicted gene 10387
15	10358535	-0.4399056	-0.1955388	0.3365866	Hmcn1	hemimentin 1
15	10340339	-0.4378502	-0.0412488	0.236903		
15	10343557	-0.43785	-0.173654	0.1795968		
15	10343308	-0.4378084	-0.2769808	-0.056518		
15	10508723	-0.4369044	-0.1437388	0.0309766	Snora61	small nucleolar RNA, H/ACA box 61
15	10378401	-0.4366566	-0.264627	0.096374		
15	10341861	-0.4348926	-0.2154898	-0.0935654		
15	10343177	-0.4342074	0.0167368	-0.0939954		
15	10358541	-0.4341392	-0.0834404	0.420207	Hmcn1	hemimentin 1
15	10344459	-0.4335802	-0.137125	0.0404724		
15	10340388	-0.4327964	-0.0308124	0.097679		
15	10547100	-0.4324998	-0.009184	0.137206	PLXND1	plexin D1
15	10343685	-0.432038	-0.0462002	0.0223228		
15	10343225	-0.4308718	-0.0753966	0.413791		
15	10338333	-0.4305648	-0.1902276	0.1351592		
15	10358547	-0.4267698	-0.0718046	0.4392614	Hmcn1	hemimentin 1
15	10341325	-0.4258618	-0.0737204	0.1687856		
15	10358490	-0.4258408	-0.089891	0.4208328	Hmcn1	hemimentin 1
15	10352918	-0.425259	-0.2145568	-0.0730966	A330023F24Rik	RIKEN cDNA A330023F24 gene
15	10449551	-0.4229138	-0.3143672	0.0472532	CPNE5	copine V
15	10580663	-0.4225344	-0.2592942	0.0045618	Ces1f (includes EG:234564)	carboxylesterase 1F
15	10587778	-0.4206114	-0.0860468	-0.0417602		
15	10342667	-0.4204194	-0.0716392	-0.0826946		
15	10339240	-0.4193576	-0.1209868	0.011484		
15	10591169	-0.4175498	-0.1241396	0.094997	MUC16	mucin 16, cell surface associated
15	10528227	-0.4168436	-0.2753578	0.0391534	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
15	10591135	-0.4163462	-0.1902936	-0.011159	FAT3	FAT tumor suppressor homolog 3 (Drosophila)
15	10338501	-0.4162972	-0.2035726	0.0611648		
15	10394538	-0.4160552	-0.052931	0.0185354	ACACA	acetyl-CoA carboxylase alpha
15	10392484	-0.4136938	-0.2394992	0.1425384	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8
15	10358559	-0.4133774	-0.0798972	0.3469512	Hmcn1	hemimentin 1
15	10339244	-0.4129868	-0.0631664	-0.0717936		
15	10449000	-0.4128266	-0.046486	-0.0525818	MSLN	mesothelin
15	10341406	-0.412467	-0.167585	0.2807686		
15	10358581	-0.4122294	-0.0816556	0.3880142	Hmcn1	hemimentin 1
15	10513437	-0.4119528	-0.1471168	-0.0803012	Mup1 (includes others)	major urinary protein 1
15	10356968	-0.411688	-0.137094	-0.019762	PAM	peptidylglycine alpha-amidating monooxygenase
15	10340403	-0.4112786	-0.2033238	-0.0733946		
15	10343682	-0.4107152	-0.232107	0.0254828		
15	10513455	-0.4100202	-0.1375302	-0.0643184	Mup1 (includes others)	major urinary protein 1
15	10339424	-0.4098396	-0.1959366	0.2119132		
15	10366864	-0.407544	-0.0953952	-0.053778	F420014N23Rik	RIKEN cDNA F420014N23 gene
15	10436941	-0.4066296	-0.1540982	-0.0755712	MRPS6	mitochondrial ribosomal protein S6
15	10380059	-0.4060166	-0.0910194	-0.056454		
15	10380061	-0.4060166	-0.0910194	-0.056454		
15	10380063	-0.4060166	-0.0910194	-0.056454		
15	10380065	-0.4060166	-0.0910194	-0.056454		
15	10341254	-0.4049014	-0.0946186	-0.0889144		
15	10588037	-0.4045118	-0.1163054	0.2173052	RBP1	retinol binding protein 1, cellular
15	10340497	-0.4044464	-0.0746	-0.045976		
15	10338177	-0.4036762	-0.178779	0.1440142		
15	10585186	-0.4033492	-0.094621	0.000394	1600029D21Rik	RIKEN cDNA 1600029D21 gene
15	10339384	-0.4020136	-0.0834362	-0.0243928		
15	10570278	-0.4001286	-0.1790364	0.1352		
15	10343660	-0.3999912	-0.2778722	0.1620338		
15	10591630	-0.3987732	-0.304261	0.2032776	DOCK6	dedicator of cytokinesis 6
15	10349571	-0.3985188	-0.2721284	0.1127192	FCAMR	Fc receptor, IgA, IgM, high affinity
15	10504234	-0.3973194	-0.1931308	0.1768128	UNC13B	unc-13 homolog B (C. elegans)
15	10339845	-0.3973138	-0.1741706	0.2427338		
15	10366293	-0.3963488	-0.2879794	0.0270198	CSR2P2	cysteine and glycine-rich protein 2
15	10338909	-0.3899306	-0.2696494	-0.0217598		
15	10338117	-0.3871986	-0.137728	-0.0670892		
15	10341661	-0.38552	-0.1830642	0.0783734		
15	10515771	-0.3840634	-0.3048904	0.1212654	TIE1	tyrosine kinase with immunoglobulin-like and EGF-like domains 1
15	10339051	-0.3828988	-0.1886708	0.1952834		
15	10493114	-0.3823254	-0.1777848	0.0885988	NES	nestin
15	10387368	-0.3806668	-0.1574054	-0.0084686	TMEM88	transmembrane protein 88
15	10548038	-0.3799928	-0.2497324	0.1918192	NTF3	neurotrophin 3
15	10342560	-0.376793	-0.2563336	0.07224		
15	10519693	-0.3758342	-0.174617	0.1351606	SEMA3D	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D
15	10566172	-0.3718938	-0.2262286	0.1303532	OR51E2	olfactory receptor, family 51, subfamily E, member 2
15	10361267	-0.3712352	-0.1984992	0.0204888		
15	10460116	-0.371235	-0.2309408	-0.095756	SOCS6	suppressor of cytokine signaling 6
15	10512145	-0.3683578	-0.2454408	0.0592752	AQP7	aquaporin 7
15	10375058	-0.368294	-0.239566	0.041034	HBA1/HBA2	hemoglobin, alpha 1
15	10478219	-0.368026	-0.2145802	0.1125184	PLCG1	phospholipase C, gamma 1
15	10375051	-0.363592	-0.218702	0.042956	HBA1/HBA2	hemoglobin, alpha 1
15	10579114	-0.3621598	-0.2284382	0.0250042	YJEFN3	Yjef N-terminal domain containing 3
15	10545742	-0.3570266	-0.2314426	-0.0289736	CD207	CD207 molecule, langerin
15	10338796	-0.3564406	-0.2639478	0.1178706		

15	10423379	-0.3512282	-0.273178	0.1013072	Tiaf2	TGF-beta1-induced anti-apoptotic factor 2
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Online Table 6. Gene list of cluster 19

Cluster	Probe Set ID	Day 4	Day 7	Day 60	Symbol	Entrez Gene Name
19	10593015	0.4421494	3.1317374	0.2995788	CD3G	CD3g molecule, gamma (CD3-TCR complex)
19	10531972	0.975506	2.7344248	0.159272	Gbp8	guanylate-binding protein 8
19	10581378	0.9756478	2.6932842	0.2039484	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10
19	10450161	0.1799426	2.6400372	1.725007	H2-Ea-ps	major histocompatibility complex, class II, DR alpha
19	10523717	0.3610268	2.5940596	1.977796	SPP1	secreted phosphoprotein 1
19	10590631	0.3531702	2.572978	0.3026312	CCR2	chemokine (C-C motif) receptor 2
19	10461721	0.6971236	2.5383322	1.0606978	MPEG1	macrophage expressed 1
19	10513739	0.5525402	2.5272676	0.2815386	TNC	tenascin C
19	10456005	0.104702	2.5244304	1.553092	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
19	10444291	0.0979178	2.511373	1.086062	H2-Ab1	major histocompatibility complex, class II, DQ beta 1
19	10541564	0.7464494	2.4722832	0.3443094	Clec4a3	C-type lectin domain family 4, member a3
19	10542164	0.5480114	2.4502562	1.1052172	CLEC12A	C-type lectin domain family 12, member A
19	10450694	1.283448	2.4501724	0.5557134	H2-T22	histocompatibility 2, T region locus 10
19	10574157	1.3049558	2.4474742	0.2223566	Nlr5	NLR family, CARD domain containing 5
19	10450154	0.0553464	2.4472182	1.5266352	H2-Aa	major histocompatibility complex, class II, DQ alpha 1
19	10450145	0.7637532	2.435735	0.2729004	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)
19	10608650	1.2253204	2.3571572	0.5479072		
19	10467136	0.9961334	2.3453586	0.0655276	CH25H	cholesterol 25-hydroxylase
19	10494271	0.8863408	2.3397738	0.9578114	CTSS	cathepsin S
19	10430344	0.7892776	2.339561	0.3294114	IL2RB	interleukin 2 receptor, beta
19	10542214	0.8568258	2.3356938	0.3147028	KLRD1	killer cell lectin-like receptor subfamily D, member 1
19	10548409	0.5555734	2.321605	0.258718	KLRC1	killer cell lectin-like receptor subfamily C, member 1
19	10545231	0.112162	2.3115278	1.2174252		
19	10450682	1.1968086	2.3070544	0.5163656	H2-T23	major histocompatibility complex, class I, E
19	10499899	0.3411854	2.2756336	0.430861	Sprr1a	small proline-rich protein 1A
19	10566358	1.4552558	2.2619232	0.3253804	Trim30a/Trim30d	tripartite motif-containing 30A
19	10358408	0.5463968	2.25218	1.0736032	RGS1	regulator of G-protein signaling 1
19	10500335	1.0418258	2.2285576	0.0730666	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)
19	10358224	0.5411394	2.2280782	0.391751	PTPRC	protein tyrosine phosphatase, receptor type, C
19	10376060	0.6354092	2.2272594	0.273665	IRF1	interferon regulatory factor 1
19	10360370	1.4681804	2.1829292	-0.0354692	BC094916/Pyhin1	pyrin and HIN domain family, member 1
19	10482802	0.1173006	2.1749958	0.1873466	CYTI1P	cytohesin 1 interacting protein
19	10483110	1.430762	2.1434404	0.2088794	IFIH1	interferon induced with helicase C domain 1
19	10391207	1.5878618	2.1416922	0.1567764	DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58
19	10360398	1.7179874	2.1286288	0.1429086	Ifi202b	interferon activated gene 202B
19	10469816	0.534669	2.114779	0.7450546	IL1RN	interleukin 1 receptor antagonist
19	10586865	0.4116198	2.1073	0.4162836	ALDH1A2	aldehyde dehydrogenase 1 family, member A2
19	10416437	0.6751552	2.096989	0.5377088	LCP1	lymphocyte cytosolic protein 1 (L-plastin)
19	10522788	0.6406626	2.0893718	1.4313376	STAP1	signal transducing adaptor family member 1
19	10608680	1.0686368	2.063397	0.5170938		
19	10574137	0.8125618	2.038502	0.1257696	Nlr5	NLR family, CARD domain containing 5
19	10541555	0.68506	2.0369386	0.2454676	Clec4a1	C-type lectin domain family 4, member a1
19	10439268	1.3933982	2.0361166	0.2693444		
19	10383198	1.3722304	2.03025	0.2341492		
19	10489107	0.9496202	2.0174686	0.193735	SAMHD1	SAM domain and HD domain 1
19	10547664	0.652098	2.0117958	-0.077252	CLEC4E	C-type lectin domain family 4, member E
19	10473356	1.2483616	2.0110876	0.2273504	UBE2L6	ubiquitin-conjugating enzyme E2L 6
19	10545672	1.073653	2.009689	-0.223924	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methylenetetrahydrofolate cyclohydrolase
19	10501063	0.92232	2.0042782	0.5883946	CD53	CD53 molecule
19	10548333	0.5087908	2.003942	0.0924392	CD69	CD69 molecule
19	10346168	0.3006652	2.0011018	0.2653532	STAT4	signal transducer and activator of transcription 4
19	10444229	-0.0841386	1.9972962	0.5102066	H2-DMa	major histocompatibility complex, class II, DM alpha
19	10383202	1.2170374	1.9899976	0.1971992		
19	10383212	1.2807078	1.9794812	0.1379936		
19	10427628	0.2020662	1.9776476	1.0536282	IL7R	interleukin 7 receptor
19	10450699	1.1703178	1.9724508	0.4997466	H2-t9	MHC class Ib T9
19	10383200	1.2727822	1.9718344	0.1916054		
19	10582997	1.0521214	1.9663418	0.2881812	CASP4	caspase 4, apoptosis-related cysteine peptidase
19	10363070	0.4972668	1.964941	0.6533532	Gp49a/Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4
19	10566050	0.8505664	1.9609576	0.1040406	IL18BP	interleukin 18 binding protein
19	10387985	0.8071282	1.9576576	0.2166224	C17orf87	chromosome 17 open reading frame 87
19	10379530	0.8658914	1.9443636	0.1128612	CCL2	chemokine (C-C motif) ligand 2
19	10383204	1.1357078	1.9425306	0.2457926		
19	10347928	1.1627542	1.9413008	0.2504984	SP110	SP110 nuclear body protein
19	10582874	1.1627542	1.9413008	0.2504984	SP110	SP110 nuclear body protein
19	10383168	1.2321966	1.9387588	0.224844		

19	10439009	1.6160874	1.9293578	0.3396058	APOD	apolipoprotein D
19	10466210	1.3308214	1.9272124	-0.2145274	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D
19	10383214	1.2460008	1.9243842	0.155819	RNF213	ring finger protein 213
19	10590623	0.1569208	1.9074108	0.3690986	CXCR6	chemokine (C-X-C motif) receptor 6
19	10444821	1.18119	1.8987912	0.345559	H2-Q8	histocompatibility 2, Q region locus 8
19	10516620	0.3329464	1.895378	-0.0414716	LCK	lymphocyte-specific protein tyrosine kinase
19	10576034	0.3441756	1.8938428	0.228497	IRF8	interferon regulatory factor 8
19	10543067	0.8924464	1.8921396	-0.1612068	ASNS	asparagine synthetase (glutamine-hydrolyzing)
19	10385504	1.3345508	1.8849688	0.0609972	993011J21Rik1 (includes others)	RIKEN cDNA 993011J21 gene 1
19	10512067	1.4561762	1.882034	0.1562328	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
19	10371082	0.2148154	1.8804068	-0.460633	ITGB1BP3	integrin beta 1 binding protein 3
19	10346799	0.0043482	1.8797438	0.1659624	ICOS	inducible T-cell co-stimulator
19	10375145	0.6974618	1.8792452	0.1815292	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)
19	10450675	1.287698	1.8782556	0.251955	H2-T24	histocompatibility 2, T region locus 24
19	10451287	1.1796362	1.876985	0.080637	ISG15	ISG15 ubiquitin-like modifier
19	10383206	1.4657144	1.8769186	0.1973942		
19	10544133	1.217127	1.866139	0.1714104	PARP12	poly (ADP-ribose) polymerase family, member 12
19	10383208	1.27534	1.8656074	0.0859574		
19	10587323	0.2530728	1.8571534	0.030345	GSTA5	glutathione S-transferase alpha 5
19	10547621	0.718058	1.854566	0.6046294	APOBEC1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1
19	10578264	0.8405288	1.8510092	0.181129	MSR1	macrophage scavenger receptor 1
19	10497358	0.440363	1.8461006	0.105642	SIRPB1	signal-regulatory protein beta 1
19	10508392	0.6191052	1.8327338	0.0518754	RNF19B	ring finger protein 19B
19	10383196	1.239303	1.8305924	0.1384022		
19	10404606	0.7732084	1.826795	0.798668	LY86	lymphocyte antigen 86
19	10416837	0.4658074	1.819301	0.0892956	IRG1	immunoresponsive 1 homolog (mouse)
19	10384458	0.4738072	1.8126064	0.5662866	PLEK	pleckstrin
19	10430174	0.9298544	1.8121148	-0.0424356	ApoB9a/Apo9b	apolipoprotein L 9b
19	10422760	0.3261818	1.8113256	0.3297336	FYB	FYN binding protein
19	10444780	0.8865558	1.8096416	0.3486722	H2-D1	major histocompatibility complex, class I, C
19	10587683	0.224268	1.8088916	0.460044	BCL2A1	BCL2-related protein A1
19	10494978	0.461454	1.8025842	0.103349	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
19	10548345	0.6456856	1.790527	0.1088762	KLRK1	killer cell lectin-like receptor subfamily K, member 1
19	10383152	1.2251342	1.7822882	0.1650364		
19	10466127	0.7595704	1.7729404	0.2949266	AW112010	expressed sequence AW112010
19	10534909	1.0012986	1.7727008	0.274811	SP110	SP110 nuclear body protein
19	10566144	1.0783222	1.765984	0.0399148	TRIM21	tripartite motif containing 21
19	10547657	0.592161	1.7624398	0.7489586	C3AR1	complement component 3a receptor 1
19	10341146	0.955206	1.757856	0.2708486		
19	10398907	0.6186054	1.7508612	0.2368952	PLD4	phospholipase D family, member 4
19	10364262	0.3280914	1.7493698	0.5955638	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
19	10383233	1.1444914	1.7484898	0.1143688	RNF213	ring finger protein 213
19	10467578	0.5865978	1.737426	0.2986214	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1
19	10538979	0.039099	1.7373972	0.0898172	CD8B	CD8b molecule
19	10351658	0.27022	1.7345502	0.348607	CD48	CD48 molecule
19	10583008	0.5963556	1.731618	0.7944984	CASP12	caspace 12 (gene/pseudogene)
19	10533213	0.952913	1.7272632	0.028116	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa
19	10579532	0.9742552	1.7251682	0.015638	BST2	bone marrow stromal cell antigen 2
19	10601456	0.4274258	1.7217426	0.0632648	Gm6377	predicted gene 6377
19	10367224	1.1219454	1.7212156	0.1063028	STAT2	signal transducer and activator of transcription 2, 113kDa
19	10473125	0.2624998	1.7191564	0.2741498	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
19	10577655	0.6809258	1.7177706	-0.0897372	IDO1	indoleamine 2,3-dioxygenase 1
19	10587331	0.2273104	1.71706	0.0388082	GSTA5	glutathione S-transferase alpha 5
19	10414360	0.2304294	1.7160434	1.2752646	LGALS3	lectin, galactoside-binding, soluble, 3
19	10420030	0.544547	1.7142812	0.1313866	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
19	10601385	0.8437128	1.7139096	0.5232028	Tlr13	toll-like receptor 13
19	10404429	0.548754	1.7086388	0.3013378	SERPIN9	serpin peptidase inhibitor, clade B (ovalbumin), member 9
19	10363082	0.674021	1.7064604	0.6561414	Gp49a/Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4
19	10466314	1.0620346	1.701901	-0.047045	Gm6545	predicted gene 6545
19	10581813	0.770091	1.701732	-0.0969206	MLKL	mixed lineage kinase domain-like
19	10532744	0.3363368	1.69874	0.2439462	SELP1G	selectin P ligand
19	10372410	0.522368	1.698527	1.1243976	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)
19	10397975	1.0263038	1.6912854	0.423526	IFI27	interferon, alpha-inducible protein 27
19	10452980	1.4950454	1.6912818	0.096311	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2
19	10385511	0.7952632	1.690896	0.2082678	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
19	10554240	1.2615106	1.690042	0.1112326	ISG20	interferon stimulated exonuclease gene 20kDa
19	10360070	0.9638368	1.6841486	0.5139922	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
19	10559486	0.318287	1.683363	0.6118422	LAIR1	leukocyte-associated immunoglobulin-like

19	10402347	1.1685306	1.668541	-0.1304298	IFI27L2	receptor 1 interferon, alpha-inducible protein 27-like 2
19	10547976	0.3606576	1.662027	0.1520756	TAPBPL	TAP binding protein-like
19	10595633	0.2980066	1.6600914	0.463966	BCL2A1	BCL2-related protein A1
19	10477250	0.593416	1.6578754	0.1589558	HCK	hemopoietic cell kinase
19	10497372	0.077279	1.6482618	0.061407	Gm5150	predicted gene 5150
19	10360373	1.4103408	1.6441048	0.2734026	Gm4955/Pydc4	predicted gene 4955
19	10341698	0.710026	1.6433962	-0.2208912		
19	10458314	0.3242682	1.6420458	0.2020784	TMEM173	transmembrane protein 173
19	10388958	0.5125318	1.6375792	0.3854556	EVI2A	ecotropic viral integration site 2A
19	10383210	1.1383424	1.6337102	0.0069638		
19	10603551	0.4223812	1.625549	1.159192	CYBB	cytochrome b-245, beta polypeptide
19	10351197	0.5833314	1.6165604	-0.1720524	SELL	selectin L
19	10430372	0.2766366	1.612696	0.2249314	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
19	10466200	0.4040966	1.6093924	0.6076166	MS4A7	membrane-spanning 4-domains, subfamily A, member 7
19	10424676	1.074176	1.60709	0.089556	LY6E	lymphocyte antigen 6 complex, locus E
19	10533198	1.2649732	1.601928	0.2665056	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
19	10385118	0.4048064	1.6018698	0.4297698	DOCK2	dedicator of cytokinesis 2
19	10446253	0.3505632	1.5963008	0.1871464	VAV1	vav 1 guanine nucleotide exchange factor
19	10525158	1.2726552	1.5929634	0.0155286	Oas1b	2'-5'-oligoadenylate synthetase 1B
19	10574163	0.7109762	1.592793	0.1357792	Nlr5	NLR family, CARD domain containing 5
19	10598004	0.072844	1.5914776	0.1603672	CCR1	chemokine (C-C motif) receptor 1
19	10601416	0.0707	1.5850616	0.146496	P2RY10	purinergic receptor P2Y, G-protein coupled, 10
19	10587690	0.2873218	1.5840334	0.422429	BCL2A1	BCL2-related protein A1
19	10516966	0.5500444	1.5819754	0.1381296	C1orf38	chromosome 1 open reading frame 38
19	10549647	0.7043544	1.5800114	0.3322452	NCR1	natural cytotoxicity triggering receptor 1
19	10356278	0.8293982	1.579104	0.2295122		
19	10444830	0.9216016	1.5748188	0.3971792	H2-Q7	major histocompatibility complex, class I, B
19	10542140	0.474192	1.5670996	0.176973	Klrb1f	killer cell lectin-like receptor subfamily B member 1F
19	10444298	-0.0366592	1.5648672	0.7938668	H2-Eb1	major histocompatibility complex, class II, DR beta 1
19	10544588	-0.0606966	1.5635748	0.2281696	Gimap3	GTPase, IMAP family member 3
19	10389134	0.7427074	1.5557914	0.2019718	SLFN13	schlafen family member 13
19	10557862	0.3038222	1.5469754	0.1986446	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)
19	10461622	0.7415382	1.5460996	-0.1543084	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
19	10381408	0.8406186	1.5359778	0.076773	IFI35	interferon-induced protein 35
19	10574151	0.7058892	1.535274	0.017785	Nlr5	NLR family, CARD domain containing 5
19	10344031	0.601693	1.5296286	0.3844464		
19	10383194	1.0963808	1.5263516	0.0543994		
19	10539135	0.3874618	1.5245522	0.4551148	CAPG	capping protein (actin filament), gelsolin- like
19	10379630	0.9251714	1.5240792	0.211215	LOC100506736/SLFN12L	schlafen family member 12-like
19	10343267	0.38988	1.5193044	0.3863932		
19	10460767	0.4964744	1.5171568	0.0798446	BATF2	basic leucine zipper transcription factor, ATF-like 2
19	10495186	0.3895426	1.5164114	0.2865824	AI504432	expressed sequence AI504432
19	10383192	1.0434578	1.5140986	-0.0689554		
19	10473809	0.6935322	1.5085088	0.3719016	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene spi1
19	10343969	0.8470774	1.5062906	0.0323934		
19	10444268	0.5573244	1.5039722	0.2411812	TAP2	transporter 2, ATP-binding cassette, sub- family B (MDR/TAP)
19	10578493	1.1026004	1.502504	0.069727	TLR3	toll-like receptor 3
19	10559467	0.2746832	1.5013596	0.3916788	Lilrb3 (includes others)	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
19	10360382	1.113058	1.4970968	-0.0960994		
19	10557591	0.2612154	1.484938	0.0962942	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)
19	10566583	0.7771216	1.484039	0.1683282	A630026L20	predicted gene 8995
19	10351691	0.1576404	1.4828854	0.0857722	SLAMF6	SLAM family member 6
19	10342250	0.6374548	1.4822284	-0.1968016		
19	10524631	1.6460816	1.4800312	-0.0082242	OASL	2'-5'-oligoadenylate synthetase-like
19	10508663	0.2615698	1.474983	0.4539704	LAPTM5	lysosomal protein transmembrane 5
19	10352000	0.2421598	1.4732024	0.1845638	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
19	10395039	1.9141296	1.4696918	0.1989334	CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
19	10385513	0.7977336	1.46827	0.1571774	9930111J21Rik2	RIKEN cDNA 9930111J21 gene 2
19	10425049	0.885278	1.4578154	0.0038998	Apo19a/Apo19b	apolipoprotein L 9b
19	10339750	0.6767434	1.4569978	0.0487598		
19	10534927	0.573481	1.456305	0.337669	PILRA	paired immunoglobulin-like type 2 receptor alpha
19	10491091	1.0070048	1.4562698	0.4677006	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
19	10343290	0.6155766	1.4531214	-0.0887452		
19	10531737	0.2531144	1.4524198	0.4214542	HPSE	heparanase
19	10392839	0.4517374	1.4475472	0.1387038	CD300E	CD300e molecule
19	10606016	0.43968	1.4448968	0.0556836	IL2RG	interleukin 2 receptor, gamma
19	10341587	0.653113	1.4434846	0.3446022		

19	10588479	0.448144	1.4411098	0.1625784	TLR9	toll-like receptor 9
19	10459772	0.3656014	1.4394276	-0.0398924	LIPG	lipase, endothelial
19	10427336	0.1455786	1.4353166	0.5366498	NCKAP1L	NCK-associated protein 1-like
19	10429128	0.2684102	1.4342246	0.154483	SLA	Src-like-adaptor
19	10385526	0.7593058	1.4337874	0.170925	9930111J21Rik2	RIKEN cDNA 9930111J21 gene 2
19	10444236	0.0472272	1.4301082	0.3940302	H2-DMb2	major histocompatibility complex, class II, DM beta
19	10404061	0.240023	1.4277124	0.060515	HIST1H2BM	histone cluster 1, H2bm
19	10593024	-0.0129024	1.4223468	0.0332308	CD3E	CD3e molecule, epsilon (CD3-TCR complex)
19	10435457	0.8965184	1.4128956	0.2355468	PARP9	poly (ADP-ribose) polymerase family, member 9
19	10347925	1.0641064	1.4110846	0.5541396	Csprs (includes others)	component of Sp100-rs
19	10343468	0.7004286	1.4107288	0.132326		
19	10487208	0.5014866	1.4104722	0.3125408	ATP8B4	ATPase, class I, type 8B, member 4
19	10446282	0.4914846	1.4084476	0.4135968	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1
19	10347915	1.1219024	1.4075254	0.5349144	Csprs (includes others)	component of Sp100-rs
19	10588786	0.6018798	1.4061173	0.1428684	UBA7	ubiquitin-like modifier activating enzyme 7
19	10432640	0.333436	1.4047486	-0.000527	BIN2	bridging integrator 2
19	10461614	0.961888	1.4014132	-0.2155936	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C
19	10338492	0.5095478	1.3989682	0.0855698		
19	10466190	0.1068396	1.3979732	0.3058532	MS4A14	membrane-spanning 4-domains, subfamily A, member 14
19	10533256	0.9298928	1.3964458	-0.0836834	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa
19	10574133	0.522839	1.3949696	0.2162864	Nlr5	NLR family, CARD domain containing 5
19	10425092	0.0750874	1.390971	0.4081618	CYTH4	cytohesin 4
19	10397645	0.4072416	1.3895768	0.2572878	GRP65	G protein-coupled receptor 65
19	10416566	0.6688464	1.3865894	0.06489	EPSTI1	epithelial stromal interaction 1 (breast)
19	10415319	1.1973094	1.384173	0.2033798	IRF9	interferon regulatory factor 9
19	10340317	0.5451872	1.382322	0.0440246		
19	10363475	0.4745612	1.3818068	-0.1199382	PRF1	perforin 1 (pore forming protein)
19	10541587	0.3294138	1.3817326	0.2952782	CLEC4A	C-type lectin domain family 4, member A
19	10486061	0.2594004	1.3733332	0.0726536	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
19	10494405	-0.020348	1.3711182	0.2621112		
19	10342553	0.5957916	1.3669464	-0.1149076		
19	10566578	1.037822	1.3646458	0.2069368	GVIN1	GTPase, very large interferon inducible pseudogene 1
19	10339951	0.3897564	1.3509698	0.0952652		
19	10408239	-0.014304	1.348348	0.256996	HIST1H3A (includes others)	histone cluster 1, H3a
19	10404065	-0.020466	1.346584	0.26231		
19	10341222	0.4446238	1.3458018	0.1773594		
19	10404049	-0.031654	1.344784	0.255568	HIST3H3	histone cluster 3, H3
19	10559446	0.1278364	1.3425096	0.1234242	Lilrb3 (includes others)	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
19	10404028	-0.021226	1.341852	0.261474		
19	10568024	0.085763	1.3407108	0.0754376	CORO1A	coronin, actin binding protein, 1A
19	10412218	0.246929	1.3405814	0.0922118	GZMK	granzyme K (granzyme 3; tryptase II)
19	10338116	0.5032076	1.3396406	0.1213958		
19	10341395	0.6270404	1.3378844	0.1173654		
19	10353844	0.2429408	1.333679	0.2992638	LINCR	neutralized homolog 3 (Drosophila) pseudogene
19	10566571	0.9780742	1.3315022	0.205392	GVIN1	GTPase, very large interferon inducible pseudogene 1
19	10551883	0.4396744	1.330637	0.6743776	TYROBP	TYRO protein tyrosine kinase binding protein
19	10374333	0.3390056	1.3290564	0.0976656	IKZF1	IKAROS family zinc finger 1 (Ikaros)
19	10574159	0.7214016	1.3265116	0.145912	Nlr5	NLR family, CARD domain containing 5
19	10408246	-0.015718	1.325692	0.245507		
19	10498345	0.0917886	1.324675	0.0081468	GPR171	G protein-coupled receptor 171
19	10403941	-0.04412	1.320704	0.255596		
19	10439527	0.3021902	1.315349	0.1007632	TIGIT	T cell immunoreceptor with Ig and ITIM domains
19	10408083	-0.007942	1.31222	0.253824		
19	10359181	1.178489	1.3080828	0.3061894	TOR3A	torsin family 3, member A
19	10541683	0.5615392	1.3078052	0.619202	C1R	complement component 1, r subcomponent
19	10465059	0.351004	1.3016886	0.0989552	CTSW	cathepsin W
19	10494402	0.018493	1.2996292	0.2561438		
19	10443980	0.0734448	1.2986444	0.3442004	MYO1F	myosin IF
19	10461636	0.9397984	1.296475	-0.2190182		
19	10439312	0.421205	1.2959762	0.2275316	CD86	CD86 molecule
19	10476945	0.1432678	1.2932402	-0.0150944	CST7	cystatin F (leukocystatin)
19	10429843	0.6822778	1.2925336	0.185145	PARP10	poly (ADP-ribose) polymerase family, member 10
19	10341905	0.3699916	1.2906664	0.1438182		
19	10424400	0.3867162	1.2881278	0.0683688	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)
19	10444068	0.387153	1.2855764	0.1565016	TAPBP	TAP binding protein (tapasin)
19	10351679	0.1049966	1.283378	0.7502694	CD84	CD84 molecule
19	10530145	0.2903852	1.2805916	0.1836964	TLR1	toll-like receptor 1
19	10593050	0.3111306	1.2747598	0.233196	IL10RA	interleukin 10 receptor, alpha
19	10482517	0.4592992	1.2700728	0.19648	NMI	N-myc (and STAT) interactor
19	10340164	0.970162	1.268731	0.136533		
19	10441003	0.1841896	1.2679018	0.386084	Runx1	runt related transcription factor 1
19	10344300	0.4637748	1.2664564	0.3330754		

19	10356262	0.7599434	1.2638648	0.3805486	Csprs (includes others)	component of Sp100-rs
19	10338280	0.767899	1.260463	0.1806542		
19	10581434	0.4151294	1.2577828	0.6114122	DPEP2	dipeptidase 2
19	10450484	0.2926204	1.2544966	0.3261892	AIFI	allograft inflammatory factor 1
19	10583669	0.2381194	1.253789	0.1980792	C19orf38	chromosome 19 open reading frame 38
19	10521667	0.327503	1.252063	0.2547964	BST1	bone marrow stromal cell antigen 1
19	10452316	0.200302	1.251358	0.455166	C3	complement component 3
19	10580754	0.540463	1.2510904	0.0598304	9330175E14Rik	RIKEN cDNA 9330175E14 gene
19	10542040	0.5443804	1.2499434	0.1510554	PARP11	poly (ADP-ribose) polymerase family, member 11
19	10420497	0.8798182	1.249821	-0.348363	PHF11	PHD finger protein 11
19	10566346	0.8833828	1.2497776	0.2051118	TRIM5	tripartite motif containing 5
19	10347948	0.7803866	1.2487958	0.2957984	Sp100	nuclear antigen Sp100
19	10339327	0.8099732	1.2386216	0.2516898		
19	10429560	0.4708498	1.238127	-0.1571372	Ly6a (includes others)	lymphocyte antigen 6 complex, locus A
19	10461765	0.5092338	1.2373714	0.1299998	LPXN	leupaxin
19	10366586	0.2604464	1.2370944	-0.032477	IFNG	interferon, gamma
19	10589884	0.674914	1.2364032	0.2063814	Bcl2a1c	B-cell leukemia/lymphoma 2 related protein A1c
19	10520452	0.3085278	1.2344378	-0.016623	IL6	interleukin 6 (interferon, beta 2)
19	10574143	0.396912	1.2337408	0.091473	Nlr5	NLR family, CARD domain containing 5
19	10542911	0.8911856	1.226798	0.221653	SAMD9L	sterile alpha motif domain containing 9-like
19	10359851	0.548288	1.223848	-0.483796	UCK2	uridine-cytidine kinase 2
19	10403871	0.3765194	1.21935	0.3465268	AOAH	acyloxyacyl hydrolase (neutrophil)
19	10381445	0.4599564	1.2148456	0.2474696	TMEM106A	transmembrane protein 106A
19	10548535	0.4885794	1.2130834	-0.0444708	Klr4 (includes others)	killer cell lectin-like receptor, subfamily A, member 4
19	10338178	1.01608	1.2127464	0.1513468		
19	10339765	0.7645518	1.2113492	0.094755		
19	10450344	0.2722964	1.2109044	0.0437848	C2	complement component 2
19	10388902	1.0430218	1.206333	0.0834354	LGALS9B	lectin, galactoside-binding, soluble, 9B
19	10440393	0.2722946	1.1941854	0.0443434	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1
19	10487823	0.6965748	1.1939224	0.1820418	SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin
19	10461558	0.3451984	1.1929978	0.2245666	SLC15A3	solute carrier family 15, member 3
19	10582985	0.4341582	1.1912892	0.3020038	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
19	10402585	0.5813128	1.1908234	0.0745218	WARS	tryptophanyl-tRNA synthetase
19	10387536	0.097804	1.1906194	0.6908104	CD68	CD68 molecule
19	10343192	0.7152414	1.1902338	0.2045428		
19	10342761	0.7804614	1.1895216	0.0579658		
19	10342539	1.0484072	1.1816892	-0.1711614		
19	10435920	0.352199	1.1808902	0.2778492		
19	10338367	0.519272	1.1806316	-0.0498678		
19	10406205	0.3361118	1.1708208	0.0557072	ERAP1	endoplasmic reticulum aminopeptidase 1
19	10466130	0.4850486	1.1697002	0.007417	MS4A8B	membrane-spanning 4-domains, subfamily A, member 8B
19	10339254	0.5823024	1.1682196	0.4186956		
19	10375443	0.359144	1.1672862	0.1080574	MED7	mediator complex subunit 7
19	10545135	0.391756	1.1655688	0.0244014	IL12RB2	interleukin 12 receptor, beta 2
19	10398052	0.4181428	1.1646914	0.122733	Serpina3g (includes others)	serine (or cysteine) peptidase inhibitor, clade A, member 3G
19	10582879	0.8689342	1.1643276	0.5951274	Csprs (includes others)	component of Sp100-rs
19	10501608	0.3361964	1.1628268	0.2990952	VCAM1	vascular cell adhesion molecule 1
19	10339726	0.7792976	1.145073	-0.0004674		
19	10342216	0.5117702	1.144153	0.2796604		
19	10343134	0.5623222	1.143999	-0.0098542		
19	10340782	0.549048	1.1399344	0.4230836		
19	10445119	0.518179	1.1362588	0.2081838	H2-M3	major histocompatibility complex, class I, G
19	10340809	0.564832	1.136208	0.103614		
19	10339017	0.4761248	1.1312168	0.0982066		
19	10450069	0.7635142	1.1293436	0.2062068	H2-K2	major histocompatibility complex, class I, B
19	10421697	0.4191708	1.115433	0.2113622	Lacc1	laccase (multicopper oxidoreductase) domain containing 1
19	10461629	0.6942788	1.1130892	0.331865	Ms4a4c (includes others)	membrane-spanning 4-domains, subfamily A, member 4C
19	10340391	0.6651832	1.1085034	0.4850126		
19	10450242	0.4702188	1.1008612	0.2129744	C4B (includes others)	complement component 4B (Chido blood group)
19	10356274	0.7974278	1.0985676	0.5549746	Csprs (includes others)	component of Sp100-rs
19	10429564	0.90183	1.09786	-0.052366	Ly6a (includes others)	lymphocyte antigen 6 complex, locus A
19	10566574	0.7283606	1.0948416	0.1557008	GVIN1	GTPase, very large interferon inducible pseudogene 1
19	10343442	0.4726248	1.09018	0.1831102		
19	10366881	0.6531048	1.0875162	0.0846756	DDIT3	DNA-damage-inducible transcript 3
19	10450723	0.4209714	1.0864318	0.308931	H2-T10/H2-T22	histocompatibility 2, T region locus 10
19	10360406	0.841702	1.081448	-0.205472	Ifi204 (includes others)	interferon activated gene 204
19	10534935	0.495244	1.0788632	0.4150748	PILRB	paired immunoglobulin-like type 2 receptor beta
19	10567580	0.4745284	1.0553076	0.5345208	IGSF6	immunoglobulin superfamily, member 6
19	10338660	0.7315254	1.03689	0.4647834		
19	10340154	0.5433788	1.0345178	0.151647		
19	10382106	0.6473176	1.0337026	0.280278	Gm885	predicted gene 885
19	10341908	0.74903	1.0101088	-0.0618252		
19	10569017	0.841266	1.008492	0.097096	IFITM3	interferon induced transmembrane protein 3 (1-8U)
19	10343761	0.5782492	0.9717006	0.5957856		

19	10475414	0.882482	0.970194	0.252234	B2M	beta-2-microglobulin
19	10339990	0.7696598	0.9679708	0.043207		

Online Table 7. Gene list of cluster 20

x	Probe Set ID	Day 4	Day 7	Day 60	Symbol	Entrez Gene Name
20	10504838	0.6466026	-0.6764438	-2.052271	NR4A3	nuclear receptor subfamily 4, group A, member 3
20	10342166	0.9021222	-0.8550704	-1.6644466		
20	10343939	0.314155	0.1882482	-1.4222714		
20	10338097	0.5650608	0.5527936	-1.2691318		
20	10359867	0.606477	-0.8260516	-1.116918	LRRC52	leucine rich repeat containing 52
20	10344291	0.4266474	0.0811516	-0.9558072		
20	10457487	0.8814756	-0.1995982	-0.9044162	mir-1	microRNA 1-1
20	10529977	0.580624	-0.635134	-0.86866	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
20	10339095	0.32861	-0.3504168	-0.8404696		
20	10343420	0.1987402	-0.1892846	-0.7776266		
20	10443463	0.6108856	0.3413	-0.7749558	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
20	10529979	0.549544	-0.499744	-0.771078	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
20	10448307	0.3367444	0.531072	-0.7708702	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A
20	10341968	0.358779	-0.0575052	-0.7682682		
20	10342975	0.1286276	-0.0392738	-0.7137612		
20	10400304	0.437786	-0.01601	-0.66923	EGLN3	egl nine homolog 3 (C. elegans)
20	10583100	0.3015062	0.2588274	-0.6682986	MMP8	matrix metalloproteinase 8 (neutrophil collagenase)
20	10343228	0.1612522	-0.2218376	-0.6650314		
20	10343840	0.1762094	-0.0432734	-0.658523		
20	10339900	0.7079828	0.5340342	-0.6476118		
20	10582916	0.2449188	0.0514598	-0.6399298		
20	10343366	0.6619412	-0.4192234	-0.6398		
20	10339167	0.4555178	-0.3477428	-0.6389084		
20	10342609	0.552077	-0.1596658	-0.5920258		
20	10342933	0.6354876	-0.229319	-0.5832938		
20	10343582	0.2264012	0.1701006	-0.577129		
20	10343410	0.372617	-0.38625	-0.5760238		
20	10344571	0.4679986	-0.4765338	-0.5749398		
20	10338949	0.2009184	0.1414942	-0.5677778		
20	10340626	0.1738014	-0.0001566	-0.567402		
20	10574023	0.471064	0.425368	-0.554394	MT2A	metallothionein 2A
20	10343628	0.4820224	-0.52959	-0.5527058		
20	10340357	0.4543644	-0.309628	-0.5450722		
20	10344013	0.3851834	-0.1298612	-0.5315274		
20	10338731	0.6644404	-0.4519762	-0.531523		
20	10419966	0.1586162	-0.1106324	-0.5313798	LOC100505868/ZFXH2	zinc finger homeobox 2
20	10436100	0.1852876	0.136416	-0.5308612	RETNLB	resistin like beta
20	10340126	0.5333784	-0.599984	-0.5293894		
20	10343871	0.2381114	0.03443	-0.5227972		
20	10344419	0.1697334	-0.0888344	-0.5221626		
20	10342575	0.259648	-0.1477532	-0.5218994		
20	10342758	0.2108672	0.2106526	-0.5181104		
20	10543017	0.5463	-0.434924	-0.517146	PDK4	pyruvate dehydrogenase kinase, isozyme 4
20	10338277	0.4394526	-0.3904224	-0.5108288		
20	10414514	0.2738508	0.410077	-0.510096	PNP	purine nucleoside phosphorylase
20	10425283	0.263011	-0.1440026	-0.4981352	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)
20	10338384	1.562577	-0.6781792	-0.4977346		
20	10343057	0.5579906	0.063359	-0.4958374		
20	10339351	0.2974774	-0.107412	-0.491899		
20	10341532	0.4281916	-0.2276126	-0.4895334		
20	10340505	0.4760996	0.4413078	-0.4864232		
20	10338864	0.3702562	-0.2694676	-0.4850074		
20	10338464	0.3137844	-0.049937	-0.472538		
20	10343925	0.9744814	-0.2944796	-0.471071		
20	10344121	1.0337716	0.030855	-0.4673632		
20	10338189	0.2269412	0.1143066	-0.4661642		
20	10339712	0.4709908	-0.1682244	-0.4658618		
20	10587639	0.187552	-0.099332	-0.46563	NT5E	5'-nucleotidase, ecto (CD73)
20	10341044	0.9763624	0.2941172	-0.4642174		
20	10339398	0.2193054	0.0181552	-0.4628092		
20	10341118	0.3467926	0.041155	-0.4624514		
20	10341975	0.23731	-0.0824482	-0.4623538		
20	10338693	0.5927138	-0.0987502	-0.4585404		
20	10341107	0.2274096	-0.1342748	-0.4556472		
20	10340452	0.2701234	-0.1106524	-0.4523214		
20	10375173	0.5234528	-0.1691866	-0.4500748		
20	10341219	0.3028466	-0.3348456	-0.4416082		
20	10339580	0.6129774	-0.2412416	-0.4385158		
20	10341764	0.1703188	-0.1097836	-0.4381568		
20	10340267	0.4720832	-0.076333	-0.4381288		
20	10339555	0.5828206	-0.0510268	-0.4361538		
20	10338102	0.3505742	0.1970672	-0.4345094		
20	10338348	0.334739	0.2341354	-0.4342006		
20	10338252	0.48856104	0.1670512	-0.4326426		
20	10342797	0.8363162	0.4265398	-0.4316902		
20	10362418	0.3127912	-0.3111002	-0.4290378	TRDN	triadin
20	10343831	0.2374426	-0.0641066	-0.4287364		
20	10338199	0.4758932	-0.1411322	-0.4264754		
20	10338799	0.383455	-0.1096402	-0.4253344		
20	10342925	0.5813664	-0.0592264	-0.4242466		

20	10341067	0.2976188	-0.1810948	-0.4210958		
20	10339142	0.2285536	-0.2278086	-0.4210024		
20	10343167	0.4315168	0.0456108	-0.4162398		
20	10340649	0.6075474	0.0939018	-0.4159858		
20	10458340	0.394086	-0.120517	-0.4154666	HBEGF	heparin-binding EGF-like growth factor
20	10478283	0.4991718	0.0184522	-0.4128608	MPHOSPH6	M-phase phosphoprotein 6
20	10339994	0.5266396	-0.4158492	-0.412145		
20	10339780	0.3365926	0.2569392	-0.4098466		
20	10338989	0.6465246	-0.6638872	-0.4060278		
20	10362428	0.53231	-0.365892	-0.403662	TRDN	triadin
20	10339958	0.2094872	-0.226427	-0.4002024		
20	10342477	0.5679884	-0.0265002	-0.3959038		
20	10343406	0.5448574	-0.1319472	-0.3946708		
20	10490946	0.230758	0.176938	-0.3917798	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1
20	10344444	0.4563744	-0.3777998	-0.3909098		
20	10598018	0.6095922	-0.0297206	-0.3900832		
20	10342072	0.2141818	-0.1634178	-0.388622		
20	10517587	0.2706716	-0.114425	-0.3876294	ALPL	alkaline phosphatase, liver/bone/kidney
20	10362416	0.6518874	-0.3528262	-0.3800158	TRDN	triadin
20	10386455	0.3108338	0.1159476	-0.3794284	RASD1	RAS, dexamethasone-induced 1
20	10340629	0.430837	-0.1919464	-0.3780716		
20	10341672	0.4958586	-0.149113	-0.3780256		
20	10341906	0.3848366	0.0241032	-0.3748144		
20	10351491	0.2311638	-0.0747234	-0.3744514	OLFML2B	olfactomedin-like 2B
20	10341943	0.465354	0.1273792	-0.3735342		
20	10342481	0.2636796	-0.107209	-0.3694492		
20	10338256	0.2001066	-0.1792948	-0.3669922		
20	10340821	0.4197158	0.3292636	-0.3663652		
20	10343663	0.2495552	-0.2222516	-0.3659642		
20	10480087	0.6360562	-0.3486038	-0.3655598	Gm13310	karyopherin (importin) alpha 2 pseudogene
20	10341258	0.5104874	0.2429788	-0.3641016		
20	10341486	0.5024092	0.3532854	-0.363378		
20	10343847	0.2309142	-0.1924114	-0.3622578		
20	10546725	0.2655284	0.0011786	-0.362254	PDZRN3	PDZ domain containing ring finger 3
20	10535759	0.2798422	-0.2407582	-0.3622442	LNK2	ligand of numb-protein X 2
20	10554839	0.237164	-0.097786	-0.361844	PICALM	phosphatidylinositol binding clathrin assembly protein
20	10508887	0.504226	0.0266234	-0.3596724	NR0B2	nuclear receptor subfamily 0, group B, member 2
20	10338912	0.2287932	0.0015392	-0.3552054		
20	10497703	0.2541964	0.1987722	-0.3546882	MRPL47	mitochondrial ribosomal protein L47
20	10338263	0.980338	-0.7446428	-0.3533042		
20	10341813	0.4079336	-0.3281372	-0.3531508		
20	10362440	0.2318646	-0.148573	-0.351924	TRDN	triadin
20	10342331	0.2835282	-0.2438488	-0.3503836		
20	10339107	0.3491866	-0.3671802	-0.3488292		
20	10568521	0.2836492	0.0567514	-0.3469452	C10orf88	chromosome 10 open reading frame 88
20	10343017	0.3203094	0.199494	-0.3462		
20	10340778	0.211222	-0.1643596	-0.3452888		
20	10339909	0.3177412	-0.0916206	-0.3419212		
20	10338241	0.2566804	-0.0654764	-0.3399122		
20	10343702	0.2664206	0.1678698	-0.3395154		
20	10338756	0.2966314	-0.0715898	-0.3386224		
20	10344054	0.2399916	-0.111099	-0.3380212		
20	10338816	0.5296906	-0.5589852	-0.3338036		
20	10492598	0.3445658	0.147439	-0.3330144	NMD3	NMD3 homolog (S. cerevisiae)
20	10342142	0.529543	-0.2637208	-0.3320708		
20	10343845	0.3095974	-0.2382986	-0.3320534		
20	10558740	0.255596	0.0360934	-0.3292526		
20	10338379	0.4398998	0.0656206	-0.3281644		
20	10338133	0.3178272	-0.15564	-0.3277312		
20	10343929	0.2806872	-0.114874	-0.3276234		
20	10339952	0.2097328	-0.0276578	-0.3263398		
20	10572161	0.3246518	0.2603094	-0.3258862	ZNF440/ZNF808	zinc finger protein 440
20	10472589	0.3723498	-0.033817	-0.3257978	PHOSPHO2	phosphatase, orphan 2
20	10386622	0.3027248	-0.1168884	-0.3255366	Gm12618	predicted gene 12618
20	10343326	0.5007962	-0.058772	-0.324937		
20	10497503	0.473796	-0.198218	-0.323924	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
20	10479761	0.6120444	-0.2749928	-0.3218364	MEIG1	meiosis expressed gene 1 homolog (mouse)
20	10448212	0.2916872	0.198233	-0.321343		
20	10392284	0.47657	-0.224428	-0.3211	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
20	10342954	0.2564738	-0.1586146	-0.3207736		
20	10343538	0.31169	-0.126509	-0.3207678		
20	10453512	0.521456	-0.21619	-0.320422	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
20	10554733	0.2926772	-0.2801242	-0.3198218	Olf292 (includes others)	olfactory receptor 295
20	10556463	0.3617934	0.0626656	-0.3192186	ARNTL	aryl hydrocarbon receptor nuclear translocator-like
20	10344136	0.6177462	-0.2347244	-0.317568		
20	10343546	0.5458966	-0.1054428	-0.3169026		
20	10397541	0.4853912	0.2960084	-0.3168666	EG544883 (includes others)	predicted gene 8300
20	10505917	0.2561528	0.0375116	-0.3160828		
20	10342637	0.2651132	-0.1432048	-0.3160302		
20	10343033	0.3045594	-0.075381	-0.3148448		
20	10338975	0.4134052	-0.3140874	-0.3117558		

20	10401829	0.4341516	0.3559566	-0.3110054	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked
20	10405160	0.2677966	-0.0544282	-0.3088274		
20	10341751	0.36525	-0.3430948	-0.3050218		
20	10338078	0.226738	0.087915	-0.3042024		
20	10446617	0.252704	-0.2106294	-0.302814		
20	10561787	0.2826048	-0.026994	-0.30199	ZNF585A	zinc finger protein 585A
20	10564015	0.2123024	-0.0919588	-0.3019384		
20	10486026	0.3478704	-0.046448	-0.300158	ZNF770	zinc finger protein 770
20	10341483	0.50961	0.4178068	-0.2993896		
20	10479833	0.2091502	-0.171265	-0.2991524	OPTN	optineurin
20	10343152	0.4707652	-0.0117906	-0.2983712		
20	10341308	0.4586628	0.4238358	-0.2976106		
20	10376555	0.3884326	-0.262665	-0.2969252	COPS3	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
20	10359888	0.2475466	-0.044394	-0.2963442	Gm5265	predicted pseudogene 5265
20	10506125	0.397109	-0.199631	-0.295652	ANGPTL3	angiopoietin-like 3
20	10340000	0.2523664	-0.0949048	-0.2953142		
20	10338699	0.3521438	-0.2200492	-0.294761		
20	10338770	0.441216	0.1014248	-0.2910876		
20	10366737	0.257942	-0.0633168	-0.2906514		
20	10338113	0.7282536	-0.0818906	-0.2896872		
20	10343263	0.2260384	0.0259664	-0.2894444		
20	10595909	0.3923746	0.267524	-0.2890164		
20	10407124	0.564428	-0.2966796	-0.2867788	PDE4D	phosphodiesterase 4D, cAMP-specific
20	10510254	0.3346426	-0.0830886	-0.2864916	AU040096/Fv1	Friend virus susceptibility 1
20	10341290	0.3884472	0.3200552	-0.2848336		
20	10338795	0.39399	0.0526006	-0.2843264		
20	10341090	0.3199266	0.1323048	-0.2833218		
20	10342652	0.4845652	0.0189762	-0.2826234		
20	10353750	0.2648568	-0.0261606	-0.2806998	BAG2	BCL2-associated athanogene 2
20	10339714	0.3777556	-0.2116314	-0.2805014		
20	10343558	0.632146	0.044108	-0.280047		
20	10342256	0.4002872	-0.0240036	-0.2792786		
20	10344513	0.665013	0.4402642	-0.2779754		
20	10340334	0.6289096	-0.1060048	-0.27795		
20	10414179	0.5251626	-0.0279104	-0.2778366		
20	10404996	0.2325064	-0.03296	-0.276548	NINJ1	ninjurin 1
20	10489343	0.3075664	-0.0994946	-0.2746374	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A
20	10539015	0.4682866	-0.114757	-0.273701		
20	10342569	0.3060498	0.1482588	-0.2733694		
20	10340813	0.4497486	-0.0036072	-0.2724442		
20	10479221	0.3039088	-0.2767886	-0.270272	2010315B03Rik (includes others)	zinc finger protein 781
20	10340042	0.3276582	-0.2271098	-0.2696182		
20	10343501	0.7053814	-0.0700242	-0.2648274		
20	10340588	0.4251332	-0.0234164	-0.2647014		
20	10606436	0.3521406	-0.159795	-0.2628976	HMGNS5	high-mobility group nucleosome binding domain 5
20	10394532	0.2352676	0.0248222	-0.2624684	UBE2F	ubiquitin-conjugating enzyme E2F (putative)
20	10344397	0.9440408	-0.0594226	-0.2610256		
20	10425299	0.3154304	-0.1615668	-0.2597062	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)
20	10342715	0.2475508	0.08976	-0.2595522		
20	10374450	0.3248384	0.0399424	-0.2575436		
20	10605828	0.32769	-0.1794206	-0.2552532	1700010D01Rik (includes others)	RIKEN cDNA 1700010D01 gene
20	10598837	0.4648872	-0.0145822	-0.253024		
20	10338337	0.394141	-0.0526072	-0.2518934		
20	10339382	0.4738318	0.13854	-0.251284		
20	10340002	0.364307	-0.3007348	-0.2512508		
20	10586170	0.247895	0.0143348	-0.2509784		
20	10338604	0.487776	0.146976	-0.250478		
20	10598041	0.649572	-0.14326	-0.249606		
20	10343819	0.317844	-0.008284	-0.2495306		
20	10343273	0.6801512	-0.4329952	-0.249347		
20	10343586	0.5869242	-0.2636704	-0.248635		
20	10342246	0.6124502	0.1023462	-0.247503		
20	10338407	0.2472068	-0.092372	-0.2462408		
20	10582969	0.2653332	-0.0190964	-0.2439236		
20	10532315	0.316247	0.0510548	-0.243059	AB010352	cDNA sequence AB010352
20	10340735	0.3456258	0.1593414	-0.242604		
20	10484584	0.3267332	-0.1513266	-0.2424556		
20	10338462	0.3350362	-0.1480482	-0.2422654		
20	10548563	0.526318	-0.040072	-0.241824	EG667723/Ptp4a1	protein tyrosine phosphatase 4a1
20	10340559	0.5259034	-0.451817	-0.2416974		
20	10604656	0.252109	0.0592874	-0.2389208	Xlr (includes others)	X-linked lymphocyte-regulated complex
20	10366407	0.2508278	0.0305574	-0.2383078	Gm10752	predicted gene 10752
20	10364091	0.6105248	-0.3406658	-0.2368674		
20	10397891	0.3968864	-0.0587104	-0.2362366	C14orf109	chromosome 14 open reading frame 109
20	10344563	0.4312332	-0.2565666	-0.236055		
20	10463068	0.510622	-0.041008	-0.236034	EG667723/Ptp4a1	protein tyrosine phosphatase 4a1
20	10418002	0.396267	0.0420786	-0.233875	EG620119	H3 histone, family 3A pseudogene
20	10342605	0.3180748	-0.0805846	-0.2338394		
20	10338726	0.326642	-0.301374	-0.2335006		
20	10344582	0.2817582	-0.1855718	-0.2329368		
20	10344566	1.7022998	-0.0414816	-0.2320412		
20	10343895	0.303694	-0.0397352	-0.2317912		

20	10343551	1.1123732	-0.525175	-0.2313878		
20	10440284	0.2962486	-0.0529352	-0.231024	C3orf38	chromosome 3 open reading frame 38
20	10603254	0.2467368	-0.0565962	-0.2309192	LARP4	La ribonucleoprotein domain family, member 4
20	10340143	0.5078258	0.053435	-0.2293402		
20	10338574	0.2973928	-0.0039226	-0.2292		
20	10461671	0.271901	-0.054972	-0.2281144	PATL1	protein associated with topoisomerase II homolog 1 (yeast)
20	10346250	0.460129	-0.2501092	-0.2277082	MSTN	myostatin
20	10409259	0.2561638	-0.1095338	-0.227662		
20	10548616	0.2869606	-0.1738994	-0.2260602		
20	10442219	0.270268	-0.001999	-0.225536	Zfp52	zinc finger protein 52
20	10371830	0.533686	-0.1496332	-0.2251336	ACTR6	ARP6 actin-related protein 6 homolog (yeast)
20	10543779	0.3486996	-0.0700148	-0.2250426	mir-29	microRNA 29a
20	10338920	0.37544	-0.102884	-0.224462		
20	10399426	0.2563668	-0.045225	-0.2232704		
20	10344506	0.377921	-0.3132704	-0.2231796		
20	10339794	0.7022134	-0.47803	-0.221982		
20	10340665	0.3950986	-0.056859	-0.2214364		
20	10343240	0.2731104	-0.121437	-0.2211664		
20	10565962	0.2612216	-0.0473884	-0.2198064	P2RY2	purinergic receptor P2Y, G-protein coupled, 2
20	10469575	0.4489004	-0.08709	-0.219806	EG667723/Ptp4a1	protein tyrosine phosphatase 4a1
20	10457400	0.318034	-0.1962598	-0.2196394		
20	10338647	0.5111746	-0.190961	-0.2194612		
20	10341566	0.6362822	0.329554	-0.2183302		
20	10339808	0.6504954	0.3666534	-0.2182886		
20	10385081	0.3495016	-0.232445	-0.2181372	ANP32C	acidic (leucine-rich) nuclear phosphoprotein 32 family, member C
20	10342901	0.5488752	0.148699	-0.2167812		
20	10340147	0.5044524	-0.0143524	-0.216544		
20	10467489	0.417562	-0.095854	-0.216514	EG667723/Ptp4a1	protein tyrosine phosphatase 4a1
20	10419116	0.2479178	-0.033169	-0.2163342	1700001F09Rik	predicted gene 8207
20	10373832	0.5112614	-0.0564748	-0.215092		
20	10395198	0.35201	-0.0940894	-0.2148404		
20	10504884	0.251631	0.0197154	-0.213143	C9orf30	chromosome 9 open reading frame 30
20	10533707	0.408492	-0.10051	-0.211133	EG667723/Ptp4a1	protein tyrosine phosphatase 4a1
20	10338838	0.3582894	-0.1862962	-0.210714		
20	10342063	0.3439312	-0.115718	-0.210568		
20	10343675	0.3843236	-0.0217372	-0.2103654		
20	10342140	0.431682	0.177564	-0.209968		
20	10344589	0.3245888	-0.0161794	-0.2099448		
20	10343223	0.2661232	-0.0698268	-0.209499		
20	10340921	0.6442204	-0.1737922	-0.207783		
20	10340756	0.4530948	-0.3905794	-0.2073322		
20	10341181	0.4758146	0.0051352	-0.2053178		
20	10338386	0.6479334	-0.0755566	-0.2052294		
20	10340834	0.331538	-0.1519852	-0.2050796		
20	10344265	0.3024488	0.0080764	-0.2047568		
20	10340332	0.3009744	0.0070794	-0.204087		
20	10341368	0.2836078	-0.0826884	-0.2030754		
20	10489870	0.4866326	-0.0004382	-0.2029494	Gm11472	ribosomal protein L17 pseudogene
20	10339630	0.64187	0.3509704	-0.2020006		
20	10426827	0.343527	-0.0979552	-0.2004002	LARP4	La ribonucleoprotein domain family, member 4
20	10442057	0.3515622	0.1166926	-0.1996802	RIOK2	RIO kinase 2 (yeast)
20	10344553	0.4116396	-0.083162	-0.1992284		
20	10405911	0.356437	-0.2154884	-0.197982	Zfp595/Zfp759	zinc finger protein 759
20	10342315	0.5383944	0.2053484	-0.1970136		
20	10342682	0.6011086	0.240776	-0.1963092		
20	10408008	0.3704206	-0.0893206	-0.1961144		
20	10339819	0.2689412	-0.03096	-0.1945246		
20	10339523	0.628278	0.064476	-0.191138		
20	10454543	0.2632724	-0.0131296	-0.189973		
20	10338935	0.5625414	-0.3714554	-0.1896158		
20	10338110	0.5843548	-0.1036262	-0.189376		
20	10340984	0.5107782	0.0501608	-0.1876676		
20	10481111	0.4071512	0.1608202	-0.1861356		
20	10604842	0.437677	0.082548	-0.1845662		
20	10608709	0.3662556	-0.0380956	-0.1843648		
20	10362434	0.386882	-0.234366	-0.183384	TRDN	triadin
20	10503180	0.3411832	-0.212259	-0.182661	CHD7	chromodomain helicase DNA binding protein 7
20	10531887	0.4279476	0.2101506	-0.1825986	SLC10A6	solute carrier family 10 (sodium/bile acid cotransporter family), member 6
20	10341553	0.272189	0.009042	-0.1822324		
20	10510191	0.8052642	0.1337214	-0.1821594	ZNF600/ZNF888	zinc finger protein 600
20	10496621	0.3214902	-0.0466086	-0.181638	GTF2B	general transcription factor IIB
20	10340155	0.704931	-0.379694	-0.18152		
20	10340187	0.5637264	-0.0756206	-0.177712		
20	10427718	0.4464534	0.1101344	-0.1774128	BRX1	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)
20	10424335	0.2650014	-0.026686	-0.177356	RNF139	ring finger protein 139
20	10532157	0.4233972	-0.1233208	-0.1773106	TMED5	transmembrane emp24 protein transport domain containing 5
20	10412607	0.2990356	-0.1969768	-0.1772468	ABHD6	abhydrolase domain containing 6
20	10384579	0.33005	-0.088416	-0.17675	UGP2	UDP-glucose pyrophosphorylase 2
20	10564448	0.315868	0.0492062	-0.1760754	ASB7	ankyrin repeat and SOCS box containing 7
20	10375893	0.286024	-0.169912	-0.174676	SAR1B	SAR1 homolog B (S. cerevisiae)
20	10547858	0.489723	-0.1406042	-0.1729604	GNB3	guanine nucleotide binding protein (G protein), beta polypeptide 3

20	10338964	0.5116012	-0.2699386	-0.1727404		
20	10338443	0.3419726	-0.0455902	-0.172658		
20	10586484	0.477402	-0.141504	-0.171782	FAM96A	family with sequence similarity 96, member A
20	10339526	0.3908352	-0.294585	-0.1693396		
20	10351430	0.446162	0.116796	-0.169288	RXRG	retinoid X receptor, gamma
20	10560089	0.3365618	-0.2127626	-0.1688942	Vmn1r86	vomeronal 1 receptor 86
20	10540544	0.445642	0.2031182	-0.1683276	THUMPD3	THUMP domain containing 3
20	10552118	0.5541726	-0.2718264	-0.1679856	Gm12755	predicted gene 12755
20	10589087	0.296672	-0.1448874	-0.1679338	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha
20	10341266	0.3106046	-0.0162336	-0.1667396		
20	10344026	0.4488932	-0.3766104	-0.166661		
20	10344208	0.3668412	-0.0422856	-0.1655322		
20	10339232	0.3956608	0.1401024	-0.1653		
20	10529730	0.3330946	-0.0648652	-0.165062		
20	10594186	0.2788388	-0.0697086	-0.164956		
20	10493086	0.3579562	-0.0752234	-0.1643782	HDGF	hepatoma-derived growth factor
20	10373355	0.335262	-0.0140498	-0.1629598	SPRYD4	SPRY domain containing 4
20	10416791	0.3449834	-0.107756	-0.1624826		
20	10490302	0.5885336	-0.324808	-0.1619158	ZNF844	zinc finger protein 844
20	10338870	0.4663534	0.0461542	-0.161914		
20	10436046	0.3651512	-0.0060084	-0.1615962		
20	10340116	0.4728642	-0.1623046	-0.1607372		
20	10341981	0.6197348	0.3130374	-0.1607192		
20	10342794	0.2735846	-0.107767	-0.1599756		
20	10578155	0.3268254	-0.1905038	-0.1588396		
20	10351259	0.2846822	-0.0805408	-0.1586188	SLC19A2	solute carrier family 19 (thiamine transporter), member 2
20	10415784	0.5427994	-0.1498442	-0.1579394	TRIM13	tripartite motif containing 13
20	10342484	0.6037316	0.1926258	-0.1578374		
20	10342994	0.5057786	-0.3300474	-0.1575352		
20	10512061	0.3318592	-0.074238	-0.1561212	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa
20	10448030	0.439968	0.0826306	-0.1547432		
20	10505532	0.3598238	0.0534804	-0.1545564		
20	10565341	0.432667	-0.1064054	-0.154162	Gm6155	predicted pseudogene 6155
20	10428066	0.463638	0.1211974	-0.1539634	1700084J12Rik	RIKEN cDNA 1700084J12 gene
20	10578763	0.5785008	0.2280154	-0.1532012	SAP30	Sin3A-associated protein, 30kDa
20	10338205	0.368721	-0.0835972	-0.1528422		
20	10460114	0.3133202	-0.022919	-0.1517882		
20	10458245	0.4079354	-0.0393346	-0.1504936		
20	10338514	0.817792	-0.25683	-0.15032		
20	10339122	0.4513984	0.0768154	-0.1502898		
20	10476941	0.3301932	-0.0286262	-0.1481326		
20	10362939	0.3512334	-0.162687	-0.1472706	EG215974	glyceraldehyde-3-phosphate dehydrogenase pseudogene
20	10338076	0.4625404	-0.2332684	-0.1470302		
20	10344160	0.48324	0.278914	-0.146742		
20	10392259	0.437614	-0.1966554	-0.1466318	SMURF2	SMAD specific E3 ubiquitin protein ligase 2
20	10564567	0.289396	-0.1234958	-0.1452768		
20	10598081	0.676514	-0.4412286	-0.1446956		
20	10340099	0.411182	0.0379058	-0.1443744		
20	10338088	0.332159	0.0363044	-0.1439792		
20	10484720	0.2896198	-0.0313542	-0.1432822	Olf1166	olfactory receptor 1166
20	10342593	0.6859476	-0.4213654	-0.1431742		
20	10583376	0.3241384	-0.1140238	-0.1428612	Olf1829	olfactory receptor 829
20	10341051	0.8256572	0.111041	-0.1425394		
20	10427603	0.2961026	-0.0359052	-0.1393286		
20	10341982	0.4710402	-0.1775274	-0.1377452		
20	10362432	0.408006	-0.135282	-0.137314	TRDN	triadin
20	10579047	0.4332096	-0.1116074	-0.1368314	LZTS1	leucine zipper, putative tumor suppressor 1
20	10574595	0.3144558	-0.1199104	-0.1365442		
20	10340680	0.5429532	-0.0747878	-0.1351196		
20	10343481	0.5149364	-0.1399546	-0.1343692		
20	10340752	0.511668	0.1071522	-0.1340268		
20	10565514	0.326048	-0.18798	-0.1326666	TMEM126A	transmembrane protein 126A
20	10598062	0.7708504	-0.2339634	-0.1322978		
20	10344252	0.332487	-0.2113676	-0.1302538		
20	10439634	0.34333	-0.0418246	-0.129813	GTPBP8	GTP-binding protein 8 (putative)
20	10468275	0.4533306	0.2081274	-0.1296886	PCGF6	polycomb group ring finger 6
20	10338120	0.439432	0.085132	-0.12876		
20	10339394	0.3739452	0.0351744	-0.1287392		
20	10341179	0.639894	-0.3670022	-0.1284212		
20	10473592	0.303059	-0.0347958	-0.1281328	Olf1183	olfactory receptor 1183
20	10343633	0.4393228	0.0870318	-0.1274854		
20	10343080	0.4145872	0.0606494	-0.126826		
20	10474477	0.3379834	-0.1013642	-0.1255444		
20	10355996	0.324212	-0.066718	-0.125184	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
20	10340586	0.5570352	0.099532	-0.1247026		
20	10420503	0.6233122	0.3045638	-0.1240812	SETDB2	SET domain, bifurcated 2
20	10450904	0.6512008	-0.1975366	-0.1238382	SCOC	short coiled-coil protein
20	10339705	0.4561256	0.052212	-0.1232954		
20	10552260	0.3187918	-0.1002628	-0.1226174		
20	10345174	0.3114848	-0.1438432	-0.1175596	Gm9884	predicted gene 9884
20	10572613	0.378118	-0.034932	-0.117492	MRPL34	mitochondrial ribosomal protein L34
20	10354732	0.4018124	-0.195804	-0.117076	HSPD1	heat shock 60kDa protein 1 (chaperonin)

20	10381345	0.3581856	-0.00755	-0.116478	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
20	10355452	0.4480898	-0.1694406	-0.1157968		
20	10528691	0.5019378	-0.135054	-0.115794	Rheb (mouse)	Ras homolog enriched in brain
20	10583347	0.3930876	0.0196402	-0.115688	CHORDC1	cysteine and histidine-rich domain (CHORD) containing 1
20	10339757	0.6614656	-0.1151198	-0.1154322		
20	10342486	0.383622	-0.206866	-0.115226		
20	10342763	0.370554	-0.025328	-0.115128		
20	10605552	0.3420016	-0.083252	-0.1148512		
20	10368739	0.3311324	0.0012366	-0.1146298	GTF3C6	general transcription factor IIIC, polypeptide 6, alpha 35kDa
20	10343509	0.4224812	0.0041972	-0.1128628		
20	10379627	0.3923338	-0.1686	-0.1118916		
20	10600588	0.4549734	-0.1500438	-0.1116676		
20	10369890	0.3422736	-0.163334	-0.1097722	CISD1	CDGSH iron sulfur domain 1
20	10340032	0.8241944	0.4563344	-0.1077386		
20	10339101	0.5539822	-0.078086	-0.10691		
20	10518679	0.5057334	-0.1409794	-0.1057906	NMNAT1	nicotinamide nucleotide adenylyltransferase 1
20	10535623	0.3988052	0.0037796	-0.1057822	1700001J03Rik (includes others)	RIKEN cDNA 1700123K08 gene
20	10342860	0.411124	-0.061116	-0.10526		
20	10369604	0.423583	-0.1665968	-0.1052346	VPS26A	vacuolar protein sorting 26 homolog A (S. pombe)
20	10341819	0.424844	-0.2266818	-0.1049486		
20	10344118	0.3174466	-0.0596546	-0.1034402		
20	10457927	0.6362774	-0.0124284	-0.1022158		
20	10342960	0.4785154	-0.2215686	-0.101964		
20	10339881	0.7222704	-0.0124696	-0.1004908		
20	10503176	0.325241	-0.0981758	-0.1001332	CHD7	chromodomain helicase DNA binding protein 7
20	10475405	0.3805114	-0.118998	-0.097606	EIF3J	eukaryotic translation initiation factor 3, subunit J
20	10339110	0.4048998	0.0436752	-0.0964794		
20	10338085	0.4394274	-0.04336	-0.0949726		
20	10503172	0.4802296	-0.2222028	-0.0926554	CHD7	chromodomain helicase DNA binding protein 7
20	10341569	0.6243144	0.0504196	-0.091793		
20	10340607	0.395543	0.0401196	-0.09132		
20	10587746	0.3757024	-0.01927	-0.091072	TMEM41B	transmembrane protein 41B
20	10339913	0.3579364	-0.0750344	-0.0904062		
20	10354418	0.3484304	-0.0598606	-0.0864406	OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A
20	10342350	0.557064	-0.1862	-0.0860212		
20	10344114	0.4212298	0.064964	-0.0848634		
20	10342646	0.6016912	0.104009	-0.083795		
20	10374793	0.6811498	0.4103276	-0.0836438	PNPT1	polyribonucleotide nucleotidyltransferase 1
20	10339698	0.6993828	-0.2716138	-0.0833668		
20	10361790	0.425616	0.02688	-0.080446	FUCA2	fucosidase, alpha-L- 2, plasma
20	10511865	0.40034	0.01834	-0.079754	PTGES3	prostaglandin E synthase 3 (cytosolic)
20	10482323	0.466557	-0.1702808	-0.0781854	PPP6C	protein phosphatase 6, catalytic subunit
20	10539649	0.3814502	0.002222	-0.075546	PTGES3	prostaglandin E synthase 3 (cytosolic)
20	10340558	0.5843748	0.1657176	-0.0751892		
20	10485811	0.3726266	-0.014166	-0.0745212	OlfR1313	olfactory receptor 1313
20	10482073	0.3703906	-0.0907354	-0.074358		
20	10456904	0.4835962	-0.1025052	-0.0722584	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2
20	10339251	0.355416	-0.036472	-0.071092		
20	10339471	0.4594668	0.011628	-0.069144		
20	10424347	0.4809562	0.0939558	-0.06528	Gm7691	ribosomal protein L17 pseudogene
20	10340870	0.6448888	0.1668276	-0.0647374		
20	10341369	0.678152	-0.13765	-0.063558		
20	10340875	0.4267644	0.022312	-0.0611472		
20	10608710	0.5257508	0.1081174	-0.0584548		
20	10385466	0.390633	-0.0190428	-0.049913	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)
20	10341729	0.5369276	0.1953082	-0.0439568		
20	10340828	0.5882534	0.0167084	-0.0371442		
20	10532989	0.5041298	0.0390602	-0.036244	GATC	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)
20	10342828	0.55565	-0.115256	-0.031172		
20	10438690	0.4602944	0.0027208	-0.0282524	RFC4	replication factor C (activator 1) 4, 37kDa
20	10343385	1.1086562	0.4540988	-0.0146048		
20	10344301	1.0129848	0.5253624	-0.0119822		
20	10400395	0.501193	0.0827344	-0.0014052	PPP2R3C	protein phosphatase 2, regulatory subunit B", gamma
20	10446771	0.505998	0.02285	0.003388	LCLAT1	lysocardiolipin acyltransferase 1
20	10447349	0.6428122	0.014972	0.009698	CRIP1	cysteine-rich PDZ-binding protein
20	10343047	0.8830632	0.3467506	0.012497		
20	10343995	0.6400986	0.060398	0.0532252		
20	10343324	0.6063256	0.0454408	0.0540828		
20	10601326	0.653302	0.0937466	0.055639	UPRT	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)
20	10338710	0.7532364	0.0567162	0.0565778		
20	10598064	1.0858592	-0.130216	0.0733384		
20	10340048	0.6877526	0.0690378	0.0796044		
20	10601328	0.9130072	0.1088154	0.094026	UPRT	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)
20	10342604	0.9727096	0.037674	0.133467		
20	10341030	0.8904632	0.156412	0.1347218		

Online Table 8. List of differentially expressed genes on 4 dpi (log ratio > 1 or < -1, P value < 0.05)

Probe Set ID	4 dpi		7 dpi		60 dpi		Symbol	Entrez Gene Name
	Log ratio	P values (t-test)	Log ratio	P values (t-test)	Log ratio	P values (t-test)		
10455970	6.6	0.00	6.8	0.00	2.8	0.00		
10608681	5.1	0.00	6.3	0.00	1.4	0.00	Gm4841	predicted gene 4841
10569102	4.1	0.00	4.6	0.00	0.1	0.72	IRF7	interferon regulatory factor 7
10462621	4.1	0.00	4.2	0.00	0.7	0.03	IFIT3	interferon-induced protein with tetratricopeptide repeats 3
10459066	3.9	0.00	6.3	0.00	1.0	0.00	Gm4841	predicted gene 4841
10376324	3.8	0.00	5.4	0.00	1.0	0.00	Gm12250	predicted gene 12250
10462623	3.7	0.00	3.8	0.00	0.4	0.18	IFIT1B	interferon-induced protein with tetratricopeptide repeats 1B
10462618	3.7	0.00	4.0	0.00	0.6	0.03	IFIT3	interferon-induced protein with tetratricopeptide repeats 3
10502791	3.4	0.00	3.7	0.00	0.6	0.02	IFI44	interferon-induced protein 44
10376326	3.4	0.00	4.9	0.00	0.7	0.01		
10455961	3.3	0.00	4.3	0.00	1.1	0.00	Iigp1	interferon inducible GTPase 1
10541307	3.2	0.00	3.5	0.00	0.2	0.15	USP18	ubiquitin specific peptidase 18
10462613	3.2	0.00	3.7	0.00	0.3	0.05	IFIT2	interferon-induced protein with tetratricopeptide repeats 2
10399710	3.0	0.00	2.9	0.00	0.3	0.13	RSAD2	radical S-adenosyl methionine domain containing 2
10531407	2.9	0.00	4.9	0.00	1.0	0.00	CXCL9	chemokine (C-X-C motif) ligand 9
10455954	2.8	0.00	3.9	0.00	0.6	0.03	Gm4951	predicted gene 4951
10461594	2.8	0.00	4.0	0.00	0.0	0.91	Ms4a4b (includes others)	membrane-spanning 4-domains, subfamily A, member 4B
10420308	2.7	0.00	5.1	0.00	0.1	0.44	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
10385500	2.6	0.00	4.3	0.00	0.4	0.06	IRGM	immunity-related GTPase family, M
10385507	2.5	0.00	5.3	0.00	0.3	0.02	9930111J21Rik1/Gm12185	predicted gene 12185
10462390	2.5	0.00	4.1	0.00	0.4	0.08	CD274	CD274 molecule
10608646	2.4	0.00	3.4	0.00	0.8	0.00		
10385533	2.4	0.00	3.9	0.00	0.6	0.04	9930111J21Rik1/Gm12185	predicted gene 12185
10496580	2.3	0.00	3.5	0.00	0.3	0.02	GBP4	guanylate binding protein 4
10385518	2.3	0.00	3.8	0.00	0.7	0.03	Tgtp1/Tgtp2	T cell specific GTPase 1
10420488	2.3	0.00	2.8	0.00	0.2	0.44	PHF11	PHD finger protein 11
10502801	2.3	0.00	2.9	0.00	0.3	0.21	IFI44L	interferon-induced protein 44-like
10531724	2.3	0.00	3.8	0.00	0.7	0.00	PLAC8	placenta-specific 8
10351873	2.3	0.00	3.2	0.00	0.2	0.09	Ifi204 (includes others)	interferon activated gene 204
10531415	2.2	0.00	3.4	0.00	0.3	0.05	CXCL10	chemokine (C-X-C motif) ligand 10
10420483	2.2	0.00	3.1	0.00	0.2	0.14	Phf11a/Phf11b	PHD finger protein 11A
10437224	2.1	0.00	2.2	0.00	0.1	0.44	Mx1/Mx2	myxovirus (influenza virus) resistance 1
10351880	2.1	0.00	2.4	0.00	0.2	0.24	Pydc3/Pydc4	pyrin domain containing 4
10455957	2.1	0.00	3.3	0.00	0.5	0.06		
10389207	2.0	0.00	3.5	0.00	0.2	0.02	CCL5	chemokine (C-C motif) ligand 5
10531994	2.0	0.00	3.2	0.00	0.2	0.26		
10434778	2.0	0.00	2.6	0.00	0.2	0.51	RTP4	receptor (chemosensory) transporter protein 4
10574145	1.9	0.00	3.3	0.00	0.4	0.01	NLRC5	NLR family, CARD domain containing 5
10524621	1.9	0.00	2.6	0.00	0.2	0.23	Oas12	2'-5' oligoadenylate synthetase-like 2
10395039	1.9	0.00	1.5	0.00	0.2	0.25	CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
10441233	1.9	0.00	2.2	0.00	0.1	0.25	Mx1/Mx2	myxovirus (influenza virus) resistance 1
10496569	1.9	0.00	3.0	0.00	0.5	0.03	GBP7	guanylate binding protein 7
10379518	1.9	0.00	3.3	0.00	-0.1	0.70	CCL7	chemokine (C-C motif) ligand 7
10379636	1.8	0.00	3.0	0.00	0.0	0.80	SLFN12L	schlafen family member 12-like
10496555	1.8	0.00	3.7	0.00	0.4	0.09	GBP2	guanylate binding protein 2, interferon-inducible
10379511	1.8	0.00	3.3	0.00	-0.1	0.43	Ccl2	chemokine (C-C motif) ligand 2
10571984	1.8	0.00	2.4	0.00	0.4	0.05	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
10574149	1.8	0.00	3.1	0.00	0.5	0.00	NLRC5	NLR family, CARD domain containing 5
10532019	1.8	0.00	3.5	0.00	0.2	0.15	Gbp6 (includes others)	guanylate binding protein 6
10531987	1.8	0.00	3.2	0.00	0.4	0.09	Gbp6 (includes others)	guanylate binding protein 6
10496592	1.8	0.00	3.3	0.00	0.5	0.05		
10393573	1.7	0.00	2.4	0.00	0.2	0.47	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein
10346191	1.7	0.00	3.0	0.00	0.4	0.00	STAT1	signal transducer and activator of transcription 1, 91kDa
10378068	1.7	0.00	2.3	0.00	0.2	0.07	XAF1	XIAP associated factor 1
10360398	1.7	0.00	2.1	0.00	0.1	0.34	Ifi202b	interferon activated gene 202B
10566366	1.7	0.00	2.3	0.00	-0.1	0.80	Trim30a/Trim30d	tripartite motif-containing 30A
10533246	1.7	0.00	2.5	0.00	0.3	0.20	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa
10490150	1.7	0.00	3.1	0.00	0.2	0.07	ZBP1	Z-DNA binding protein 1
10538590	1.7	0.00	2.7	0.00	0.3	0.14	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
10344566	1.7	0.01	0.0	0.93	-0.2	0.58		
10574098	1.7	0.00	2.7	0.00	0.5	0.00	NLRC5	NLR family, CARD domain containing 5
10450075	1.7	0.00	2.7	0.00	0.7	0.00	HLA-B	major histocompatibility complex,

10450325	1.7	0.00	3.3	0.00	0.7	0.00	CFB	class I, B
10444814	1.6	0.00	2.7	0.00	0.7	0.00	HLA-B	complement factor B major histocompatibility complex, class I, B
10524631	1.6	0.00	1.5	0.00	0.0	0.92	OASL	2'-5'-oligoadenylate synthetase-like
10439009	1.6	0.00	1.9	0.00	0.3	0.16	APOD	apolipoprotein D
10563597	1.6	0.00	2.7	0.00	-0.2	0.23	Saa3	serum amyloid A 3
10391207	1.6	0.00	2.1	0.00	0.2	0.25	DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58
10496539	1.6	0.00	2.6	0.00	0.5	0.01	GBP5	guanylate binding protein 5
10338384	1.6	0.02	-0.7	0.24	-0.5	0.21		
10398075	1.5	0.00	2.3	0.00	0.9	0.01	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
10375515	1.5	0.00	3.0	0.00	0.2	0.02		
10452980	1.5	0.00	1.7	0.00	0.1	0.52	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2
10574102	1.5	0.00	2.3	0.00	0.4	0.01	NLRC5	NLR family, CARD domain containing 5
10439249	1.5	0.00	2.6	0.00	0.3	0.06	PARP14	poly (ADP-ribose) polymerase family, member 14
10360370	1.5	0.00	2.2	0.00	0.0	0.85	Ifi204 (includes others)	interferon activated gene 204
10512470	1.5	0.00	2.7	0.00	0.9	0.00	CD72	CD72 molecule
10383206	1.5	0.00	1.9	0.00	0.2	0.40		
10512067	1.5	0.00	1.9	0.00	0.2	0.27	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
10566358	1.5	0.00	2.3	0.00	0.3	0.07	Trim30a/Trim30d	tripartite motif-containing 30A
10547740	1.4	0.04	0.2	0.86	1.7	0.04	C1S	complement component 1, s subcomponent
10483110	1.4	0.00	2.1	0.00	0.2	0.12	IFIH1	interferon induced with helicase C domain 1
10360373	1.4	0.00	1.6	0.00	0.3	0.07	Pydc3/Pydc4	pyrin domain containing 4
10531980	1.4	0.00	2.8	0.00	0.4	0.03	Gbp6 (includes others)	guanylate binding protein 6
10439268	1.4	0.00	2.0	0.00	0.3	0.07	DTX3L	deltex 3-like (Drosophila)
10444244	1.4	0.00	2.8	0.00	0.3	0.01	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
10531420	1.4	0.00	2.8	0.00	0.1	0.28	Cxcl11	chemokine (C-X-C motif) ligand 11
10383198	1.4	0.00	2.0	0.00	0.2	0.28		
10574135	1.4	0.00	2.8	0.00	0.4	0.03	NLRC5	NLR family, CARD domain containing 5
10379633	1.4	0.00	2.6	0.00	0.0	0.98	S1fn1	schlafen 1
10385504	1.3	0.00	1.9	0.00	0.1	0.67	Gm5431	predicted gene 5431
10574104	1.3	0.00	2.5	0.00	0.4	0.00	NLRC5	NLR family, CARD domain containing 5
10466210	1.3	0.00	1.9	0.00	-0.2	0.25	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
10552406	1.3	0.00	4.0	0.00	0.2	0.05	NKG7	natural killer cell group 7 sequence
10412211	1.3	0.00	2.7	0.00	0.0	0.64	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
10574157	1.3	0.00	2.4	0.00	0.2	0.06	NLRC5	NLR family, CARD domain containing 5
10450675	1.3	0.00	1.9	0.00	0.3	0.06	H2-T24	histocompatibility 2, T region locus 24
10450694	1.3	0.00	2.5	0.00	0.6	0.00	H2-T22	histocompatibility 2, T region locus 22
10383212	1.3	0.00	2.0	0.00	0.1	0.08	Rnf213	ring finger protein 213
10383208	1.3	0.00	1.9	0.00	0.1	0.52		
10383200	1.3	0.00	2.0	0.00	0.2	0.26		
10525158	1.3	0.00	1.6	0.00	0.0	0.92	Oas1b	2'-5'-oligoadenylate synthetase 1B
10574139	1.3	0.00	2.5	0.00	0.4	0.00	NLRC5	NLR family, CARD domain containing 5
10533198	1.3	0.00	1.6	0.00	0.3	0.11	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
10554240	1.3	0.00	1.7	0.00	0.1	0.17	ISG20	interferon stimulated exonuclease gene 20kDa
10473356	1.2	0.00	2.0	0.00	0.2	0.16	UBE2L6	ubiquitin-conjugating enzyme E2L 6
10383214	1.2	0.00	1.9	0.00	0.2	0.15	Rnf213	ring finger protein 213
10389231	1.2	0.00	2.7	0.00	0.5	0.20	CCL3L1/CCL3L3	chemokine (C-C motif) ligand 3-like 1
10383196	1.2	0.00	1.8	0.00	0.1	0.40	Rnf213	ring finger protein 213
10444258	1.2	0.00	3.1	0.00	0.3	0.00	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8
10383168	1.2	0.00	1.9	0.00	0.2	0.04		
10608650	1.2	0.00	2.4	0.00	0.5	0.00		
10383152	1.2	0.00	1.8	0.00	0.2	0.18	Rnf213	ring finger protein 213
10544133	1.2	0.00	1.9	0.00	0.2	0.10	PARP12	poly (ADP-ribose) polymerase family, member 12
10383202	1.2	0.00	2.0	0.00	0.2	0.11	Rnf213	ring finger protein 213
10415319	1.2	0.00	1.4	0.00	0.2	0.15	IRF9	interferon regulatory factor 9
10450682	1.2	0.00	2.3	0.00	0.5	0.00	HLA-E	major histocompatibility complex, class I, E
10444821	1.2	0.00	1.9	0.00	0.3	0.02	H2-Q5	histocompatibility 2, Q region locus 5
10451287	1.2	0.00	1.9	0.00	0.1	0.54		
10359181	1.2	0.00	1.3	0.00	0.3	0.03	TOR3A	torsin family 3, member A
10450699	1.2	0.00	2.0	0.00	0.5	0.00	HLA-F	major histocompatibility complex, class I, F
10402347	1.2	0.00	1.7	0.00	-0.1	0.44	IFI27L2	interferon, alpha-inducible protein 27- like 2

10347928	1.2	0.00	1.9	0.00	0.3	0.13	SP110	SP110 nuclear body protein
10582874	1.2	0.00	1.9	0.00	0.3	0.13	SP110	SP110 nuclear body protein
10383233	1.1	0.00	1.7	0.00	0.1	0.33	Rnf213	ring finger protein 213
10383210	1.1	0.00	1.6	0.00	0.0	0.92	Rnf213	ring finger protein 213
10351509	1.1	0.00	3.2	0.00	0.6	0.01	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)
10383204	1.1	0.00	1.9	0.00	0.2	0.12	Rnf213	ring finger protein 213
10398039	1.1	0.00	3.1	0.00	0.3	0.02		
10367224	1.1	0.00	1.7	0.00	0.1	0.48	STAT2	signal transducer and activator of transcription 2, 113kDa
10347915	1.1	0.00	1.4	0.00	0.5	0.02	Csprs (includes others)	component of Sp100-rs
10360382	1.1	0.00	1.5	0.00	-0.1	0.38	Ifi204 (includes others)	interferon activated gene 204
10590635	1.1	0.00	3.1	0.00	0.5	0.03	CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene)
10598013	1.1	0.00	3.1	0.00	0.5	0.03	CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene)
10578493	1.1	0.00	1.5	0.00	0.1	0.39	TLR3	toll-like receptor 3
10598976	1.1	0.01	3.3	0.00	0.2	0.48	TIMP1	TIMP metalloproteinase inhibitor 1
10383194	1.1	0.01	1.5	0.00	0.1	0.70	Rnf213	ring finger protein 213
10598064	1.1	0.04	-0.1	0.71	0.1	0.86		
10566144	1.1	0.00	1.8	0.00	0.0	0.72	TRIM21	tripartite motif containing 21
10360173	1.1	0.00	2.7	0.00	0.5	0.01	SLAMF7	SLAM family member 7
10424676	1.1	0.00	1.6	0.00	0.1	0.52	LY6E	lymphocyte antigen 6 complex, locus E
10545672	1.1	0.00	2.0	0.00	-0.2	0.02	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methylenetetrahydrofolate cyclohydrolase
10608680	1.1	0.00	2.1	0.00	0.5	0.00	H2-T22	histocompatibility 2, T region locus 22
10347925	1.1	0.00	1.4	0.00	0.6	0.02	Csprs (includes others)	component of Sp100-rs
10466314	1.1	0.00	1.7	0.00	0.0	0.67		
10582997	1.1	0.00	2.0	0.00	0.3	0.09	CASP4	caspase 4, apoptosis-related cysteine peptidase
10383192	1.0	0.00	1.5	0.00	-0.1	0.56		
10388902	1.0	0.00	1.2	0.00	0.1	0.24	LGALS9	lectin, galactoside-binding, soluble, 9
10500335	1.0	0.00	2.2	0.00	0.1	0.31	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)
10566578	1.0	0.00	1.4	0.00	0.2	0.19	Gm8979	very large inducible GTPase 1 pseudogene
10344121	1.0	0.01	0.0	0.94	-0.5	0.44		
10397975	1.0	0.00	1.7	0.00	0.4	0.00	IFI27	interferon, alpha-inducible protein 27
10517165	1.0	0.00	3.0	0.00	1.0	0.00	Cd52	CD52 antigen
10338178	1.0	0.00	1.2	0.00	0.2	0.61		
10344301	1.0	0.04	0.5	0.24	0.0	0.98		
10491091	1.0	0.01	1.5	0.00	0.5	0.06	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
10534909	1.0	0.00	1.8	0.00	0.3	0.02	SP110	SP110 nuclear body protein
10467136	1.0	0.00	2.3	0.00	0.1	0.56	CH25H	cholesterol 25-hydroxylase
10566571	1.0	0.00	1.3	0.00	0.2	0.17		
10341044	1.0	0.02	0.3	0.55	-0.5	0.48		
10581378	1.0	0.00	2.7	0.00	0.2	0.01	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10
10531972	1.0	0.00	2.7	0.00	0.2	0.18	Gbp8	guanylate-binding protein 8
10343925	1.0	0.03	-0.3	0.46	-0.5	0.14		
10579532	1.0	0.00	1.7	0.00	0.0	0.89	BST2	bone marrow stromal cell antigen 2
10340164	1.0	0.01	1.3	0.00	0.1	0.72		
10406928	1.0	0.00	2.8	0.00	0.9	0.01	CD180	CD180 molecule
10360070	1.0	0.00	1.7	0.00	0.5	0.01	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
10461614	1.0	0.00	1.4	0.00	-0.2	0.22	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C
10533213	1.0	0.00	1.7	0.00	0.0	0.84	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa
10584047	-1.0	0.03	-0.5	0.08	-0.3	0.18	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif, 8
10340043	-1.0	0.03	-0.3	0.37	0.0	0.90		
10585390	-1.0	0.00	-0.2	0.45	-0.2	0.72	Sln	sarcophilin
10463551	-1.0	0.02	-0.8	0.37	-0.4	0.25	ELOVL3	ELOVL fatty acid elongase 3
10558673	-1.0	0.01	-0.5	0.32	-0.1	0.87	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1
10490913	-1.0	0.04	-0.4	0.56	-0.6	0.10	CA3	carbonic anhydrase III, muscle specific
10581605	-1.0	0.00	0.0	0.94	0.0	0.88	HP	haptoglobin
10340401	-1.1	0.00	-0.2	0.52	0.2	0.65		
10341006	-1.2	0.01	0.6	0.28	0.8	0.11		
10438801	-1.3	0.03	-0.7	0.34	-0.3	0.74	FGF12	fibroblast growth factor 12
10343452	-1.4	0.02	0.4	0.31	0.5	0.51		
10438813	-1.5	0.02	-0.3	0.67	-0.3	0.70	Mir690	microRNA 690
10495306	-1.5	0.04	-0.8	0.38	-0.2	0.83	MYBPHL	myosin binding protein H-like
10384044	-1.5	0.05	-1.1	0.35	-0.3	0.74	MYL7	myosin, light chain 7, regulatory
10559698	-1.6	0.01	-0.5	0.42	0.2	0.80	SGK110	putative uncharacterized serine/threonine-protein kinase SgK110-like

Online Table 9. List of differentially expressed genes on 7 dpi (log ratio > 1 or < -1, P value < 0.05)

Probe Set ID	4 dpi		7 dpi		60 dpi		Symbol	Entrez Gene Name
	Log ratio	P values (t-test)	Log ratio	P values (t-test)	Log ratio	P values (t-test)		
10455970	6.6	0.00	6.8	0.00	2.8	0.00		
10459066	3.9	0.00	6.3	0.00	1.0	0.00	Gm4841	predicted gene 4841
10608681	5.1	0.00	6.3	0.00	1.4	0.00	Gm4841	predicted gene 4841
10376324	3.8	0.00	5.4	0.00	1.0	0.00	Gm12250	predicted gene 12250
10385507	2.5	0.00	5.3	0.00	0.3	0.02	9930111J21Rik1/Gm12185	predicted gene 12185
10420308	2.7	0.00	5.1	0.00	0.1	0.44	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
10531407	2.9	0.00	4.9	0.00	1.0	0.00	CXCL9	chemokine (C-X-C motif) ligand 9
10376326	3.4	0.00	4.9	0.00	0.7	0.01		
10569102	4.1	0.00	4.6	0.00	0.1	0.72	IRF7	interferon regulatory factor 7
10385500	2.6	0.00	4.3	0.00	0.4	0.06	IRGM	immunity-related GTPase family, M
10455961	3.3	0.00	4.3	0.00	1.1	0.00	Iigp1	interferon inducible GTPase 1
10462621	4.1	0.00	4.2	0.00	0.7	0.03	IFIT3	interferon-induced protein with tetratricopeptide repeats 3
10462390	2.5	0.00	4.1	0.00	0.4	0.08	CD274	CD274 molecule
10461594	2.8	0.00	4.0	0.00	0.0	0.91	Ms4a4b (includes others)	membrane-spanning 4-domains, subfamily A, member 4B
10462618	3.7	0.00	4.0	0.00	0.6	0.03	IFIT3	interferon-induced protein with tetratricopeptide repeats 3
10552406	1.3	0.00	4.0	0.00	0.2	0.05	NKG7	natural killer cell group 7 sequence
10385533	2.4	0.00	3.9	0.00	0.6	0.04	9930111J21Rik1/Gm12185	predicted gene 12185
10455954	2.8	0.00	3.9	0.00	0.6	0.03	Gm4951	predicted gene 4951
10462623	3.7	0.00	3.8	0.00	0.4	0.18	IFIT1B	interferon-induced protein with tetratricopeptide repeats 1B
10531724	2.3	0.00	3.8	0.00	0.7	0.00	PLAC8	placenta-specific 8
10385518	2.3	0.00	3.8	0.00	0.7	0.03	Tgtp1/Tgtp2	T cell specific GTPase 1
10502791	3.4	0.00	3.7	0.00	0.6	0.02	IFI44	interferon-induced protein 44
10496555	1.8	0.00	3.7	0.00	0.4	0.09	GBP2	guanylate binding protein 2, interferon-inducible
10462613	3.2	0.00	3.7	0.00	0.3	0.05	IFIT2	interferon-induced protein with tetratricopeptide repeats 2
10496580	2.3	0.00	3.5	0.00	0.3	0.02	GBP4	guanylate binding protein 4
10389207	2.0	0.00	3.5	0.00	0.2	0.02	CCL5	chemokine (C-C motif) ligand 5
10532019	1.8	0.00	3.5	0.00	0.2	0.15	Gbp6 (includes others)	guanylate binding protein 6
10541307	3.2	0.00	3.5	0.00	0.2	0.15	USP18	ubiquitin specific peptidase 18
10379535	0.8	0.00	3.5	0.00	0.9	0.01	Ccl8	chemokine (C-C motif) ligand 8
10608646	2.4	0.00	3.4	0.00	0.8	0.00		
10531415	2.2	0.00	3.4	0.00	0.3	0.05	CXCL10	chemokine (C-X-C motif) ligand 10
10598976	1.1	0.01	3.3	0.00	0.2	0.48	TIMP1	TIMP metalloproteinase inhibitor 1
10379511	1.8	0.00	3.3	0.00	-0.1	0.43	Ccl2	chemokine (C-C motif) ligand 2
10574145	1.9	0.00	3.3	0.00	0.4	0.01	NLRC5	NLR family, CARD domain containing 5
10379518	1.9	0.00	3.3	0.00	-0.1	0.70	CCL7	chemokine (C-C motif) ligand 7
10455957	2.1	0.00	3.3	0.00	0.5	0.06		
10450325	1.7	0.00	3.3	0.00	0.7	0.00	CFB	complement factor B
10496592	1.8	0.00	3.3	0.00	0.5	0.05		
10351509	1.1	0.00	3.2	0.00	0.6	0.01	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)
10531994	2.0	0.00	3.2	0.00	0.2	0.26		
10351873	2.3	0.00	3.2	0.00	0.2	0.09	Ifi204 (includes others)	interferon activated gene 204
10531987	1.8	0.00	3.2	0.00	0.4	0.09	Gbp6 (includes others)	guanylate binding protein 6
10420483	2.2	0.00	3.1	0.00	0.2	0.14	Phf11a/Phf11b	PHD finger protein 11A
10444258	1.2	0.00	3.1	0.00	0.3	0.00	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8
10593015	0.4	0.00	3.1	0.00	0.3	0.11	CD3G	CD3g molecule, gamma (CD3-TCR complex)
10590635	1.1	0.00	3.1	0.00	0.5	0.03	CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene)
10598013	1.1	0.00	3.1	0.00	0.5	0.03	CCR5	chemokine (C-C motif) receptor 5 (gene/pseudogene)
10490150	1.7	0.00	3.1	0.00	0.2	0.07	ZBP1	Z-DNA binding protein 1
10398039	1.1	0.00	3.1	0.00	0.3	0.02		
10574149	1.8	0.00	3.1	0.00	0.5	0.00	NLRC5	NLR family, CARD domain containing 5
10517165	1.0	0.00	3.0	0.00	1.0	0.00	Cd52	CD52 antigen
10379636	1.8	0.00	3.0	0.00	0.0	0.80	SLFN12L	schlafen family member 12-like
10496569	1.9	0.00	3.0	0.00	0.5	0.03	GBP7	guanylate binding protein 7
10346191	1.7	0.00	3.0	0.00	0.4	0.00	STAT1	signal transducer and activator of transcription 1, 91kDa
10375515	1.5	0.00	3.0	0.00	0.2	0.02		
10399710	3.0	0.00	2.9	0.00	0.3	0.13	RSAD2	radical S-adenosyl methionine domain containing 2
10502801	2.3	0.00	2.9	0.00	0.3	0.21	IFI44L	interferon-induced protein 44-like
10461605	0.8	0.00	2.9	0.00	0.2	0.00	Ms4a4b (includes others)	membrane-spanning 4-domains, subfamily A, member 4B
10444244	1.4	0.00	2.8	0.00	0.3	0.01	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
10406928	1.0	0.00	2.8	0.00	0.9	0.01	CD180	CD180 molecule
10531980	1.4	0.00	2.8	0.00	0.4	0.03	Gbp6 (includes others)	guanylate binding protein 6
10574135	1.4	0.00	2.8	0.00	0.4	0.03	NLRC5	NLR family, CARD domain containing 5
10420488	2.3	0.00	2.8	0.00	0.2	0.44	PHF11	PHD finger protein 11
10531420	1.4	0.00	2.8	0.00	0.1	0.28	Cxcl11	chemokine (C-X-C motif) ligand 11

10538590	1.7	0.00	2.7	0.00	0.3	0.14	HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
10531972	1.0	0.00	2.7	0.00	0.2	0.18	Gbp8	guanylate-binding protein 8
10574098	1.7	0.00	2.7	0.00	0.5	0.00	NLRC5	NLR family, CARD domain containing 5
10450075	1.7	0.00	2.7	0.00	0.7	0.00	HLA-B	major histocompatibility complex, class I, B
10512470	1.5	0.00	2.7	0.00	0.9	0.00	CD72	CD72 molecule
10444814	1.6	0.00	2.7	0.00	0.7	0.00	HLA-B	major histocompatibility complex, class I, B
10412211	1.3	0.00	2.7	0.00	0.0	0.64	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
10563597	1.6	0.00	2.7	0.00	-0.2	0.23	Saa3	serum amyloid A 3
10581378	1.0	0.00	2.7	0.00	0.2	0.01	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10
10389231	1.2	0.00	2.7	0.00	0.5	0.20	CCL3L1/CCL3L3	chemokine (C-C motif) ligand 3-like 1
10360173	1.1	0.00	2.7	0.00	0.5	0.01	SLAMF7	SLAM family member 7
10450161	0.2	0.19	2.6	0.00	1.7	0.00	HLA-DRA	major histocompatibility complex, class II, DR alpha
10434778	2.0	0.00	2.6	0.00	0.2	0.51	RTP4	receptor (chemosensory) transporter protein 4
10379633	1.4	0.00	2.6	0.00	0.0	0.98	Sfn1	schlafen 1
10496539	1.6	0.00	2.6	0.00	0.5	0.01	GBP5	guanylate binding protein 5
10523717	0.4	0.03	2.6	0.00	2.0	0.00	SPP1	secreted phosphoprotein 1
10590631	0.4	0.00	2.6	0.00	0.3	0.10	CCR2	chemokine (C-C motif) receptor 2
10439249	1.5	0.00	2.6	0.00	0.3	0.06	PARP14	poly (ADP-ribose) polymerase family, member 14
10524621	1.9	0.00	2.6	0.00	0.2	0.23	Oas12	2'-5' oligoadenylate synthetase-like 2
10574139	1.3	0.00	2.5	0.00	0.4	0.00	NLRC5	NLR family, CARD domain containing 5
10461721	0.7	0.00	2.5	0.00	1.1	0.00	MPEG1	macrophage expressed 1
10513739	0.6	0.00	2.5	0.00	0.3	0.14	TNC	tenascin C
10456005	0.1	0.47	2.5	0.00	1.6	0.00	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
10444291	0.1	0.46	2.5	0.00	1.1	0.00	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
10541564	0.7	0.00	2.5	0.00	0.3	0.07	Clec4a3	C-type lectin domain family 4, member a3
10574104	1.3	0.00	2.5	0.00	0.4	0.00	NLRC5	NLR family, CARD domain containing 5
10533246	1.7	0.00	2.5	0.00	0.3	0.20	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa
10542164	0.5	0.00	2.5	0.00	1.1	0.00	CLEC12A	C-type lectin domain family 12, member A
10450694	1.3	0.00	2.5	0.00	0.6	0.00	H2-T22	histocompatibility 2, T region locus 22
10574157	1.3	0.00	2.4	0.00	0.2	0.06	NLRC5	NLR family, CARD domain containing 5
10450154	0.1	0.69	2.4	0.00	1.5	0.00	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1
10450145	0.8	0.00	2.4	0.00	0.3	0.00	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9
10351880	2.1	0.00	2.4	0.00	0.2	0.24	Pydc3/Pydc4	pyrin domain containing 4
10571984	1.8	0.00	2.4	0.00	0.4	0.05	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60
10608650	1.2	0.00	2.4	0.00	0.5	0.00		
10393573	1.7	0.00	2.4	0.00	0.2	0.47	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein
10467136	1.0	0.00	2.3	0.00	0.1	0.56	CH25H	cholesterol 25-hydroxylase
10378068	1.7	0.00	2.3	0.00	0.2	0.07	XAF1	XIAP associated factor 1
10494271	0.9	0.00	2.3	0.00	1.0	0.01	CTSS	cathepsin S
10430344	0.8	0.00	2.3	0.00	0.3	0.00	IL2RB	interleukin 2 receptor, beta
10574102	1.5	0.00	2.3	0.00	0.4	0.01	NLRC5	NLR family, CARD domain containing 5
10542214	0.9	0.00	2.3	0.00	0.3	0.01	KLRD1	killer cell lectin-like receptor subfamily D, member 1
10548409	0.6	0.00	2.3	0.00	0.3	0.04	KLRC1	killer cell lectin-like receptor subfamily C, member 1
10566366	1.7	0.00	2.3	0.00	-0.1	0.80	Trim30a/Trim30d	tripartite motif-containing 30A
10545231	0.1	0.56	2.3	0.00	1.2	0.02		
10398075	1.5	0.00	2.3	0.00	0.9	0.01	SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 3
10450682	1.2	0.00	2.3	0.00	0.5	0.00	HLA-E	major histocompatibility complex, class I, E
10499899	0.3	0.02	2.3	0.00	0.4	0.00	Spr1a	small proline-rich protein 1A
10566358	1.5	0.00	2.3	0.00	0.3	0.07	Trim30a/Trim30d	tripartite motif-containing 30A
10358408	0.5	0.00	2.3	0.00	1.1	0.00	RGS1	regulator of G-protein signaling 1
10500335	1.0	0.00	2.2	0.00	0.1	0.31	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)
10358224	0.5	0.00	2.2	0.00	0.4	0.02	PTPRC	protein tyrosine phosphatase, receptor type, C
10376060	0.6	0.01	2.2	0.00	0.3	0.02	IRF1	interferon regulatory factor 1
10441233	1.9	0.00	2.2	0.00	0.1	0.25	Mx1/Mx2	myxovirus (influenza virus) resistance 1

10437224	2.1	0.00	2.2	0.00	0.1	0.44	Mx1/Mx2	myxovirus (influenza virus) resistance 1
10360370	1.5	0.00	2.2	0.00	0.0	0.85	Ifi204 (includes others)	interferon activated gene 204
10482802	0.1	0.41	2.2	0.00	0.2	0.32	CYTIP	cytohesin 1 interacting protein
10483110	1.4	0.00	2.1	0.00	0.2	0.12	IFIH1	interferon induced with helicase C domain 1
10391207	1.6	0.00	2.1	0.00	0.2	0.25	DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58
10360398	1.7	0.00	2.1	0.00	0.1	0.34	Ifi202b	interferon activated gene 202B
10469816	0.5	0.00	2.1	0.00	0.7	0.01	IL1RN	interleukin 1 receptor antagonist
10586865	0.4	0.05	2.1	0.00	0.4	0.01	ALDH1A2	aldehyde dehydrogenase 1 family, member A2
10416437	0.7	0.00	2.1	0.00	0.5	0.03	LCP1	lymphocyte cytosolic protein 1 (L-plastin)
10522788	0.6	0.00	2.1	0.00	1.4	0.00	STAP1	signal transducing adaptor family member 1
10608680	1.1	0.00	2.1	0.00	0.5	0.00	H2-T22	histocompatibility 2, T region locus 22
10574137	0.8	0.00	2.0	0.00	0.1	0.05	NLRC5	NLR family, CARD domain containing 5
10541555	0.7	0.00	2.0	0.00	0.2	0.10	Clec4a1	C-type lectin domain family 4, member a1
10439268	1.4	0.00	2.0	0.00	0.3	0.07	DTX3L	deltex 3-like (Drosophila)
10383198	1.4	0.00	2.0	0.00	0.2	0.28		
10489107	0.9	0.00	2.0	0.00	0.2	0.11	SAMHD1	SAM domain and HD domain 1
10547664	0.7	0.01	2.0	0.00	-0.1	0.75	CLEC4E	C-type lectin domain family 4, member E
10473356	1.2	0.00	2.0	0.00	0.2	0.16	UBE2L6	ubiquitin-conjugating enzyme E2L 6
10545672	1.1	0.00	2.0	0.00	-0.2	0.02	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methylenetetrahydrofolate cyclohydrolase
10501063	0.9	0.00	2.0	0.00	0.6	0.03	CD53	CD53 molecule
10548333	0.5	0.02	2.0	0.00	0.1	0.18	CD69	CD69 molecule
10346168	0.3	0.02	2.0	0.00	0.3	0.00	STAT4	signal transducer and activator of transcription 4
10444229	-0.1	0.50	2.0	0.00	0.5	0.00	HLA-DMA	major histocompatibility complex, class II, DM alpha
10383202	1.2	0.00	2.0	0.00	0.2	0.11	Rnf213	ring finger protein 213
10383212	1.3	0.00	2.0	0.00	0.1	0.08	Rnf213	ring finger protein 213
10427628	0.2	0.09	2.0	0.00	1.1	0.00	IL7R	interleukin 7 receptor
10450699	1.2	0.00	2.0	0.00	0.5	0.00	HLA-F	major histocompatibility complex, class I, F
10383200	1.3	0.00	2.0	0.00	0.2	0.26		
10582997	1.1	0.00	2.0	0.00	0.3	0.09	CASP4	caspase 4, apoptosis-related cysteine peptidase
10363070	0.5	0.00	2.0	0.00	0.7	0.04	Gp49a/Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4
10566050	0.9	0.00	2.0	0.00	0.1	0.08	IL18BP	interleukin 18 binding protein
10387985	0.8	0.00	2.0	0.00	0.2	0.07	SCIMP	SLP adaptor and CSK interacting membrane protein
10379530	0.9	0.00	1.9	0.00	0.1	0.52	CCL2	chemokine (C-C motif) ligand 2
10383204	1.1	0.00	1.9	0.00	0.2	0.12	Rnf213	ring finger protein 213
10347928	1.2	0.00	1.9	0.00	0.3	0.13	SP110	SP110 nuclear body protein
10582874	1.2	0.00	1.9	0.00	0.3	0.13	SP110	SP110 nuclear body protein
10383168	1.2	0.00	1.9	0.00	0.2	0.04		
10439009	1.6	0.00	1.9	0.00	0.3	0.16	APOD	apolipoprotein D
10466210	1.3	0.00	1.9	0.00	-0.2	0.25	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
10383214	1.2	0.00	1.9	0.00	0.2	0.15	Rnf213	ring finger protein 213
10590623	0.2	0.12	1.9	0.00	0.4	0.03	CXCR6	chemokine (C-X-C motif) receptor 6
10444821	1.2	0.00	1.9	0.00	0.3	0.02	H2-Q5	histocompatibility 2, Q region locus 5
10516620	0.3	0.01	1.9	0.00	0.0	0.71	LCK	lymphocyte-specific protein tyrosine kinase
10576034	0.3	0.01	1.9	0.00	0.2	0.01	IRF8	interferon regulatory factor 8
10543067	0.9	0.00	1.9	0.00	-0.2	0.35	ASNS	asparagine synthetase (glutamine-hydrolyzing)
10385504	1.3	0.00	1.9	0.00	0.1	0.67	Gm5431	predicted gene 5431
10512067	1.5	0.00	1.9	0.00	0.2	0.27	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
10371082	0.2	0.17	1.9	0.00	-0.5	0.03	NMRK2	nicotinamide riboside kinase 2
10346799	0.0	0.94	1.9	0.00	0.2	0.05	ICOS	inducible T-cell co-stimulator
10375145	0.7	0.00	1.9	0.00	0.2	0.21	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa)
10450675	1.3	0.00	1.9	0.00	0.3	0.06	H2-T24	histocompatibility 2, T region locus 24
10451287	1.2	0.00	1.9	0.00	0.1	0.54		
10383206	1.5	0.00	1.9	0.00	0.2	0.40		
10544133	1.2	0.00	1.9	0.00	0.2	0.10	PARP12	poly (ADP-ribose) polymerase family, member 12
10383208	1.3	0.00	1.9	0.00	0.1	0.52		
10587323	0.3	0.07	1.9	0.00	0.0	0.65		
10547621	0.7	0.00	1.9	0.00	0.6	0.06	APOBEC1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1
10578264	0.8	0.00	1.9	0.00	0.2	0.43	MSR1	macrophage scavenger receptor 1
10497358	0.4	0.01	1.8	0.00	0.1	0.29	Sirpb1a (includes others)	signal-regulatory protein beta 1A
10508392	0.6	0.00	1.8	0.00	0.1	0.47	RNF19B	ring finger protein 19B

10383196	1.2	0.00	1.8	0.00	0.1	0.40	Rnf213	ring finger protein 213
10404606	0.8	0.01	1.8	0.00	0.8	0.01	LY86	lymphocyte antigen 86
10416837	0.5	0.00	1.8	0.00	0.1	0.51	Irg1	immunoresponsive gene 1
10384458	0.5	0.02	1.8	0.00	0.6	0.04	PLEK	pleckstrin
10430174	0.9	0.00	1.8	0.00	0.0	0.72	ApoI9a/ApoI9b	apolipoprotein L 9b
10422760	0.3	0.01	1.8	0.00	0.3	0.08	FYB	FYN binding protein
10444780	0.9	0.00	1.8	0.00	0.3	0.00	HLA-B	major histocompatibility complex, class I, B
10587683	0.2	0.03	1.8	0.00	0.5	0.02	BCL2A1	BCL2-related protein A1
10494978	0.5	0.01	1.8	0.00	0.1	0.37	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
10548345	0.6	0.00	1.8	0.00	0.1	0.44		
10383152	1.2	0.00	1.8	0.00	0.2	0.18	Rnf213	ring finger protein 213
10466127	0.8	0.01	1.8	0.00	0.3	0.02	AW112010	expressed sequence AW112010
10534909	1.0	0.00	1.8	0.00	0.3	0.02	SP110	SP110 nuclear body protein
10566144	1.1	0.00	1.8	0.00	0.0	0.72	TRIM21	tripartite motif containing 21
10547657	0.6	0.01	1.8	0.00	0.7	0.04	C3AR1	complement component 3a receptor 1
10341146	1.0	0.07	1.8	0.00	0.3	0.23		
10398907	0.6	0.00	1.8	0.00	0.2	0.15	PLD4	phospholipase D family, member 4
10364262	0.3	0.00	1.7	0.00	0.6	0.05	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)
10383233	1.1	0.00	1.7	0.00	0.1	0.33	Rnf213	ring finger protein 213
10467578	0.6	0.00	1.7	0.00	0.3	0.00	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1
10538979	0.0	0.62	1.7	0.00	0.1	0.22	CD8B	CD8b molecule
10351658	0.3	0.03	1.7	0.00	0.3	0.02	CD48	CD48 molecule
10583008	0.6	0.00	1.7	0.00	0.8	0.00	CASP12	caspase 12 (gene/pseudogene)
10533213	1.0	0.00	1.7	0.00	0.0	0.84	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa
10579532	1.0	0.00	1.7	0.00	0.0	0.89	BST2	bone marrow stromal cell antigen 2
10601456	0.4	0.00	1.7	0.00	0.1	0.39	Gm6377	predicted gene 6377
10367224	1.1	0.00	1.7	0.00	0.1	0.48	STAT2	signal transducer and activator of transcription 2, 113kDa
10473125	0.3	0.00	1.7	0.00	0.3	0.01	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
10577655	0.7	0.00	1.7	0.00	-0.1	0.46	IDO1	indoleamine 2,3-dioxygenase 1
10587331	0.2	0.09	1.7	0.00	0.0	0.49		
10414360	0.2	0.02	1.7	0.00	1.3	0.00	LGALS3	lectin, galactoside-binding, soluble, 3
10420030	0.5	0.00	1.7	0.00	0.1	0.17	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
10601385	0.8	0.00	1.7	0.00	0.5	0.05	Tlr13	toll-like receptor 13
10404429	0.5	0.01	1.7	0.00	0.3	0.21	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9
10363082	0.7	0.00	1.7	0.00	0.7	0.03	Gp49a/Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4
10466314	1.1	0.00	1.7	0.00	0.0	0.67		
10581813	0.8	0.00	1.7	0.00	-0.1	0.44	MLKL	mixed lineage kinase domain-like
10532744	0.3	0.01	1.7	0.00	0.2	0.02	SELPLG	selectin P ligand
10372410	0.5	0.00	1.7	0.00	1.1	0.00	GLIPR1	GLI pathogenesis-related 1
10397975	1.0	0.00	1.7	0.00	0.4	0.00	IFI27	interferon, alpha-inducible protein 27
10452980	1.5	0.00	1.7	0.00	0.1	0.52	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2
10385511	0.8	0.00	1.7	0.00	0.2	0.12	Psme2b	protease (prosome, macropain) activator subunit 2B
10554240	1.3	0.00	1.7	0.00	0.1	0.17	ISG20	interferon stimulated exonuclease gene 20kDa
10360070	1.0	0.00	1.7	0.00	0.5	0.01	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
10559486	0.3	0.04	1.7	0.00	0.6	0.01	LAIR1	leukocyte-associated immunoglobulin-like receptor 1
10402347	1.2	0.00	1.7	0.00	-0.1	0.44	IFI27L2	interferon, alpha-inducible protein 27-like 2
10547976	0.4	0.03	1.7	0.00	0.2	0.16	TAPBPL	TAP binding protein-like
10595633	0.3	0.00	1.7	0.00	0.5	0.01	BCL2A1	BCL2-related protein A1
10477250	0.6	0.00	1.7	0.00	0.2	0.27	HCK	hemopoietic cell kinase
10497372	0.1	0.25	1.6	0.00	0.1	0.61	Gm5150	predicted gene 5150
10360373	1.4	0.00	1.6	0.00	0.3	0.07	Pydc3/Pydc4	pyrin domain containing 4
10341698	0.7	0.03	1.6	0.00	-0.2	0.30		
10458314	0.3	0.11	1.6	0.00	0.2	0.22	TMEM173	transmembrane protein 173
10388958	0.5	0.00	1.6	0.00	0.4	0.08		
10383210	1.1	0.00	1.6	0.00	0.0	0.92	Rnf213	ring finger protein 213
10603551	0.4	0.01	1.6	0.00	1.2	0.00	CYBB	cytochrome b-245, beta polypeptide
10351197	0.6	0.01	1.6	0.00	-0.2	0.37	SELL	selectin L
10430372	0.3	0.04	1.6	0.00	0.2	0.05	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
10466200	0.4	0.00	1.6	0.00	0.6	0.01	MS4A7	membrane-spanning 4-domains, subfamily A, member 7
10424676	1.1	0.00	1.6	0.00	0.1	0.52	LY6E	lymphocyte antigen 6 complex, locus E
10533198	1.3	0.00	1.6	0.00	0.3	0.11	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa
10385118	0.4	0.00	1.6	0.00	0.4	0.01	DOCK2	dedicator of cytokinesis 2
10446253	0.4	0.00	1.6	0.00	0.2	0.05	VAV1	vav 1 guanine nucleotide exchange factor
10525158	1.3	0.00	1.6	0.00	0.0	0.92	Oas1b	2'-5' oligoadenylate synthetase 1B
10574163	0.7	0.00	1.6	0.00	0.1	0.09	NLRC5	NLR family, CARD domain

10598004	0.1	0.63	1.6	0.00	0.2	0.15	CCR1	containing 5
10601416	0.1	0.53	1.6	0.00	0.1	0.20	P2RY10	chemokine (C-C motif) receptor 1 purinergic receptor P2Y, G-protein coupled, 10
10587690	0.3	0.00	1.6	0.00	0.4	0.01	BCL2A1	BCL2-related protein A1
10516966	0.6	0.01	1.6	0.00	0.1	0.20	THEMIS2	thymocyte selection associated family member 2
10549647	0.7	0.00	1.6	0.00	0.3	0.02	NCR1	natural cytotoxicity triggering receptor 1
10356278	0.8	0.00	1.6	0.00	0.2	0.02	SP110	SP110 nuclear body protein
10444830	0.9	0.00	1.6	0.00	0.4	0.00	H2-K2/H2-Q9	histocompatibility 2, K region locus 2
10542140	0.5	0.01	1.6	0.00	0.2	0.19	Klrb1f	killer cell lectin-like receptor subfamily B member 1F
10444298	0.0	0.66	1.6	0.00	0.8	0.00	HLA-DRB1	major histocompatibility complex, class II, DR beta 1
10544588	-0.1	0.52	1.6	0.00	0.2	0.02	GIMAP5	GTPase, IMAP family member 5
10389134	0.7	0.01	1.6	0.00	0.2	0.07	SLFN13	schlafen family member 13
10557862	0.3	0.01	1.5	0.00	0.2	0.28	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)
10461622	0.7	0.00	1.5	0.00	-0.2	0.34	Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B
10381408	0.8	0.00	1.5	0.00	0.1	0.31	IFI35	interferon-induced protein 35
10574151	0.7	0.00	1.5	0.00	0.0	0.86	NLRC5	NLR family, CARD domain containing 5
10344031	0.6	0.01	1.5	0.00	0.4	0.15		
10383194	1.1	0.01	1.5	0.00	0.1	0.70	Rnf213	ring finger protein 213
10539135	0.4	0.01	1.5	0.00	0.5	0.04	CAPG	capping protein (actin filament), gelsolin-like
10379630	0.9	0.00	1.5	0.00	0.2	0.05	Slnf2	schlafen 2
10343267	0.4	0.13	1.5	0.00	0.4	0.15		
10460767	0.5	0.01	1.5	0.00	0.1	0.31	BATF2	basic leucine zipper transcription factor, ATF-like 2
10495186	0.4	0.00	1.5	0.00	0.3	0.02	A1504432	expressed sequence A1504432
10383192	1.0	0.00	1.5	0.00	-0.1	0.56		
10473809	0.7	0.00	1.5	0.00	0.4	0.08	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene
10343969	0.8	0.04	1.5	0.00	0.0	0.92		
10444268	0.6	0.00	1.5	0.00	0.2	0.00	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
10578493	1.1	0.00	1.5	0.00	0.1	0.39	TLR3	toll-like receptor 3
10559467	0.3	0.02	1.5	0.00	0.4	0.06		
10360382	1.1	0.00	1.5	0.00	-0.1	0.38	Ifi204 (includes others)	interferon activated gene 204
10557591	0.3	0.02	1.5	0.00	0.1	0.24	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)
10566583	0.8	0.00	1.5	0.00	0.2	0.16	Gm8995	predicted gene 8995
10351691	0.2	0.02	1.5	0.00	0.1	0.15	SLAMF6	SLAM family member 6
10342250	0.6	0.05	1.5	0.00	-0.2	0.67		
10524631	1.6	0.00	1.5	0.00	0.0	0.92	OASL	2'-5'-oligoadenylate synthetase-like
10508663	0.3	0.05	1.5	0.00	0.5	0.02	LAPTM5	lysosomal protein transmembrane 5
10352000	0.2	0.14	1.5	0.00	0.2	0.17	KMO	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
10395039	1.9	0.00	1.5	0.00	0.2	0.25	CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial
10385513	0.8	0.00	1.5	0.00	0.2	0.15	9930111J21Rik2	RIKEN cDNA 9930111J21 gene 2
10425049	0.9	0.00	1.5	0.00	0.0	0.97	Apo9a/Apo9b	apolipoprotein L 9b
10339750	0.7	0.00	1.5	0.00	0.0	0.84		
10534927	0.6	0.01	1.5	0.00	0.3	0.03	PILRA	paired immunoglobulin-like type 2 receptor alpha
10491091	1.0	0.01	1.5	0.00	0.5	0.06	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
10343290	0.6	0.11	1.5	0.01	-0.1	0.85		
10531737	0.3	0.03	1.5	0.00	0.4	0.00	HPSE	heparanase
10392839	0.5	0.00	1.4	0.00	0.1	0.04	CD300E	CD300e molecule
10606016	0.4	0.01	1.4	0.00	0.1	0.75	IL2RG	interleukin 2 receptor, gamma
10341587	0.7	0.02	1.4	0.00	0.3	0.21		
10588479	0.4	0.01	1.4	0.00	0.2	0.04	TLR9	toll-like receptor 9
10459772	0.4	0.04	1.4	0.00	0.0	0.66	LIPG	lipase, endothelial
10427336	0.1	0.27	1.4	0.00	0.5	0.01	NCKAP1L	NCK-associated protein 1-like
10429128	0.3	0.06	1.4	0.00	0.2	0.22	SLA	Src-like-adaptor
10385526	0.8	0.00	1.4	0.00	0.2	0.13		
10444236	0.0	0.56	1.4	0.00	0.4	0.00	HLA-DMB	major histocompatibility complex, class II, DM beta
10404061	0.2	0.05	1.4	0.00	0.1	0.65	HIST1H2BB	histone cluster 1, H2bb
10593024	0.0	0.92	1.4	0.00	0.0	0.60	CD3E	CD3e molecule, epsilon (CD3-TCR complex)
10435457	0.9	0.00	1.4	0.00	0.2	0.08	PARP9	poly (ADP-ribose) polymerase family, member 9
10347925	1.1	0.00	1.4	0.00	0.6	0.02	Csprs (includes others)	component of Sp100-rs
10343468	0.7	0.02	1.4	0.00	0.1	0.40		
10487208	0.5	0.00	1.4	0.00	0.3	0.05	ATP8B4	ATPase, class I, type 8B, member 4
10446282	0.5	0.01	1.4	0.00	0.4	0.04	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1
10347915	1.1	0.00	1.4	0.00	0.5	0.02	Csprs (includes others)	component of Sp100-rs
10588786	0.6	0.00	1.4	0.00	0.1	0.00		
10432640	0.3	0.02	1.4	0.00	0.0	0.99		
10461614	1.0	0.00	1.4	0.00	-0.2	0.22	Ms4a6c	membrane-spanning 4-domains,

10338492	0.5	0.00	1.4	0.00	0.1	0.68		subfamily A, member 6C
10466190	0.1	0.40	1.4	0.00	0.3	0.14	MS4A14	membrane-spanning 4-domains, subfamily A, member 14
10533256	0.9	0.00	1.4	0.00	-0.1	0.61	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa
10574133	0.5	0.01	1.4	0.00	0.2	0.07	NLRC5	NLR family, CARD domain containing 5
10425092	0.1	0.41	1.4	0.00	0.4	0.03	CYTH4	cytohesin 4
10397645	0.4	0.02	1.4	0.00	0.3	0.07	GPR65	G protein-coupled receptor 65
10407327	-0.2	0.33	1.4	0.00	0.2	0.30	EMB	embigin
10416566	0.7	0.00	1.4	0.00	0.1	0.30	Eps11	epithelial stromal interaction 1 (breast)
10415319	1.2	0.00	1.4	0.00	0.2	0.15	IRF9	interferon regulatory factor 9
10340317	0.5	0.03	1.4	0.00	0.0	0.84		
10363475	0.5	0.01	1.4	0.00	-0.1	0.28	PRF1	perforin 1 (pore forming protein)
10541587	0.3	0.08	1.4	0.00	0.3	0.12	CLEC4A	C-type lectin domain family 4, member A
10486061	0.3	0.01	1.4	0.00	0.1	0.33	RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
10494405	0.0	0.86	1.4	0.00	0.3	0.09		
10342553	0.6	0.02	1.4	0.00	-0.1	0.48		
10566578	1.0	0.00	1.4	0.00	0.2	0.19	Gm8979	very large inducible GTPase 1 pseudogene
10339951	0.4	0.12	1.4	0.00	0.1	0.65		
10408239	0.0	0.90	1.3	0.00	0.3	0.08	HIST2H3C (includes others)	histone cluster 2, H3c
10404065	0.0	0.86	1.3	0.00	0.3	0.08		
10341222	0.4	0.01	1.3	0.00	0.2	0.27		
10404049	0.0	0.78	1.3	0.00	0.3	0.09		
10559446	0.1	0.35	1.3	0.00	0.1	0.38	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
10404028	0.0	0.86	1.3	0.00	0.3	0.08		
10568024	0.1	0.07	1.3	0.00	0.1	0.48	CORO1A	coronin, actin binding protein, 1A
10412218	0.2	0.07	1.3	0.00	0.1	0.38	GZMK	granzyme K (granzyme 3; tryptase II)
10338116	0.5	0.01	1.3	0.00	0.1	0.25		
10341395	0.6	0.01	1.3	0.00	0.1	0.25		
10353844	0.2	0.05	1.3	0.00	0.3	0.00	Neur3	neutralized homolog 3 homolog (Drosophila)
10566571	1.0	0.00	1.3	0.00	0.2	0.17		
10551883	0.4	0.02	1.3	0.00	0.7	0.01	TYROBP	TYRO protein tyrosine kinase binding protein
10362350	-0.1	0.59	1.3	0.00	0.1	0.60	THEMIS	thymocyte selection associated
10374333	0.3	0.00	1.3	0.00	0.1	0.19	IKZF1	IKAROS family zinc finger 1 (Ikaros)
10574159	0.7	0.00	1.3	0.00	0.1	0.07	NLRC5	NLR family, CARD domain containing 5
10408246	0.0	0.89	1.3	0.00	0.2	0.09		
10498345	0.1	0.38	1.3	0.00	0.0	0.92	GPR171	G protein-coupled receptor 171
10403941	0.0	0.71	1.3	0.00	0.3	0.09		
10439527	0.3	0.01	1.3	0.00	0.1	0.40	TIGIT	T cell immunoreceptor with Ig and ITIM domains
10408083	0.0	0.94	1.3	0.00	0.3	0.09		
10359181	1.2	0.00	1.3	0.00	0.3	0.03	TOR3A	torsin family 3, member A
10541683	0.6	0.02	1.3	0.00	0.6	0.01		
10465059	0.4	0.00	1.3	0.00	0.1	0.45	CTSW	cathepsin W
10494402	0.0	0.87	1.3	0.00	0.3	0.06		
10443980	0.1	0.40	1.3	0.00	0.3	0.11	MYO1F	myosin IF
10461636	0.9	0.00	1.3	0.00	-0.2	0.24		
10439312	0.4	0.00	1.3	0.00	0.2	0.08	CD86	CD86 molecule
10476945	0.1	0.39	1.3	0.00	0.0	0.88	CST7	cystatin F (leukocystatin)
10564539	0.2	0.06	1.3	0.00	-0.2	0.10	MCTP2	multiple C2 domains, transmembrane 2
10429843	0.7	0.00	1.3	0.00	0.2	0.01	PARP10	poly (ADP-ribose) polymerase family, member 10
10341905	0.4	0.14	1.3	0.00	0.1	0.61		
10424400	0.4	0.01	1.3	0.00	0.1	0.56	MYC	v-myc avian myelocytomatosis viral oncogene homolog
10538187	-0.1	0.47	1.3	0.00	3.2	0.00	GPNUMB	glycoprotein (transmembrane) nmb
10444068	0.4	0.00	1.3	0.00	0.2	0.03	TAPBP	TAP binding protein (tapasin)
10351679	0.1	0.40	1.3	0.00	0.8	0.02	CD84	CD84 molecule
10557895	0.1	0.60	1.3	0.00	1.3	0.01	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)
10530145	0.3	0.07	1.3	0.00	0.2	0.23	TLR1	toll-like receptor 1
10408202	0.0	0.74	1.3	0.00	0.2	0.08	HIST2H3C (includes others)	histone cluster 2, H3c
10593050	0.3	0.02	1.3	0.00	0.2	0.00	IL10RA	interleukin 10 receptor, alpha
10482517	0.5	0.01	1.3	0.00	0.2	0.12	NMI	N-myc (and STAT) interactor
10340164	1.0	0.01	1.3	0.00	0.1	0.72		
10441003	0.2	0.05	1.3	0.00	0.4	0.03	RUNX1	runt-related transcription factor 1
10344300	0.5	0.23	1.3	0.01	0.3	0.01		
10356262	0.8	0.01	1.3	0.00	0.4	0.09	Csprs (includes others)	component of Sp100-rs
10338280	0.8	0.01	1.3	0.00	0.2	0.51		
10581434	0.4	0.01	1.3	0.00	0.6	0.02	DPEP2	dipeptidase 2
10568714	-0.1	0.48	1.3	0.00	0.1	0.09	MKI67	antigen identified by monoclonal antibody Ki-67

10450484	0.3	0.03	1.3	0.00	0.3	0.04	AIF1	allograft inflammatory factor 1
10583669	0.2	0.08	1.3	0.00	0.2	0.01	C19orf38	chromosome 19 open reading frame 38
10521667	0.3	0.01	1.3	0.00	0.3	0.11	BST1	bone marrow stromal cell antigen 1
10452316	0.2	0.08	1.3	0.00	0.5	0.01	C3	complement component 3
10580754	0.5	0.01	1.3	0.00	0.1	0.68	9330175E14Rik	RIKEN cDNA 9330175E14 gene
10542040	0.5	0.01	1.2	0.00	0.2	0.03	PARP11	poly (ADP-ribose) polymerase family, member 11
10420497	0.9	0.01	1.2	0.00	-0.3	0.08	Phf11c	PHD finger protein 11C
10566346	0.9	0.00	1.2	0.00	0.2	0.25	TRIM5	tripartite motif containing 5
10347948	0.8	0.00	1.2	0.00	0.3	0.06	Sp100	nuclear antigen Sp100
10548552	0.2	0.22	1.2	0.00	0.0	0.66	Klra2	killer cell lectin-like receptor, subfamily A, member 2
10339327	0.8	0.02	1.2	0.00	0.3	0.42		
10429560	0.5	0.00	1.2	0.00	-0.2	0.20	Ly6a (includes others)	lymphocyte antigen 6 complex, locus A
10461765	0.5	0.00	1.2	0.00	0.1	0.25	LPXN	leupaxin
10366586	0.3	0.02	1.2	0.00	0.0	0.73	IFNG	interferon, gamma
10589884	0.7	0.00	1.2	0.00	0.2	0.25	Bcl2a1c	B cell leukemia/lymphoma 2 related protein A1c
10520452	0.3	0.08	1.2	0.00	0.0	0.88	IL6	interleukin 6 (interferon, beta 2)
10574143	0.4	0.07	1.2	0.00	0.1	0.36	NLRC5	NLR family, CARD domain containing 5
10457168	-0.2	0.57	1.2	0.00	0.2	0.16	CD226	CD226 molecule
10542911	0.9	0.00	1.2	0.00	0.2	0.12	SAMD9L	sterile alpha motif domain containing 9-like
10359851	0.5	0.01	1.2	0.00	-0.5	0.00	UCK2	uridine-cytidine kinase 2
10403871	0.4	0.00	1.2	0.00	0.3	0.01	AOAH	acyloxyacyl hydrolase (neutrophil)
10381445	0.5	0.00	1.2	0.00	0.2	0.03	TMEM106A	transmembrane protein 106A
10548535	0.5	0.00	1.2	0.00	0.0	0.82	Klra4 (includes others)	killer cell lectin-like receptor, subfamily A, member 4
10338178	1.0	0.00	1.2	0.00	0.2	0.61		
10339765	0.8	0.02	1.2	0.00	0.1	0.62		
10450344	0.3	0.07	1.2	0.00	0.0	0.70	C2	complement component 2
10388902	1.0	0.00	1.2	0.00	0.1	0.24	LGALS9	lectin, galactoside-binding, soluble, 9
10497364	0.2	0.03	1.2	0.00	0.0	0.58	Sirpb1a (includes others)	signal-regulatory protein beta 1A
10440393	0.3	0.03	1.2	0.00	0.0	0.51	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1
10487823	0.7	0.00	1.2	0.00	0.2	0.07	SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin
10461558	0.3	0.02	1.2	0.00	0.2	0.11	SLC15A3	solute carrier family 15 (oligopeptide transporter), member 3
10582985	0.4	0.00	1.2	0.00	0.3	0.05	CASP1	caspase 1, apoptosis-related cysteine peptidase
10402585	0.6	0.00	1.2	0.00	0.1	0.58	WARS	tryptophanyl-tRNA synthetase
10387536	0.1	0.19	1.2	0.00	0.7	0.02	CD68	CD68 molecule
10343192	0.7	0.01	1.2	0.02	0.2	0.49		
10342761	0.8	0.01	1.2	0.00	0.1	0.77		
10342539	1.0	0.07	1.2	0.02	-0.2	0.68		
10408077	0.1	0.47	1.2	0.00	0.2	0.35	HIST1H2AD	histone cluster 1, H2ad
10435920	0.4	0.03	1.2	0.00	0.3	0.14	CD200R1L	CD200 receptor 1-like
10338367	0.5	0.01	1.2	0.00	0.0	0.79		
10390707	-0.1	0.15	1.2	0.00	0.2	0.12	TOP2A	topoisomerase (DNA) II alpha 170kDa
10519951	0.0	0.88	1.2	0.00	0.3	0.01	GSAP	gamma-secretase activating protein
10414548	0.1	0.43	1.2	0.00	0.1	0.46	RNASE6	ribonuclease, RNase A family, k6
10406205	0.3	0.00	1.2	0.00	0.1	0.45	ERAP1	endoplasmic reticulum aminopeptidase 1
10430302	0.2	0.00	1.2	0.00	0.3	0.11	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
10466130	0.5	0.00	1.2	0.00	0.0	0.91	MS4A8	membrane-spanning 4-domains, subfamily A, member 8
10415015	0.0	0.71	1.2	0.00	-0.1	0.53	Trav7-4	T cell receptor alpha variable 7-4
10339254	0.6	0.08	1.2	0.01	0.4	0.26		
10375443	0.4	0.01	1.2	0.01	0.1	0.37	HAVCR2	hepatitis A virus cellular receptor 2
10545135	0.4	0.00	1.2	0.00	0.0	0.78	IL12RB2	interleukin 12 receptor, beta 2
10398052	0.4	0.00	1.2	0.00	0.1	0.26	Serpina3h	serine (or cysteine) peptidase inhibitor, clade A, member 3H
10582879	0.9	0.00	1.2	0.00	0.6	0.00	Csprs (includes others)	component of Sp100-rs
10356020	-0.1	0.32	1.2	0.00	0.4	0.02	DOCK10	dedicator of cytokinesis 10
10501608	0.3	0.00	1.2	0.00	0.3	0.05	VCAM1	vascular cell adhesion molecule 1
10449303	0.2	0.07	1.2	0.00	0.0	0.59	BAK1	BCL2-antagonist/killer 1
10387890	0.1	0.24	1.2	0.00	0.4	0.03	CXCL16	chemokine (C-X-C motif) ligand 16
10606058	0.0	0.81	1.2	0.00	0.0	0.91	CXCR3	chemokine (C-X-C motif) receptor 3
10384154	0.3	0.00	1.1	0.00	0.2	0.04	MYO1G	myosin IG
10390640	0.2	0.02	1.1	0.00	-0.1	0.19	IKZF3	IKAROS family zinc finger 3 (Aiolos)
10339726	0.8	0.00	1.1	0.00	0.0	1.00		
10342216	0.5	0.00	1.1	0.00	0.3	0.10		
10485405	0.2	0.03	1.1	0.00	0.2	0.22	CD44	CD44 molecule (Indian blood group)
10343134	0.6	0.00	1.1	0.00	0.0	0.95		
10340782	0.5	0.05	1.1	0.00	0.4	0.23		
10344149	0.3	0.25	1.1	0.00	-0.8	0.02		
10445119	0.5	0.01	1.1	0.00	0.2	0.03	HLA-G	major histocompatibility complex, class I, G
10340809	0.6	0.00	1.1	0.00	0.1	0.30		
10425066	0.1	0.03	1.1	0.00	0.2	0.26	CSF2RB	colony stimulating factor 2 receptor,

								beta, low-affinity (granulocyte-macrophage)
10339017	0.5	0.17	1.1	0.00	0.1	0.72		
10450069	0.8	0.00	1.1	0.00	0.2	0.01	H2-K2/H2-Q9	histocompatibility 2, K region locus 2
10567825	0.1	0.10	1.1	0.00	0.1	0.34	LAT	linker for activation of T cells
10350516	0.1	0.43	1.1	0.00	-0.2	0.17	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
10355967	0.1	0.06	1.1	0.00	0.1	0.22	AP1S3	adaptor-related protein complex 1, sigma 3 subunit
10374236	0.4	0.01	1.1	0.00	-0.2	0.01	UPP1	uridine phosphorylase 1
10466410	0.1	0.24	1.1	0.00	-0.1	0.22	PSAT1	phosphoserine aminotransferase 1
10342565	0.4	0.33	1.1	0.00	-0.1	0.83		
10421697	0.4	0.01	1.1	0.00	0.2	0.03	LACC1	laccase (multicopper oxidoreductase) domain containing 1
10497831	-0.3	0.03	1.1	0.00	0.1	0.27	CCNA2	cyclin A2
10461629	0.7	0.00	1.1	0.00	0.3	0.00	Ms4a4b (includes others)	membrane-spanning 4-domains, subfamily A, member 4B
10559454	0.2	0.10	1.1	0.00	0.3	0.02	Pira11	paired-Ig-like receptor A11
10542981	0.2	0.07	1.1	0.00	0.1	0.63	GMFG	glia maturation factor, gamma
10404063	0.2	0.18	1.1	0.00	0.1	0.63	Hist1h2ab (includes others)	histone cluster 1, H2ab
10340391	0.7	0.04	1.1	0.01	0.5	0.17		
10360306	0.2	0.16	1.1	0.00	0.3	0.01	SLAMF8	SLAM family member 8
10394054	0.3	0.02	1.1	0.00	0.0	0.99	CD7	CD7 molecule
10482929	0.0	0.62	1.1	0.00	0.2	0.03	LY75	lymphocyte antigen 75
10574141	0.4	0.01	1.1	0.00	0.0	0.74	NLRC5	NLR family, CARD domain containing 5
10351099	0.3	0.07	1.1	0.00	0.0	0.67	TNFSF18	tumor necrosis factor (ligand) superfamily, member 18
10450242	0.5	0.00	1.1	0.00	0.2	0.10	C4A/C4B	complement component 4B (Chido blood group)
10425053	0.3	0.00	1.1	0.00	0.3	0.07	NCF4	neutrophil cytosolic factor 4, 40kDa
10356274	0.8	0.00	1.1	0.00	0.6	0.00	Csprs (includes others)	component of Sp100-rs
10429564	0.9	0.00	1.1	0.00	-0.1	0.59	Ly6a (includes others)	lymphocyte antigen 6 complex, locus A
10489127	0.3	0.05	1.1	0.00	0.3	0.06	RBL1	retinoblastoma-like 1 (p107)
10566574	0.7	0.00	1.1	0.00	0.2	0.36	Gvin1 (includes others)	GTPase, very large interferon inducible 1
10343442	0.5	0.17	1.1	0.01	0.2	0.43		
10544273	0.2	0.13	1.1	0.00	0.4	0.09	CLEC5A	C-type lectin domain family 5, member A
10366881	0.7	0.00	1.1	0.00	0.1	0.18	DDIT3	DNA-damage-inducible transcript 3
10538753	0.2	0.16	1.1	0.00	0.1	0.42		
10450723	0.4	0.01	1.1	0.00	0.3	0.04	H2-T10	histocompatibility 2, T region locus 10
10347335	0.2	0.08	1.1	0.00	0.4	0.03	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1
10360406	0.8	0.00	1.1	0.00	-0.2	0.16	Ifi204 (includes others)	interferon activated gene 204
10408572	0.3	0.20	1.1	0.01	0.0	0.92		
10487480	-0.1	0.29	1.1	0.00	0.2	0.02	BUB1	BUB1 mitotic checkpoint serine/threonine kinase
10534935	0.5	0.01	1.1	0.00	0.4	0.02	PILRB	paired immunoglobulin-like type 2 receptor beta
10454782	0.3	0.05	1.1	0.00	0.1	0.59	EGR1	early growth response 1
10531370	0.1	0.30	1.1	0.00	0.3	0.05	NAAA	N-acylthanolamine acid amidase
10574155	0.4	0.03	1.1	0.00	0.1	0.64	NLRC5	NLR family, CARD domain containing 5
10340949	0.4	0.10	1.1	0.01	0.1	0.64		
10497349	0.2	0.02	1.1	0.00	0.0	0.49	Sirpb1a (includes others)	signal-regulatory protein beta 1A
10569020	0.3	0.21	1.1	0.00	0.1	0.19	Ifitm6	interferon induced transmembrane protein 6
10425410	0.2	0.11	1.1	0.00	0.1	0.52	GRAP2	GRB2-related adaptor protein 2
10393449	0.3	0.03	1.1	0.00	-0.1	0.23	SOC3	suppressor of cytokine signaling 3
10475517	0.1	0.22	1.1	0.00	0.0	0.95	C15orf48	chromosome 15 open reading frame 48
10343490	0.5	0.15	1.1	0.00	-0.5	0.18		
10554789	0.2	0.06	1.1	0.00	0.1	0.48	CTSC	cathepsin C
10356248	0.4	0.01	1.1	0.00	0.3	0.01	C130026I21Rik (includes others)	RIKEN cDNA C130026I21 gene
10567580	0.5	0.01	1.1	0.00	0.5	0.05	IGSF6	immunoglobulin superfamily, member 6
10385428	0.2	0.00	1.1	0.00	0.2	0.04	ITK	IL2-inducible T-cell kinase
10489891	0.4	0.00	1.1	0.00	0.1	0.39	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5
10548375	0.0	0.88	1.1	0.00	1.2	0.00	CLEC7A	C-type lectin domain family 7, member A
10538290	0.3	0.00	1.1	0.00	0.1	0.43	SNX10	sorting nexin 10
10481949	0.1	0.26	1.1	0.00	0.0	0.65	TRAF1	TNF receptor-associated factor 1
10435704	0.2	0.10	1.0	0.00	-0.1	0.66	CD80	CD80 molecule
10538135	0.1	0.43	1.0	0.00	0.0	0.91	GIMAP7	GTPase, IMAP family member 7
10487011	0.0	0.72	1.0	0.00	0.5	0.02	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)
10487597	0.1	0.67	1.0	0.00	0.0	0.77	IL1B	interleukin 1, beta
10601581	0.5	0.00	1.0	0.00	0.1	0.02		
10500677	0.0	0.85	1.0	0.00	-0.1	0.18	CD2	CD2 molecule
10481627	0.8	0.00	1.0	0.00	-0.8	0.00	LCN2	lipocalin 2
10548892	0.2	0.05	1.0	0.00	0.2	0.02	ARHGDB	Rho GDP dissociation inhibitor

10582862	0.4	0.01	1.0	0.00	0.2	0.35	SP140	(GDI) beta SP140 nuclear body protein
10340154	0.5	0.01	1.0	0.00	0.2	0.44		
10382106	0.6	0.00	1.0	0.00	0.3	0.12	Milr1	mast cell immunoglobulin like receptor 1
10595148	0.1	0.57	1.0	0.00	0.0	0.72		
10547985	0.0	0.88	1.0	0.00	0.0	0.97	CD27	CD27 molecule
10357875	-0.3	0.26	1.0	0.00	0.2	0.31	BTG2	BTG family, member 2
10413047	0.0	0.81	1.0	0.00	0.3	0.05	PLAU	plasminogen activator, urokinase
10344052	0.6	0.22	1.0	0.02	0.0	0.91		
10562637	-0.1	0.33	1.0	0.00	-0.2	0.07	Ccnb1/Gm5593	cyclin B1
10341593	0.4	0.08	1.0	0.00	0.1	0.62		
10559478	0.4	0.04	1.0	0.00	0.1	0.32	LILRB3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3
10366848	0.1	0.09	1.0	0.00	0.1	0.48	B4GALNT1	beta-1,4-N-acetyl-galactosaminyl transferase 1
10411739	0.0	0.84	1.0	0.00	-0.2	0.02	Ccnb1/Gm5593	cyclin B1
10342412	0.4	0.11	1.0	0.00	0.4	0.10		
10368144	0.1	0.10	1.0	0.00	0.0	0.73	TNFAIP3	tumor necrosis factor, alpha-induced protein 3
10490903	0.3	0.01	1.0	0.00	0.2	0.08	CA13	carbonic anhydrase XIII
10444824	0.4	0.00	1.0	0.00	0.3	0.01	HLA-B	major histocompatibility complex, class I, B
10480035	0.4	0.00	1.0	0.00	0.1	0.10	PFKFB3	6-phosphofructo-2-kinase/fructose- 2,6-biphosphatase 3
10344592	-0.5	0.12	1.0	0.01	0.1	0.84		
10547590	0.4	0.01	1.0	0.00	0.1	0.51	KLRG1	killer cell lectin-like receptor subfamily G, member 1
10471929	0.0	0.88	1.0	0.00	0.1	0.26	ARHGAP15	Rho GTPase activating protein 15
10510260	0.1	0.74	1.0	0.00	-0.2	0.39	Nppb	natriuretic peptide type B
10341908	0.7	0.01	1.0	0.00	-0.1	0.85		
10569017	0.8	0.00	1.0	0.00	0.1	0.15	IFITM2	interferon induced transmembrane protein 2
10554162	0.0	0.64	1.0	0.00	-0.2	0.19		
10405587	0.0	0.72	1.0	0.00	0.2	0.06	TGFBI	transforming growth factor, beta- induced, 68kDa
10433507	0.1	0.50	1.0	0.00	0.1	0.56	CIITA	class II, major histocompatibility complex, transactivator
10587339	0.1	0.13	1.0	0.00	0.1	0.17		
10367532	0.1	0.50	1.0	0.00	0.0	0.56	TESPA1	thymocyte expressed, positive selection associated 1
10566333	0.6	0.00	1.0	0.00	0.1	0.12	TRIM5	tripartite motif containing 5
10597648	0.4	0.00	1.0	0.00	0.1	0.01	MYD88	myeloid differentiation primary response 88
10390763	0.1	0.49	1.0	0.00	-0.1	0.50	CCR7	chemokine (C-C motif) receptor 7
10360158	0.3	0.03	1.0	0.00	0.3	0.05	LY9	lymphocyte antigen 9
10338225	0.4	0.10	1.0	0.00	0.5	0.05		
10347933	0.4	0.02	1.0	0.00	0.2	0.37	SP140	SP140 nuclear body protein
10342214	0.2	0.60	1.0	0.00	-0.1	0.71		
10351667	-0.1	0.82	1.0	0.00	0.1	0.35	SLAMF1	signaling lymphocytic activation molecule family member 1
10450374	0.3	0.09	1.0	0.00	0.1	0.33		
10601424	0.2	0.27	1.0	0.00	0.0	0.83	GPR174	G protein-coupled receptor 174
10344407	0.2	0.48	1.0	0.00	0.4	0.03		
10515836	0.0	0.77	1.0	0.00	-0.1	0.16	Ccnb1/Gm5593	cyclin B1
10342377	-0.1	0.78	1.0	0.01	0.5	0.05		
10541605	0.5	0.02	1.0	0.00	0.1	0.77	CLEC6A	C-type lectin domain family 6, member A
10504755	0.3	0.01	1.0	0.00	0.1	0.20	BC057193	cDNA sequence BC057193
10548415	0.4	0.02	1.0	0.00	-0.1	0.40	Klri1	killer cell lectin-like receptor family I member 1
10340199	0.1	0.84	1.0	0.00	-0.5	0.08		
10356866	0.0	0.71	1.0	0.00	0.0	1.00	PDCD1	programmed cell death 1
10363161	0.3	0.06	1.0	0.00	0.2	0.18	TMEM229B	transmembrane protein 229B
10507908	0.0	0.66	1.0	0.00	0.0	0.77	FHL3	four and a half LIM domains 3
10343761	0.6	0.03	1.0	0.00	0.6	0.06		
10475414	0.9	0.00	1.0	0.00	0.3	0.01	B2M	beta-2-microglobulin
10361133	0.5	0.00	1.0	0.00	0.0	0.96		
10339990	0.8	0.00	1.0	0.00	0.0	0.84		
10508734	0.0	0.85	1.0	0.00	0.5	0.02	PTAFR	platelet-activating factor receptor
10536898	0.2	0.02	1.0	0.00	0.1	0.28	IRF5	interferon regulatory factor 5
10582868	0.2	0.12	1.0	0.00	0.1	0.51		
10407985	0.1	0.33	1.0	0.01	0.1	0.67	GPR141	G protein-coupled receptor 141
10338478	0.3	0.29	1.0	0.02	0.2	0.41		
10461723	0.1	0.50	1.0	0.00	0.0	0.77	FAM111A	family with sequence similarity 111, member A
10342606	0.4	0.15	1.0	0.01	0.3	0.28		
10608649	0.6	0.00	1.0	0.00	0.1	0.21		
10351792	0.3	0.04	1.0	0.00	0.3	0.01	SLAMF9	SLAM family member 9
10601421	0.3	0.01	1.0	0.01	-0.1	0.82	A630033H20Rik	RIKEN cDNA A630033H20 gene
10474875	-0.3	0.03	1.0	0.00	0.1	0.48	CASC5	cancer susceptibility candidate 5
10349401	0.0	0.66	1.0	0.00	0.2	0.16	GPR39	G protein-coupled receptor 39
10430190	0.0	0.69	1.0	0.00	0.2	0.07	Apo110a (includes others)	apolipoprotein L 11a
10586448	0.0	0.79	1.0	0.00	0.3	0.12	KIAA0101	KIAA0101
10594053	0.6	0.01	1.0	0.00	0.0	0.88	PML	promyelocytic leukemia
10602385	-0.1	0.69	-1.0	0.00	0.1	0.63	PFKFB1	6-phosphofructo-2-kinase/fructose- 2,6-biphosphatase 1

10340749	0.2	0.58	-1.0	0.05	-0.4	0.31		
10339035	-0.2	0.53	-1.0	0.00	0.0	0.86		
10338755	0.3	0.35	-1.0	0.00	-0.3	0.32		
10436095	-0.2	0.52	-1.0	0.03	0.7	0.02	Retnla	resistin like alpha
10354299	0.1	0.58	-1.1	0.00	-0.6	0.00	Mettl21e	methyltransferase like 21E
10344113	-0.4	0.37	-1.1	0.02	0.0	0.91		
10340272	-0.6	0.18	-1.1	0.04	0.2	0.67		
10342598	0.3	0.58	-1.1	0.05	-0.1	0.82		
10341361	0.0	0.97	-1.1	0.01	-0.5	0.09		
10341762	-0.3	0.43	-1.1	0.05	0.5	0.28		
10340062	0.0	0.95	-1.2	0.00	-0.8	0.02		
10518526	-0.5	0.04	-1.3	0.00	0.3	0.24	ANGPTL7	angiotensin-like 7

Online Table 10. List of differentially expressed genes on 60 dpi (log ratio > 1 or < -1, P value < 0.05)

Probe Set ID	4 dpi		7 dpi		60 dpi		Symbol	Entrez Gene Name
	Log ratio	P values (t-test)	Log ratio	P values (t-test)	Log ratio	P values (t-test)		
10583056	0.0	0.83	0.2	0.24	3.5	0.00	MMP12	matrix metalloproteinase 12 (macrophage elastase)
10538187	-0.1	0.47	1.3	0.00	3.2	0.00	GNPMB	glycoprotein (transmembrane) nmb
10511779	0.2	0.14	0.4	0.05	3.0	0.00	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2
10455970	6.6	0.00	6.8	0.00	2.8	0.00		
10545237	-0.1	0.46	-0.1	0.74	2.1	0.05		
10523717	0.4	0.03	2.6	0.00	2.0	0.00	SPP1	secreted phosphoprotein 1
10450161	0.2	0.19	2.6	0.00	1.7	0.00	HLA-DRA	major histocompatibility complex, class II, DR alpha
10547740	1.4	0.04	0.2	0.86	1.7	0.04	C1S	complement component 1, s subcomponent
10545173	-0.1	0.56	0.6	0.06	1.6	0.01		
10456005	0.1	0.47	2.5	0.00	1.6	0.00	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain
10450154	0.1	0.69	2.4	0.00	1.5	0.00	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1
10494262	-0.4	0.05	0.1	0.31	1.5	0.00	CTSK	cathepsin K
10522788	0.6	0.00	2.1	0.00	1.4	0.00	STAP1	signal transducing adaptor family member 1
10608681	5.1	0.00	6.3	0.00	1.4	0.00	Gm4841	predicted gene 4841
10403021	0.1	0.20	0.3	0.01	1.4	0.00		
10531126	-0.3	0.21	0.5	0.00	1.3	0.00	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
10338640	1.0	0.16	-0.3	0.64	1.3	0.02		
10557895	0.1	0.60	1.3	0.00	1.3	0.01	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)
10414360	0.2	0.02	1.7	0.00	1.3	0.00	LGALS3	lectin, galactoside-binding, soluble, 3
10545231	0.1	0.56	2.3	0.00	1.2	0.02		
10403038	-0.1	0.07	0.4	0.01	1.2	0.01		
10548375	0.0	0.88	1.1	0.00	1.2	0.00	CLEC7A	C-type lectin domain family 7, member A
10603551	0.4	0.01	1.6	0.00	1.2	0.00	CYBB	cytochrome b-245, beta polypeptide
10372410	0.5	0.00	1.7	0.00	1.1	0.00	GLIPR1	GLI pathogenesis-related 1
10455961	3.3	0.00	4.3	0.00	1.1	0.00	Iigp1	interferon inducible GTPase 1
10542164	0.5	0.00	2.5	0.00	1.1	0.00	CLEC12A	C-type lectin domain family 12, member A
10444291	0.1	0.46	2.5	0.00	1.1	0.00	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
10358408	0.5	0.00	2.3	0.00	1.1	0.00	RGS1	regulator of G-protein signaling 1
10461721	0.7	0.00	2.5	0.00	1.1	0.00	MPEG1	macrophage expressed 1
10545247	0.3	0.10	0.4	0.05	1.1	0.02		
10427628	0.2	0.09	2.0	0.00	1.1	0.00	IL7R	interleukin 7 receptor
10376324	3.8	0.00	5.4	0.00	1.0	0.00	Gm12250	predicted gene 12250
10531407	2.9	0.00	4.9	0.00	1.0	0.00	CXCL9	chemokine (C-X-C motif) ligand 9
10545198	-0.3	0.15	0.0	0.98	1.0	0.01		
10517165	1.0	0.00	3.0	0.00	1.0	0.00	Cd52	CD52 antigen
10459066	3.9	0.00	6.3	0.00	1.0	0.00	Gm4841	predicted gene 4841
10494271	0.9	0.00	2.3	0.00	1.0	0.01	CTSS	cathepsin S
10339525	0.0	0.97	0.2	0.59	1.0	0.01		
10344291	0.4	0.55	0.1	0.90	-1.0	0.01		
10546432	0.2	0.51	-0.6	0.03	-1.0	0.00	ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9
10343814	0.1	0.85	-0.3	0.66	-1.0	0.01		
10359867	0.6	0.06	-0.8	0.00	-1.1	0.00	LRRC52	leucine rich repeat containing 52
10338097	0.6	0.34	0.6	0.12	-1.3	0.02		
10343939	0.3	0.42	0.2	0.62	-1.4	0.01		
10504838	0.6	0.03	-0.7	0.00	-2.1	0.00	NR4A3	nuclear receptor subfamily 4, group A, member 3

Online Table 11. Top networks identified by IPA of microarray data of heart samples from TMEV-infected mice*

ID	Associated Network Functions	Score[†]
4 dpi		
1	Infectious Disease, Antimicrobial Response, Inflammatory Response	43
2	Antimicrobial Response, Inflammatory Response, Infectious Disease	43
3	Infectious Disease, Humoral Immune Response, Protein Synthesis	34
4	Cell-To-Cell Signaling and Interaction, Cellular Movement, Immune Cell Trafficking	31
5	Dermatological Diseases and Conditions, Cellular Movement, Immune Cell Trafficking	23
7 dpi		
1	Infectious Disease, Cellular Function and Maintenance, Antimicrobial Response	47
2	Cell Death and Survival, Antigen Presentation, Protein Synthesis	38
3	Lymphoid Tissue Structure and Development, Tissue Morphology, Antimicrobial Response	35
4	Infectious Disease, Antimicrobial Response, Inflammatory Response	35
5	Infectious Disease, Cell Death and Survival, Cell-To-Cell Signaling and Interaction	33
60 dpi		
1	Cellular Function and Maintenance, Inflammatory Response, Cellular Movement	33
2	Cellular Movement, Immune Cell Trafficking, Hematological System Development and Function	12
3	Ophthalmic Disease, DNA Replication, Recombination, and Repair, Cell Death and Survival	2
4	Cellular Assembly and Organization, Neurological Disease, Cardiovascular Disease	2

*Genes were clustered by Ingenuity Pathway Analysis (IPA) Network Generation Algorithm.

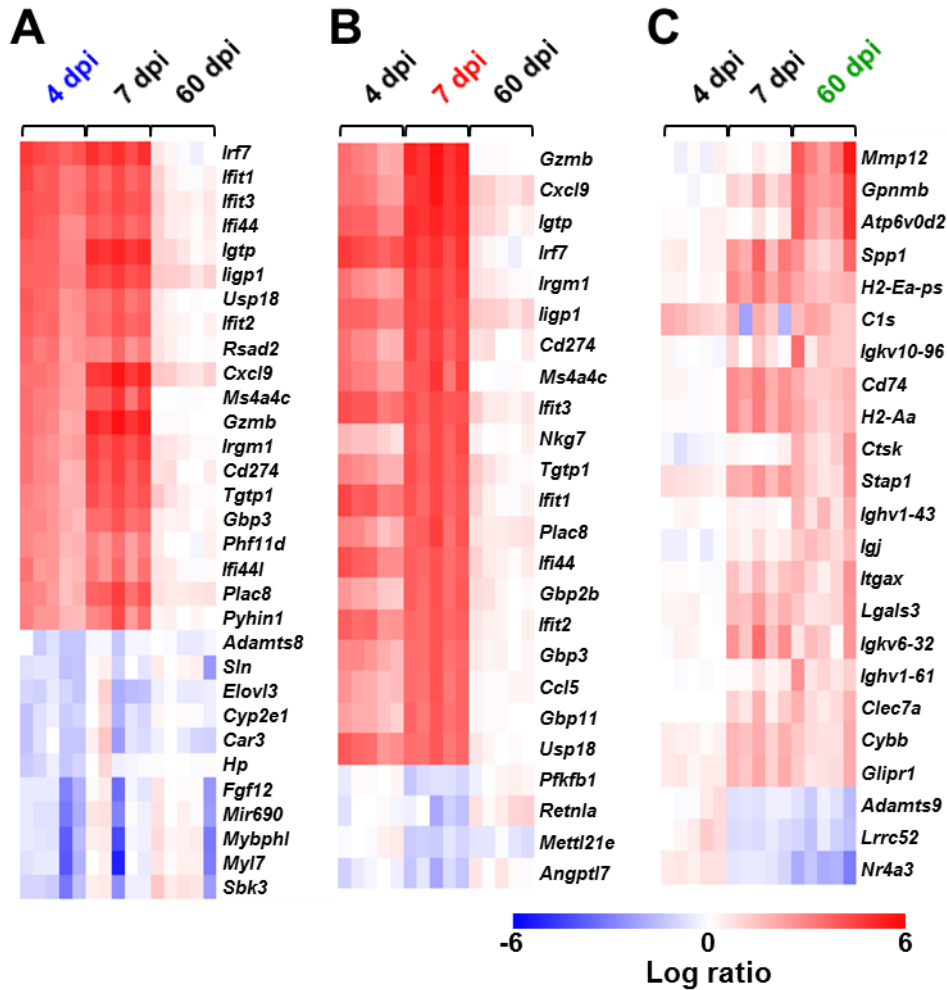
[†]Network score was calculated based on the right-tailed Fisher's Exact Test that takes into account: 1) the number of Network Eligible molecules in the network, 2) size of the network, 3) the total number of Network Eligible molecules in the given dataset, and 4) the number of molecules in the IPA database that could potentially be included in the networks.

Online Table 12. Top toxicity functions (cardiotoxicity)

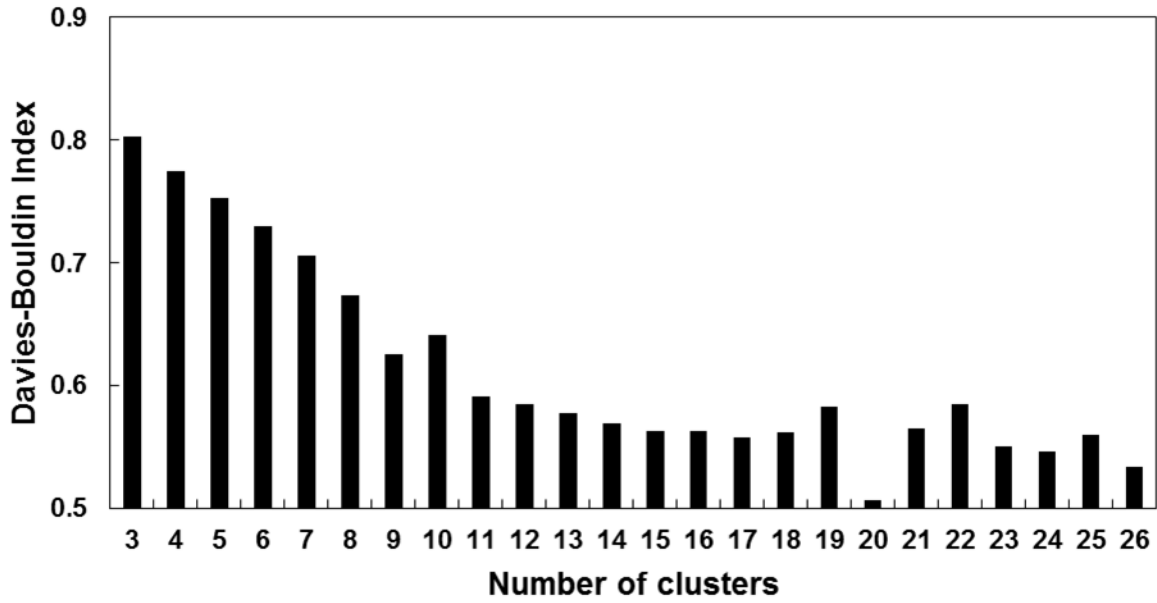
Name	<i>P</i> value	# of molecules	Molecules
4 dpi			
1 Cardiac Inflammation	0.0001 – 0.22	4	<i>Ccl2, Ccl3, Ccr5, Tlr3</i>
2 Cardiac Infarction	0.01 – 0.01	3	<i>Ccl2, Ccl3, Stat1</i>
3 Cardiac Dysfunction	0.01 – 0.01	2	<i>Ccl2, Timp1</i>
4 Cardiac Output	0.03 – 0.16	1	<i>Tnfsf10</i>
5 Pulmonary Hypertension	0.03 – 0.03	1	<i>Tnfsf10</i>
7 dpi			
1 Cardiac Inflammation	7E-11 – 0.57	11	<i>Ccl2, Ccl3, Ccr2, Ccr5, Ifng, Itgal, Itgam, Itgb2, Prf1, Stat4, Tlr3</i>
2 Cardiac Infarction	0.0003 – 0.15	8	<i>Ccl2, Ccl3, Cd44, Cybb, Fcer1g, Il6, Stat1, Lck</i>
3 Cardiac Dysfunction	0.001 – 0.07	5	<i>Ccl2, Cybb, Plau, Timp1, Ifng</i>
4 Cardiac Dilation	0.002 – 0.002	5	<i>Ccna2, Ifng, Plau, Spp1, Timp1</i>
5 Cardiac Necrosis/Cell Death	0.003 – 0.005	8	<i>Casp1, Cybb, Il1b, Il1rn, Lcn2, Sprr1a, Stat1, Tnfaip3</i>
60 dpi			
1 Cardiac Dysfunction	0.005 – 0.005	2	<i>Cybb, Ppargc1a</i>
2 Cardiac Fibrosis	0.01 – 0.01	2	<i>Cybb, Spp1</i>
3 Cardiac Dilation	0.07 – 0.07	1	<i>Spp1</i>
4 Cardiac Infarction	0.10 – 0.10	1	<i>Cybb</i>
5 Cardiac Necrosis/Cell Death	0.15 – 0.15	1	<i>Cybb</i>

Cardiotoxicities were ranked by IPA. *P* values were calculated by Fisher's Exact Test.

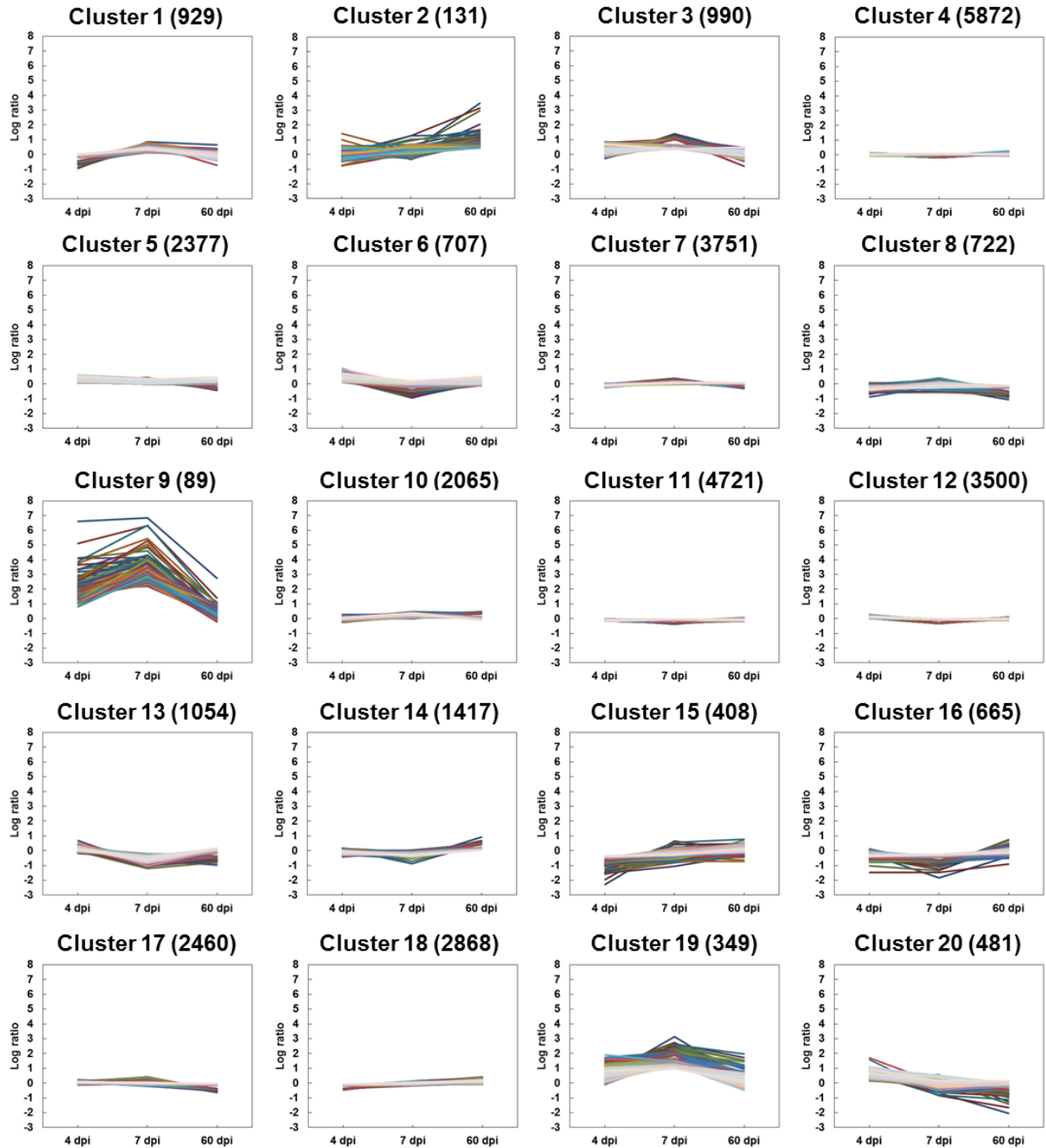
V. Online Figures



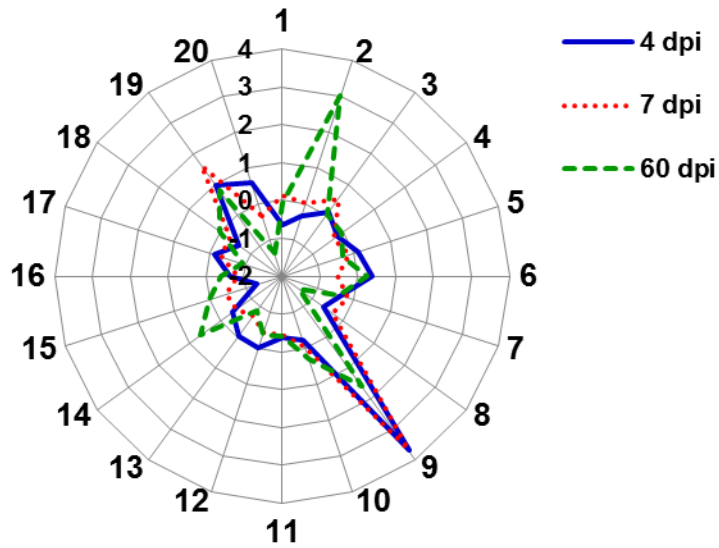
Online Figure 1. Heat maps of most highly up- or down-regulated genes in the hearts of TMEV-infected mice on 4 (A), 7 (B), and 60 dpi (C). A) On 4 dpi, 20 upregulated and 16 downregulated genes. B) On 7 dpi, 20 upregulated and 7 downregulated genes. C) On 60 dpi, 20 upregulated and 4 downregulated genes. Gene expression patterns of (A) and (B) were similar between 4 and 7 dpi, while those in (C) were similar between 7 and 60 dpi. Red, blue, and white indicate upregulation, downregulation, and no change, compared with control mice, respectively. Each column represents the data from one mouse. $n = 5/\text{dpi}$. A list of abbreviations of genes is shown in Online Table 1.



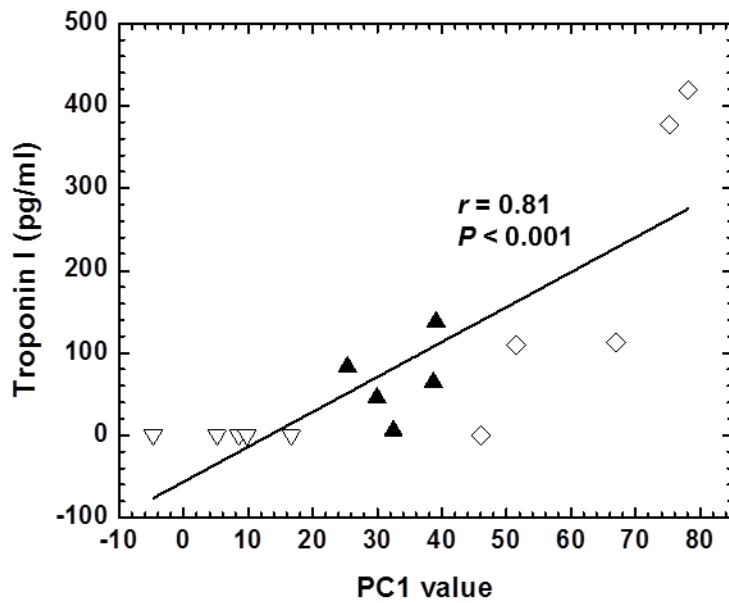
Online Figure 2. Davies-Bouldin index of k -means clustering for microarray data of the hearts from TMEV-infected mice (total number of mice = 15, five mice/dpi). We used Davies-Bouldin index to determine the optimum number of clusters in k -means clustering and obtained the lowest score (0.51) when microarray data were separated into 20 clusters.



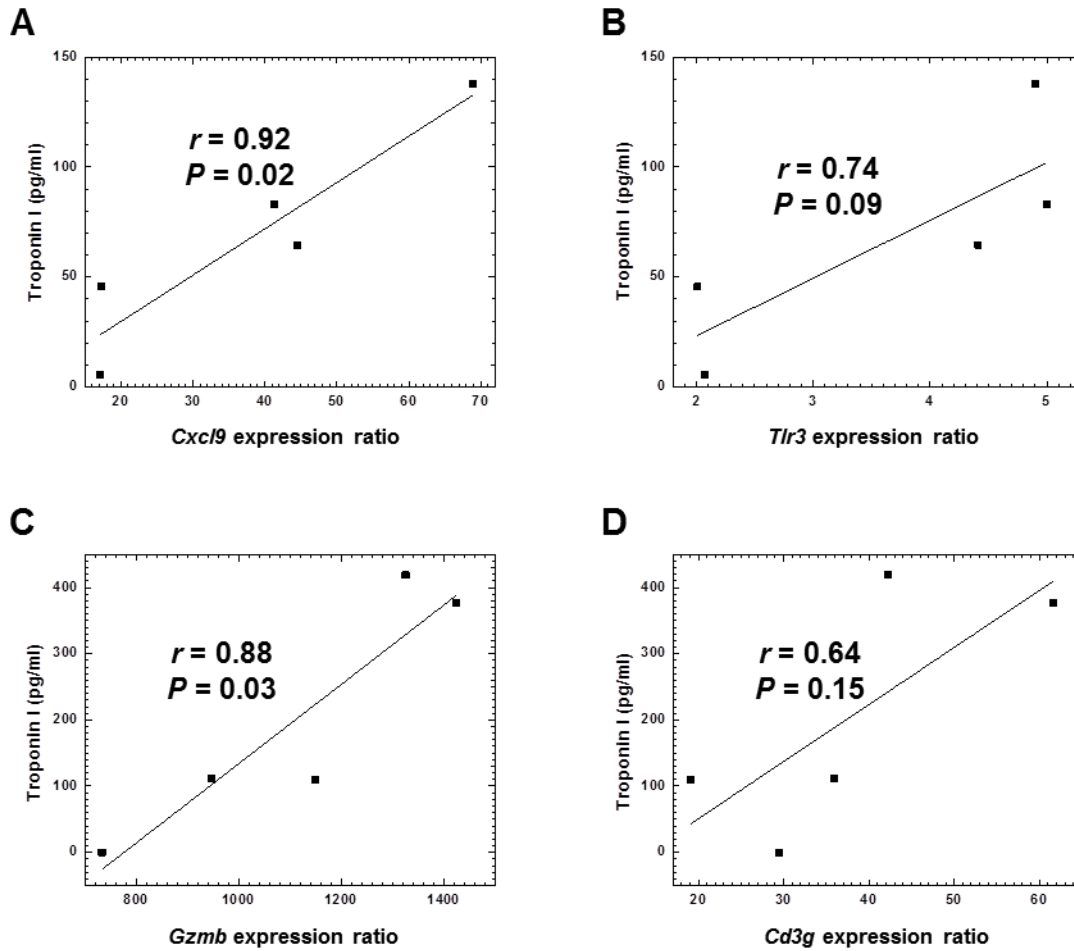
Online Figure 3. The gene expression patterns of 20 clusters separated by *k*-means clustering. Graphs were drawn using the genes of top 80, middle 80, and bottom 80 (total 240 genes) in each cluster. The number next to a cluster number indicated the number of genes in each cluster.



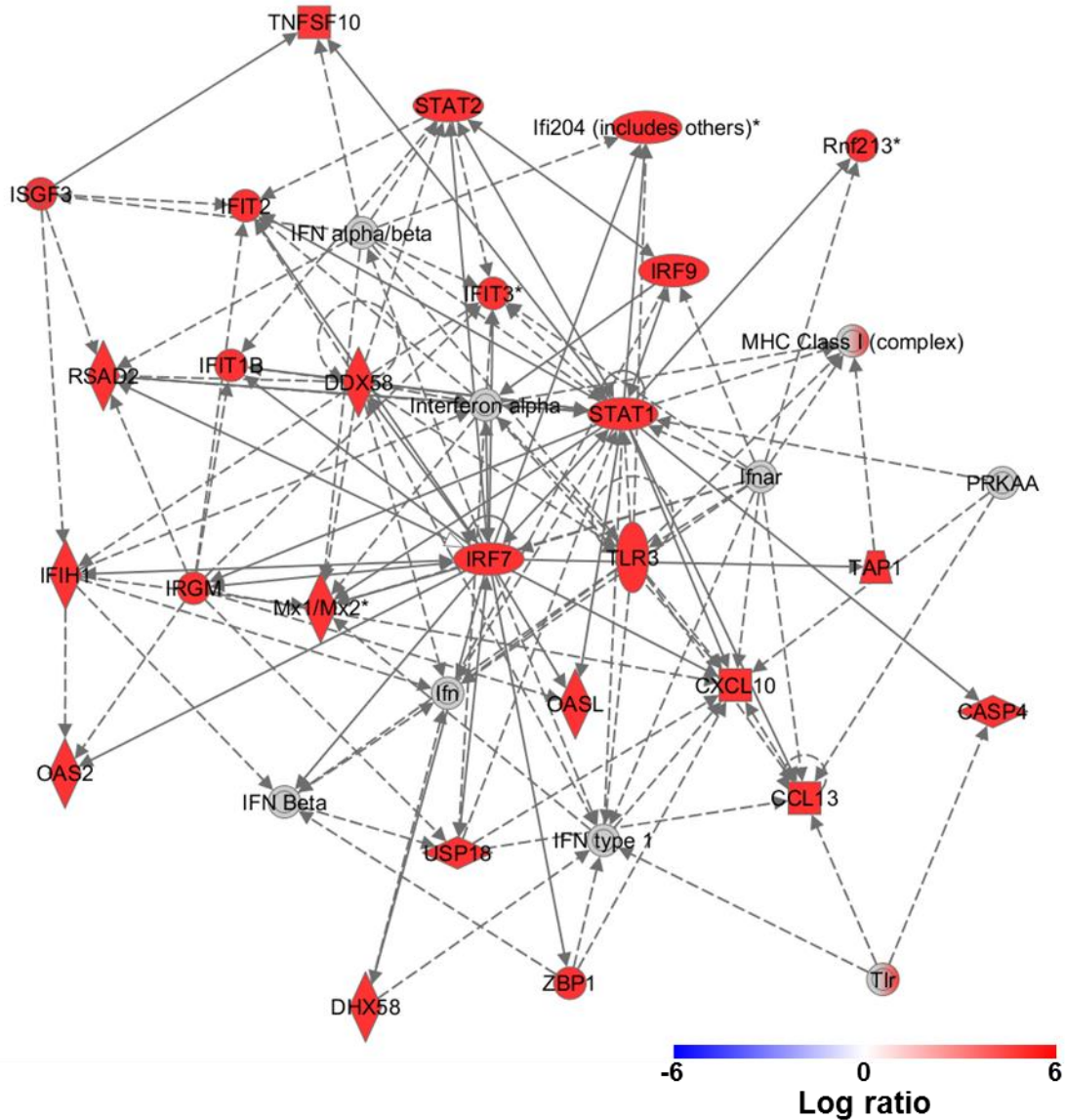
Online Figure 4. Radar chart of expression patterns of cluster center genes of 20 clusters by *k*-means clustering. Clusters 2, 9, and 19 included cardiac remodeling-, innate immunity-, and acquired immunity-related genes, respectively. The number at each vertex is the cluster number (1 to 20), while the numbers along the axis (-2 to 4) are log ratios, compared with age-matched controls.



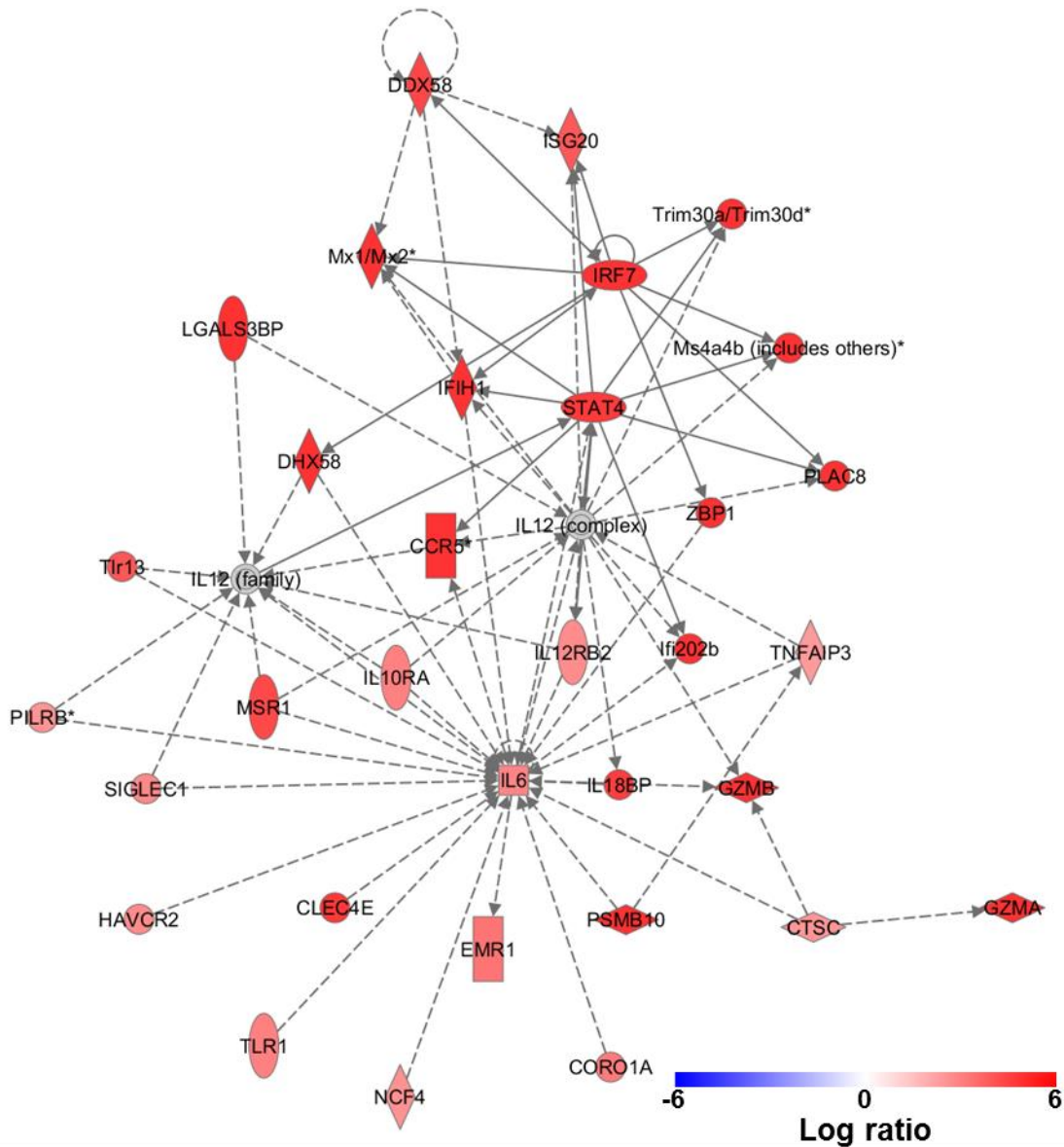
Online Figure 5. Correlation between disease activity and PC1 values. As an indicator of disease activity, cardiac troponin I levels in sera determined by ELISA were used. The PC1 values were calculated using microarray data by R and R package ‘prcomp’. There was a strong correlation between troponin levels and PC1 values ($r = 0.81$, $P < 0.001$). This suggested that the PC1 value reflected the disease activity. ▽: 60 days post infection (dpi), ▲: 4 dpi, ◇: 7 dpi.



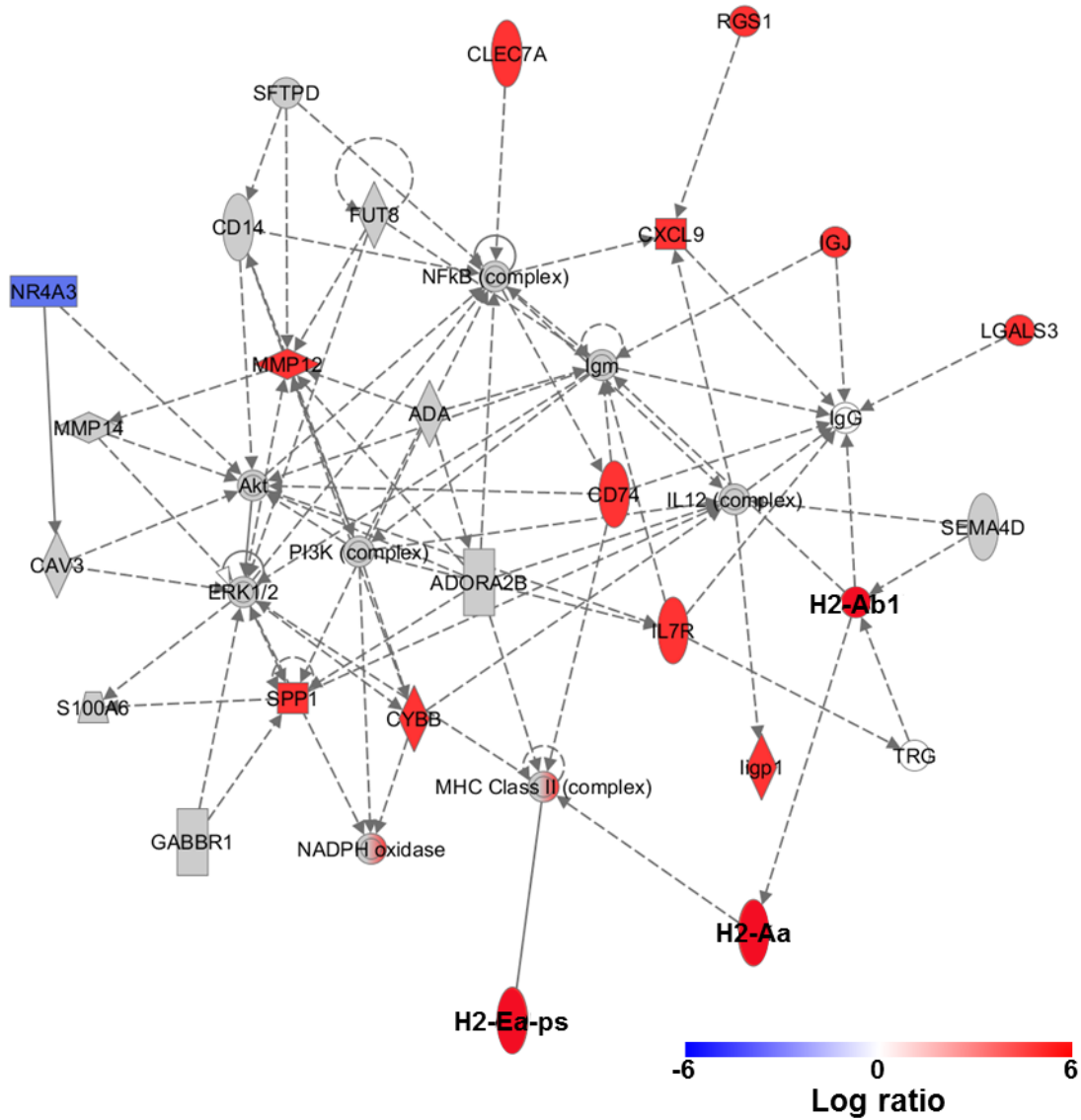
Online Figure 6. Correlations between serum troponin I levels and gene expression ratios (real-time PCR). There were strong correlations between troponin I levels and gene expression ratios of Chemokine (C-X-C motif) ligand 9 (*Cxcl9*) (A) or toll-like receptor 3 (*Tlr3*) (B) on 4 dpi. There was also a strong correlation between troponin I levels and gene expression ratios of granzyme B (*Gzmb*) (C), but not CD3 γ subunit (*Cd3g*) (D), on 7 dpi.



Online Figure 7. The network associated with ‘Infectious Disease’, ‘Antimicrobial Response’, and ‘Inflammatory Response’. This is the top network listed on Ingenuity Pathway Analysis® (IPA) on 4 dpi. Red nodes indicate genes upregulated in the hearts of TMEV-infected mice compared with control mice. Gray nodes indicate genes whose expression levels were less than 2-fold or *P* values were more than 0.05. *P* values were determined comparing the signal values of each probe between five samples from infected mice and five samples from age-matched controls, using Student *t* test.

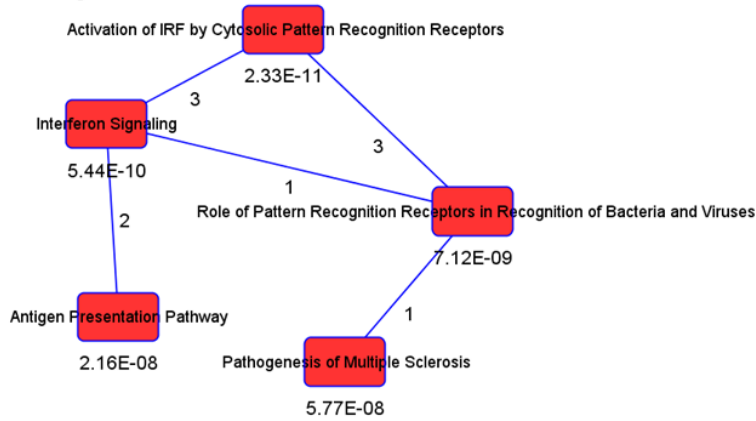


Online Figure 8. The network associated with ‘Infectious Disease’, ‘Cellular Function and Maintenance’, and ‘Antimicrobial Response’. This is the top network listed on IPA on 7 dpi. Red nodes indicate genes upregulated in the hearts of TMEV-infected mice compared with control mice. Gray nodes indicate genes whose expression levels were less than 2-fold or P values were more than 0.05. P values were determined comparing the signal values of each probe between five samples from infected mice and five samples from age-matched controls, using Student t test.

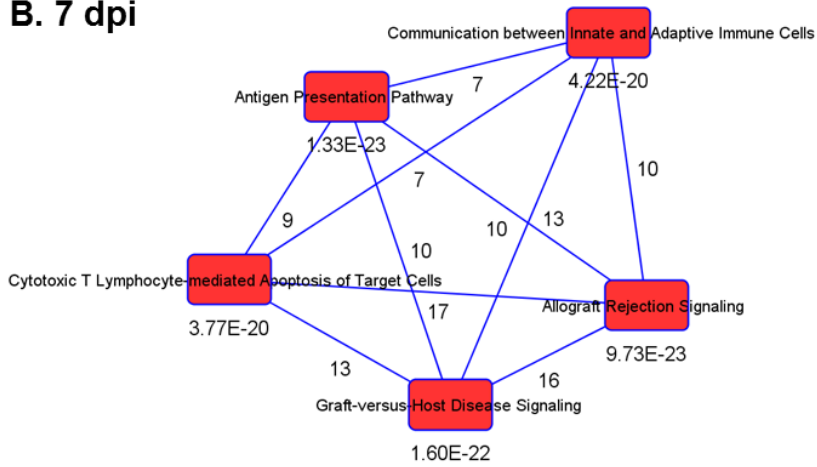


Online Figure 9. The network associated with ‘Cellular Function and Maintenance’, ‘Inflammatory Response’, and ‘Cellular Movement’. This is the top network listed on IPA on 60 dpi. Red nodes indicate genes upregulated in the hearts of TMEV-infected mice compared with control mice. Blue nodes indicate downregulated genes. Gray nodes indicate genes whose expression levels were less than 2-fold or *P* values were more than 0.05. *P* values were determined comparing the signal values of each probe between five samples from infected mice and five samples from age-matched controls, using Student *t* test.

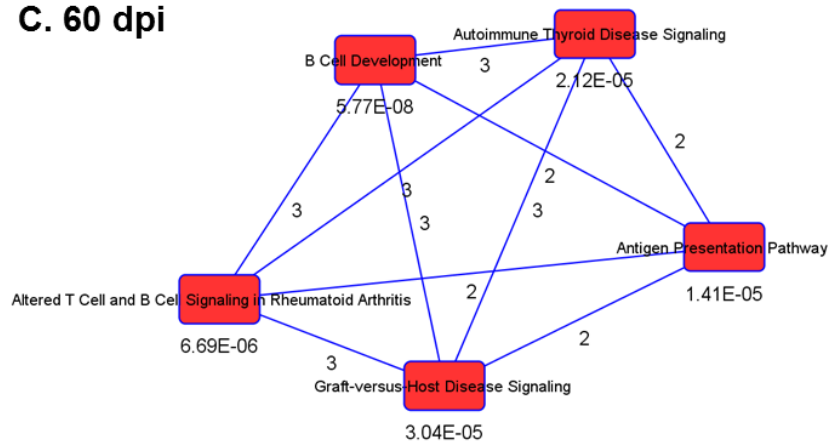
A. 4 dpi



B. 7 dpi



C. 60 dpi



Online Figure 10. The top 5 canonical pathways ranked by IPA on 4 (A), 7 (B), and 60 dpi (C). The numbers on the lines indicate the number of overlapped genes between two pathways. The values under the nodes indicate *P* values calculated by Fisher's Exact Test.