Supplementary Information Titles

Journal: Nature Medicine	

Article Title:	**Host mediated regulation of superinfection in malaria**
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Supplementary Item & Number	**Title or Caption**
Supplementary Figure 1	Inhibition of *Plasmodium* liver infection by an ongoing malaria blood-stage infection results in small EEFs that fail to develop.
Supplementary Figure 2	Infection of both mouse primary hepatocytes and hepatoma cells by *P. berghei* sporozoites is unaffected by co-culture with iRBCs.
Supplementary Figure 3	No support for a role of adaptive immunity or aspects of innate immunity in inhibition of *Plasmodium* liver infection by an ongoing malaria blood-stage infection.
Supplementary Figure 4	Reduced level of apoptosis observed in *P. berghei* NK65 blood-stage infected caspase-3 deficient mice.
Supplementary Figure 5	Hepcidin, Id1 and iron and malaria infections.
Supplementary Figure 6	Model predictions for age-related incidence and multiplicity of infections.
Supplementary Table 1	Differentially expressed (DE) transcripts during blood-stage, liver stage or Reinfection.
Supplementary Methods	Methods

Supplementary Material - Methods

Real time *in vivo* imaging luminescent *Plasmodium*. Naïve mice (control) and blood stage infected (PbA in Fig. 1A and PbNK in Fig. 1B and Fig. 1C), were intra-peritoneally injected with 200µl of anaesthesia mixture (80 mg/kg Ketamine and 10 mg/kg Xylazine) diluted in PBS in order to allow each mouse exposure to 15 *Anopheles* mosquitoes infected with luciferase expressing *P. berghei* (parasite line 354cl4). After 30 minutes of mosquito bites, mice were shaved in the abdomen. Forty h post-infection for Fig. 1A and 1B and 6 days post-infection for Fig. 1C, D-luciferin dissolved in PBS (150 mg/kg; Caliper Life Sciences, USA) was injected subcutaneously in the neck. Animals were anesthetized again as described above for the whole duration of measurements (performed within 5 to 10 minutes after the injection of D-luciferin). Bioluminescence imaging was acquired with a 12.5 cm field of view (FOV), medium binning factor and an exposure time of 180 seconds. Luciferase activity in animals was visualized through imaging of whole bodies using the i*n vivo* IVIS® Lumina Imaging System [1].

qReal-Time PCR quantification of liver infection. Livers were collected and homogenized in denaturing solution (4 M guanidine thiocyanate; 25mM sodium citrate pH 7, 0.5% N-Lauroylsarcosineand, 0.7% β-Mercaptoethanol in DEPC-treated water). Total RNA was extracted using RNeasy Mini kit (Qiagen), and then reverse transcribed into cDNA using Transcriptor First Strand cDNA Synthesis kit (Roche), according to the manufacturers' protocols. Infection load in the liver was determined as previously described by qRT-PCR using classic PbA 18S *rRNA* [2] specific primers or *gfp* specific primers (*gfp* expression correlates with PbA 18S *rRNA*, fig. S1). qRT-PCR reactions used Power SYBR Green PCR Master Mix (Applied Biosystems) and were performed according to the manufacturer's instructions on an ABI Prism 7000 system (Applied Biosystems). Relative amounts of PbA 18S *rRNA* and *gfp* mRNA were calculated against the Hypoxanthine Guanine Phosphoribosyltransferase (*hprt*) housekeeping gene, following a prime denaturation of 10 minutes at 95°C, then 50 cycles of 95°C for 15 seconds and 60°C for 1 minute. PbA 18S *rRNA*, *gfp* and *hprt* specific primer sequences were:

5’-CGG CTT AAT TTG ACT CAA CAC G-3’ and 5’-TTA GCA TGC CAG AGT CTC GTT C-3’ for PbA 18S *rRNA*, 5’- GTC AGT GGA GAG GGT GAA GG– 3’ and 5’ – ACT TCA GCA CGT GTC TTG TAG TTC – 3’ for *gfp* and 5’ – TGC TCGAGA TGT GAT GAA GG – 3´ and 5’ – TCC CCT GTT GAC TGG TCA TT – 3’ for mouse *hprt*. External standardization was performed using plasmids encoding the full-length genes cDNA cloned in TOPO TA (Invitrogen).

Chloroquine treatment. Mice infected 4 days previously with *P. berghei* NK65 and control mice received 0.8 mg of chloroquine (CQ) by intra-peritoneal injection for 1 or 2 days before re-infection, a protocol leading to decrease in peripheral blood parasitaemia until zero by day 2 of treatment.

Cells. Huh7 cells, a human hepatoma cell line, were cultured in RPMI (Gibco/Invitrogen) medium supplemented with 10% fetal calf serum (FCS, Gibco/Invitrogen), 1% penicillin/streptomycin (pen/strep, Gibco/Invitrogen), 1% glutamine (Gibco/Invitrogen) at pH 7 and maintained at 37°C with 5% CO_2.

Isolation of murine primary hepatocytes. Mouse primary hepatocytes were isolated as previously describe [3]. Briefly, cells were initially obtained by perfusion of mouse liver lobules with liver perfusion medium and liver digest medium (Gibco/Invitrogen) at 37°C using a peristaltic pump. Hepatocytes were then purified using a 1.12 g/ml, 1.08 g/ml and 1.06g/ml Percoll gradient. Cells were cultured in William´s E medium containing 4% FCS, 1% pen/strep in 24-well plates coated with 0.2% Gelatine in PBS. Cells were maintained in culture at 37°C and 5% CO_2.

Sporozoite infection and development in contact with infected blood. Mouse primary hepatocytes and Huh7 cells, a human hepatoma cell line, were cultured as described above in complete William’s E or RPMI (Gibco/Invitrogen) in transwell system plates (COSTAR/Corning). In the lower chamber, liver-derived cells were infected with 20,000 *P. berghei* ANKA sporozoites, and allowed to share medium with upper chambers containing serum (CTRL), non-infected blood (NI) or blood containing 6 x 10^5 *P. berghei* NK65 iRBCs (PbNK), new serum was added every 12h. After 36h of co-culture, hepatoma cells were collected and treated for FACS analysis and primary hepatocytes were fixed in 4% paraformaldehyde for 10 minutes, washed three times in PBS, and later permeabilized and blocked 1h in 0.3% Triton X-100 (Calbiochem) and 1% Bovine Serum Albumin (Sigma) to avoid non-specific reactivity. Coverslips were then incubated 1h at 4°C in the same solution containing anti-GFP IgG Alexa flour 488 congugate antibody (Invitrogen), Alexa 594 phaloidin (Invitrogen) and DAPI (Sigma). After mounting coverslips on slides, EEFs were counted using the Leica DM5000B Widefield Fluorescence Microscope, and the sizes of 20 randomly chosen EEFs of each coverslip were measured using a Zeiss LSM 510 META Point Scanning Confocal Microscope. All immunofluorescence-stained images were analysed using the ImageJ 1.42b software.

Fluorescence activated cell sorting (FACS) analysis of sporozoite infection. FACS analysis of sporozoite-infected Huh7 hepatoma cell cultures at 36h post-sporozoite addition was performed to determine the percentage of parasite-containing cells and parasite-GFP intensity within infected cells. Cell samples for FACS analysis were processed as previously described [4].

Transcription profiling. Total RNA from livers of naïve mice (control group), mice infected with 10^6 *P. berghei* NK65 iRBCs for 7 days (Blood stage group, BS), mice infected with 5x10^4 *P. berghei* ANKA-GFP sporozoites for 40h (Liver stage group, LS), and mice infected with 10^6 *P. berghei* NK65 iRBCs for 7 days then re-infected with 5x10^4 *P. berghei* ANKA-GFP sporozoites for 40h (Reinfection group, Reinf) was extracted using RNeasy Mini kit (Qiagen), following the manufacturer's instructions. Three biological replicates were analysed for each group. RNA quality and quantity was assessed on a Bioanalyser nanochip (Agilent). Total RNA was reverse transcribed and end-labelled as cRNA using the GeneChip WT Amplified Double-Stranded cDNA Synthesis Kit and the GeneChip WT Terminal Labeling Kit as recommended by Affymetrix. Hybridisation to an Affymetrix Mouse Gene 1.0 ST Array was carried out at 45°C for 16h under rotation (60 rpm). Arrays were washed on an Affymetrix FS450 and scanned using an Affymetrix Genechip Scanner 3000 7G. Fluorescence intensities were background adjusted, quantile normalised and median polished into expression values using the robust multi-array averaging program RMA [5] in R/Bioconductor suite [6] (software package: affy [7]) To assess significance and differential expression (DE), each infected group was compared to the non-infected group, and out of 28815 main probesets represented on the array, 6273 transcript clusters were classified as significant (F-test, $p<0.05$) with 1704 being DE at a fold change of 2 (software packages: limma [8] and gplots). Each cluster separated from the non-hierarchical clustering was subjected to a Gene Ontology Biological Process enrichment analysis using a hypergeometric test (software package: GOstats [9]. Original data was submitted to Array Express and is accessible in the reviewer's user account: Username: Reviewer_E-TABM-839, and Password: 1257429875724.

Depletions using monoclonal antibodies. (**i**) IL-6. Mice infected with *P. berghei* NK65 and control mice received 1 mg of IL-6 specific monoclonal antibody (clone MP520F3, Rat IgG1) 3h, 3 days, and 5 days after inoculation with infected blood, a protocol leading to IL-6 depletion at the time of sporozoite infection, 7 days post- *P. berghei* NK65 infection.

(**ii**) IFNγ. Mice infected with *P. berghei* NK65 and control mice received 0.4 mg of IFNγ specific monoclonal antibody (clone R46A2, Rat IgG1) 1, 2 and 3 days, after inoculation with infected blood, a protocol leading IFNγ depletion at the time of sporozoite infection, 5 days post-*P. berghei* NK65 infection.

(**iii**) TNFα. Mice infected with *P. berghei* NK65 and control mice received 0.4 mg of TNF specific monoclonal antibody (clone XT3.11, Rat IgG1) 4 and 6 days after inoculation of infected blood, a protocol leading to TNFα depletion at the time of sporozoite infection, 5 days post-*P. berghei* NK65 infection.

Nω-Nitro-L-arginine methyl ester hydrochloride treatment. Mice infected with *P. berghei* NK65 and control mice received 50mg/kg of Nω-Nitro-L-arginine methyl ester hydrochloride (L-

NAME, Sigma) 3, 4, 5 and 6 days after inoculation of infected blood, a protocol leading to NOS inhibition at the time of sporozoite infection, 7 days post- *P. berghei* NK65 infection.

S-methyl-isothiourea treatment. Mice infected with *P. berghei* NK65 and control mice received 100 μg of S-methyl-isothiourea (SMT, Sigma) 3, 4, 5 and 6 days after inoculation of infected blood, a protocol leading to iNOS inhibition at the time of sporozoite infection, 7 days post- *P. berghei* NK65 infection.

C3a receptor antagonist treatment. C5a deficient (B10.D2-Hc0.H2d.H2-T18c/oSnJ) naïve or *P. berghei* NK65 infected mice received 0.5 mg of C3a receptor antagonist (SB290157, Calbiochem) 4h before sporozoite re-infection, 5 days post-*P. berghei* NK65 infection.

N-Acetyl Cysteine treatment. Mice infected with *P. berghei* NK65 and control mice received 20mg/kg of N-Acetyl Cystein treatment (NAC, Zambon) 2h after inoculation of infected blood, and every 12h for the course of the experiment. Three days post-blood stage infection all mice were infected with *gfp*-expressing *P. berghei* sporozoites and 40h later livers were collected.

Splenectomy. Intra-peritoneal injection of 250 µl of anaesthesia mixture (80 mg/kg Ketamine and 10 mg/kg Xylazine) was administered to mice 10 to 15 min before surgery. After observing the animals for response to anaesthesia, the animals were laid on their right side; and the fur removed with a razor. A 1.5 to 2 cm long skin incision was made in the left hypochondrium, the connective tissue under the skin was loosened and another incision in the peritoneal wall was made. Gently the spleen was pulled onto the exterior surface of the peritoneum. The artery, attached to the hilum of the spleen, close to the stomach was tied off with a single knot using 3-0 plain CATGUT suture. The efferent venule attached at the other end of the spleen was tied off similarly by a single knot using 3-0 plain CATGUT. Cutting away the mesentery and connective tissue, the spleen was removed. Peritoneal wall and underlying muscles were closed with plain CATGUT (3-0) and the skin incisions closed with wound clips. Mice with accessorial spleen were excluded from the study. The control group underwent a sham surgery and they were maintained in the same conditions.

***In vitro* hepcidin induction.** Mouse primary hepatocytes were cultured in the presence of solely medium or medium with added serum collected from non-infected and *P. berghei* NK65 infected mice, new serum was added every 12h. All these three conditions were tested in the presence of Dorsomorphin or IL-6 specific monoclonal antibody (clone MP520F3, Rat IgG1). After 24h culture cells were washed and collected for RNA extraction and measurement of hepcidin expression.

Total non-heme iron quantification. Total non-heme iron was measured as described previously [10], in brief after drying samples (spleens and primary hepatocytes) for 48h at 45°C, tissues were weighed, and digested for 48h in 10% trichloroacetic acid/10% HCl at 65°C. Two hundred microliters of the extract were then added to 1 ml of chromogen solution (0.01% bathophenanthroline-disulfonic acid, 0.1% thioglycolic acid, 2.5 M sodium acetate) and after 15 minutes of incubation, absorbance was measured at 535 nm. A standard curve performed for known iron concentrations between 10 and 500 μg/ml revealed a linearity of response with a slope of ~1. Samples were diluted appropriately to fall within the linear range. Values were expressed as % of control, in micrograms of iron per gram of dry weight.

HAMP1 peptide *in vivo* treatment. Mice were treated with 40μg of hamp1 peptide (Peptide, Japan) 20h prior to sporozoite infection and 20h after sporozoite infection. All mice were then infected with $2x10^4$ *P. berghei* ANKA (1.49L) sporozoites, and 40h later livers were collected and liver infection was determined by expression of PbA 18S *rRNA*.

HAMP adenovirus *in vivo* infection. Mice were infected with adenoviral $5x10^{11}$ pu of pAd.CMV.GFP (control) or pAd.CMV.Hamp.ires.GFP.Wpre (HAMP.adV) kindly provided by Stefano Rivella for (Weill Cornell Medical College, USA) 48h prior to sporozoite infection, hepcidin expression was 2 fold upregulated by the Hamp.adv compared to uninfected and GFP.adv control groups. All mice were then infected with $2x10^4$ *P. berghei* ANKA (1.49L) sporozoites, and 40h later livers were collected and liver infection was determined by expression of PbA 18S *rRNA*.

HAMP transgenic mice and *Plasmodium* liver infection. Wild-type and transgenic mice containing an over-expression of *hamp1* [11] were infected with $3x10^4$ *P. berghei* ANKA (1.49L) sporozoites, hepcidin expression was 2 fold upregulated by the transgene compared to wild-type control groups, and 40h later livers were collected and liver infection was determined by expression of PbA 18S *rRNA*.

Tunel detection of apoptosis. Liver tissues were harvested from wild type and caspase 3-deficient mice infected with *P. berghei* NK65 for 8 days along with non-infected wild type mice. Tissues were frozen in OCT freezing medium and then sliced into 16 μm sections using a cryostat. Analysis of DNA fragmentation by transferase-mediated dUTP nick-end labelling (TUNEL) was performed using the In Situ Cell Death Detection kit, POD and DAB Substrate kits (Roche, USA) following the manufacturer's instructions, and later stained with DAPI (Sigma) for general nuclei count. Sections were imaged on a Zeiss LSM 510 META Point Scanning Confocal Microscope. Quantification of positive cells was determined counting a total of 1000 cells/section and calculating the proportion of stained nuclei. Images of immunofluorescence-stained sections were analysed using the ImageJ 1.42b software.

Model description. A stochastic, individual-based model was used to follow a cohort of N individuals for up to 20 years in a low, medium and high transmission setting (with according annual EIR of 2, 20 and 200, respectively). At each time point t_i the probability of an individual becoming infected, P, is given as the product of the probability of being bitten by an infected mosquito, p_{bite} (=1-1/EIR), times the probability of this bite leading to successful blood stage infection which itself is dependent on the immune history of the host, p_{imm}, and the parasite density of a possible ongoing infection, p_{dens}. That is, $P(\text{infection}) = P(p_{bite} \cap p_{imm} \cap p_{dens})$. We assumed that the average parasite density per infection decreases with age [12-14] given as

$\pi_{age} = \pi_{\max}(1 + k\exp(-age))$, and that mean parasitaemia level also decreases over the course of infection [15]; for simplicity we assumed this to be linear although the actual functional form does not change the results presented here. We further assumed that there exists a threshold parasite density, p_{crit}, above which the host is mostly protected from super-infections. This threshold density then defines the probability of a successful inoculation as a function of infection length and is given as $p_{dens} = \prod_i \left(1 + \exp(\tau_i - \Delta t_i)^{\beta}\right)^{-1}$, where i is the number of concurrent infections, Δt_i is the time since infection i, and $\tau_i = T_i(1 - \pi_{crit} / \pi_{\max})$ is the time when the probability of a new blood stage infection is approximately half; $1/T_i$ is the clearance rate of infection i. For reasons of simplicity and because we are here more concerned with the inhibitory effect on new liver-stage infections, we do not take into account the full complexity of super-infections (see e.g. [16]) and assume infections and their respective clearance rates to be independent. A graphical representation of the relationship between parasitaemia and probability of infection is given in Supplementary Figure 7. Finally we assumed acquired immunity to be driven by exposure, or rather the number of life-time blood stage infections. We chose this to be non-linear to take into account antigenic diversity of and immunity against the various life-stages of the parasite; again, the exact functional form does not have a significant effect on the results presented. The probability of an infection not being blocked by immunity is then given as $p_{imm} = \prod_{i=1..n} \sqrt{\frac{D-i}{D}}$, where n is the life-time number of blood stage infections and D can be understood as a measure of antigenic diversity and which defines the rate of acquired protection with infection history (see SI). We also considered maternal protection during the first few months of life to examine if this could explain the observed patterns in the number and multiplicities of infections (MOI). This was done by including a time-dependent probability of infection $p_{mat} = 1/(1 + \exp(-0.05(t - 90)))$. However, apart from an initial drop in the resulting number of infections and MOI in the <1 year old age class (see Fig. S11) this had no effect on the overall model predictions and was thus dropped from the subsequent analyses. The parameter values used for the simulations are as follows: N=500, p_0=5000, k=2, b=2, p_{crit}=3000, T~normal(100) and D=500. Note, our results are robust to a wide range of parameter values; however, we do not attempt to fit the outcome to actual epidemiological data but here are more concerned with the qualitative behaviour of the model.

Statistical analysis. All experiments were performed with a minimum number of 5 mice per group, and all shown results are one representative of at least three independent experiments, or the cumulative result of at least three independent experiments. In all bar graphs, bars represent average and error bars represent standard deviation. Significance is indicated by * and its value is identified in every graph. For samples in which n > 5, statistical analysis was performed using unpaired Student t or variance (ANOVA) parametric tests. Normal distributions were confirmed using the Kolmogorov-Smirnov test.

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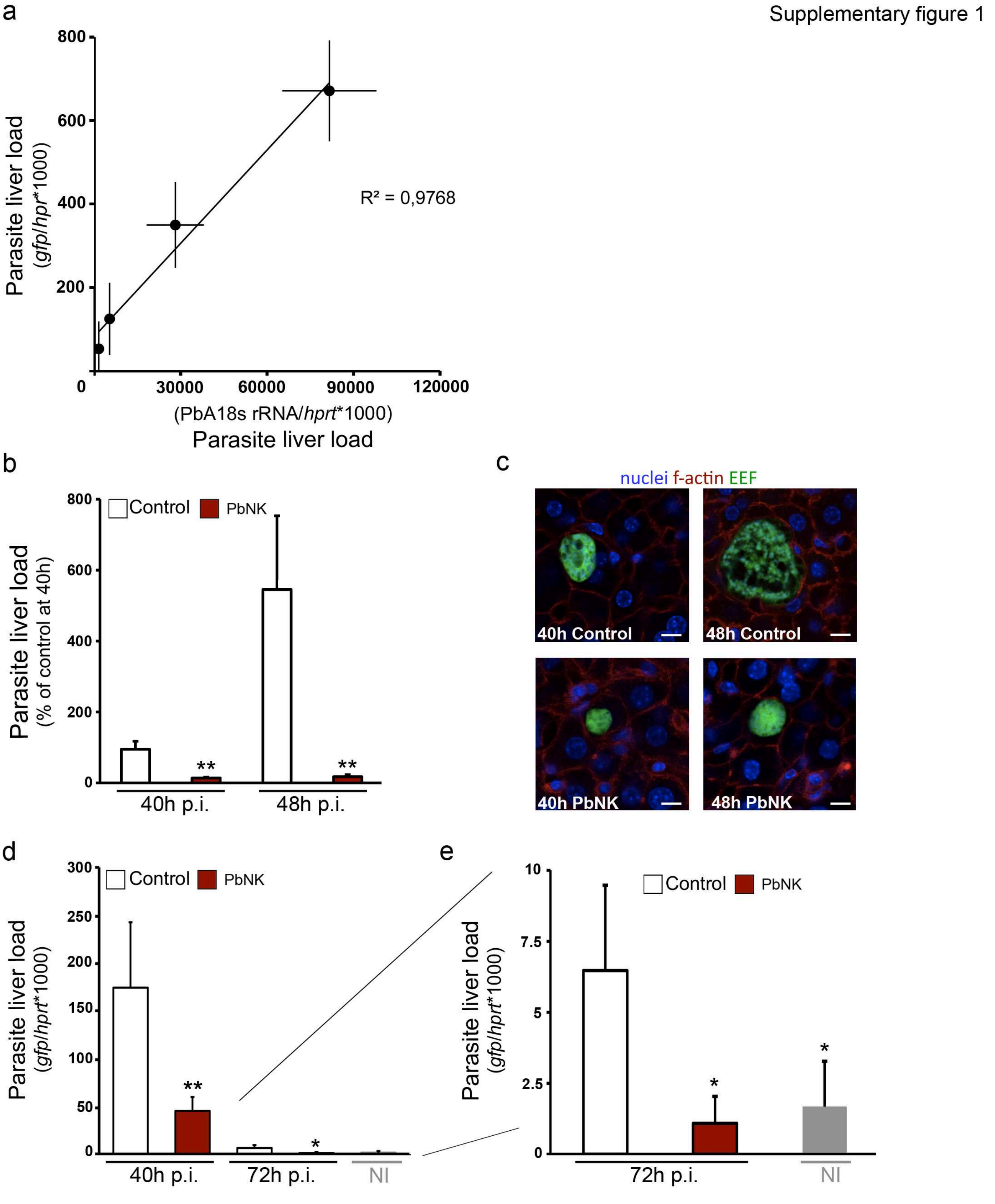
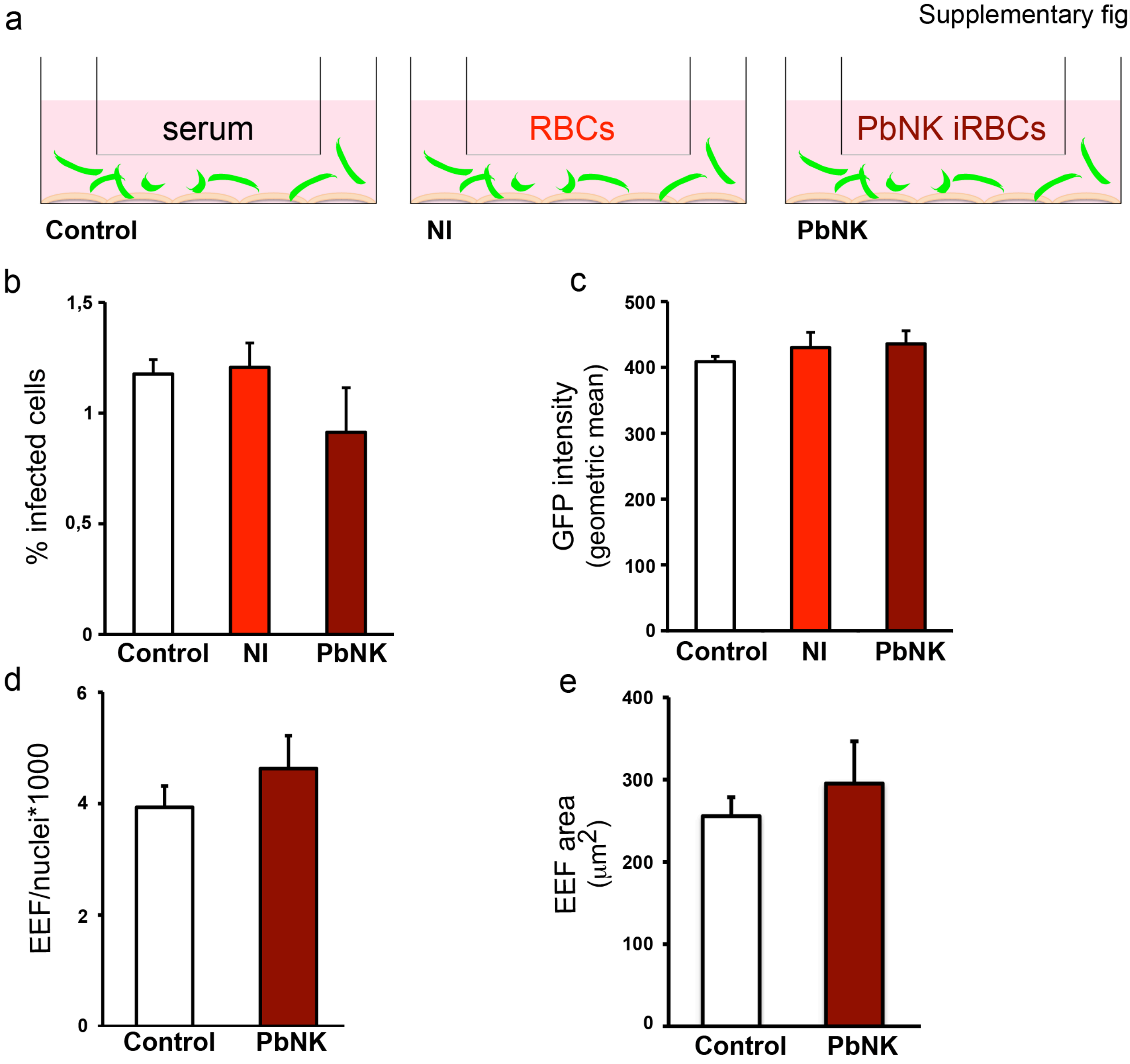
Supplementary figure 1



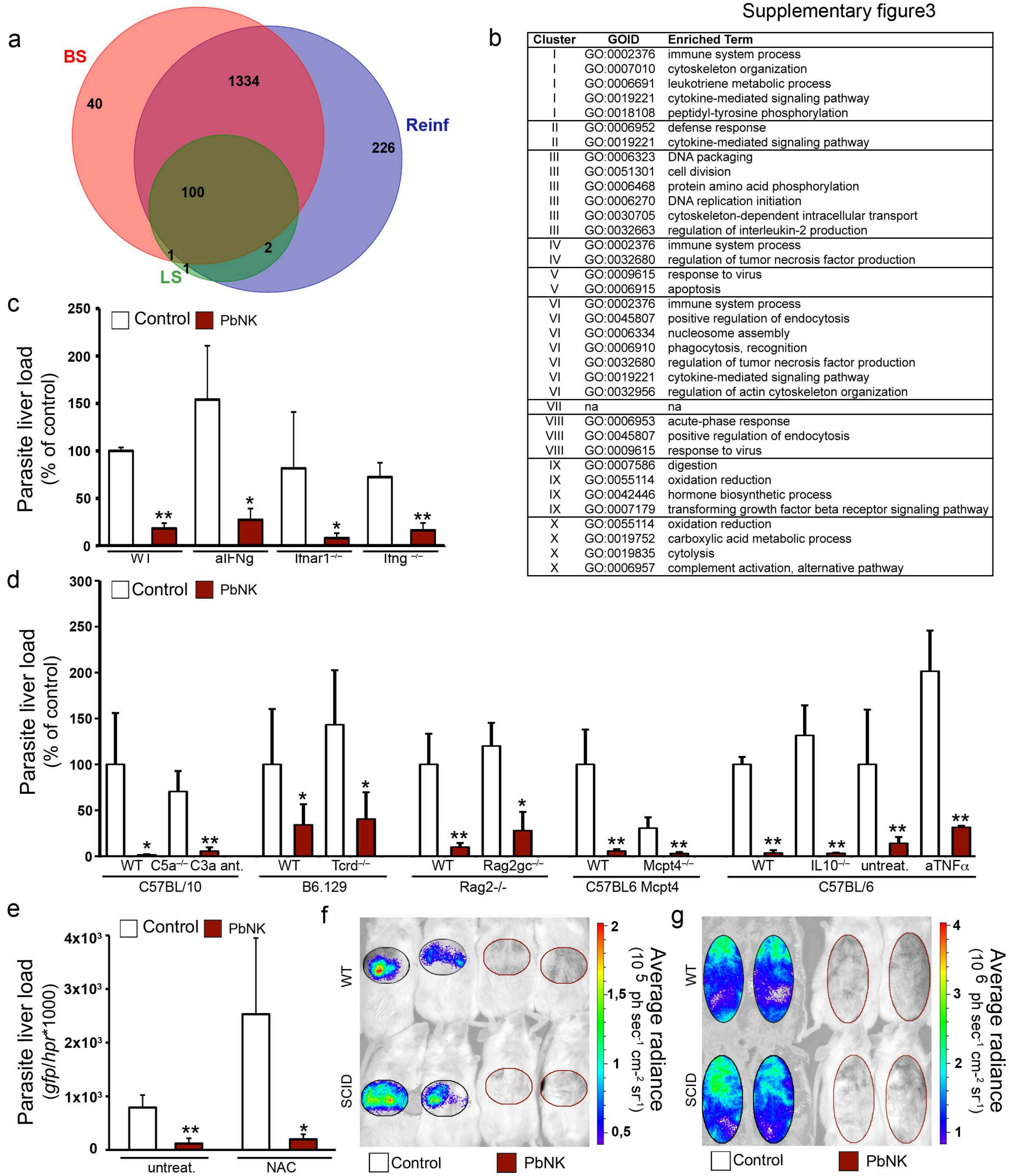
Supplementary Figure 1. (**a**) Correlation between expression levels of 18S rRNA and *gfp* cDNA in mouse livers, 40h post 5 x 10^3, 2 x 10^4, 5 x 10^4 and 1.5 x 10^5 *P. berghei* ANKA-GFP sporozoite injection. Dots show the average expression of 4 mice and the black line represents the positive correlation between the two parameters measured. (**b**) *Plasmodium* liver load 40 and 48h post 5 x 10^4 *P. berghei* ANKA-GFP sporozoite injection into naïve mice (control) and mice infected 5 days previously with 10^6 *P. berghei* NK65 (PbNK). (**c**) Representative EEFs in liver sections of naïve mice (Control) or mice infected 5 days previously with 10^6 *P. berghei* NK65 iRBCs (PbNK), 40 and 48h post 5 x 10^4 *P. berghei* ANKA-GFP expressing sporozoite infection. (Bar = 10µm.). (**d**) *Plasmodium* liver load 40 and 72h post 5 x 10^4 *P. berghei* ANKA-GFP sporozoite injection into naïve mice (Control) and mice infected 5 days previously with 10^6 *P. berghei* NK65 (PbNK), compared to a non-infected group (NI). (**e**) Magnification of 72h post infection of 5 x 10^4 *P. berghei* ANKA-GFP sporozoite injection into naïve mice (Control) and mice infected 5 days previously with 10^6 *P. berghei* NK65 (PbNK), and non infected control group shown in (c). (*$P < 0.01$, Ttest). Results are expressed as mean ± s.d. of 3 independent infections each counting with a minimum of 5 mice per group.

Supplementary figure 2



Supplementary Figure 2. (**a**) Effect of *Plasmodium* iRBC supernatants on sporozoite hepatocyte infection. Primary hepatocytes grown in the lower chamber of a transwell system where infection by sporozoites (green crescents) takes place, contacting with medium (Control), non-infected blood (NI) or blood containing 6 x 10^5 *P. berghei* NK65 iRBCs (PbNK) within the upper chamber. (**b**) Sporozoite infection (% infected cells) in the three conditions described above 36h post-2 x 10^4 *P. berghei* ANKA GFP expressing sporozoite addition, measured by FACS. (**c**) EEF development (GFP intensity) in the three conditions described above 36h post-2 x 10^4 *P. berghei* ANKA GFP expressing sporozoite addition, quantified by FACS. (**d**) Sporozoite infection (EEF/1000 nuclei) of mouse primary hepatocytes isolated from naive mice (control) and mice infected 5 to 7 days previously with 6 x 10^5 *P. berghei* NK65 iRBCs (PbNK), 48h post-2 x 10^4 *P. berghei* ANKA GFP expressing sporozoite addition, analysed by wide field microscopy. (**e**) EEF development (EEF area) in mouse primary hepatocytes isolated from naive mice (control) and mice infected 5 to 7 days previously with 6 x 10^5 *P. berghei* NK65 iRBCs (PbNK), 48h post-2 x 10^4 *P. berghei* ANKA GFP expressing sporozoite addition, analysed by confocal microscopy.

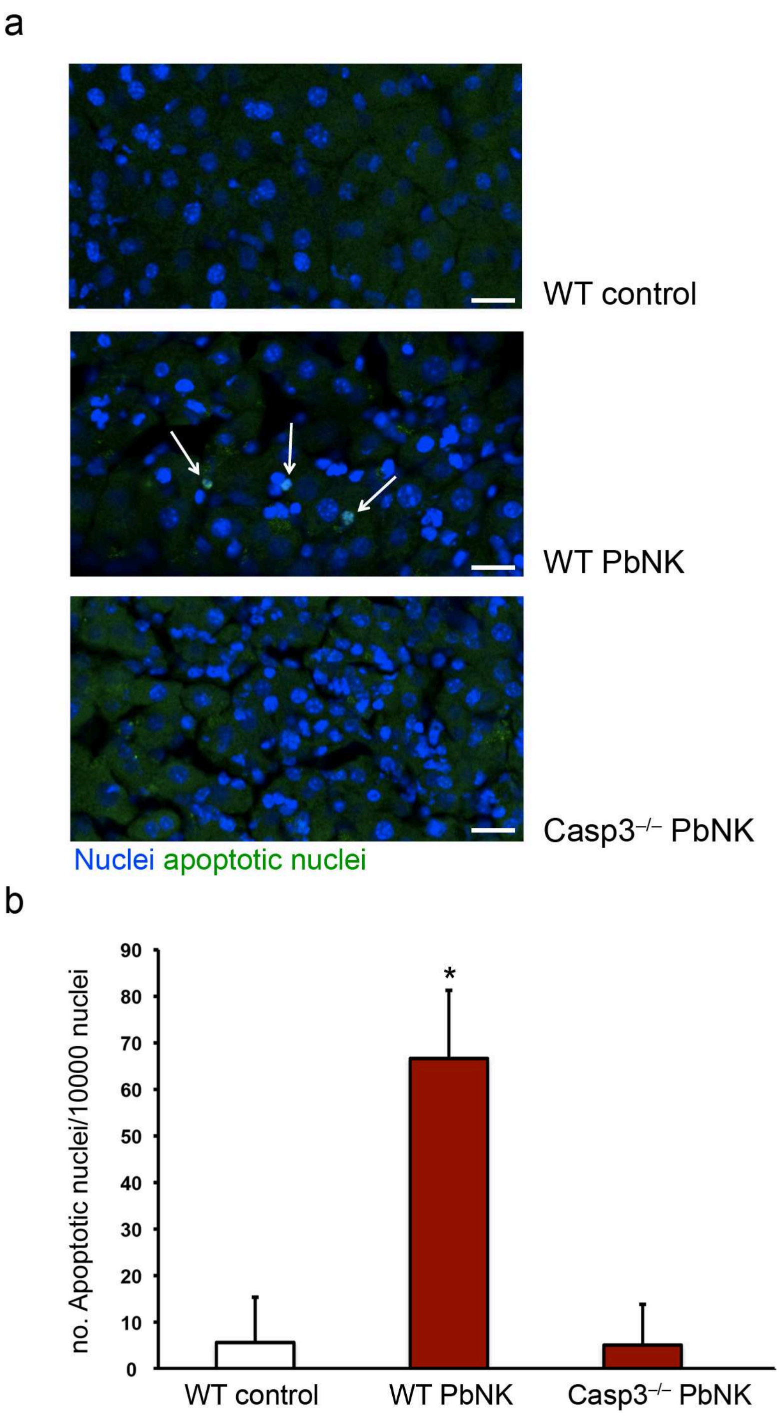
Supplementary figure3



Cluster	GOID	Enriched Term
I	GO:0002376	immune system process
I	GO:0007010	cytoskeleton organization
I	GO:0006691	leukotriene metabolic process
I	GO:0019221	cytokine-mediated signaling pathway
I	GO:0018108	peptidyl-tyrosine phosphorylation
II	GO:0006952	defense response
II	GO:0019221	cytokine-mediated signaling pathway
III	GO:0006323	DNA packaging
III	GO:0051301	cell division
III	GO:0006468	protein amino acid phosphorylation
III	GO:0006270	DNA replication initiation
III	GO:0030705	cytoskeleton-dependent intracellular transport
III	GO:0032663	regulation of interleukin-2 production
IV	GO:0002376	immune system process
IV	GO:0032680	regulation of tumor necrosis factor production
V	GO:0009615	response to virus
V	GO:0006915	apoptosis
VI	GO:0002376	immune system process
VI	GO:0045807	positive regulation of endocytosis
VI	GO:0006334	nucleosome assembly
VI	GO:0006910	phagocytosis, recognition
VI	GO:0032680	regulation of tumor necrosis factor production
VI	GO:0019221	cytokine-mediated signaling pathway
VI	GO:0032956	regulation of actin cytoskeleton organization
VII	na	na
VIII	GO:0006953	acute-phase response
VIII	GO:0045807	positive regulation of endocytosis
VIII	GO:0009615	response to virus
IX	GO:0007586	digestion
IX	GO:0055114	oxidation reduction
IX	GO:0042446	hormone biosynthetic process
IX	GO:0007179	transforming growth factor beta receptor signaling pathway
X	GO:0055114	oxidation reduction
X	GO:0019752	carboxylic acid metabolic process
X	GO:0019835	cytolysis
X	GO:0006957	complement activation, alternative pathway

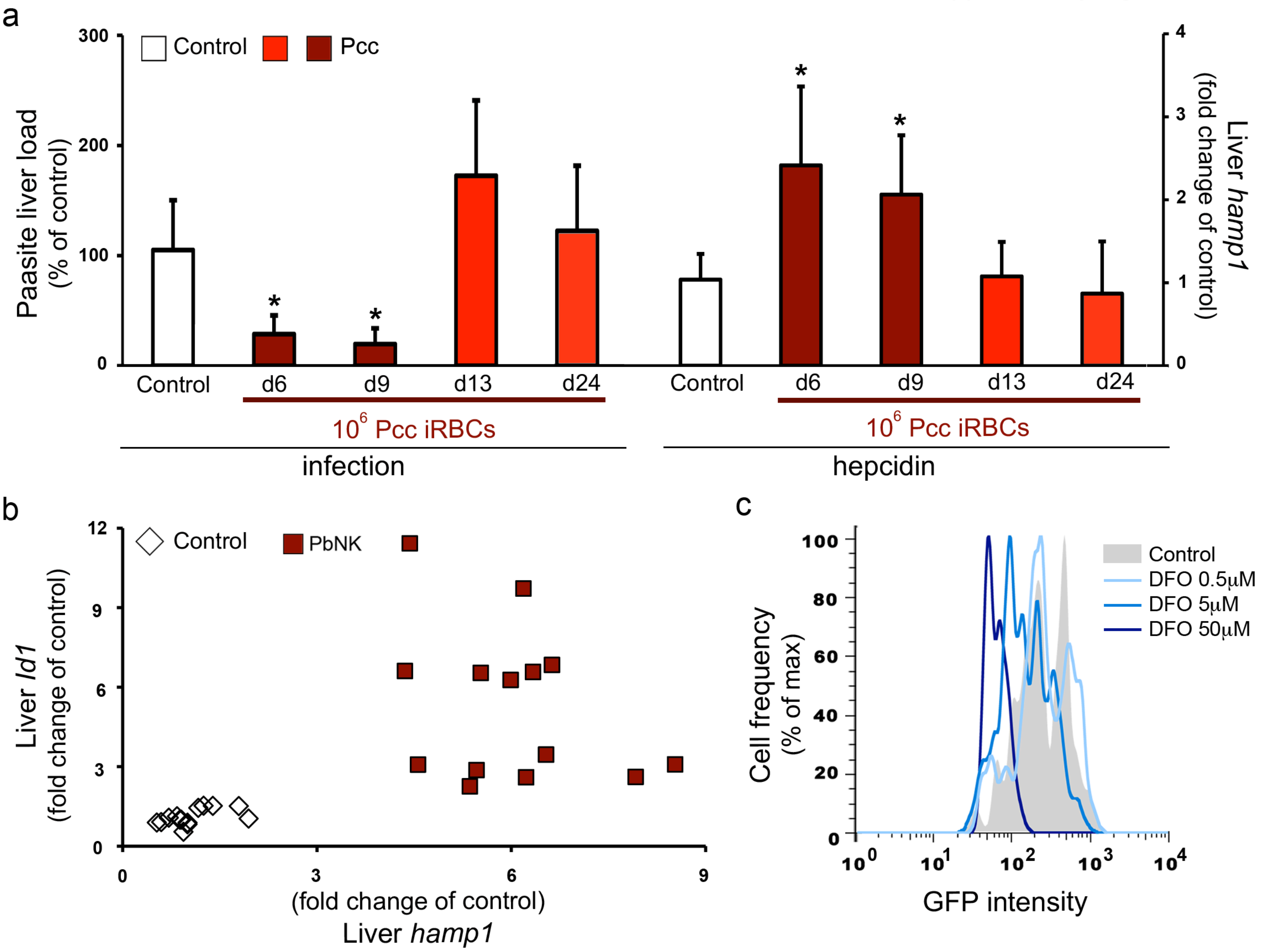
Supplementary Figure 3. (**a**) Microarray data analysis of liver RNA and targeting of hit molecules. Venn diagram showing the proportion of differentially expressed (DE) transcripts. Numbers are indicated for each group. (**b**) Gene Ontology enrichment a*Plasmodium* load measurement after sporozoite infection of naïve mice (Control) or mice previously infected with *P. berghei* NK65 (PbNK). (**c**) 40h post 5 x 10^4 ANK PbA-GFP sporozoite injection of mice infected 5 days before with 10^6 iRBCs of PbNK iRBCs, with and without IFNg monoclonal antibody (aIFNg) and using mice deficient for interferon alpha receptor 1 (Ifnar1$^{-/-}$), and mice deficient for Interferon γ (Ifng$^{-/-}$). (**d**) 40h post 5 x 10^4 PbA-GFP sporozoite injection of mice infected 5 days beforewith 10^6 PbNK iRBCs, using mice with different and genotypes, complement factor deficint C5a$^{-/-}$ mice treated with C3a antagonist SB 290157 (C5a$^{-/-}$C3a ant.), TCR delta deficient (Tcrd$^{-/-}$) , Rag2gc deficient, mastocyte deficient (Mcpt4$^{-/-}$), IL-10 deficient (IL10$^{-/-}$) and after monoclonal antibody treatment (aTNFα), all compared to respective background littermates. (**e**) 40h post 5 x 10^4 PbA-GFP sporozoite injection of mice infected 3 days before with 10^6 PbNK iRBCs, treated with N-acyl.cystein (NAC). (**f**) 40h after luciferase-expressing PbA infective mosquito bites of mice infected 8 days before with 10^6 PbNK iRBCs. (**g**) as in (d) but 3 days later. (*$P < 0.05$, **$P < 0.01$, Ttest) Results are expressed as the mean ± s.d. of 3 independent infections each counting with a minimum of 5 mice per group.

Supplementary figure 4

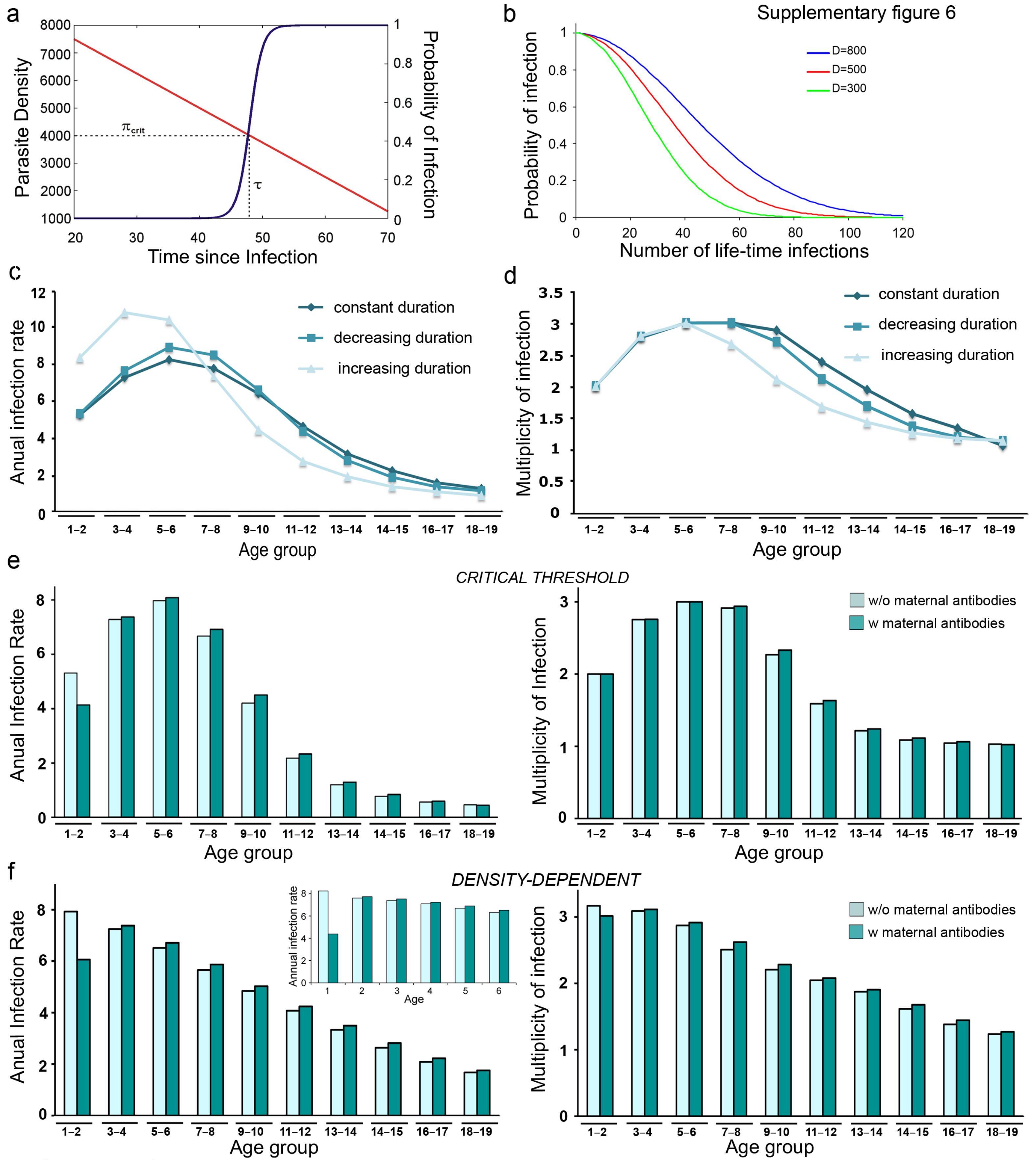


Supplementary Figure 4. Blood stage induced apoptosis in caspase 3-deficient mice. (**a**) Apoptosis in liver sections of naïve wild-type C57BL/6 mice (WT control), wild-type C57BL/6 mice infected 6 days previously with 10^6 *P. berghei* NK65 iRBCs (WT PbNK) and caspase3-deficient mice infected 6 days previously with 10^6 *P. berghei* NK65 iRBCs (Casp3-/- PbNK). (bar =20µm). (**b**) Quantification of apoptotic nuclei in liver sections of naïve wild-type C57BL/6 mice (WT control), wild-type C57BL/6 mice infected 6 days previously with 10^6 *P. berghei* NK65 iRBCs (WT PbNK) and caspase3 deficient mice infected 6 days previously with 10^6 *P. berghei* NK65 iRBCs (Casp3 -/- PbNK) (*P <0.05 Ttest). Results are expressed as the mean ± s.d. of 3 independent infections each counting with a minimum of 5 mice per group.

Supplementary Figure 5



Supplementary Figure 5. (**a**) *Plasmodium* liver load (left axis), and relative hepcidin expression levels (right axis), 40h post 7 x 10^4 *P. berghei* ANKA-GFP sporozoite injection into naïve mice (Control), mice infected 6, 9, 13 and 24 days previously with 10^6 *P. chabaudi* AS iRBCs (Pcc). (*P <0.05, Ttest) (**b**) Liver Id1 and hepcidin expression levels, 40h post 5 x 10^4 *P. berghei* ANKA-GFP sporozoite injection into naïve mice (control), mice infected 4 days previously with 10^6 *P. berghei NK65* (PbNK). (**c**) Effect of various concentrations of DFO on *P. berghei* ANKA-GFP EEF development inside Huh7 hepatoma cells, 36h after-2 x 10^4 *P. berghei* ANKA-GFP expressing sporozoite addition. The graphs show one representative data set of triplicate samples.



Supplementary Figure 6. (**a**) Functional relationship between parasite density and probability of infection. As the level of parasitaemia of an ongoing infection (red line) remains above a critical threshold density, πcrit, the probability of establishing a new blood stage infection (blue line) is extremely low but significantly increases as soon as the parasitaemia level falls below this threshold. (**b**) Acquired immunity as a function of infection history. The probability of infection is dependent on the total number of blood-stage infections experienced by the host and D, which can generally be understood as a proxy for antigenic diversity, where greater D requires more infections to gain protection. (**c** and **d**)Model behaviour under changes in duration of infections. The model was tested under three different assumptions concerning the duration of infection: (i) constant over age (T=100), (ii) decreasing with age (T=100-2*age), or (iii) increasing with age (T=60+2*age). Shown are the age-related annual infection rates (**c**) and multiplicity of infections (**d**) under these assumptions, clearly demonstrating a qualitative invariance of the model's behaviour to the underlying assumption about the period of infection. (**d** and **f**) Effect of maternally derived protection. Assuming that individuals are protected from clinical infections (and high parasitaemia episodes) for the first 3-6 months of live due to maternal antibodies can lead to a small decline in the rate of clinical infections in the youngest age classes but no significant difference in the multiplicity of infection (MOI). (**e**) The overall qualitative behaviour, i.e. the initial increase in both infection rate and MOI followed by a steady decrease with age, is preserved when assuming maternal protection within the critical threshold model. (**f**) Including this maternal effect within the density-dependent model does result in a decrease in annual infection rate and MOI in the youngest age class although this is entirely due to the temporary protection of the <1 year olds.

Supplementary table 1. Differentially expressed (DE) transcripts organised as toptable (sorted by log odds that a transcript is DE = B column). Cluster Nb corresponds to the clusters found in the non-hierarchical clustering and used for GO enrichment analysis. GO annotation for each transcript is also added, as well as if the transcript detected is a full length or partial or even if it's an EST. All trancripts are significant at p.value adjusted for multiple testing p<0.05. Transcript Cluster ID is the Affymetrix accession number. logFC is the log base of the fold change. Grey highlighted rows correspond to genes mentioned in the text.

Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (G**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10345436	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10345675	-0.601415904	-4.795082462	0.35401	-5.448006231	-1.400368093	0.620039438	5.596311087		Npas2	neuronal PAS dom	two-component ser	full-length
10345762	0.458723039	-6.626551458	0.596520253	-5.34801059	1.502116908	-2.596326751	9.483007998	Cluster II	Il1r1	interleukin 1 recept	signal transducer a	full-length
10345824	1.568464859	4.074662933	0.265663926	-5.607002262	1.295822929	1.686074687	5.127333798	Cluster I	Il18rap	interleukin 18 recep	receptor activity ///	full-length
10346168	1.528045861	8.174531437	-0.201671997	-5.425216669	1.529619231	7.753375662	4.854649429		Stat4	signal transducer a	DNA binding /// trar	full-length
10346191	2.245572797	11.23540134	1.660163087	7.406066781	2.746698753	13.22610923	10.57502395	Cluster VI	Stat1	signal transducer a	DNA binding /// trar	full-length
10346222	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10346365	1.238860264	-0.384631353	0.009722207	-6.39106834	0.658326799	-4.736829807	4.835880402	Cluster III	Sgol2	shugoshin-like 2 (S	chromosome, centr	full-length
10346410	-1.305856453	1.39552679	-0.106658749	-6.27740713	-1.639414101	3.314302862	11.56194851		Aox3	aldehyde oxidase 3	aldehyde oxidase a	full-length
10346783	1.116786756	0.770029106	0.124253399	-6.206669298	1.164535111	0.791102651	5.177951702		Cd28	CD28 antigen	positive regulation	full-length
10346799	1.244777455	5.865333743	-0.020208044	-6.381216662	1.316080191	6.070957486	5.841575758		Icos	inducible T-cell co-	protein binding /// ir	full-length
10347222	1.009351426	1.168341395	0.326829754	-4.859414166	0.924341947	-0.013352143	8.293681242		---	---	---	est
10347277	-1.090022407	-0.823040232	-0.184213474	-6.096532361	-2.386674567	6.773248621	10.61137768		Igfbp2	insulin-like growth f	regulation of cell gr	full-length
10347291	0.684676664	-3.650414189	-0.094564517	-6.302858742	1.340719157	1.206746426	3.806800288		Il8rb	interleukin 8 recept	signal transducer a	full-length
10347335	2.278314362	14.57719563	0.422528475	-2.126773417	2.527775954	15.41483684	8.624475088		Slc11a1	solute carrier family	transporter activity	full-length
10347928	1.356642952	7.36001555	0.234880094	-4.994067087	1.407440196	7.355674074	5.476680342		---	---	---	partial
10347933	1.560499279	6.143283378	0.187881662	-5.807803663	1.868274434	7.797119961	6.667701127		Sp140 /// A530032	Sp140 nuclear bod	zinc ion binding ///	full-length
10347948	0.918196146	1.354902028	0.505754699	-2.585760485	1.058910266	2.385416972	7.573024817		Sp100	nuclear antigen Sp	DNA binding /// bin	full-length
10348244	1.738001686	9.469374676	0.004353374	-6.391323262	1.688241862	8.692895905	7.214365916	Cluster I	Inpp5d	inositol polyphosph	inositol or phospha	full-length
10348702	-0.50596952	-4.628101337	-0.052503521	-6.357725144	-1.407190544	2.760263873	9.348201241	Cluster X	Agxt	alanine-glyoxylate	catalytic activity ///	full-length
10349661	1.680824552	5.144786193	0.344731087	-5.0546373	2.1352932	7.455580651	5.887134529		5430435G22Rik	RIKEN cDNA 5430	nucleotide binding	full-length
10349968	1.427600734	-0.256316403	0.068122624	-6.364326118	2.314194199	4.136204015	5.932215742		Chi3l1	chitinase 3-like 1	catalytic activity ///	full-length
10350136	1.561697103	8.093157466	-0.06927187	-6.276654408	1.507842033	7.249358357	8.901392019	Cluster I	Csrp1	cysteine and glycin	protein binding /// n	full-length
10350247	1.080375795	1.055258105	0.454354862	-4.033226296	1.244611762	2.057660348	5.607917906		Kif21b	kinesin family mem	nucleotide binding	full-length
10350630	1.321470502	2.276906762	0.020093247	-6.387016139	0.848068004	-1.996823983	6.659460595	Cluster III	Fam129a	family with sequen	negative regulation	full-length
10350733	-0.014113415	-7.278357094	0.16497872	-6.177300387	-1.350982589	0.234568256	9.176120665		Rgs16	regulator of G-prot	signal transducer a	full-length
10350838	2.551290618	6.695762609	0.432454803	-5.179335221	2.393876047	5.539023704	7.445096409		2810417H13Rik	RIKEN cDNA 2810	nucleus /// mitocho	full-length
10351182	1.485107925	0.586966806	-0.100790127	-6.324957052	2.329459636	4.808263004	6.004016261		Sele	selectin, endothelia	binding /// protein b	full-length
10351197	2.334114146	7.154491617	-0.152993339	-6.179350612	2.888676791	9.229972691	6.692433976		Sell	selectin, lymphocyt	binding /// protein b	full-length
10351206	0.867361333	-1.321676529	0.069243969	-6.332462495	1.370177033	2.501456826	5.60655358	Cluster IV	Selp	selectin, platelet	glycoprotein bindin	full-length
10351293	-0.751052198	-1.808340459	-0.493701816	-3.56027995	-1.287103194	2.689000294	6.018635441		Dpt	dermatopontin	protein binding /// e	full-length
10351380	0.892956567	-1.943854175	-0.269983577	-5.703569557	2.049555665	5.672559586	7.378538886		Ildr2	immunoglobulin-lik	---	full-length
10351477	1.186634491	-0.272682983	-0.142762829	-6.219802944	1.242948217	-0.218601857	4.006053373	Cluster I	Sh2d1b1	SH2 domain protei	phosphotyrosine bi	full-length
10351509	2.841819489	15.45932015	0.441521476	-2.71974558	3.075590109	16.01124046	8.983862863		Fcgr4	Fc receptor, IgG, lo	receptor activity ///	full-length
10351603	1.556326916	8.473372975	0.036801279	-6.356666839	1.567628491	8.125526096	6.86342467		Arhgap30	Rho GTPase activ	molecular_function	full-length
10351644	1.615634983	5.124579543	-0.060886902	-6.34198717	1.737446201	5.515617234	5.609582963		Cd244	CD244 natural kille	receptor activity ///	full-length
10351658	2.522447918	13.90759518	-0.061766518	-6.298054647	2.512707559	13.46627181	7.006319409	Cluster VI	Cd48	CD48 antigen	protein binding /// p	full-length
10351679	1.394320753	5.462182946	-0.139351858	-6.02873136	1.30283081	4.28572126	6.883782526		Cd84	CD84 antigen	receptor activity ///	full-length
10351691	1.100684335	6.257330663	0.161952271	-5.52191284	0.960231284	4.301727566	4.757971483		Slamf6	SLAM family mem	receptor activity ///	full-length
10351792	1.561576307	10.34337334	0.258436141	-4.377862172	1.720155183	11.07417637	6.657600169		Slamf9	SLAM family mem	membrane /// integ	full-length
10351825	1.811187972	10.84318358	-0.251028138	-4.801401858	1.721957093	9.813086611	7.474558649		Tagln2	transgelin 2	muscle developme	full-length
10351867	1.072097677	3.083283713	-0.185203377	-5.708429779	0.982535182	1.793274685	5.170416975		Aim2	absent in melanom	protein binding /// n	full-length
10351873	2.28142115	6.700626036	1.029071192	-0.608596332	2.554497554	7.581962168	6.396509508		Pyhin1	pyrin and HIN dom	protein binding /// n	full-length
10352344	-1.015213476	2.301230637	-0.448676484	-3.251060095	-2.205925589	10.6731044	8.451798175		---	---	---	predicted
10352439	-1.236846041	5.695558624	-0.092604521	-6.176952776	-1.567998449	8.006570776	6.38606834		Susd4	sushi domain conta	membrane /// integ	full-length
10352548	-0.919126119	0.551804675	-0.095255508	-6.238161762	-1.330436461	3.885246873	8.765617624		Slc30a10	solute carrier family	plasma membrane	full-length

10352709	1.188215565	0.683735867	-0.102366216	-6.282188557	0.613764117	-4.320271609	5.275984687	Cluster III	Nsl1	NSL1, MIND kineto	nucleus /// cell cycl	full-length
10353181	-0.68800574	0.532026627	-0.134953538	-5.859787627	-1.547971544	8.910071712	10.62300121		Lactb2	lactamase, beta 2	mitochondrion /// zi	full-length
10353420	1.620406997	3.571632592	0.060811008	-6.354586927	1.496507151	2.336163727	6.817711044		Mcm3	minichromosome m	nucleotide binding /	full-length
10354003	0.945108111	0.700823085	-0.025335671	-6.381057958	1.067995612	1.492002814	4.89286009		Mgat4a	mannoside acetylgl	extracellular region	full-length
10354472	1.096688317	4.972609226	-0.320481857	-3.981673445	1.262847229	6.138668628	6.764435211		Gls	glutaminase	neurological contro	full-length
10354588	1.46491064	10.83786926	-0.317822901	-3.033637799	1.494521959	10.65226473	8.308846166		Stk17b	serine/threonine kir	nucleotide binding /	full-length
10354768	1.091393952	3.806670901	0.083653963	-6.231178029	0.815462021	0.486796789	7.973761064		Akr1b3	aldo-keto reductase	aldehyde reductase	full-length
10355162	1.152675424	1.960371794	0.247095105	-5.556749701	1.014798475	0.361323767	5.673447408		Plekhm3	pleckstrin homology	intracellular signalir	full-length
10356020	1.865246671	10.11537985	0.098354227	-6.164735859	1.659987366	8.300379508	6.989028641		Dock10	dedicator of cytokin	guanyl-nucleotide e	full-length
10356082	0.553155346	-3.21849284	0.035106609	-6.369913882	1.099866905	2.08600168	8.757588006	Cluster IV	Plscr1	phospholipid scram	calcium ion binding	full-length
10356248	0.869490439	8.300054267	0.169772364	-4.402490107	1.076243774	10.4037186	4.76004335		C130026I21Rik ///	RIKEN cDNA C130	---	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**ene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10356269	0.923575905	-2.532104671	0.075702059	-6.346734144	1.195167635	-0.896646034	6.380586917		A530032D15Rik	RIKEN cDNA A530	---	full-length
10356278	1.135509064	8.92492463	0.256884186	-3.612150977	1.427116847	11.22217422	6.950308132	Cluster IV	Sp110 /// MGC118	Sp110 nuclear bod	DNA binding /// bin	full-length
10356293	1.29886182	8.832593564	0.40383995	-1.926843486	1.257892917	8.021437883	5.615639076		A630001G21Rik	RIKEN cDNA A630	---	full-length
10356593	-1.108556479	3.457428402	-0.155972915	-5.897857779	-1.477516015	6.219126636	7.862908758		Hes6	hairy and enhancer	DNA binding /// trar	full-length
10356762	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10357003	-0.381223971	-6.393638041	0.202990275	-6.134720024	-1.362877505	-0.696793284	6.758321153		Rnf152	ring finger protein 1	protein binding /// z	full-length
10357242	-0.549853945	-4.593855377	0.005344403	-6.391486617	-1.053276575	-0.696939613	11.7567844		Dbi	diazepam binding i	acyl-CoA binding //	full-length
10357261	4.526537759	17.07484221	0.233843469	-5.700442254	4.310452098	16.17993199	9.380993706		Marco	macrophage recept	receptor activity ///	full-length
10357298	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10357332	0.872655299	6.257582797	0.12059409	-5.618529154	1.034816739	7.802282788	10.28407466		Actr3	ARP3 actin-related	nucleotide binding /	full-length
10357436	1.963521823	7.583204295	0.066898253	-6.329278606	1.761095853	5.895875753	7.150609625		Mcm6	minichromosome m	nucleotide binding /	full-length
10357472	1.269732834	8.768783458	-0.01878545	-6.377311439	2.039226378	13.99596486	6.988309214		Cxcr4	chemokine (C-X-C	patterning of blood	full-length
10357604	1.452698965	5.903257289	-0.016276289	-6.386718335	2.184763448	10.25673191	8.603072906		Ikbke	inhibitor of kappaB	nucleotide binding /	full-length
10357875	1.820055808	0.11500494	0.274601404	-6.099217696	1.695533034	-0.845038051	6.818474213		Btg2	B-cell translocation	protein binding /// tr	full-length
10357878	0.963253546	-3.794594483	-0.176076967	-6.244602029	1.735995154	0.187034967	7.161137143	Cluster IV	Adora1	adenosine A1 rece	adenosine receptor	full-length
10358027	0.664333066	-4.926673837	0.146848774	-6.258821933	1.131375739	-2.232432656	5.272792099		Elf3	E74-like factor 3	DNA binding /// trar	full-length
10358224	2.579933642	14.87817004	0.173498235	-5.601379677	2.608336334	14.62734008	8.427281409	Cluster VI	Ptprc	protein tyrosine ph	activation of MAPK	full-length
10358389	1.578881287	3.646778056	0.019463212	-6.387709407	1.208079639	0.568838403	6.440332482		Rgs2	regulator of G-prote	signal transducer a	full-length
10358408	0.920727537	-2.083180418	-0.471844374	-4.644021144	1.077097369	-1.198922602	5.267976285		Rgs1	regulator of G-prote	signal transducer a	full-length
10358434	2.059111457	11.14202971	0.030870844	-6.369631359	1.993117365	10.32807003	7.00380142		Pla2g4a	phospholipase A2,	phospholipase activ	full-length
10358454	1.812480084	1.721865529	0.03895128	-6.383256522	2.101723556	2.829483671	10.23263092		Rbm3	RNA binding motif	nucleotide binding /	full-length
10358476	1.379392915	6.202294558	0.139347025	-5.971022388	1.921470187	9.654226163	8.433181645		Prg4	proteoglycan 4 (me	extracellular region	full-length
10359161	1.945498921	12.69735625	0.311962195	-3.730795685	2.047679482	12.89993494	7.781374022		Soat1	sterol O-acyltransfe	sterol O-acyltransfe	full-length
10359582	0.763183298	-6.566799093	-0.33640944	-6.250606425	2.239576201	-3.015820247	8.760436618		Fmo2	flavin containing m	magnesium ion bin	full-length
10359593	2.369822837	-4.969049554	0.093358349	-6.38761594	4.832316558	-0.926295075	6.589762045		Fmo3	flavin containing m	monooxygenase ac	full-length
10359642	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10359890	2.188209014	3.088687425	0.061358334	-6.372806062	1.754502657	0.514259396	5.670234685		Nuf2	NUF2, NDC80 kine	chromosome, centr	full-length
10359970	0.789262932	-2.728299611	0.152339065	-6.159535033	1.054601546	-0.873397667	6.628030778		Nos1ap	nitric oxide synthas	PDZ domain bindin	full-length
10360040	1.315938931	6.835291013	-0.063282427	-6.282707146	1.149575594	4.872577046	7.178272194	Cluster I	Fcgr3	Fc receptor, IgG, lo	antibody-dependen	full-length
10360070	2.547024871	14.06393917	0.2510721	-4.985737813	2.622844323	14.01947442	10.10560572	Cluster VI	Fcer1g	Fc receptor, IgE, hi	positive regulation	full-length
10360158	2.332627992	14.53317849	0.080131645	-6.188239089	2.310602555	14.03489461	6.714514011		Ly9	lymphocyte antigen	protein binding /// c	full-length
10360173	2.252196952	3.221698512	-0.480984069	-5.349661773	2.864306529	5.43212602	5.84719144		Slamf7	SLAM family memb	receptor activity ///	full-length
10360306	2.077551657	9.355413266	-0.197062217	-5.765270951	2.763899434	12.34053829	6.205779542		Slamf8	SLAM family memb	membrane /// integ	full-length
10360328	1.347003667	-0.940922403	0.056457287	-6.373757653	2.137773995	3.041491689	10.1167251		Apcs	serum amyloid P-c	calcium ion binding	full-length
10360367	1.151856355	1.81323835	1.178350132	2.484207364	1.7610862	5.960798547	6.198808716		---	---	---	partial
10360370	1.145955613	-3.02483614	0.356977878	-5.852968498	0.637235509	-5.808802792	4.070470875		BC094916	cDNA sequence B	protein binding /// n	full-length
10360373	1.071424452	-2.210477258	1.389919613	0.466021514	1.621751532	0.908252189	4.98433849		---	---	---	partial
10360377	1.647610747	5.456112424	0.886601735	-0.091752475	2.04723578	7.521415775	8.119960418		AI607873	expressed sequen	---	full-length
10360382	1.758429232	7.172285646	0.947215281	1.155794289	1.978064747	8.116221071	7.764202583		Mnda /// Ifi204	myeloid cell nuclea	transcription cofact	full-length
10360391	0.87578147	-2.242859167	1.022394879	-0.408489897	1.070141006	-1.026252448	7.600846508		Ifi203	interferon activated	protein binding /// n	full-length
10360406	2.975243539	8.612193504	0.667704224	-3.764111831	3.54843202	10.27631824	6.758379305		Ifi205	interferon activated	protein binding /// n	full-length
10360506	1.086485113	4.229990997	0.039557383	-6.352234248	1.050079467	3.448331077	6.251975011	Cluster III	Akt3	thymoma viral prot	nucleotide binding /	full-length
10360631	-0.334255269	-6.187614199	-0.029165998	-6.38298082	-1.251190712	0.713158533	10.58090668		Cabc1	chaperone, ABC1	nucleotide binding /	full-length

10361065	1.021558326	9.833413408	0.036670075	-6.290455906	1.229659351	11.6238222	7.104265134	Cluster IV	Mfsd7b	major facilitator sup	in utero embryonic	full-length
10361091	1.674577616	2.134704173	0.163999254	-6.201950598	2.057733114	3.885549776	6.493619283		Atf3	activating transcript	DNA binding /// trar	full-length
10361110	1.093713695	2.102786385	0.144630165	-6.051862863	0.711368331	-2.025103631	5.019566964		Dtl	denticleless homolo	nucleus /// cytoplas	full-length
10361133	1.270400628	3.490397665	-0.08169506	-6.284784032	1.615537793	5.718403967	6.621638214		---	---	---	---
10361246	-1.75170692	4.275116517	-1.118186675	0.425096	-2.251807281	6.676837589	7.833937967		G0s2	G0/G1 switch gene	cell cycle	full-length
10361375	1.755301447	2.168553775	0.45695988	-5.149253852	1.284054021	-1.063411423	5.455597213	Cluster I	Fbxo5	F-box protein 5	mitotic metaphase /	full-length
10361790	1.040729629	0.466361906	0.01122691	-6.390137714	0.731817461	-2.672183103	7.423174497		Fuca2	fucosidase, alpha-L	catalytic activity /// a	full-length
10361807	0.887436856	0.854722358	0.179105892	-5.791389203	1.120879743	2.783145423	5.959132819		Hivep2	human immunodefi	nucleic acid binding	full-length
10361887	-0.689250152	2.114803956	-0.105101445	-5.942570265	-1.15350809	7.35416531	9.413311509		Perp	PERP, TP53 apopt	protein binding /// m	full-length
10362091	-0.51324539	-5.169196626	-0.162036674	-6.154990654	-1.849444783	4.077323332	7.61060347		Raet1d /// Raet1e /	retinoic acid early tr	plasma membrane	full-length
10362129	0.487609316	-4.263344469	0.179583748	-5.906685703	1.166097385	2.022981371	10.41536753		Vnn3	vanin 3	extracellular space	full-length
10362138	-1.634332453	2.246424186	-0.24072564	-5.960956874	-1.839373457	3.06586999	9.223019333		Vnn1	vanin 1	acute inflammatory	full-length
10362350	1.209549714	2.180574811	0.11380783	-6.214781546	1.078234223	0.679443774	4.57014725		E430004N04Rik	RIKEN cDNA E430	---	full-length
10362379	-0.740247154	-1.957657115	-0.109991365	-6.219360426	-1.399339963	3.509962107	8.903988682		Echdc1	enoyl Coenzyme A	catalytic activity /// r	full-length
10362538	-0.646404854	-3.491254958	-0.173009186	-6.045660615	-1.09355326	0.103497855	5.887827853		Lama4	laminin, alpha 4	blood vessel develo	full-length
10362596	1.046466734	0.987280822	-0.086459512	-6.284241421	0.857183867	-1.124638987	7.675973755	Cluster III	Fyn	Fyn proto-oncogene	nucleotide binding /	full-length
10362896	1.010778356	-1.943995819	-0.560584606	-4.320939134	0.793963923	-3.775034488	5.84573092	Cluster III	Cd24a	CD24a antigen	response to hypoxia	full-length
10362904	-0.610620913	-1.457964983	-0.098446486	-6.16118027	-1.071905703	3.424141321	8.380765767	Cluster X	Rtn4ip1	reticulon 4 interacti	protein binding /// m	full-length
10363005	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10363070	3.489822096	9.876060996	0.326670844	-5.727656711	4.126552251	11.45311271	7.562396819		Gp49a	glycoprotein 49 A	membrane /// integr	full-length
10363082	2.794059814	7.532401052	0.21255272	-6.088575369	3.394983507	9.398446859	7.256798107	Cluster VI	Lilrb4	leukocyte immunog	receptor activity ///	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**ene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10363161	1.591120189	6.88086314	0.100984784	-6.201482788	1.659545777	6.936467473	7.047246907		---	---	---	partial
10363475	1.189894173	-0.770349478	0.351689864	-5.517933047	1.538587996	1.183020883	5.976169472		Prf1	perforin 1 (pore forr	calcium ion binding	full-length
10363561	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10(	---	est
10363669	0.543098373	-5.667227879	-0.340521201	-5.727814419	1.322457655	-1.167289663	8.936570341		Dnajc12	DnaJ (Hsp40) hom	molecular_function	full-length
10364262	2.826728451	16.24887648	-0.079894243	-6.205906576	2.973509212	16.47996796	8.480707392	Cluster VI	Itgb2	integrin beta 2	receptor activity ///	full-length
10364593	1.863987541	10.26143735	-0.055613942	-6.316406268	1.868118108	9.85939879	7.09953153	Cluster I	Cnn2	calponin 2	actin binding /// calr	full-length
10364950	1.105789686	-4.201914788	-0.14180972	-6.329457361	2.404728971	1.20972625	8.011268438		Gadd45b	growth arrest and D	activation of MAPK	full-length
10365482	0.574366458	-0.126839786	-0.060035708	-6.25717396	1.570778565	10.36624007	7.852668869		Timp3	tissue inhibitor of m	enzyme inhibitor ac	full-length
10366476	-1.354729312	3.504230558	0.050727062	-6.355216601	-2.544360843	10.31164239	8.322779568		Ptprb	protein tyrosine pho	protein tyrosine pho	full-length
10366886	1.0240414	4.432962946	0.017081966	-6.383152745	0.931961095	3.008474954	6.416521213		Arhgap9	Rho GTPase activa	GTPase activator a	full-length
10367066	-2.265239313	3.66888708	-0.193218274	-6.198425349	-3.269151426	7.370115533	8.30989025	Cluster IX	Sdr9c7	4short chain dehyd	catalytic activity ///	full-length
10367634	0.932606492	2.159433981	0.212462986	-5.42106521	1.230785411	4.694440457	6.511553206		Akap12	A kinase (PRKA) ar	protein binding /// c	full-length
10367734	1.014488874	3.420266068	0.268527662	-4.801532655	1.048606128	3.362041571	5.524470178		Ust	uronyl-2-sulfotransf	Golgi apparatus ///	full-length
10367805	1.650803283	4.77429189	0.002199906	-6.391732273	1.59701093	3.992150593	5.474218023		9130014G24Rik	RIKEN cDNA 9130	---	partial
10367816	1.838134186	5.505616267	0.104769138	-6.270527901	1.216782423	0.795283394	5.364307106		---	---	---	predicted
10368144	1.880001717	-0.141165237	0.325852217	-6.029337638	2.899248002	3.73822324	7.20719571		Tnfaip3	tumor necrosis fact	DNA binding /// pro	full-length
10368644	1.707112856	2.090415316	0.200074166	-6.123929484	2.301219589	4.853888231	6.725260485		Fam26f	family with sequenc	membrane /// integr	full-length
10368675	1.372548595	6.2349302	-0.028293408	-6.373609003	1.268834334	4.920684017	8.483214743		Marcks	myristoylated alanir	actin binding /// pro	full-length
10368713	-0.729881771	-0.051802218	-0.080669603	-6.238910697	-1.369861596	6.035555939	9.257790419		AI317395	expressed sequenc	sugar:hydrogen syr	full-length
10368947	1.164132296	2.358447877	0.586831506	-2.514625144	1.728132635	6.244155232	8.448273162		Aim1	absent in melanom	molecular_function	full-length
10369264	-0.664503812	-4.498074544	-0.145277744	-6.233065128	-1.872858588	3.204607579	8.504763706		Oit3	oncoprotein induce	calcium ion binding	full-length
10369290	0.797558457	-6.058145688	0.661217888	-5.550172703	2.094584762	-1.7784914	7.882915674		Ddit4	DNA-damage-induc	molecular_function	full-length
10369541	0.902230137	4.111263221	0.068612148	-6.224606006	1.032014275	5.174419469	6.363685635		Hk1	hexokinase 1	nucleotide binding /	full-length
10369615	1.832506603	11.36015098	-0.084495753	-6.177584313	2.036507757	12.20430104	10.03750933		Srgn	serglycin	ossification /// prote	full-length
10369815	1.526985135	1.762301183	0.19953856	-6.081041485	0.792120564	-3.710461741	6.320725725	Cluster III	Cdc2a	cell division cycle 2	nucleotide binding /	full-length
10370339	1.197304332	1.141454085	0.138605444	-6.17553227	1.1821282	0.647100424	6.368579705		Trpm2	transient receptor p	receptor activity /// i	full-length
10370946	1.290354763	7.790552998	0.091132483	-6.117999678	1.364359874	8.011843291	7.401956996		Mobkl2a	MOB1, Mps One Bi	protein binding /// z	full-length
10371054	-0.792592944	6.747548816	-0.312281575	-1.543713231	-1.001532463	9.058771803	9.764962308		Creb3l3	cAMP responsive e	DNA binding /// trar	full-length
10371591	1.18092784	5.150213285	0.116859855	-6.054457252	0.79095565	0.608438401	4.785507696		4930547N16Rik	RIKEN cDNA 4930	DNA binding /// nuc	full-length
10371607	1.782829489	8.375094421	0.233546586	-5.407862883	2.28492287	10.89748787	7.138551976		1200002N14Rik	RIKEN cDNA 1200	lysosome /// autoph	full-length
10371662	2.900484713	7.616295235	0.218421418	-6.090319858	3.230321953	8.448960992	6.919085471		Spic	Spi-C transcription	DNA binding /// trar	full-length
10371796	-0.637548342	-2.786021194	-0.102915726	-6.231268045	-1.151396731	1.806726418	7.347246192		Slc17a8	solute carrier family	transporter activity /	full-length
10371846	1.231010175	7.231056845	-0.151037827	-5.667263652	1.233488813	6.822111734	6.894045396		Apaf1	apoptotic peptidase	nucleotide binding /	full-length

10371970	-0.410972989	-4.248045702	0.078744354	-6.256010746	-1.654345506	7.809346945	10.99451669	Cluster X	Amdhd1	amidohydrolase do	iron ion binding /// c	full-length
10372028	-1.058169955	2.398480302	-0.054300529	-6.336309284	-1.483127529	5.633603911	7.615402266		Plxnc1	plexin C1	receptor activity ///	full-length
10372177	-0.532103302	-1.529807826	-0.345591142	-3.446203596	-1.067759855	4.779974404	6.702880178		Tmtc2	transmembrane an	binding /// membran	full-length
10372324	-0.524425534	-6.215835438	-0.100929981	-6.35023252	-1.153293513	-3.476009927	7.315046123		Syt1	synaptotagmin I	transporter activity /	full-length
10372410	1.962854789	14.90729117	-0.075229842	-6.122958795	1.82496027	13.66420586	5.768514647		Glipr1	GLI pathogenesis-r	extracellular region	full-length
10372648	1.64329724	6.325026331	-0.032900656	-6.374366025	1.43231003	4.356750009	10.3580629		Lyz2	lysozyme 2	lysozyme activity ///	full-length
10372716	0.920126308	7.341540095	-0.081965306	-5.992443829	1.138885077	9.423468345	10.67557607		Rap1b	RAS related protein	nucleotide binding /	full-length
10372781	2.105091219	8.900567408	0.352950236	-4.724246551	2.420479379	10.13091087	6.98071657	Cluster VI	Irak3	interleukin-1 recept	nucleotide binding /	full-length
10372831	-0.366265715	-5.705678145	-0.374942938	-4.793464895	-1.06407414	0.231104729	5.863238486		Tbc1d30	TBC1 domain famil	Rab GTPase activa	partial
10373054	-0.677718443	-0.607918476	-0.254837324	-4.983276414	-1.173153616	4.406199234	5.933289485		Slc26a10	solute carrier family	transporter activity /	partial
10373197	-1.012609869	3.953512817	-0.321656049	-4.019567799	-0.255764436	-5.790502085	9.254078765		Inhbc	inhibin beta-C	hormone activity ///	full-length
10373325	-0.858355708	-0.46298624	-0.071927876	-6.311386459	-1.706323831	6.152539739	7.546581133		Gpr182	G protein-coupled r	signal transducer a	full-length
10373334	-1.392349111	-4.159252343	-0.354926384	-6.144812829	-3.108649354	1.549614482	11.02856138	Cluster IX	Hsd17b6	hydroxysteroid (17-	catalytic activity /// e	full-length
10373407	1.183128152	4.766522979	-0.135089993	-5.975228098	1.210366106	4.596887709	7.677344106		Mbc2	membrane bound C	membrane /// integr	full-length
10374183	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	predicted
10374236	1.082967561	0.108769141	-0.078166782	-6.323746361	1.600189571	3.581772438	6.047462293		Upp1	uridine phosphoryla	catalytic activity /// u	full-length
10374333	1.712968256	10.47807967	0.010290408	-6.388603786	1.990403633	11.85054124	6.025749216	Cluster I	Ikzf1	IKAROS family zinc	nucleic acid binding	full-length
10374352	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10374842	1.240939914	2.843331599	-0.084037245	-6.286844123	0.825835549	-1.294966867	5.03492856	Cluster III	Ccdc88a	coiled coil domain c	regulation of protein	full-length
10375065	1.456871655	4.851211078	0.438049206	-3.910302045	1.857819427	7.191718798	5.783462051		Sh3pxd2b	SH3 and PX domai	protein binding /// c	full-length
10375083	1.47394103	5.59971414	0.00550984	-6.391255605	1.433739267	4.864753323	6.743067489		Stk10	serine/threonine kir	nucleotide binding /	full-length
10375145	2.196852134	14.89080491	0.154794919	-5.527258491	2.311834375	15.11137589	7.70870904	Cluster VI	Lcp2	lymphocyte cytosol	protein binding /// c	full-length
10375324	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10375443	1.641451406	10.12203555	0.342129426	-3.525647257	1.753040767	10.47997449	5.628203496		Havcr2	hepatitis A virus cel	receptor activity ///	full-length
10375472	1.552143994	2.11048047	0.165447208	-6.168561526	1.134191285	-1.119213371	8.248047736		Timd4	T-cell immunoglobu	membrane /// integr	full-length
10375515	2.163320003	8.343374057	1.0206651	0.87964578	2.878337614	11.31430543	7.98201593		Ifi47 /// Olfr56	interferon gamma in	endoplasmic reticul	full-length
10375704	-0.594441182	-2.772098413	-0.217833598	-5.601141092	-1.482968028	5.271349894	7.589326709		3010026O09Rik	RIKEN cDNA 3010	---	full-length
10376060	1.843935277	6.317100379	0.18700999	-5.959483611	1.93189853	6.42150479	8.934093717	Cluster I	Irf1	interferon regulator	DNA binding /// trar	full-length
10376094	-0.624635402	-3.992569208	-0.0540101	-6.360940626	-1.130227665	-0.109979543	7.852882164		---	---	---	est
10376324	3.58629976	9.882140173	2.107233713	4.067294086	4.783493732	12.90275301	9.063691189		OTTMUSG000000	predicted gene, OT	---	full-length
10376326	2.423222592	12.94644092	1.803062145	8.835895185	3.056565883	15.29314886	10.25251441		Igtp /// Iigp2	interferon gamma in	GTPase activity ///	full-length

Affymetrix ID	BS/Non Inf.		LS/Non Inf.		ReINF/Non Inf.		Average	Cluster	Gene	Gene	Gene Ontology (GO	Transcript
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10376459	0.961331072	6.784603893	0.111535496	-5.786359065	1.00358155	6.850207737	6.438140325		OTTMUSG000000	predicted gene, OT	---	est
10376868	1.591914123	6.092440238	0.281838315	-5.199372816	1.40095067	4.23908462	6.280057207		Trpv2	transient receptor p	ion channel activity	full-length
10377265	0.942198022	0.486583777	0.019760394	-6.385516741	1.027666852	0.92710934	5.781217238		Pik3r5	phosphoinositide-3-	nucleus /// cytoplas	full-length
10377405	1.865137577	5.143414988	0.133920715	-6.212208372	1.428693823	1.899420406	6.25133693		Aurkb	aurora kinase B	nucleotide binding /	full-length
10377439	0.232662313	-6.99085316	0.415530918	-5.531526463	1.157581454	-2.616593463	6.846480927		Per1	period homolog 1 (I	two-component ser	full-length
10378068	1.581144999	6.385460143	1.998100913	8.587921138	1.848288823	7.765228547	7.159940547	Cluster V	Xaf1	XIAP associated fa	nucleus /// cytoplas	full-length
10378216	1.422618765	5.59110259	0.21731545	-5.555746516	1.397747953	4.967898054	5.792143921		Atp2a3	ATPase, Ca++ tran	nucleotide binding /	full-length
10378385	-1.07461346	-2.778868455	-0.000252509	-6.391790625	-1.442749025	-0.897472939	6.359157411		Spata22	spermatogenesis a	---	full-length
10378572	-0.705770047	-4.803373921	0.23019386	-6.088224483	-1.909553634	2.057567954	10.40341831		Tlcd2	TLC domain contai	membrane /// integr	full-length
10379511	1.966443803	-1.805702183	0.090508217	-6.374345808	3.052353723	1.689273299	6.598362357	Cluster VI	Ccl2	chemokine (C-C m	G-protein-coupled r	full-length
10379518	1.133878564	-3.696256706	0.07166272	-6.373371737	1.996043296	0.136329844	6.175795342	Cluster II	Ccl7	chemokine (C-C m	cytokine activity ///	full-length
10379530	0.791371974	-3.783133729	-0.015423917	-6.390091529	1.829506656	2.627194333	4.578959959	Cluster II	Ccl12	chemokine (C-C m	cytokine activity ///	full-length
10379535	1.584947677	7.125922051	0.107671717	-6.164970074	1.69700124	7.488912684	4.281286028	Cluster I	Ccl8	chemokine (C-C m	cytokine activity ///	full-length
10379615	0.821428303	1.539505649	1.055279843	4.374243239	1.192390482	5.060238797	7.57563771		Slfn5	schlafen 5	nucleotide binding /	full-length
10379630	2.533280086	8.816292331	0.797448229	-1.856306275	2.862628874	9.837658605	7.890803406		Slfn2	schlafen 2	negative regulation	full-length
10379633	2.058122405	0.994984416	0.795818624	-4.367711997	2.944921854	4.275221911	5.999187408		Slfn1	schlafen 1	G1/S transition of m	full-length
10379636	1.616899303	-0.757859217	0.27328985	-6.09189986	2.625558883	3.518960356	5.436920306		Slfn4	schlafen 4	---	full-length
10379646	0.944728061	2.242020862	0.558149814	-1.595456678	1.002172616	2.446667565	5.968986553		Slfn3	schlafen 3	negative regulation	full-length
10379721	1.189204782	-1.786203663	-0.035181415	-6.384540312	1.322808382	-1.279876661	5.531307805	Cluster I	Ccl4	chemokine (C-C m	cytokine activity ///	full-length
10379727	1.730466441	12.55887777	0.150101175	-5.511781817	1.930974581	13.45820118	9.847081292		OTTMUSG000000	predicted gene, OT	---	full-length
10380566	-0.89420656	3.179791791	0.084601416	-6.175226146	-1.013180753	4.105959481	5.871579626		Phospho1 /// Abi3	phosphatase, orpha	magnesium ion bin	full-length
10380571	1.703075558	8.768440781	-0.001720336	-6.3917234	1.600568673	7.604699712	6.434065744		Gngt2	guanine nucleotide	signal transducer a	full-length
10381072	1.40332835	3.727326683	0.328250893	-5.049644893	1.228483902	1.941921279	6.072626386	Cluster III	Cdc6	cell division cycle 6	nucleotide binding /	full-length

10381387	-1.195230754	-0.362150293	-0.254322056	-5.878686617	-2.371967117	6.267681109	11.83997744		G6pc	glucose-6-phospha	catalytic activity ///	full-length
10381514	-0.671256707	-0.689955674	-0.115432964	-6.076654319	-1.373420774	6.175937106	7.372488574		Cd300lg	CD300 antigen like	receptor activity ///	full-length
10381588	0.800235002	6.950372262	0.071194392	-6.018682223	1.016219219	9.327053297	11.47042852		Grn	granulin	blastocyst hatching	full-length
10381708	1.180230383	1.975381799	0.262133753	-5.496949833	1.405109577	3.375636805	5.575184047		Fmnl1	formin-like 1	actin binding /// pro	full-length
10381809	1.103158855	7.367009489	0.191495566	-4.9859428	1.426749919	9.974346778	7.271567779		Itgb3	integrin beta 3	receptor activity /// i	full-length
10382106	1.992028991	7.568821326	0.325980552	-5.087704377	2.151038093	8.035907293	6.701270724		Gm885	gene model 885, (	extracellular region	full-length
10382271	-0.277664227	-6.523456235	-0.001800876	-6.391758082	-1.114225444	-0.428514439	7.364389253		Arsg	arylsulfatase G	catalytic activity ///	full-length
10382438	1.34328317	10.67344314	-0.226129352	-4.218138081	1.220631538	9.103606688	7.15321494	Cluster I	Cd300a	CD300A antigen	DNA binding /// rec	full-length
10382532	1.055830526	-4.333466296	-0.477270362	-5.693782454	2.024011731	-0.203438738	7.11095152		Slc16a5	solute carrier family	---	full-length
10383152	1.418770227	6.507303881	2.192405812	10.50640326	2.044228831	10.37704321	9.644297057		---	---	---	partial
10383168	1.490500526	6.67682517	2.15467087	10.05104298	2.033536025	9.900379192	9.837844354		---	---	---	partial
10383192	1.35905021	4.719314619	2.071940942	8.959127911	2.077220639	9.187727499	8.684434569		---	---	---	partial
10383194	1.391641572	4.789091982	2.024667161	8.580936049	1.948620432	8.223494762	9.864739093		---	---	---	partial
10383196	1.567901683	6.723583211	2.157004688	9.643522439	1.96193122	8.917694279	8.892665308		---	---	---	partial
10383198	1.61574014	6.838241853	2.161775081	9.481035537	2.10055242	9.49118417	9.823970862		---	---	---	partial
10383200	1.574268366	6.124748376	2.206625429	9.33819291	2.039170261	8.707840906	8.952714283		---	---	---	partial
10383202	1.623369752	8.690550066	2.210102957	11.02299423	2.092909436	11.28972542	9.977040214		---	---	---	partial
10383204	1.547985395	7.511593612	2.21166423	10.57872862	2.078258436	10.57039772	9.081417163		---	---	---	partial
10383206	1.579579841	6.825879742	2.344417795	10.39647201	2.236424433	10.49882322	9.365484694		---	---	---	partial
10383208	1.255452005	0.631817021	1.904109723	5.060843454	1.931205565	4.645691756	7.767187752		---	---	---	partial
10383210	1.35328663	6.799857288	2.076120554	10.6630425	2.017349605	11.08972709	9.491558493		---	---	---	partial
10383212	1.460430637	6.40381905	2.183797038	10.13994933	2.125101266	10.38706652	9.905593156		---	---	---	partial
10383214	1.403403128	7.930134961	2.138613293	11.42024444	1.969024763	11.52866311	9.841506825		Rnf213	ring finger protein 2	---	partial
10383233	1.325744716	6.693197561	2.008067158	10.47307902	1.899945089	10.50628882	9.881494571		Rnf213	ring finger protein 2	---	partial
10383395	-0.509778151	-1.397085802	0.024269993	-6.371029983	-1.016118758	4.895077022	10.00298178		Slc25a10	solute carrier family	binding /// mitochor	full-length
10383502	1.406111692	4.943938216	0.227526952	-5.556069307	2.262143321	10.0415289	7.173573762		Slc16a3	solute carrier family	transporter activity	full-length
10383556	-0.340877279	-4.87544513	-0.085035956	-6.218597911	-1.007937443	2.787015437	7.137788823		BC032265	cDNA sequence B	kinase activity /// tra	full-length
10383564	-0.61448859	-0.257887293	-0.104022915	-6.054494658	-1.267579849	6.853098886	6.636475529		Fn3k	fructosamine 3 kin	soluble fraction /// c	full-length
10384154	1.967312651	10.83032492	-0.138384508	-5.943958918	2.050799907	10.90309524	6.403158349		Myo1g	myosin IG	nucleotide binding	full-length
10384373	1.975806708	3.162585665	0.312916632	-5.804256112	1.701763906	1.258214588	5.190272439		Fignl1	fidgetin-like 1	nucleotide binding	full-length
10384378	-0.733861122	-2.131301216	-0.098594134	-6.257001035	-1.119022157	1.08392066	9.164559336	Cluster X	Ddc	dopa decarboxylas	catalytic activity ///	full-length
10384458	3.165962824	14.67055603	0.103335959	-6.203425002	3.752989775	16.27588698	7.875501065		Plek	pleckstrin	intracellular signali	full-length
10385118	2.180841882	9.945359245	0.294795069	-5.063000387	2.058639798	8.82897407	6.924710381	Cluster I	Dock2	dedicator of cyto-ki	membrane raft pola	full-length
10385236	1.091424672	3.909354003	0.12805245	-6.01465206	0.786205394	0.239389138	8.125265415		Akr1b3	aldo-keto reductas	aldehyde reductase	full-length
10385248	1.289603378	2.079562322	0.199087121	-5.93484672	1.018511523	-0.496219458	3.892145997		Hmmr	hyaluronan mediat	receptor activity ///	full-length
10385391	1.768715548	10.40944604	0.122359588	-5.98683602	2.161546179	12.38634957	6.654200439		Cyfip2	cytoplasmic FMR1	molecular_function	full-length
10385428	1.09630116	9.09056877	0.067982989	-6.1283278	1.17772544	9.510600581	5.80265477	Cluster III	Itk	IL2-inducible T-cell	nucleotide binding	full-length
10385500	1.89722396	7.387294162	1.545956735	5.183620549	2.606642781	10.71931804	10.04014577	Cluster VI	Irgm1	immunity-related G	nucleotide binding	full-length
10385504	1.570955825	-0.409868479	1.129342508	-2.149194545	1.737524383	0.123854686	5.701314774		EG432555	predicted gene, EG	---	full-length
10385507	0.624544378	1.911396748	0.082886949	-6.061980009	1.09839234	7.697454988	4.871835754		---	---	---	predicted
10385513	1.87147335	11.07906977	0.827327434	2.339016976	1.727180237	9.694656539	7.209400817		9930111J21Rik ///	RIKEN cDNA 9930	---	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10385518	4.546315414	16.60680771	1.885822012	6.255855848	5.170872358	17.72414045	9.176843692	Cluster VIII	Tgtp	T-cell specific GTP	GTPase activity ///	full-length
10385526	1.814934235	10.68956465	0.779302152	1.781196203	1.687242294	9.391274569	7.152753182		9930111J21Rik ///	RIKEN cDNA 9930	---	full-length
10385533	4.273880337	16.52872138	1.635440815	5.400330775	4.968870374	17.89159697	9.588838281	Cluster VIII	Tgtp	T-cell specific GTP	GTPase activity ///	full-length
10385542	-0.070151101	-7.228573715	-0.093014875	-6.303769248	-1.145567281	-0.142437489	6.647123073		Btnl9	butyrophilin-like 9	membrane /// integ	full-length
10385747	0.609016939	-0.712901442	0.147992268	-5.78034716	1.009216143	3.794825596	6.594592237		Phf15	PHD finger protein	protein binding /// z	full-length
10385814	-0.803806754	-0.694799364	-0.222745146	-5.604240096	-1.612201881	5.941651306	5.970543864		Leap2	liver-expressed ant	extracellular region	full-length
10385872	-1.355691427	6.58797815	-0.36634407	-3.711515267	-0.819101918	0.830814953	7.326963237	Cluster X	Slc22a5	solute carrier family	nucleotide binding	full-length
10385941	0.974132651	1.654862104	-0.079748518	-6.270677366	1.173052781	3.154185805	7.000225866		Tnip1	TNFAIP3 interactin	nucleus /// cytoplas	full-length
10386652	-0.996211169	3.930222866	-0.171561116	-5.60218059	-1.353678598	6.951578396	10.68909927	Cluster X	Aldh3a2	aldehyde dehydrog	aldehyde dehydrog	full-length
10387536	2.030701703	13.99935585	0.074793699	-6.178372531	2.087236709	13.931892	9.319713129		Cd68	CD68 antigen	lysosome /// endos	full-length
10387821	1.371964504	3.117001144	-0.15153186	-6.101819317	1.186375541	1.254658929	5.625007224		Alox12	arachidonate 12-lip	arachidonate 12-lip	full-length
10387890	0.990819115	1.344020075	-0.133899396	-6.086538261	1.183769232	2.738125304	6.997679828	Cluster IV	Cxcl16	chemokine (C-X-C	low-density lipoprot	full-length
10387985	1.133220648	1.904214037	0.373329116	-4.588198202	1.514570878	4.552717001	6.00226295		A430084P05Rik	RIKEN cDNA A430	membrane /// integ	full-length

10388254	-0.924423784	-0.066490249	-0.158772845	-6.029782049	-1.082751974	1.02103159	6.99445857	Cluster X	Aspa	aspartoacylase	aminoacylase activ	full-length
10388545	1.563280718	5.874953765	0.051834398	-6.347719357	2.005928056	8.336088805	6.379464514		Abr	active BCR-related	guanyl-nucleotide e	full-length
10388834	-0.996006349	3.708003305	-0.119470869	-6.012155086	-1.125839763	4.625815973	5.334581833		Slc13a2	solute carrier family	transporter activity /	full-length
10388958	1.947611678	14.61597744	0.218921957	-4.465806934	1.900282657	13.9398213	5.944090119		Evi2b /// Evi2a	ecotropic viral integ	membrane /// integr	full-length
10389134	1.493285921	5.309575499	1.606629716	6.123745662	1.434916318	4.443909464	6.658812368		Slfn9	schlafen 9	nucleus	full-length
10389143	1.186781313	0.751254378	0.809723921	-1.655485832	1.745034567	4.290075812	5.88579375		Slfn8	schlafen 8	---	full-length
10389207	3.716420785	19.3673981	-0.31227799	-3.960604353	3.466792941	18.35100876	8.705297218		Ccl5	chemokine (C-C mo	cytokine activity ///	full-length
10389222	3.026076712	15.04294057	0.079962802	-6.259577713	3.34017426	15.82161349	9.346184162	Cluster VI	Ccl6	chemokine (C-C mo	cytokine activity ///	full-length
10389231	3.683332876	5.958010909	0.224943937	-6.241327809	4.214842774	7.077988055	6.760123827		Ccl3	chemokine (C-C mo	cytokine activity ///	full-length
10389261	0.001174274	-7.279970578	0.072915931	-6.315146967	-1.263014481	2.456286747	7.233731466		OTTMUSG000000	predicted gene, OT	membrane /// integr	partial
10389606	1.164228284	-0.712097807	0.167480865	-6.170804287	0.857750529	-3.235842233	5.093231743		Prr11	proline rich 11	---	full-length
10390186	1.294572607	1.131487866	0.101216438	-6.292453201	1.231112258	0.291784605	7.417077977	Cluster III	Abi3	ABI gene family, me	molecular_function	full-length
10390640	1.742359822	6.121824829	-0.137820004	-6.134166337	1.876718523	6.543531527	5.273988617		Ikzf3	IKAROS family zinc	nucleic acid binding	full-length
10390691	-0.803763522	-5.495063916	-0.310089453	-6.101455779	-2.20259578	0.344776126	9.463424518		Nr1d1 /// Thra	nuclear receptor su	DNA binding /// tran	full-length
10390707	2.774201802	5.731240285	0.261495857	-6.052437602	2.434168612	3.860717015	6.535280504		Top2a	topoisomerase (DN	nucleotide binding /	full-length
10391207	0.786058486	4.391660712	1.731465742	11.88019373	0.886289086	5.301715261	7.698706802		Dhx58	DEXH (Asp-Glu-X-I	nucleotide binding /	full-length
10391301	0.777641281	1.722013077	0.280568908	-4.347442513	1.057840044	4.54479799	10.18687501	Cluster II	Stat3	signal transducer a	temperature homeo	full-length
10391461	1.42091858	9.015926383	0.160499497	-5.565966602	1.390575661	8.327973051	5.29610825		Brca1	breast cancer 1	condensed chromo	full-length
10392142	0.916798156	-0.008067696	-0.444486993	-3.926278691	1.121382105	1.50418196	6.093784094		Cd79b	CD79B antigen	transmembrane rec	full-length
10392522	-0.977191331	-3.073158683	-0.136005362	-6.282258866	-1.354364023	-1.013591263	9.924223409		Abca8a	ATP-binding casset	nucleotide binding /	full-length
10392796	1.168013368	3.311884815	0.108847487	-6.176332493	1.253312408	3.652527883	5.595038043		Cd300lb	CD300 antigen like	receptor activity ///	full-length
10392808	1.451453647	2.779988711	-0.042090474	-6.37265396	1.215462683	0.642803467	7.657685187	Cluster I	4732429D16Rik	RIKEN cDNA 4732	receptor activity ///	full-length
10392815	1.711074121	11.98604065	0.076017385	-6.170995216	1.732503323	11.71831981	7.336673965	Cluster I	Cd300a /// AF2517	CD300A antigen ///	DNA binding /// rec	full-length
10392825	1.138292597	4.835141703	0.028551094	-6.370801478	1.070260306	3.743326226	6.555058249		RP23-331L12.8 ///	CMRF-35-like mole	molecular_function	full-length
10392834	1.086404843	4.339119619	-0.042103909	-6.346087178	1.103433823	4.091269021	6.607936086		RP23-331L12.8 ///	CMRF-35-like mole	molecular_function	full-length
10392839	2.595166456	14.80435953	0.118924858	-6.01732804	2.777867661	15.22357452	8.049746496	Cluster VI	Cd300e	CD300e antigen	receptor activity ///	full-length
10392845	2.394464465	5.669463728	0.335926505	-5.670238858	3.218570833	8.671290607	6.547312912	Cluster VI	Cd300lf	CD300 antigen like	receptor activity ///	full-length
10393341	1.149121609	4.773528908	0.138608494	-5.928036632	1.322266484	5.92524287	7.661117494		Rhbdf2	rhomboid 5 homolo	endoplasmic reticul	full-length
10393449	0.773793266	-1.327426713	0.056670133	-6.341897585	1.119473844	1.608358209	6.989372155	Cluster III	Socs3	suppressor of cytok	regulation of cell gr	full-length
10393754	1.76581318	15.22034632	0.054534265	-6.206338935	1.962221976	16.07704213	11.50216721	Cluster I	Actg1	actin, gamma, cyto	nucleotide binding /	full-length
10394054	1.138933719	3.636753121	0.01336199	-6.388100847	0.783656441	-0.392064577	5.983748651		Cd7	CD7 antigen	receptor activity /// i	full-length
10394068	1.194806982	-0.716258774	0.560962999	-4.358271053	1.124746572	-1.533316933	5.059150181		Sectm1a	secreted and transr	extracellular region	full-length
10394593	2.213459504	12.79084346	0.450407523	-2.481493959	2.348283286	13.08903361	7.819887087		Fam49a	family with sequenc	---	full-length
10394674	-1.78352182	-1.779570122	-1.903208928	-0.608438617	-0.806442524	-5.880105734	8.610149583		---	---	---	partial
10394978	1.422706486	2.329722983	0.154469197	-6.150267775	1.032896095	-0.995206251	7.3537293		Rrm2	ribonucleotide redu	ribonucleoside-diph	full-length
10395039	0.785167927	-1.769653404	2.097353396	7.791693477	1.424408161	3.340787627	7.435309179		Cmpk2	cytidine monophos	nucleotide binding /	full-length
10395259	1.147507637	1.122438025	0.682585815	-2.275930359	2.121606291	7.336951906	9.953764182		Nampt	nicotinamide phosp	cytoplasm /// NAD b	full-length
10395273	1.434576677	-1.136793428	1.045593913	-2.586198095	1.882236995	0.894947699	6.321739011		Gdap10	ganglioside-induce	---	full-length
10395275	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10395770	0.88012766	2.629449619	0.144009567	-5.824810786	1.044751718	4.03732745	7.199263659		Srp54c /// 1700047	signal recognition p	---	full-length
10395780	0.88012766	2.629449619	0.144009567	-5.824810786	1.044751718	4.03732745	7.199263659		Srp54c /// 1700047	signal recognition p	---	full-length
10395805	0.857542087	0.778533572	0.190979028	-5.678863099	1.053741675	2.415419716	8.681631134		1700047I17Rik1	RIKEN cDNA 1700	---	full-length
10396402	1.071638349	3.567697856	0.12287853	-6.052783996	0.883471046	1.204768584	7.291487619	Cluster III	Prkch	protein kinase C, et	nucleotide binding /	full-length
10396919	0.627693376	-4.51854092	0.386769507	-5.236817828	1.480509428	1.34874753	8.8702687		4933426M11Rik	RIKEN cDNA 4933	---	full-length
10397145	-0.785886437	1.715537389	-0.34024313	-3.624202176	-1.405160143	7.65954487	7.820804004	Cluster X	Acot2	acyl-CoA thioestera	carboxylesterase ac	full-length
10397148	-2.679519424	6.530530195	-0.54174295	-4.770249546	-3.901762127	10.52782823	6.949443915		Acot1	acyl-CoA thioestera	long-chain fatty aci	full-length
10397346	0.609271995	-4.869318125	0.355101232	-5.495958959	1.020338138	-2.250238417	6.13773868		Fos	FBJ osteosarcoma	DNA binding /// tran	full-length
10397359	1.023215347	5.934855567	-0.235162539	-4.539232816	0.959111414	4.78198452	5.964798568		Batf	basic leucine zippe	DNA binding /// tran	full-length
10397541	0.514786118	-5.27349734	0.016220665	-6.389525982	1.001801681	-1.939870303	9.123939191		Eif1a /// EG266459	eukaryotic translati	RNA binding /// tran	full-length
10397543	0.608812509	-4.836788785	-0.030946735	-6.384367374	1.102969378	-1.607158422	9.157370996		Eif1a /// EG266459	eukaryotic translati	RNA binding /// tran	full-length
10397645	2.130857952	12.58583067	-0.093987929	-6.151396124	2.343083731	13.31014553	6.70528544		Gpr65	G-protein coupled r	signal transducer a	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (G**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10398011	-4.236418831	5.376953055	-0.384729327	-6.094998667	-4.724305998	6.18582556	7.794616807		Serpina4-ps1	serine (or cysteine)	---	full-length
10398039	3.024887823	13.52453352	0.836000377	0.071615834	3.302049243	14.16722273	8.690266092		Serpina3g /// Serpi	serine (or cysteine)	endopeptidase inhi	full-length
10398069	0.65095769	-4.996485966	0.17085164	-6.211545304	1.354842259	-0.814721316	11.97186424		Serpina3m	serine (or cysteine)	endopeptidase inhi	full-length

10398075	0.748148429	-3.85597004	0.177316848	-6.151647049	1.294419992	-0.27651097	12.42849654		Serpina3n	serine (or cysteine)	endopeptidase inhil	full-length
10398267	1.328113799	6.655897573	0.201848204	-5.40605402	1.67139821	8.915702252	7.749627151		Evl	Ena-vasodilator sti	actin binding /// pro	full-length
10398299	-0.414113476	-2.189107046	-0.20713247	-4.759823898	-1.042064259	6.336871498	12.00415093		AI132487	expressed sequenc	transporter activity	full-length
10398665	1.395080545	6.346715589	-0.31897107	-4.437423227	1.431343308	6.210618629	8.046413842		Tnfaip2	tumor necrosis fact	angiogenesis /// mu	full-length
10398907	2.196906967	11.39213238	0.287734017	-4.83075924	1.988957712	9.779246239	7.792405489		Pld4	phospholipase D fa	catalytic activity ///	full-length
10399005	1.842722128	10.4411117	-0.098534411	-6.14552749	1.595845627	8.301758115	7.507792165		Crip1	cysteine-rich protei	zinc ion binding ///	full-length
10399087	2.356759165	5.831690596	0.113892433	-6.299233731	1.671018599	1.738825877	5.411149749		Ncapg2	non-SMC condensi	inner cell mass cell	full-length
10399178	1.127067018	0.335031041	0.125455748	-6.222959443	1.071082224	-0.47018502	5.622974669		Cdca7l	cell division cycle a	protein binding /// n	full-length
10399354	-0.366255893	-5.727432216	-0.070370004	-6.329168453	-1.100725263	0.469744695	6.011129199		---	---	---	est
10399360	0.614127492	-3.247146272	0.004575843	-6.391491767	1.037108548	0.461916687	7.695296935		Rhob	ras homolog gene f	nucleotide binding	full-length
10399457	1.137965692	5.430766007	0.017209863	-6.383292704	0.838680136	1.770338843	7.990043937		Akr1b3	aldo-keto reductase	aldehyde reductase	full-length
10399540	1.426207631	8.458097486	0.199326442	-5.268516067	1.260744555	6.585677966	6.026872392		Pqlc3	PQ loop repeat con	membrane /// integ	full-length
10399710	1.240784794	-0.157267941	2.363898115	6.433481636	2.023616548	4.32671077	8.643245448	Cluster VII	Rsad2	radical S-adenosyl	catalytic activity /// i	full-length
10399924	1.740633292	11.10230928	0.00089324	-6.391765136	1.874917551	11.57004594	6.058329615		Pik3cg	phosphoinositide-3	inositol or phospha	full-length
10400023	1.28835144	0.936101917	-0.237037464	-5.88057061	1.13988572	-0.527390172	7.295455465		Tspan13	tetraspanin 13	membrane /// integ	full-length
10400357	0.708757144	-0.140400459	0.205382859	-5.425680148	1.012749728	2.929153795	7.299846646		Baz1a	bromodomain adja	nuclear chromosom	full-length
10400510	-1.29696058	3.316803279	-0.318007458	-5.028716076	-2.109816912	8.38905659	6.358353593		Clec14a	C-type lectin domai	binding /// sugar bir	full-length
10400589	1.161950156	-0.53727765	-0.193614134	-6.084822032	0.812132146	-3.428831083	3.987229999		C79407	expressed sequenc	---	full-length
10400844	-0.323514574	-4.337820223	-0.046856844	-6.316685667	-1.088399635	5.522330055	11.1221662		Pygl	liver glycogen phos	nucleotide binding	full-length
10401160	1.225138039	1.313716903	-0.160927964	-6.104791485	1.228739332	0.963635091	6.56918436		6330442E10Rik	RIKEN cDNA 6330	membrane /// integ	full-length
10401829	0.595803589	-4.749467229	-0.025635437	-6.386243133	1.097266459	-1.314144536	8.497319048		Eif1a /// EG266459	eukaryotic translati	RNA binding /// trar	full-length
10402268	1.493248649	12.7635069	0.010006908	-6.385967906	1.512831697	12.51011842	10.81436756		Lgmn	legumain	cysteine-type endo	full-length
10402347	1.24179531	9.379263728	0.592324645	1.736052766	1.157023561	8.110260294	6.430070166		Ifi27	interferon, alpha-in	aging /// response t	full-length
10402428	-0.839393488	-0.577386966	0.000339599	-6.391789134	-1.723276604	6.368210274	7.875891223		Serpina12	serine (or cysteine)	endopeptidase inhil	full-length
10402585	0.921100346	5.661194202	-0.044298367	-6.302820047	1.339516934	9.599457844	8.611743433		Wars	tryptophanyl-tRNA	nucleotide binding	full-length
10402708	1.18918105	0.969065702	0.029781478	-6.381872439	0.655028302	-3.831718517	7.671534298		Ckb	creatine kinase, bra	nucleotide binding	full-length
10402864	2.412037407	8.105508827	0.014681937	-6.389599134	2.523119293	8.202195067	6.248789458	Cluster VI	Igh /// Igh-6 /// Igh-	immunoglobulin he	activation of MAPK	full-length
10402991	2.399502366	3.94282047	-0.331881645	-5.870341475	2.157094225	2.41403181	6.467209059		---	---	---	partial
10403006	1.620561415	-1.344328757	0.135290938	-6.327309011	0.777842614	-5.545859126	3.798757982		---	---	---	partial
10403009	2.389924278	-0.977717719	-0.691308212	-5.591200369	2.05812809	-2.423139364	5.082742289		---	---	---	full-length
10403011	2.111400194	2.704021211	0.118904277	-6.320955827	1.778406131	0.628485928	3.842409925		---	---	---	partial
10403015	4.337803737	9.685338007	-0.545166827	-5.273574212	4.120459401	8.643590934	6.744391441		---	---	---	partial
10403018	4.21655688	8.942663514	-0.873432448	-3.98083219	3.951374756	7.743953801	7.37883165		---	---	---	partial
10403021	4.287390512	7.729487478	-0.046014356	-6.385402761	3.997255288	6.48350264	5.800215116		---	---	---	partial
10403028	3.752118089	10.65221645	-0.075561169	-6.355007032	3.266736604	8.574404045	4.964840004		---	---	---	partial
10403031	1.92222016	-0.917950971	0.035480886	-6.388269904	1.989601566	-0.968703829	4.68986167		---	---	---	partial
10403034	5.189469753	13.669253	-0.195840125	-6.179949344	5.241060299	13.38871935	7.401476571		Igh	immunoglobulin he	---	full-length
10403036	1.638535218	-0.450231253	-0.145283652	-6.301570293	1.428014942	-1.881517886	3.831466274		Igh	immunoglobulin he	---	full-length
10403038	3.048582165	12.45499113	0.123845885	-6.191691887	2.520318938	9.76137894	4.406416528		---	---	---	partial
10403043	3.894345847	11.19214841	-0.024815067	-6.387748467	3.908256773	10.81170244	7.674871583	Cluster VIII	---	---	---	partial
10403046	0.566215986	-5.515228577	0.011803673	-6.390935091	1.168699793	-2.048141491	3.878503935		---	---	---	partial
10403048	4.330384989	13.11068604	-0.272816451	-5.867690611	4.278419591	12.56065952	7.978757401	Cluster VIII	---	---	---	partial
10403054	3.276720893	10.2179919	-0.033339043	-6.383043153	3.208850097	9.539312284	7.262290059		---	---	---	partial
10403060	3.474690349	12.27257273	-0.044089698	-6.372591976	3.290268835	11.20381827	6.407605945		---	---	---	partial
10403063	4.290722601	11.40701745	-0.062370461	-6.370010917	4.405231237	11.30132205	6.63507977		Igh	immunoglobulin he	---	full-length
10403069	4.49697847	12.13711639	-0.217895463	-6.123392072	4.354255691	11.33444869	5.151612048		---	---	---	partial
10403073	2.553319795	1.452620719	0.394920598	-5.986090858	2.532027782	0.992309655	3.791517751		---	---	---	partial
10403079	3.862783219	9.268242166	-0.237930472	-6.124018497	3.559129045	7.8684451	6.34304094		---	---	---	partial
10403108	1.178575616	5.298144584	0.116595453	-6.045838055	0.925758752	2.292751768	9.558395208		Hmgn2	high mobility group	chromatin /// DNA b	full-length
10403352	1.26068969	3.913274215	-0.134064248	-6.080144249	1.790123181	7.446241723	7.597721323		Klf6	Kruppel-like factor	nucleic acid binding	full-length
10403743	-1.350960195	4.66877051	-0.69941719	-0.919781683	-1.901696051	8.157441671	6.548072685		Inhba	inhibin beta-A	receptor binding ///	full-length
10403842	1.463572157	9.408897112	-0.095184702	-6.086984176	1.520993538	9.435594404	5.951190619		Elmo1	engulfment and cel	protein binding /// c	full-length
10403871	1.692428397	8.281319133	0.117035347	-6.106640473	1.713700433	7.995078383	6.294626442		Aoah	acyloxyacyl hydrola	lipid metabolic proc	full-length
10403938	1.011035303	3.641839976	0.039051838	-6.35186637	0.792729324	0.792897986	10.80120072	Cluster III	Hist1h2ai /// Hist1h	histone cluster 1, H	nucleosome /// DN	full-length
10403941	2.656640354	11.07813234	0.233534434	-5.677809695	2.344801224	9.161492735	10.27607897	Cluster VI	Hist1h3i /// Hist2h3	histone cluster 1, H	nucleosome /// DN	full-length
10403943	1.120615391	1.549044076	0.203522352	-5.828277997	0.828974157	-1.472093356	7.723914203	Cluster III	Hist1h2bm	histone cluster 1, H	nucleosome /// DN	full-length

10403948	1.004053745	0.761116453	-0.088212161	-6.275957082	0.611647463	-3.381911426	9.427372087		LOC665622 /// Hist	H2b histone family	nucleosome /// DNA	full-length
10403955	1.037873776	3.422236924	0.025148054	-6.376685124	0.797657686	0.415266552	11.02750983	Cluster III	RP23-480B19.10 //	similar to histone 2a	nucleosome /// DNA	full-length
10403957	1.083932352	2.622156242	0.037934599	-6.364773774	0.806643561	-0.548756545	9.955015714	Cluster III	Hist1h4i /// Hist1h4	histone cluster 1, H	nucleosome /// DNA	full-length
10403978	1.057983377	1.071912872	-0.05369897	-6.350260663	0.67753786	-2.862977282	9.612201009		LOC665622 /// Hist	H2b histone family	nucleosome /// DNA	full-length
10404026	1.004131759	3.186191256	0.015980321	-6.3855548	0.778642822	0.292649043	11.05200557	Cluster III	Hist1h2ai /// Hist1h2	histone cluster 1, H	nucleosome /// DNA	full-length

Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GO**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10404028	2.603618434	10.85407752	0.248023803	-5.589892243	2.304269785	8.970109424	10.36666004	Cluster VI	Hist1h3i /// Hist1h3	histone cluster 1, H	nucleosome /// DNA	full-length
10404045	1.042313045	3.499200285	0.015822981	-6.385770926	0.79826785	0.449626287	10.84549605	Cluster III	Hist1h2ai /// Hist1h2	histone cluster 1, H	nucleosome /// DNA	full-length
10404049	2.749791353	10.85610984	0.264904828	-5.572538312	2.420768202	8.909123131	10.35790962	Cluster VI	Hist1h3i /// Hist2h3	histone cluster 1, H	nucleosome /// DNA	full-length
10404061	1.060988666	-0.478686811	0.269557393	-5.690363293	0.943211155	-1.757122982	5.224189199	Cluster III	Hist1h2bb	histone cluster 1, H	nucleosome /// DNA	full-length
10404063	2.178380614	3.680430705	0.057091388	-6.37324649	1.390160901	-0.992441981	4.158456098		Hist1h2ab	histone cluster 1, H	nucleosome /// DNA	full-length
10404065	2.726411915	11.08407653	0.250747507	-5.613465591	2.416737208	9.218562981	10.49620367	Cluster VI	Hist1h3i /// Hist2h3	histone cluster 1, H	nucleosome /// DNA	full-length
10404067	1.033673356	3.385528424	0.031752827	-6.367696583	0.784845383	0.272698487	10.22968492	Cluster III	Hist1h4m /// Hist1h4	histone cluster 1, H	nucleosome /// DNA	full-length
10404069	1.626035492	3.747389607	-0.104516501	-6.279660429	1.1859411	0.215485721	7.752394477		Hist1h1a	histone cluster 1, H	nucleosome /// DNA	full-length
10404097	-0.900095184	2.929042522	0.005478626	-6.390922106	-1.101639355	4.690669101	9.493295348		Slc17a3	solute carrier family	---	full-length
10404132	-0.897137612	-4.390626389	0.000504039	-6.391789858	-1.653929598	-0.644467084	9.930473069	Cluster X	Cmah	cytidine monophosp	iron ion binding /// c	full-length
10404152	1.570728718	6.644797174	-0.062726013	-6.318808392	1.744170892	7.427818227	5.893428157		Fam65b	family with sequenc	binding	full-length
10404389	1.165804227	4.369368097	-0.258682058	-5.033796989	1.429154956	6.229401636	4.70963077	Cluster IV	Irf4	interferon regulator	DNA binding /// tran	full-length
10404422	0.818703961	1.349662037	0.111271679	-6.082772061	1.222765064	5.160686433	7.079824406		Serpinb6b	serine (or cysteine)	---	full-length
10404429	1.143220679	3.127847614	0.145216577	-6.010205264	1.517787696	5.818186752	6.642140254		Serpinb9	serine (or cysteine)	protein binding /// a	full-length
10404439	0.937929806	0.19623511	0.113369739	-6.199085796	1.212375807	2.284911638	4.997937458		Serpinb9b	serine (or cysteine)	protein binding /// cy	full-length
10404496	-0.353015577	-5.823868425	-0.08940307	-6.290799673	-1.01561348	-0.244164602	10.21135598	Cluster X	Nqo2	NAD(P)H dehydrog	dihydronicotinamide	full-length
10404606	1.774521878	7.451937686	0.345994823	-4.641714074	1.555228036	5.505739165	9.058640403	Cluster I	Ly86	lymphocyte antigen	protein binding /// e	full-length
10404874	-0.778647753	4.735822104	-0.150221369	-5.273121148	-1.013959411	7.31448221	7.084982906		Mylip	myosin regulatory li	molecular_function	full-length
10405216	1.677566478	8.248008208	0.053573833	-6.330259197	1.57094802	7.046848368	6.416556822	Cluster I	Syk	spleen tyrosine kina	nucleotide binding /	full-length
10405587	1.038529572	6.280423137	0.01178464	-6.386231903	1.219639924	7.711946634	9.217578351		Tgfbi	transforming growth	protein binding /// e	full-length
10405753	-0.77841468	-2.779502736	-0.030464808	-6.38222512	-1.40252469	1.793414342	11.10209971	Cluster X	Me1	malic enzyme 1, NA	catalytic activity /// r	full-length
10406407	-0.132794714	-7.17789115	-0.046992785	-6.379220837	-1.401069646	-0.928053055	10.06352336		Arrdc3	arrestin domain con	molecular_function	full-length
10406417	1.605874795	13.36525042	0.007367722	-6.388768671	1.777866237	14.17400532	11.60114828		Actg1	actin, gamma, cytop	nucleotide binding /	full-length
10406676	-1.141512845	3.74917922	-0.428593424	-3.370723353	-1.448358048	5.968348952	6.521617429		Lhfpl2	lipoma HMGIC fusi	membrane /// integr	full-length
10406817	0.530953684	-3.325505291	0.086399273	-6.254219671	1.044105157	1.797532176	7.554511623		Enc1	ectodermal-neural c	actin binding /// prot	full-length
10406928	2.56849209	17.16581422	0.110748034	-5.894686271	2.826397166	17.91298073	7.022083842	Cluster VI	Cd180	CD180 antigen	receptor activity ///	full-length
10406982	0.643151629	-3.557585931	0.851854434	-0.996312857	1.323500189	1.85478772	5.314655354		Adamts6	a disintegrin-like an	molecular_function	full-length
10407327	2.4935708	4.607925365	-0.330479742	-5.851719965	2.86552595	5.739516162	5.758154418		Emb	embigin	membrane /// integr	full-length
10407481	1.775358402	11.34963967	-0.110298871	-6.008675967	2.194438508	13.46550743	7.321659514		Pfkp	phosphofructokinas	nucleotide binding /	full-length
10407792	1.517900535	4.38555468	-0.212925213	-5.812571708	1.830979119	6.061363868	6.519176974		Gpr137b-ps /// Gpr1	G protein-coupled r	molecular_function	full-length
10407803	1.159358544	1.522383585	0.258624353	-5.563763527	1.288877063	2.187174401	6.007661361		Gpr137b	G protein-coupled r	molecular_function	full-length
10407985	2.412308373	4.233311296	0.153448223	-6.271724004	3.103360856	6.641294408	4.742868145		Gpr141	G protein-coupled r	signal transducer a	full-length
10408072	1.010068222	3.503430192	0.03156476	-6.366298409	0.787498501	0.618477156	11.07846573	Cluster III	Hist1h2ai /// Hist1h2	histone cluster 1, H	nucleosome /// DNA	full-length
10408074	1.030828203	3.296861972	0.050982006	-6.330548389	0.796721123	0.358431987	10.20357844	Cluster III	Hist1h4m /// Hist1h4	histone cluster 1, H	nucleosome /// DNA	full-length
10408077	1.28868286	2.58698012	-0.02905779	-6.380638533	0.987583699	-0.325216131	6.156464837	Cluster III	Hist1h2ak	histone cluster 1, H	nucleosome /// DNA	full-length
10408081	2.812923756	10.96193489	0.184656867	-5.99155171	2.552592512	9.375854526	8.758656865	Cluster VI	Hist1h1b	histone cluster 1, H	nucleosome /// DNA	full-length
10408083	2.649884886	10.95584562	0.243234839	-5.631898033	2.332684904	9.007990185	10.26776855	Cluster VI	Hist1h3i /// Hist2h3	histone cluster 1, H	nucleosome /// DNA	full-length
10408085	1.018184824	3.369328625	0.020011024	-6.381947355	0.797077252	0.539189499	10.80013262	Cluster III	Hist1h2ai /// Hist1h2	histone cluster 1, H	nucleosome /// DNA	full-length
10408092	1.083932352	2.622156242	0.037934599	-6.364773774	0.806643561	-0.548756545	9.955015714	Cluster III	Hist1h4i /// Hist1h4	histone cluster 1, H	nucleosome /// DNA	full-length
10408094	1.022867933	3.591068061	0.03605511	-6.358838125	0.793267193	0.645735645	10.8471452	Cluster III	RP23-480B19.10 //	similar to histone 2a	nucleosome /// DNA	full-length
10408111	1.012918984	3.362643784	0.021968165	-6.379821143	0.78275691	0.413990572	11.02689464	Cluster III	Hist1h2ai /// Hist1h2	histone cluster 1, H	nucleosome /// DNA	full-length
10408118	1.045914804	3.491040544	0.033613183	-6.36489555	0.813642892	0.587064081	10.79949939	Cluster III	Hist1h2ag /// Hist1h	histone cluster 1, H	nucleosome /// mol	full-length
10408200	1.421810245	2.668680891	0.063709336	-6.347161071	1.234249764	0.879564021	7.385365586	Cluster III	Hist1h4f	histone cluster 1, H	nucleosome /// DNA	full-length
10408202	2.674371361	10.21067781	0.217988415	-5.853739131	2.336739279	8.177992903	10.18473722	Cluster VI	Hist1h3i /// Hist1h3	histone cluster 1, H	nucleosome /// DNA	full-length
10408239	2.689368252	11.19583886	0.2518841	-5.572018029	2.369072959	9.256003265	10.46535703	Cluster VI	Hist1h3i /// Hist1h3	histone cluster 1, H	nucleosome /// DNA	full-length
10408243	1.06134143	3.663048314	0.094210028	-6.182863685	0.839327786	0.892430554	9.94395126	Cluster III	Hist1h4m /// Hist1h4	histone cluster 1, H	nucleosome /// DNA	full-length
10408246	2.608984263	10.81349922	0.240695322	-5.641715772	2.297328517	8.86930596	10.36360744	Cluster VI	Hist1h3a /// Hist1h3	histone cluster 1, H	nucleosome /// DNA	full-length
10408251	-0.2257751	-6.707382349	0.2214465	-5.853433258	-1.183883458	0.66171065	9.185585321		Slc17a4	solute carrier family	transporter activity /	full-length
10408600	1.014257298	1.833239822	-0.129014317	-6.092824855	0.679061019	-2.010586481	8.283333601		Serpinb6a	serine (or cysteine)	endopeptidase inhib	full-length

10408693	1.673038375	-3.326360576	-0.367135822	-6.143816796	2.777961747	0.187511219	5.712335758		F13a1	coagulation factor	protein-glutamine g	full-length
10408838	-0.524174474	-4.823580402	-0.08751202	-6.311645142	-1.679538688	3.772874628	11.37920873	Cluster X	Elovl2	elongation of very	very-long-chain fatt	full-length
10408850	1.068925592	6.055389156	-0.148033571	-5.640923679	1.062705125	5.560992577	7.079941882	Cluster III	Nedd9	neural precursor ce	regulation of cell gr	full-length
10408861	-0.724048852	0.223769085	-0.042286803	-6.346006033	-1.027027005	3.282750419	9.509372748		9530008L14Rik	RIKEN cDNA 9530	membrane /// integ	full-length
10409240	1.846269208	10.08405799	0.020260726	-6.381842135	2.038492694	10.84060835	6.461892809		Sema4d	sema domain, imm	receptor binding ///	full-length
10409376	1.897247082	8.304814493	0.108437502	-6.194868798	2.158847792	9.402381432	6.988596414		Hk3	hexokinase 3	nucleotide binding	full-length
10409567	1.862487502	6.317365676	0.178774213	-6.003206374	2.088668809	7.209941214	6.060815846		Tifab	TRAF-interacting p	---	full-length
10409866	1.208470232	5.332220193	0.199139508	-5.469044371	0.621620548	-1.513341107	5.914253402		Ctla2b	cytotoxic T lympho	cysteine protease i	partial
10409876	1.782509988	6.502418331	0.153153368	-6.068572673	1.853597947	6.521443825	6.039876641		Ctla2a	cytotoxic T lympho	molecular_function	full-length
10410452	-1.363159492	-3.494152106	-0.000896818	-6.391788824	-1.761729846	-2.095708147	9.460559388	Cluster IX	Srd5a1	steroid 5 alpha-red	3-oxo-5-alpha-ster	full-length
10410560	1.081985533	2.452804367	-0.012822341	-6.388788134	0.807327052	-0.666580287	5.630000489		Trip13	thyroid hormone re	nucleotide binding	full-length
10410650	-0.926630249	2.300887814	-0.419003046	-3.136384648	-1.09240193	3.615806155	7.123835428		Zfp825	zinc finger protein	nucleus /// zinc ion	full-length
10410927	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10410931	1.729542495	-0.511448571	0.13312081	-6.324653275	2.028486224	0.551234424	5.144738856		Vcan	versican	binding /// calcium i	full-length
10411359	1.792012955	6.978017219	-0.07141986	-6.314801607	1.729926972	6.140992556	6.998276701		Plp2	proteolipid protein	membrane /// integ	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**ene Ontology (GO**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10411595	0.995286333	4.561796084	0.170330472	-5.521789554	1.023057653	4.444672927	6.222896902		Naip2	NLR family, apopto	nucleotide binding	full-length
10411633	1.216206039	3.137363684	0.223687191	-5.614918129	0.798239658	-1.180420403	4.881047026		Naip1	NLR family, apopto	nucleotide binding	full-length
10411668	-0.666225565	-2.620722632	-0.216683234	-5.733106596	-1.269379597	2.602566946	7.487831736		Ocln	occludin	structural molecule	full-length
10411728	1.451033253	1.804600321	0.119610032	-6.265273963	0.9970172	-1.839213113	4.183971695	Cluster III	Cenph	centromere protein	kinetochore /// kine	full-length
10411739	2.488172416	6.804383	-0.196357992	-6.103639215	2.251759816	5.237689133	5.870559277		Ccnb1	cyclin B1	in utero embryonic	full-length
10412036	-0.45115032	-3.217020777	-0.178401881	-5.59231414	-1.052625319	3.759644386	7.912664386		Apoo /// Apoo-ps	apolipoprotein O ///	membrane /// integ	full-length
10412123	1.543574131	9.569308021	0.02091855	-6.377881983	1.504395589	8.832488827	6.384197149		Ncf2	neutrophil cytosolic	acrosome /// bindin	full-length
10412211	3.430390235	13.31908536	0.140570235	-6.15684091	3.700117919	13.81842533	6.319758208		Gzma	granzyme A	serine-type endope	full-length
10412218	1.181816292	8.48809159	0.008615211	-6.388436167	1.121690893	7.441785754	5.296097447		Gzmk	granzyme K	serine-type endope	full-length
10412345	1.465779112	9.024957918	-0.249636416	-4.645848949	1.655868631	10.04537423	6.361684057		Parp8	poly (ADP-ribose) p	NAD+ ADP-ribosylt	full-length
10412607	-1.390891779	5.89759731	-0.186542311	-5.703454918	-1.901624217	9.11239537	8.903904949		Abhd6	abhydrolase domai	catalytic activity ///	full-length
10413047	2.023844067	7.40783395	-0.105536554	-6.250558974	1.876070715	6.100702814	6.515110578		Plau	plasminogen activa	response to hypoxi	full-length
10414163	-0.650084089	-1.517696827	-0.041309231	-6.355975999	-1.022002646	2.19609727	7.170806772		Lrit1	leucine-rich repeat,	protein binding /// e	full-length
10414262	2.263078432	10.0681886	-0.162422298	-5.980443354	2.249403484	9.566477115	6.70650711		Ear2	eosinophil-associat	nucleic acid bindin	full-length
10414360	2.866730502	14.22814816	0.205413917	-5.589846347	3.111773911	14.80785711	8.184513738		Lgals3	lectin, galactose bi	skeletal developme	full-length
10414548	1.7722049	7.615476489	-0.110031642	-6.185366188	1.597444896	5.984295756	6.257220313		Rnase6	ribonuclease, RNa	nucleic acid bindin	full-length
10415052	1.035300964	3.884063216	0.053241695	-6.317947871	1.439530205	7.169420941	8.987358541		Mmp14	matrix metallopepti	metalloendopeptida	full-length
10415279	-1.417876186	4.879359713	-0.151605523	-6.01772778	-1.947796403	8.094265501	9.114115085		1110028A07Rik	RIKEN cDNA 1110	endoplasmic reticul	full-length
10416023	0.79672943	-5.581003887	0.381567119	-5.972973563	1.911733017	-1.04828725	6.708502695		Scara5	scavenger receptor	scavenger receptor	full-length
10416037	1.172340705	-2.285815974	-0.130575577	-6.302769279	0.157812195	-7.210773537	4.67100739	Cluster III	Pbk	PDZ binding kinase	nucleotide binding	full-length
10416071	-0.862731701	0.370234525	-0.249172111	-5.32468896	-1.072324622	2.082431628	5.70183682		Chrna2	cholinergic recepto	receptor activity ///	full-length
10416334	0.874771103	1.612933129	0.109396373	-6.114949803	1.065961839	3.234381088	6.69580545		Dok2	docking protein 2	MAPKKK cascade	full-length
10416340	1.081198624	-1.600153237	0.019538754	-6.388948473	0.505563684	-5.723286941	5.335315329		Gfra2	glial cell line derive	receptor activity ///	full-length
10416437	0.794454397	6.789689158	-0.127875889	-5.272202635	1.102540119	10.22162057	10.33094596		Lcp1	lymphocyte cytosol	ruffle /// phagocytic	full-length
10416566	1.322241611	9.197014321	0.28737806	-3.688190184	1.163299783	7.256789524	5.869620573		Epsti1	epithelial stromal in	molecular_function	full-length
10416696	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10416698	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10416700	1.153499881	-0.967828384	0.036114042	-6.381788513	0.454941109	-5.964796962	5.994365929		Pcdh17	protocadherin 17	calcium ion binding	full-length
10416837	3.07736229	4.602021016	-0.156371507	-6.309598454	3.595138698	5.920929812	6.674863917		Irg1	immunoresponsive	propionate catabol	full-length
10417787	1.03790217	4.597224852	0.033164717	-6.35919191	0.963873257	3.380243395	6.872385087		Gng2	guanine nucleotide	GTPase activity ///	full-length
10418410	1.140518857	5.790194814	0.039110906	-6.345359269	1.282549077	6.704151981	8.09274887	Cluster IV	Prkcd	protein kinase C, d	nucleotide binding	full-length
10418434	0.751164488	0.185850163	0.1290006	-6.009389634	1.098754735	3.565523283	12.51440271		Itih3	inter-alpha trypsin i	endopeptidase inhi	full-length
10418848	1.328702946	3.511998235	0.123193638	-6.170419061	1.081487982	1.031975639	6.231075677		Wdfy4	WD repeat and FY	---	partial
10418868	1.422117113	2.724279327	0.109568469	-6.259320022	1.004862074	-0.901366629	6.763233079		---	---	---	predicted
10418917	-0.755013901	-0.988783226	-0.140704078	-6.048236209	-1.107546431	2.168480798	8.049869819		2200001I15Rik	RIKEN cDNA 2200	---	full-length
10419082	-0.6305862	1.790460819	-0.025557435	-6.361065288	-1.089073786	7.342468881	10.41096244		5730469M10Rik	RIKEN cDNA 5730	extracellular region	full-length
10419154	1.824621031	9.835061402	-0.003448791	-6.391507718	1.624689193	8.02836958	5.73450307		Ear2 /// Ear1 /// Ear	eosinophil-associat	nucleic acid bindin	full-length
10419156	2.046706297	6.699734101	-0.002442783	-6.391724781	1.813061987	4.896932944	6.271160705		Ear2 /// Ear1 /// Ear	eosinophil-associat	nucleic acid bindin	full-length
10419296	1.160290348	2.779568821	-0.000876063	-6.391777978	1.012340426	1.029637081	5.684902209		Wdhd1	WD repeat and HM	DNA binding /// nuc	full-length

10419323	1.570038014	4.452191649	0.107457158	-6.247385138	1.396478739	2.787233013	5.686657303		Dlgap5	discs, large (Droso	nucleus /// cytoplas	full-length
10419563	-4.085458832	1.162971677	-3.094252761	-0.608404836	-4.114620294	0.854708968	6.062411127		Rnase1	ribonuclease, RNas	nucleic acid binding	full-length
10419854	1.860609124	11.21372998	0.109706572	-6.05332113	2.135477046	12.44323259	7.533482936		Slc7a8	solute carrier family	amine transmembra	full-length
10420023	-0.581250126	-3.027489904	0.168097551	-5.925138904	-1.113826155	2.0241902	8.178549003		Fam158a	family with sequenc	---	full-length
10420198	2.085226247	11.00553043	0.220196085	-5.396477187	1.870699525	9.283001959	6.89746141		Ripk3	receptor-interacting	nucleotide binding /	full-length
10420308	4.739648816	15.47432623	0.287669311	-5.67388678	5.280516687	16.36105088	7.145009835	Cluster VIII	Gzmb	granzyme B	serine-type endope	full-length
10420426	1.333050422	-0.877488785	-0.116986967	-6.311886325	0.866736596	-4.056564519	4.420003638		F630043A04Rik	RIKEN cDNA F630	---	full-length
10420483	1.947397729	3.932709116	0.885863718	-2.234253083	2.322103987	5.456833953	5.23748241		Phf11 /// EG62870	PHD finger protein	---	full-length
10420488	0.952217941	0.999543106	0.757201147	-0.368515922	1.522709011	5.518553136	6.957555637		D14Ertd668e /// Se	DNA segment, Chr	DNA binding /// nuc	full-length
10420935	-0.855791201	6.976219728	-0.045933479	-6.252867676	-1.142308166	9.948892794	11.52961769		Ephx2	epoxide hydrolase	magnesium ion bin	full-length
10421029	1.292894468	2.541242522	0.229578766	-5.739790672	0.724769138	-2.76271783	5.279592811	Cluster III	Cdca2	cell division cycle a	molecular_function	full-length
10421293	1.071854084	6.256505287	-0.191568099	-5.146468318	1.062085568	5.723218877	6.540193183		Ppp3cc	protein phosphatas	phosphoprotein ph	full-length
10421309	0.227183247	-6.912292179	-0.031222194	-6.384823978	1.024446085	-2.446551362	10.22480952		Slc39a14	solute carrier family	zinc ion transmem	full-length
10421648	-2.500849101	4.458013489	-0.984584126	-2.79072219	-2.913221775	5.738994633	8.878193232		Slc25a30	solute carrier family	transporter activity /	full-length
10421697	1.484596241	6.320152516	0.245565075	-5.299841049	1.981364073	9.266597797	7.938886558		9030625A04Rik	RIKEN cDNA 9030	---	full-length
10422247	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10422493	1.086765034	3.9468177	0.196985869	-5.520065782	1.073495126	3.4024823	5.979377752		Gpr18	G protein-coupled r	signal transducer a	full-length
10422608	1.359864788	0.278290709	0.083418859	-6.340687954	1.200894381	-1.134943011	6.618715783		Oxct1	3-oxoacid CoA tran	mitochondrion /// m	full-length
10422635	-1.626773115	2.936619132	-0.074116017	-6.343219375	-1.908887909	4.2347417	9.704342597		C6	complement comp	---	full-length
10422748	-1.011501279	-0.785611259	0.011821303	-6.390333294	-1.153547347	0.000170563	11.49263507	Cluster X	C9	complement comp	extracellular region	full-length
10422760	2.121215255	7.029865932	0.255835346	-5.713117689	2.025042928	6.064795188	7.013326301	Cluster I	Fyb	FYN binding protei	nucleus /// cytoplas	full-length
10422822	-1.206566678	-2.683148725	-0.20630745	-6.206349742	-2.006593534	1.152124436	10.37370014		Lifr	leukemia inhibitory	receptor activity ///	full-length
10423005	-1.268627979	7.644371912	-0.065733874	-6.246618518	-1.654735772	10.36084297	10.05926814		Ugt3a1	UDP glycosyltransf	metabolic process /	full-length
10423090	-0.584527936	-0.364574257	-0.046189538	-6.318594351	-1.14144221	6.0795235	10.06168223		Amacr	alpha-methylacyl-C	catalytic activity ///	full-length
10424188	1.099818259	0.81327286	0.215750749	-5.827923196	0.849252223	-1.733229611	5.293418537		Mtbp	Mdm2, transforme	protein binding /// u	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**ene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10424377	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	predicted
10424400	1.610728559	10.97211977	-0.214528029	-4.881263666	1.531018796	9.939740787	7.262905063		Myc	myelocytomatosis	B cell apoptosis ///	full-length
10424676	1.052586866	6.445673286	0.70662265	2.558853264	1.134407823	6.877828367	11.9742688		Ly6e	lymphocyte antigen	in utero embryonic	full-length
10424683	0.680433621	-2.168893491	0.180955747	-5.884155585	1.229363994	2.726397924	4.004173444		---	---	---	partial
10424929	-0.998410269	1.88880566	-0.217485487	-5.542763879	-1.582949172	6.464582555	7.827781599		Adck5	aarF domain contai	protein kinase activ	full-length
10425049	0.802535498	4.2800802	1.271031507	8.941546977	1.280955908	9.227511735	11.38494442		Apol9a /// Apol9b	apolipoprotein L 9a	---	full-length
10425053	1.729952914	8.949268103	-0.170188032	-5.762671008	1.883960136	9.530800042	6.415382968		Ncf4	neutrophil cytosolic	protein binding /// c	full-length
10425066	1.906754174	6.726485865	-0.222096142	-5.787643546	2.025385409	6.993058303	7.134698146	Cluster VI	Csf2rb	colony stimulating f	receptor activity ///	full-length
10425092	2.280002693	9.931153201	0.314661185	-5.015310279	2.095910028	8.500293091	7.435875071		Cyth4	cytohesin 4	guanyl-nucleotide	full-length
10425161	1.586039166	6.770286803	-0.025656783	-6.379493761	1.262811319	3.793621814	9.472872593		Lgals1	lectin, galactose bi	sugar binding /// ga	full-length
10425321	2.359205695	12.27425151	0.577242047	-1.600399795	2.625105992	13.13843722	7.136738212		Apobec3	apolipoprotein B m	nucleus /// cytoplas	full-length
10425410	1.314826364	7.082891176	0.155745747	-5.730231913	1.383186644	7.239569793	5.64960807		Grap2	GRB2-related adap	protein binding	full-length
10425866	1.93690622	8.29320546	0.170449924	-5.935240245	2.00834374	8.286921127	7.008517122		Parvg	parvin, gamma	actin binding /// pro	full-length
10426479	1.202293745	3.566087177	-0.134437048	-6.069095759	1.13784037	2.5816952	7.757515217		Ano6	anoctamin 6	ion channel activity	full-length
10426557	-0.664617276	3.666589984	-0.147451612	-5.184896407	-1.012275101	7.999980883	7.948039329		Pfkm	phosphofructokinas	nucleotide binding /	full-length
10426812	-0.78627222	3.822985401	-0.18258336	-5.04568881	-1.457251204	10.50940482	10.78864991	Cluster X	Gpd1	glycerol-3-phospha	catalytic activity ///	full-length
10427035	1.548274755	4.369321786	0.077880269	-6.314560799	1.614198121	4.407623523	6.596011679		Nr4a1	nuclear receptor su	DNA binding /// tran	full-length
10427336	2.297149129	15.3541954	0.006939591	-6.389948784	2.219440645	14.57756846	7.860930127		Nckap1l	NCK associated pr	---	full-length
10427389	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10427918	1.647756833	4.706411184	-0.034922552	-6.377142404	1.491600492	3.214037644	6.441586478		Fam105a	family with sequenc	---	full-length
10428302	-0.66476758	-3.510747169	-0.447684593	-4.47299739	-1.40431655	2.200637139	7.722891507		Klf10	Kruppel-like factor	nucleic acid binding	full-length
10428534	1.230721493	2.022701269	-0.099879238	-6.263690921	1.492373113	3.622334505	4.545753771		Trps1	trichorhinophalang	DNA binding /// tran	full-length
10428536	1.173417702	5.027733779	0.17016661	-5.702411122	1.036177173	3.258060786	5.254332809		Trps1	trichorhinophalang	DNA binding /// tran	full-length
10428604	1.024609234	8.174936914	-0.048400533	-6.259554433	0.666046338	2.920149523	7.10136318		Tnfrsf11b	tumor necrosis fact	receptor activity ///	full-length
10428763	1.186061874	-3.273003811	0.116283731	-6.340629484	0.911263413	-4.841234148	6.009052725		Atad2	ATPase family, AA	nucleotide binding /	full-length
10428983	1.547352456	11.61627575	-0.0529457	-6.267778264	1.723037128	12.48585871	8.19133647		Fam49b	family with sequenc	---	full-length
10429114	0.843720289	-2.300373089	-0.059888565	-6.355637103	1.14649618	-0.193742168	5.915243503		Tmem71	transmembrane pr	membrane /// integ	full-length
10429128	2.274439678	10.66625231	0.314793578	-4.846605702	2.589163657	11.79410151	7.45697743		Sla	src-like adaptor	protein binding /// c	full-length
10429520	0.904149481	-0.805158109	-0.155648568	-6.084393203	1.006937077	-0.230461318	6.828532686		Ly6d	lymphocyte antigen	plasma membrane	full-length

10429560	2.740088064	10.05264577	0.255904825	-5.71161494	3.816276419	13.58972306	5.42516361		Ly6i	lymphocyte antigen	plasma membrane	full-length
10429564	2.792793476	16.13039233	0.936583426	3.783099915	3.147798147	17.14835405	11.10187085		Ly6a	lymphocyte antigen	intracellular /// plas	full-length
10429568	3.903071062	18.98967398	0.380013251	-3.477026386	4.237746196	19.59639302	9.071093523		Ly6c1 /// Ly6c2	lymphocyte antigen	external side of pla	full-length
10429573	3.476367095	17.78210874	0.60820174	-0.585117848	3.847649503	18.5930618	8.008440878		Ly6c1 /// Ly6c2	lymphocyte antigen	external side of pla	full-length
10429580	2.215200895	1.475479852	-0.362685906	-5.936812267	2.916592948	3.912943175	5.453274242		---	---	---	partial
10429843	0.933719421	0.94340034	0.815581567	0.328018928	1.166511672	2.767214847	7.421057387		Plec1	plectin 1	actin binding /// ins	full-length
10429968	-1.049741368	-3.626065877	0.216135939	-6.194115942	-1.525858686	-1.378619994	10.01580257		---	---	---	---
10430006	-0.495407831	-6.310103402	-0.218492002	-6.196643202	-1.511554154	-1.587997882	9.554130242		Slc39a4	solute carrier family	zinc ion transmem	full-length
10430174	0.813447524	4.696158923	1.415581923	10.14043318	1.308066779	9.76851272	11.22478343		Apol9a /// Apol9b	apolipoprotein L 9a	---	full-length
10430190	1.793706532	6.791595894	0.312972565	-5.094409772	2.754514976	11.43760276	5.561483606		Apol11b /// Apol10	apolipoprotein L 11	---	full-length
10430201	0.908113346	4.069556212	0.040095645	-6.335382948	1.016784774	4.892590066	9.663875234		Myh9	myosin, heavy poly	microfilament moto	full-length
10430302	1.642667929	5.684467469	0.040162886	-6.368582884	1.929517323	7.101505619	6.621200507		Csf2rb2	colony stimulating f	receptor activity ///	full-length
10430344	1.773893886	8.510522376	0.026059524	-6.378125638	2.041793245	9.748070163	6.242377276		Il2rb	interleukin 2 recept	receptor activity ///	full-length
10430372	2.356779373	14.12524268	0.397363153	-2.900269987	2.305409345	13.47082264	8.233053659		Rac2	RAS-related C3 bo	nucleotide binding	full-length
10430883	-1.047927229	-3.528717329	0.379529775	-5.779138658	-1.675249468	-0.451770473	10.36108874		Cyp2d13	cytochrome P450,	cellular_componen	full-length
10430892	-0.267030392	-6.711542289	0.525859136	-4.465499643	-1.205247289	-0.704870828	10.1082096		Pcdhb11	protocadherin beta	calcium ion binding	full-length
10430899	-1.20078454	-1.542695619	0.134669255	-6.281586281	-2.032357736	2.923284374	8.485597411	Cluster IX	Cyp2d40	cytochrome P450,	---	full-length
10430904	-0.611650983	-2.341066847	-0.010963009	-6.389506336	-1.155953887	2.941862537	10.33625098		---	---	---	partial
10430931	1.786420227	8.269244146	0.22041239	-5.526380937	1.620620088	6.699616855	6.080490153	Cluster I	Nfam1	Nfat activating mol	molecular_function	full-length
10431546	-0.909327214	-1.776217319	0.18291382	-6.063964627	-1.547981039	2.664256955	8.506278506		Tymp /// Sco2	thymidine phospho	phosphorylase acti	full-length
10431872	1.26960455	1.018309237	-0.23140574	-5.881270033	1.147737299	-0.266249765	5.155475309		---	---	---	partial
10431874	1.538111842	9.419460569	-0.043139759	-6.333899359	1.717680682	10.30623093	6.037791985		Slc38a1	solute carrier family	membrane fraction	full-length
10432511	2.2759967	6.936479599	0.091173195	-6.314569412	1.711152513	3.333622363	6.290527884		Racgap1	Rac GTPase-activ	GTPase activator a	full-length
10432636	-0.53183503	-5.387373287	4.32E-05	-6.391790956	-1.018097195	-2.303196747	9.476271372		BC004728	cDNA sequence B	plasma membrane	full-length
10432640	2.145925805	7.12745468	-0.261422383	-5.68895799	2.094982276	6.418167717	7.135877657		---	---	---	partial
10432652	-2.541275397	0.393581144	-1.61182399	-2.35885849	-2.77506375	0.842114527	7.353592002		Ela1	elastase 1, pancre	---	full-length
10432939	-1.415889356	10.91091988	-0.341996978	-2.403031563	-0.590071913	0.792018067	10.84800121	Cluster X	Csad	cysteine sulfinic aci	catalytic activity ///	full-length
10432957	1.575497878	6.506125438	-0.205156464	-5.671731085	1.698094196	6.939848612	6.027632194		Itgb7	integrin beta 7	receptor activity ///	full-length
10433101	1.030580787	-2.033582306	0.090472388	-6.332318552	1.596089379	1.364320075	5.661803673		Gpr84	G protein-coupled	signal transducer a	full-length
10433735	1.378627975	7.379630497	0.188260762	-5.484326686	1.684348665	9.307476613	6.482743374		Abcc1	ATP-binding casse	nucleotide binding	full-length
10434758	0.580173832	0.525794994	-0.092041411	-6.039331398	1.040674558	6.249793159	9.169413185		St6gal1	beta galactoside al	beta-galactoside al	full-length
10434778	1.164211571	1.217438448	1.912801615	6.447257235	1.754136705	5.105514517	9.343740496		Rtp4	receptor transporte	membrane /// integ	full-length
10434934	-0.735430377	-3.593990416	-0.286133147	-5.704773775	-1.657121029	2.713407549	9.968215809	Cluster X	Bdh1	3-hydroxybutyrate	catalytic activity ///	full-length
10435457	0.733701773	0.471035525	1.05869792	4.408213097	1.26171546	5.700377006	8.942648337		Parp9	poly (ADP-ribose)	NAD+ ADP-ribosylt	full-length
10435497	0.840393984	-4.854990028	0.265618131	-6.113254154	1.439997034	-2.05928526	3.690222975		Stfa2l1 /// Stfa2	stefin A2 like 1 /// s	endopeptidase inhi	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (G**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10435565	2.118670158	14.63681336	-0.078426115	-6.151882504	2.388575717	15.66108625	8.017027176	Cluster VI	Hcls1	hematopoietic cell	protein binding /// n	full-length
10435907	1.137228931	7.590647098	0.119600689	-5.818721563	1.131593214	7.099930266	4.37228433		Cd200r1	CD200 receptor 1	receptor activity ///	full-length
10435982	1.139697524	2.421238288	-0.082183192	-6.282205141	1.333608487	3.662721335	5.016592127	Cluster I	Btla	B and T lymphocyt	immune response-	full-length
10436100	1.483165239	-3.597910256	0.321480112	-6.170924156	2.556185498	0.103284521	4.850677062		Retnlg	resistin like gamma	molecular_function	full-length
10436106	1.609248187	1.952511182	0.019067187	-6.389072194	1.07740903	-1.922040583	5.497935674		C330027C09Rik	RIKEN cDNA C330	binding /// cytoplas	full-length
10436978	0.844551139	-4.29407099	-0.115553492	-6.323497693	1.86717129	1.186841856	5.120377719		Cbr3	carbonyl reductase	---	full-length
10437224	0.67795618	-5.559988253	2.587550364	4.115099316	1.208721174	-3.140620739	5.972771953		Mx2	myxovirus (influenz	nucleotide binding	full-length
10437243	1.494147386	7.548485342	0.303145268	-4.489128824	1.192269125	4.550219778	5.505725786		Mefv	Mediterranean feve	actin binding /// pro	full-length
10437945	1.438997105	1.064231298	0.075313832	-6.347711692	1.328534745	-0.038151357	6.325926571		Mcm4	minichromosome m	nucleotide binding	full-length
10438405	3.793517437	11.51244062	-0.311239036	-5.720525578	3.384348722	9.724402542	7.433082037		Igl-V1 /// Igl	immunoglobulin lan	antigen binding ///	full-length
10438415	2.692160172	6.66508726	-0.509884173	-4.91758581	2.783897874	6.620156263	5.557052576		---	---	---	full-length
10438445	1.650281535	11.35443274	-0.090257428	-6.092694159	1.753479806	11.66012571	7.434939334		Klhl6	kelch-like 6 (Droso	protein binding	full-length
10438575	-0.651281857	-4.509626477	-0.276353644	-5.816010114	-1.741230199	2.626230711	10.9737441	Cluster X	Ehhadh	enoyl-Coenzyme A	catalytic activity ///	full-length
10438738	1.95955977	-1.819883289	1.224124976	-3.79214633	0.488786556	-6.863029562	7.521272229	Cluster V	Bcl6	B-cell leukemia/lym	negative regulation	full-length
10438769	-0.609206284	-2.987142496	-0.039229795	-6.367534987	-1.305938773	3.248975228	9.693129707		Cldn1	claudin 1	structural molecule	full-length
10439058	1.272480571	5.58471622	0.344789341	-4.064409219	1.277104278	5.19957192	5.622702681		Lrrc33	leucine rich repeat	protein binding /// m	full-length
10439249	1.225533971	3.703155898	1.552382127	6.288628331	1.732563042	7.166766675	8.945483224		Parp14	poly (ADP-ribose)	nucleic acid bindin	full-length
10439312	1.295640362	3.849878185	0.063191162	-6.32575349	1.157028518	2.258181535	6.586548231		Cd86	CD86 antigen	receptor activity ///	full-length
10439404	-1.420205888	5.718266346	-0.583330793	-1.863455399	-1.194287735	3.392406453	5.834661297		100043264	predicted gene, 10	---	predicted

10439527	0.986353752	2.09576891	0.225737883	-5.42420748	1.290267116	4.526853121	6.389275095		---	---	---	full-length
10439744	1.193169229	6.178703303	0.021058749	-6.378587814	0.927791694	2.99304501	3.828303882		Cd96	CD96 antigen	protein binding /// c	full-length
10439881	0.670296656	0.064387487	0.251914691	-4.776490916	1.040337068	4.059055892	5.343532932		---	---	---	partial
10439936	1.327683691	0.578624727	0.350405118	-5.449953694	1.936093129	3.996942922	7.028171883		Nfkbiz	nuclear factor of ka	nucleus /// transcrip	full-length
10440300	0.970398965	2.948684415	0.1248742	-6.013260486	1.136971735	4.230922188	7.762257944		---	---	---	predicted
10440393	1.813030098	7.274848612	0.12383542	-6.156689703	1.988844689	7.924075991	5.972900831		Samsn1	SAM domain, SH3	phosphotyrosine bi	full-length
10440522	1.061569281	7.647075554	0.009812308	-6.387118429	1.306168803	9.665498522	7.442104091		Adamts1	a disintegrin-like an	ovulation from ovar	full-length
10440926	-0.730450912	-1.613874102	-0.379667111	-4.393785977	-1.231441682	2.78551659	6.504875978		Dnajc28	DnaJ (Hsp40) hom	heat shock protein	full-length
10440993	0.553798819	-1.620679833	0.058772008	-6.294993536	1.247367826	5.947926272	8.441396538		Rcan1	regulator of calcine	nucleus /// cytoplas	full-length
10441003	1.467312988	5.043473827	0.622949423	-2.035383266	1.632652295	5.819753451	5.946737289	Cluster I	Runx1	runt related transcri	skeletal developme	full-length
10441233	1.042584165	-2.008507551	0.966942459	-1.808183612	1.221457362	-1.103928663	5.589674728	Cluster II	Mx1	myxovirus (influenz	nucleotide binding /	full-length
10441361	-0.628859043	0.047844825	-0.398622887	-2.585916729	-1.021802147	4.541085297	5.445934645		Tiam2	T-cell lymphoma in	receptor signaling p	full-length
10441601	1.137106413	4.244098688	0.085218782	-6.225399888	1.218684854	4.585331255	5.804234343		Tagap	T-cell activation Rh	---	full-length
10442098	0.9470498	4.262143823	-0.00906041	-6.389035714	1.149402355	6.002258103	4.614580712		Fpr2 /// Fpr3	formyl peptide rece	receptor activity ///	full-length
10442606	1.347603682	-0.110750903	0.378821541	-5.473021452	1.155741532	-1.707655103	7.267708466		4930528F23Rik	RIKEN cDNA 4930	---	full-length
10442625	-1.008179153	5.601682035	-0.218639592	-4.802736484	-0.86053821	3.441296404	9.118478135		Igfals	insulin-like growth f	protein binding /// e	full-length
10442914	-0.806079874	1.327970344	-0.107640869	-6.094542454	-1.035237931	3.48200314	10.2427874		0610011F06Rik	RIKEN cDNA 0610	---	full-length
10443463	1.116339342	-4.162703907	1.272916374	-2.681979523	1.532028425	-2.548109102	8.267880863	Cluster V	Cdkn1a	cyclin-dependent ki	cyclin-dependent p	full-length
10443730	1.6752258	8.974323352	0.106839958	-6.118742667	1.650767198	8.367697238	8.447230901		Abcg1	ATP-binding casse	nucleotide binding /	full-length
10443764	0.88208584	0.127953849	0.268166663	-5.275570726	1.221441554	2.917036825	6.920328836		Slc37a1	solute carrier family	---	full-length
10443786	-0.488119484	-4.520128068	0.084788926	-6.292102023	-1.286835541	2.457956343	7.607760304		Pde9a	phosphodiesterase	catalytic activity ///	full-length
10443836	0.864536336	1.465230914	0.121145583	-6.056092927	1.002230624	2.555497193	5.961292748		Rrp1b	ribosomal RNA pro	nucleus /// rRNA pr	full-length
10443898	-0.564475587	-2.973481986	0.07682544	-6.283677695	-1.046567765	1.779365605	10.62785536	Cluster X	Cyp4f15	cytochrome P450,	---	full-length
10443980	2.807198761	11.58492488	0.307279841	-5.228752089	3.009101677	11.99783168	6.887715013	Cluster VI	Myo1f	myosin IF	nucleotide binding /	full-length
10444068	1.110043185	9.90380278	0.304817358	-2.139339066	1.262867881	11.01791592	10.50675251	Cluster IV	Tapbp	TAP binding protei	antigen processing	full-length
10444229	1.538799059	2.96358935	-0.022498278	-6.386746025	1.26504782	0.635380733	6.84628491	Cluster I	H2-DMa	histocompatibility 2	antigen processing	full-length
10444236	1.867965994	5.087384876	-0.105858405	-6.280452517	1.691874842	3.585444112	7.196002519	Cluster I	H2-DMb1 /// H2-DM	histocompatibility 2	antigen processing	full-length
10444244	2.253832491	13.54040651	1.098758596	5.241919839	2.47518143	14.25438161	8.580041007	Cluster VI	Tap1	transporter 1, ATP-	nucleotide binding /	full-length
10444258	1.759586238	11.20261837	0.445329104	-1.966995805	1.807238065	11.10001196	8.799732379	Cluster I	Psmb8	proteasome (proso	endopeptidase acti	full-length
10444291	1.729824887	0.501948001	0.051561251	-6.379081369	1.529533146	-0.924148656	9.949317767	Cluster I	H2-Ab1	histocompatibility 2	antigen processing	full-length
10444298	1.745536388	0.773882442	0.10836264	-6.333537829	1.388321374	-1.538200176	9.037003517	Cluster I	H2-Eb1	histocompatibility 2	antigen processing	full-length
10444658	1.92353341	13.49327829	0.041243965	-6.324665745	1.949141623	13.25033413	7.841183657		Clic1	chloride intracellula	ion channel activity	full-length
10444780	1.116713311	8.885819095	0.236922926	-3.903065777	1.209096829	9.397593004	11.90527292	Cluster IV	H2-L /// H2-D1	histocompatibility 2	antigen processing	full-length
10444814	1.717967204	12.05353506	0.598490967	0.957517097	1.885178339	12.75020032	9.175239684		H2-gs10	MHC class I like pr	---	full-length
10444821	0.939938356	5.917446337	0.159602031	-5.318010524	1.092127239	7.21432325	8.485113558		H2-Q8	histocompatibility 2	antigen processing	full-length
10444824	1.958447916	12.37890343	0.686998568	1.251912658	2.100595626	12.80481473	9.3866276		H2-Q6	histocompatibility 2	---	full-length
10444890	0.928000385	-2.199603921	0.028948862	-6.384590474	1.241732482	-0.204161819	5.461780087		Ier3	immediate early res	membrane /// integ	full-length
10444932	1.164149321	6.628000446	0.013307231	-6.385797616	1.303363068	7.506895204	5.881660628		2310014H01Rik	RIKEN cDNA 2310	actin binding /// cyt	full-length
10445112	2.695343423	11.05281754	0.263542537	-5.52294313	3.810465874	14.76184318	6.219396373		Ubd	ubiquitin D	protein modificatio	full-length
10445119	1.04391677	6.564373615	0.536043628	0.313442151	1.019416455	5.862735232	6.222411154	Cluster II	H2-M3	histocompatibility 2	positive regulation	full-length
10445241	1.091650194	5.492444062	0.106449746	-6.043893597	1.335262391	7.375209601	7.61061741		Tnfrsf21	tumor necrosis fact	receptor activity ///	full-length
10445251	-0.957473618	1.445027622	-0.229031824	-5.462220276	-2.548435268	12.07420049	6.821117462		Gpr110	G protein-coupled r	signal transducer a	full-length
10445293	2.597943739	6.273633851	0.102181672	-6.325396585	3.414066046	9.034155329	8.39096902		Pla2g7	phospholipase A2,	catalytic activity ///	full-length
10445558	-0.366454339	-5.097320127	-0.098063851	-6.214061825	-1.162403961	2.924133919	6.614634118		BC048355	cDNA sequence B	nucleus	full-length
10445746	0.806177275	-3.454580589	0.068235373	-6.355879639	1.261100799	-0.528303057	4.565014359		Trem1	triggering receptor	receptor activity ///	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**RelNF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10445753	1.619310014	8.982910475	-0.02521188	-6.375166223	1.968813272	10.88338154	5.481639646		Trem3	triggering receptor	receptor activity ///	full-length
10445758	2.202413808	5.551881484	0.157430348	-6.20054181	2.053987135	4.352216969	8.582157902		Treml4	triggering receptor	receptor activity	full-length
10445767	1.142791353	4.780923528	-0.11186211	-6.08226432	1.162963531	4.553126171	5.391907312		Treml2	triggering receptor	receptor activity ///	full-length
10445774	1.632568301	10.29291321	0.307130971	-3.909793386	1.897367839	11.66636032	6.66909564		B430306N03Rik	RIKEN cDNA B430	receptor activity	full-length
10445953	1.285630581	-1.104195277	0.002144214	-6.3917635	0.681576887	-5.096418656	7.833197683		Emr4	EGF-like module c	signal transducer a	full-length
10446074	1.84919339	4.228934577	0.066122449	-6.353639697	1.556929345	2.016450175	5.736139862		Uhrf1	ubiquitin-like, conta	DNA binding /// pro	full-length
10446253	2.416270656	16.83445264	0.270581787	-3.739976463	2.548274287	17.10200665	7.212046424	Cluster VI	Vav1	vav 1 oncogene	guanyl-nucleotide e	full-length
10446282	1.817628491	3.966384337	0.203117831	-6.045194989	1.429124188	1.106045818	9.015923298		Emr1	EGF-like module c	signal transducer a	full-length
10446553	1.696078557	3.73612301	0.15928452	-6.155224252	1.492977432	2.005561634	6.210383606		Epb4.1l3	erythrocyte protein	actin binding /// stru	full-length

10446763	1.040612358	0.883048197	-0.160040717	-6.034289016	0.820366752	-1.516584123	7.123892691		Lbh	limb-bud and heart	nucleus /// cytoplas	full-length
10446777	-1.314377083	6.496499735	-0.032488626	-6.364445976	-1.967182876	10.82140006	9.002762177		Ehd3	EH-domain contain	nucleotide binding /	full-length
10447594	1.077240247	8.639261007	-0.068179549	-6.13734935	0.892801713	6.021598788	9.265479972		Dynlt1	dynein light chain T	motor activity /// pro	full-length
10447602	1.362442951	8.318672971	-0.056076953	-6.288679699	1.728194691	10.71604293	7.683696716		Ezr	ezrin	uropod /// binding //	full-length
10448124	1.84971366	12.59073734	0.050281436	-6.299352475	1.872339655	12.32516804	8.589630726		Fpr1	formyl peptide rece	signal transducer a	full-length
10448202	1.474491973	7.365051521	-0.13348706	-5.978127105	1.613011144	7.982870378	10.10265422		Tpm4	tropomyosin 4	podosome /// actin	full-length
10448230	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10448459	0.622563169	-1.870014438	-0.140834804	-5.989796554	1.257347869	4.355249583	7.818047307		Tbc1d24	TBC1 domain famil	GTPase activator a	full-length
10448495	-1.048742287	3.292366096	-0.099381637	-6.169932139	-1.03593091	2.758030804	8.485406504		1600002H07Rik	RIKEN cDNA 1600	---	full-length
10448743	-1.046059865	1.295290595	-0.369021164	-4.568129456	-1.316198435	3.22824763	8.32627698		Fahd1	fumarylacetoacetat	magnesium ion bin	full-length
10448836	-0.628883761	-1.89736954	-0.061295895	-6.315806959	-1.136990017	3.123449747	7.602567725		Tmem204	transmembrane pro	plasma membrane	full-length
10449245	-1.52714552	-0.81982212	-1.364572295	-1.020621308	-1.554591665	-1.007746616	4.234351713		Pdia2	protein disulfide iso	protein disulfide iso	full-length
10449303	1.459481097	7.986613753	0.160025886	-5.72989637	1.521415596	8.041762046	7.468885339	Cluster I	Bak1	BCL2-antagonist/ki	leukocyte homeosta	full-length
10449452	0.425254568	-6.742409127	0.291791721	-6.139494578	1.50885449	-2.742396815	9.737641753		Fkbp5	FK506 binding prot	peptidyl-prolyl cis-tr	full-length
10449467	-2.976818582	-0.140743959	-2.251997949	-1.62300943	-3.114758703	-0.09488016	6.862724585	Cluster IX	Clps	colipase, pancreati	extracellular region	full-length
10449661	-1.322487467	-2.808061345	-1.067383792	-3.262600432	-1.344559211	-2.976617171	5.494785472		Tff2	trefoil factor 2 (spas	extracellular region	full-length
10449940	-0.663751654	-5.413127876	-0.037718489	-6.385013037	-1.170424698	-2.913895192	10.43354049		Cyp4f14	cytochrome P450, f	monooxygenase ac	full-length
10449999	-0.568707892	-4.954648352	-0.124265085	-6.263641049	-1.172172603	-0.806645416	5.728844895	Cluster X	Zfp101	zinc finger protein 1	nucleus /// zinc ion	full-length
10450038	-1.084090052	5.905961098	0.040502657	-6.335583062	-1.141852127	6.068547082	10.1315938		Angptl4	angiopoietin-like 4	molecular_function	full-length
10450145	2.224036882	10.14892722	0.766885223	-0.419926507	2.232775249	9.766777477	9.552751845	Cluster VI	Psmb9	proteasome (proso	endopeptidase acti	full-length
10450154	1.781179563	2.565847473	0.142451308	-6.25343954	1.560339179	0.871080556	9.776977452	Cluster I	H2-Aa	histocompatibility 2	antigen processing	full-length
10450374	2.753912984	16.68917607	0.137785926	-5.782590813	3.014837951	17.37761257	7.68058165		D17H6S56E-5	DNA segment, Chr	viral envelope	full-length
10450444	-0.529028937	-1.236852552	-0.119045341	-5.925283139	-1.062774729	5.209401157	11.07881118		Apom	apolipoprotein M	lipid transporter act	full-length
10450484	1.864623454	10.67698524	0.295030777	-4.435563708	1.811529301	9.904895662	7.08047346		Aif1	allograft inflammat	ruffle /// phagocytic	full-length
10450496	1.209220542	3.373026756	0.133406239	-6.08840054	1.176595196	2.680858979	6.878429881		Lst1	leukocyte specific t	cell morphogenesis	full-length
10450501	1.388657468	-1.69357711	0.127770731	-6.32026928	1.767491387	-0.038330006	6.031594066	Cluster I	Tnf	tumor necrosis fact	negative regulation	full-length
10450605	1.051051005	2.006754686	-0.075890648	-6.290500457	1.024801778	1.369728755	10.22799912		Tubb5	tubulin, beta 5	nucleotide binding /	full-length
10450694	1.065670646	7.588421198	0.407249012	-1.255608631	1.247634657	9.013140486	10.39271794		H2-T22 /// H2-T10 /	histocompatibility 2	---	full-length
10450723	1.017640367	3.681471217	0.21419331	-5.29301222	1.199098109	5.060544231	7.350323445		H2-T10	histocompatibility 2	---	full-length
10451287	1.114592054	5.548027878	2.074627428	11.36409224	1.731285738	10.26737958	7.168436177	Cluster V	Isg15	ISG15 ubiquitin-like	protein binding /// e	full-length
10451291	-1.672034169	-1.063243468	0.169395974	-6.290202535	-2.528055825	2.383176819	7.648587551		Slc22a7	solute carrier family	transporter activity /	full-length
10451547	1.176487677	6.941068383	0.008923698	-6.389004134	0.937952507	3.967852619	7.000322959		LOC100043385	similar to high mobi	---	predicted
10451710	1.060420785	1.297030788	-0.086357382	-6.280344749	1.155286951	1.751393194	5.912516755		Rftn1	raftlin lipid raft linke	plasma membrane	full-length
10451763	1.158463494	8.849173736	0.397086782	-1.265514311	1.573490688	12.07652456	5.862075776	Cluster IV	Satb1	special AT-rich seq	negative regulation	full-length
10451818	-0.557483652	-5.641007735	0.185635208	-6.193987114	-1.142967074	-2.395816037	5.900782627		Sult1c2	sulfotransferase fa	lysosome /// sulfotr	full-length
10451860	1.14950815	-1.958999026	-0.041857059	-6.381308529	0.785037415	-4.495987602	6.171729564		Pot1b	protection of telome	---	full-length
10451943	-1.292386352	7.402881626	0.070658898	-6.236838815	-0.830772865	2.125779261	8.122545322		2310076L09Rik	RIKEN cDNA 2310	lipid particle	full-length
10451953	0.533754077	-4.939084752	0.219410937	-5.945842178	1.227093599	0.17755241	11.66407445		Lrg1	leucine-rich alpha-2	---	full-length
10452485	1.158274696	6.728270418	-0.017372424	-6.381295007	0.926607147	3.80546563	7.421783188		Rab31	RAB31, member R	nucleotide binding /	full-length
10452648	0.909831128	1.699191068	-0.146326532	-5.932436194	1.156704831	3.781208669	6.581575019		Emilin2	elastin microfibril in	protein binding /// e	full-length
10452815	0.781862172	2.295412921	0.476011874	-1.355438582	1.492665557	9.119355363	10.54554979		Xdh	xanthine dehydroge	catalytic activity ///	full-length
10452854	-0.446130636	-3.498379396	-0.06521775	-6.286834203	-1.336961577	6.017332606	6.613266776	Cluster X	Srd5a2	steroid 5 alpha-red	3-oxo-5-alpha-stero	full-length
10452980	0.340660131	-4.574525934	1.366669388	7.178056379	0.603188415	-1.306160147	7.859384946	Cluster V	Eif2ak2	eukaryotic translati	nucleotide binding /	full-length
10453026	-0.685062641	-2.399017438	-0.039515203	-6.368558001	-1.005421042	0.370667686	9.892991383		Prkd3	protein kinase D3	nucleotide binding /	full-length
10453715	1.35016213	2.114359991	0.054259669	-6.359561198	0.958024768	-1.351737691	5.742254083		---	---	---	predicted
10453759	-1.170810218	0.588275263	-0.476649319	-4.339477997	-1.413902429	2.031303689	4.43268366		---	---	---	partial
10453867	0.655264614	-0.748175409	-0.26664891	-4.817654109	1.243094241	5.238921274	6.710269372		Rbbp8	retinoblastoma bin	G1/S transition of m	full-length
10454015	-0.871376232	1.668428467	0.088286103	-6.206696209	-1.933692664	10.16739805	10.83023706		Ttc39c	tetratricopeptide re	---	full-length
10454030	-1.206890922	-0.554437758	0.13846418	-6.245033191	-1.341446145	0.016250529	5.323092408		Cabyr	calcium-binding tyr	calcium ion binding	full-length
10454039	0.672727362	-0.233349604	-0.000740622	-6.391776242	1.369675423	6.734141625	8.525794132		Impact	imprinted and ancie	negative regulation	full-length
10454198	-0.25571687	-6.726122153	0.149296221	-6.202441512	-1.082621247	-1.339316554	11.0708006		Rnf125	ring finger protein 1	protein binding /// in	full-length
10454286	0.889876374	2.818490152	0.007151272	-6.39030832	1.127503152	4.957484853	7.994471029	Cluster III	Mapre2	microtubule-associa	protein binding /// c	full-length
10454709	1.453795038	4.123534883	-0.011948442	-6.389808561	0.888271299	-1.012255619	5.56699016		Kif20a	kinesin family mem	nucleotide binding /	full-length
10454782	1.191071214	-2.197848419	0.387252547	-5.652790303	0.175704232	-7.182433741	6.342220951		Egr1	early growth respo	negative regulation	full-length
10455015	1.47775062	8.801267107	0.254587809	-4.668396143	1.067578069	4.63066707	8.0078		---	---	---	est
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**ene Ontology (G**	**Transcript**

Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10455533	0.868053987	-2.646055581	0.211225323	-6.017591434	1.34779765	0.555832597	8.171033047		Eif1a	eukaryotic translati	RNA binding /// tra	full-length
10455647	1.28908237	7.802257566	-0.02802723	-6.365287186	1.295906803	7.430902085	6.356141617		Tnfaip8	tumor necrosis fact	cytoplasm /// apopt	full-length
10455813	1.042615551	1.258528139	-0.207285159	-5.759194567	0.787890443	-1.539186826	6.624766481		Lmnb1	lamin B1	structural molecule	full-length
10455957	1.228499573	-2.049942331	0.918374836	-3.095310448	1.129406287	-2.917315854	8.233767417		EG546714	predicted gene, EG	---	predicted
10455961	0.973753612	5.825855848	0.689825577	2.553688931	1.194675558	7.756570169	11.75968432	Cluster II	Iigp1	interferon inducible	nucleotide binding /	full-length
10455970	3.272123556	3.106863243	2.366983416	0.556761766	2.39864889	-0.276163304	7.629838105		BC023105	cDNA sequence B	---	full-length
10456005	1.906401481	4.444146892	-0.087041604	-6.327223531	1.660904883	2.565145607	9.479464669	Cluster I	Cd74	CD74 antigen (inva	protein binding /// ly	full-length
10456071	1.254429206	1.550943468	0.127525146	-6.209808044	0.92648035	-1.483078306	9.441390094	Cluster III	Csf1r	colony stimulating f	nucleotide binding /	full-length
10456357	0.732353659	-0.4544337	0.000659012	-6.391781621	1.051817519	2.605674884	6.103746176		Pmaip1	phorbol-12-myrista	release of cytochro	full-length
10456400	1.511840537	9.106229913	-0.023930567	-6.374247237	1.458426761	8.248203534	7.80170063		Tubb6	tubulin, beta 6	nucleotide binding /	full-length
10456439	1.038815639	1.456804159	0.043036283	-6.361794384	0.967170909	0.406176038	5.981632074		Cep192	centrosomal protei	---	full-length
10456490	1.362927519	3.819536648	-0.144124763	-6.088736815	0.88243054	-0.765061376	4.492004888		---	---	---	partial
10457203	0.887243	-3.311661423	0.448152814	-5.169530402	1.391802431	-0.295499764	7.659872894		---	---	---	---
10457225	1.042965395	3.727663792	0.272724841	-4.754082964	0.935865319	2.191428658	6.629561266	Cluster III	Map3k8	mitogen-activated	nucleotide binding /	full-length
10457640	1.766205164	12.36880803	-0.045977242	-6.310062738	1.685490718	11.3941297	8.192710744		S100a11	S100 calcium bindi	calcium ion binding	full-length
10457667	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	predicted
10457733	1.310877363	6.550059153	0.223214134	-5.197133877	1.083995375	3.99633491	5.6671515		B4galt6	UDP-Gal:betaGlcN	magnesium ion bin	full-length
10458046	-0.692366194	-2.638876933	-0.228675127	-5.717051552	-1.144826369	1.160379293	6.707875805		D0H4S114	DNA segment, hum	protein binding /// re	full-length
10458278	2.88946772	11.26483061	0.160347903	-6.088556817	2.726849578	10.1479584	6.174965608		2010001M09Rik	RIKEN cDNA 2010	extracellular region	full-length
10458314	1.820156211	11.07918591	-0.124488953	-5.95013044	2.033083822	11.98239557	7.740144556	Cluster VI	Tmem173	transmembrane pro	mitochondrion /// m	full-length
10458340	0.779021062	2.320414196	-0.045037402	-6.322516351	1.044641716	5.049250291	6.079460435		Hbegf	heparin-binding EG	angiogenesis /// bla	full-length
10458382	1.303677249	4.29049128	0.268385575	-5.22200767	2.250380673	10.17444272	6.276383122	Cluster II	Cd14	CD14 antigen	response to molecu	full-length
10458843	-1.027330326	1.619987067	0.070378766	-6.307340577	-1.310938743	3.734443542	6.20611498		Sema6a	sema domain, trans	protein binding /// p	full-length
10459066	1.413742363	2.652464028	0.117368028	-6.240331859	1.541241429	3.149062751	4.994741396		---	---	---	predicted
10459236	-0.942963626	1.381434336	-0.092825411	-6.22677121	-1.19250182	3.376459606	8.709411828		Grpel2	GrpE-like 2, mitoch	adenyl-nucleotide e	full-length
10459262	-0.960949779	-0.942274679	-0.159489743	-6.114745609	-1.113951862	-0.023249367	7.002665501		Ablim3	actin binding LIM p	actin binding /// cyt	full-length
10459288	1.121728749	0.689450788	0.165160023	-6.076361076	1.639125835	4.149407807	6.297768645		Adrb2	adrenergic recepto	regulation of syste	full-length
10459730	2.004408	7.668119055	-0.195526197	-5.88938663	1.741821677	5.619259765	7.171460388		Me2	malic enzyme 2, N	catalytic activity ///	full-length
10459772	-0.926197054	0.915833683	0.003018151	-6.391624795	-1.24308936	3.491993345	6.56049869		Lipg	lipase, endothelial	catalytic activity /// l	full-length
10460085	0.882051065	5.746516892	-0.012190411	-6.384284576	1.086416057	7.720325926	9.272447403		Cndp2	CNDP dipeptidase	carboxypeptidase a	full-length
10460146	2.250913326	2.412004711	0.059582889	-6.376941991	2.041796383	1.059745966	6.583268641		---	---	---	full-length
10460237	1.125442816	7.430854889	0.332366426	-2.928025072	1.153976715	7.289873574	8.794796532	Cluster IV	Unc93b1	unc-93 homolog B1	toll-like receptor sig	full-length
10460263	-0.478392862	-3.07952269	-0.101029642	-6.142835435	-1.331749178	5.970229776	9.517888132		Acy3	aspartoacylase (am	aminoacylase activ	full-length
10460371	0.898761692	0.497229079	0.119736701	-6.142769834	1.057017722	1.668668494	6.884615332		Ptprcap	protein tyrosine ph	receptor activity ///	full-length
10460738	1.565712565	5.523393684	0.416068478	-4.159825389	1.024589445	0.702085325	5.374752519	Cluster III	Cdca5	cell division cycle a	protein binding /// n	full-length
10460767	0.898531108	-1.671882528	0.296258034	-5.524086354	1.508888154	2.666001465	6.208407445		Batf2	basic leucine zippe	DNA binding /// tra	full-length
10460833	0.943922605	4.354992011	0.091671677	-6.109206054	1.123645645	5.878419729	8.121066044		Ehd1	EH-domain contain	nucleotide binding /	full-length
10461093	1.105770262	10.51195464	0.211369247	-3.765326494	1.197818958	11.04302345	6.680104296		Pla2g16	phospholipase A2,	cell cycle /// membr	full-length
10461558	2.171567819	12.46742094	0.467328335	-2.31169033	2.601261152	14.20921947	8.63452774		Slc15a3	solute carrier family	transporter activity /	full-length
10461587	4.986026362	14.12293561	0.308831262	-5.793669366	5.582581523	15.06649976	7.4441669		Ms4a4a	membrane-spannin	---	predicted
10461594	2.764149806	7.858323095	0.27394531	-5.857398646	3.749211828	11.04920377	6.943540494		Ms4a4c	membrane-spannin	---	full-length
10461605	2.486652415	12.07357334	0.130498929	-6.081305996	2.295308095	10.6967029	5.02248326		Ms4a4b	membrane-spannin	integral to plasma	full-length
10461614	3.005638696	13.11957774	0.931254233	0.726433031	3.471796862	14.43011497	8.154908608		Ms4a6c	membrane-spannin	receptor activity ///	full-length
10461622	3.08140971	16.13744997	0.691568798	0.208163853	3.519260077	17.30465695	7.270745875		Ms4a6b	membrane-spannin	receptor activity ///	full-length
10461629	0.66855835	-0.432177206	0.279351606	-4.630511398	1.190946775	4.952325326	7.022685378		Ms4a4d	membrane-spannin	receptor activity ///	full-length
10461636	1.18485248	-1.921413322	0.085748966	-6.350059998	1.620200185	0.333688934	3.924021196		---	---	---	partial
10461721	2.32020093	15.30679273	0.825915541	3.666249959	2.390656823	15.2852448	10.20896729		Mpeg1	macrophage expres	membrane /// integ	full-length
10461723	2.167127194	7.035772671	0.430812048	-4.691492474	2.014024203	5.764240224	6.292205917		4632417K18Rik	RIKEN cDNA 4632	---	full-length
10461728	-1.282115485	7.573415088	-0.096198335	-6.094603805	-1.760492633	10.90386251	10.35804535		EG240549	predicted gene, EG	mitochondrion /// ac	partial
10461758	-1.732729513	11.64315163	-0.334417932	-3.283600113	-2.025166293	13.09186593	10.6983087		Keg1	kidney expressed g	mitochondrion /// m	full-length
10461765	1.440459759	3.217757914	-0.013640667	-6.389569013	1.410298081	2.592934444	6.209711351		Lpxn	leupaxin	cytoplasm /// zinc i	full-length
10462390	2.78736912	7.599532313	0.775383673	-3.163467931	3.649312795	10.35956334	7.636047052	Cluster VI	Cd274	CD274 antigen	receptor activity ///	full-length
10462587	1.241155049	1.291163073	0.254200485	-5.718085891	1.136471006	0.099733469	5.633073219		Stambpl1	Stam binding protei	ubiquitin thiolestera	full-length
10462613	1.481593963	3.548550631	1.427163311	3.495300107	2.140806913	7.252784224	7.577183261		Ifit2	interferon-induced	binding	full-length
10462618	1.643328326	3.983910463	2.172402121	6.958525221	2.406819727	7.886113643	8.213695562		Ifit3	interferon-induced	binding	full-length

10462621	1.016066162	-1.484637326	1.556727505	2.789006417	1.831845084	3.672854343	6.558230946		I830012O16Rik	RIKEN cDNA I830	---	full-length
10462623	1.502610045	-1.588776881	3.279459828	6.062178747	2.744289084	3.666860788	9.156570455		Ifit1	interferon-induced	binding	full-length
10462632	1.211612221	-0.646460284	0.084111167	-6.338830602	0.89008632	-3.205491742	4.435083209	Cluster III	Kif20b	kinesin family mem	nucleotide binding /	full-length
10462796	1.949836308	5.330300999	0.168039	-6.126082081	1.688314515	3.337025651	5.591551463		Kif11	kinesin family mem	nucleotide binding /	full-length
10462866	1.698659084	2.283098604	0.005554961	-6.391569759	1.475073982	0.529925732	4.599056155		Cep55	centrosomal protei	cell cycle /// mitosis	full-length
10462973	1.552265653	0.62779366	0.125931711	-6.295661154	1.779368023	1.555252371	5.511968544	Cluster I	Hells	helicase, lymphoid	nucleotide binding /	full-length
10463005	-1.459398902	-4.001793044	-0.870568473	-5.070524843	-3.129780099	1.457991661	5.52921232	Cluster IX	Cyp2c55	cytochrome P450, f	monooxygenase ac	full-length
10463027	-0.983422604	-2.75436647	-0.17209444	-6.201753452	-1.279543596	-1.123991437	11.96096848	Cluster X	Cyp2c29	cytochrome P450, f	monooxygenase ac	full-length
10463068	0.202965545	-6.768781974	-0.00677407	-6.391213266	1.008750636	-0.352968694	10.93024361		Ptp4a1 /// OTTMUS	protein tyrosine pho	phosphoprotein pho	full-length

Affymetrix ID	BS/Non Inf.		LS/Non Inf.		ReINF/Non Inf.		Average	Cluster	Gene	Gene	Gene Ontology (GC	Transcript
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10463070	1.851418807	12.17021593	0.219214337	-4.926429659	2.094441463	13.23135304	8.300668322		Entpd1	ectonucleoside tripl	magnesium ion bin	full-length
10463355	1.896568656	4.348092119	-0.093226557	-6.318303974	2.015494634	4.597023092	7.335570164		Scd2	stearoyl-Coenzyme	stearoyl-CoA 9-des	full-length
10463551	-3.778744336	0.657105352	0.081357533	-6.384930272	-7.195495181	7.104959929	9.731111606		Elovl3	elongation of very l	endoplasmic reticul	full-length
10463599	0.962307916	0.594554029	-0.03889199	-6.367971666	1.330756305	3.444241594	7.444765308	Cluster IV	Nfkb2	nuclear factor of ka	follicular dendritic c	full-length
10464298	-5.019751004	0.498481042	-3.975832135	-0.801956694	-5.217591789	0.488279426	5.901841059	Cluster IX	Pnlip	pancreatic lipase	extracellular region	full-length
10464313	-4.298474148	0.315037232	-3.268070107	-1.240065595	-4.503162864	0.375957815	5.221192186		Pnliprp1	pancreatic lipase re	catalytic activity /// t	full-length
10464328	-2.432258263	-0.908025131	-1.693042019	-2.687408316	-2.223599598	-1.931458134	5.520067273	Cluster IX	Pnliprp2	pancreatic lipase-re	catalytic activity /// t	full-length
10464560	1.16299988	4.050699056	-0.097901372	-6.189758525	1.073422767	2.789021084	7.189839358		Aldh3b1	aldehyde dehydrog	aldehyde dehydrog	full-length
10464704	0.907255821	4.686385504	0.074167598	-6.177971817	1.066498292	6.07916918	8.301217309	Cluster III	Adrbk1	adrenergic recepto	nucleotide binding /	full-length
10465059	1.096519691	4.612765503	-0.085178679	-6.200944504	1.08448577	4.073277639	5.421677934		Ctsw	cathepsin W	cysteine-type endo	full-length
10465342	-1.030317076	-3.660503511	-0.036995235	-6.385763289	-1.210736937	-2.949198917	10.69867225	Cluster X	Tm7sf2	transmembrane 7 s	endoplasmic reticul	full-length
10465587	1.693444407	10.16831283	0.141495409	-5.831405298	1.660797507	9.506948997	7.135438697		Fermt3	fermitin family hom	podosome /// protei	full-length
10465726	1.266580355	-1.923794803	-0.035823943	-6.385403647	1.48012551	-1.030583758	5.451900449		BC014805	cDNA sequence BC	---	full-length
10465734	1.234841551	-2.295982004	0.116043769	-6.328475035	0.964728751	-4.065823039	5.546187899		AB056442	cDNA sequence AB	---	full-length
10465742	-1.652954084	-0.511806952	-0.241430159	-6.153243457	-1.879630775	0.266971906	10.67638585		C730048C13Rik	RIKEN cDNA C730	---	full-length
10465764	-1.549367591	-0.972624885	-0.211213408	-6.204957696	-1.688484504	-0.593303224	11.5481997		C730048C13Rik	RIKEN cDNA C730	---	full-length
10465861	1.420603863	1.488995167	0.049373406	-6.37052516	1.092265265	-1.21461469	5.742649765	Cluster III	Incenp	inner centromere p	chromosome, centr	full-length
10465895	-0.388577034	-6.39511119	0.019503233	-6.389465314	-1.35490416	-0.912751916	11.49938431	Cluster X	Fads2	fatty acid desaturas	stearoyl-CoA 9-des	full-length
10465912	1.2510891	7.293768951	0.178868904	-5.416912513	1.01190233	4.457976935	6.334800086		Fen1	flap structure speci	magnesium ion bin	full-length
10466008	0.047934143	-7.212090541	-0.099807486	-6.109104588	-1.209288871	5.748787635	10.90647859		Dak	dihydroxyacetone k	nucleotide binding /	full-length
10466127	1.636619087	11.47631202	0.257247423	-4.222471216	1.933210124	13.05105344	11.34075692		AW112010	expressed sequenc	---	full-length
10466130	1.964495058	4.084074589	0.099449656	-6.317541531	2.015519363	3.946387798	7.008094963		Ms4a8a	membrane-spannin	receptor activity ///	full-length
10466172	1.203360755	0.750695256	0.059652656	-6.354770095	1.217319074	0.489085458	4.431061248		Ms4a1	membrane-spannin	receptor activity ///	full-length
10466200	1.132298365	6.563814791	0.030523931	-6.358896858	1.546320833	9.794466161	4.694239761		Ms4a7	membrane-spannin	---	full-length
10466210	3.112205938	14.63853373	0.555739886	-2.325161784	3.99165371	17.14472217	7.628667648		Ms4a6d	membrane-spannin	receptor activity ///	full-length
10466410	1.013903475	1.988581452	0.026857268	-6.378115492	1.620792135	6.674923436	6.044552992		Psat1	phosphoserine ami	catalytic activity /// p	full-length
10466606	1.902520436	12.56719753	-0.140914062	-5.737640384	1.823147699	11.64457879	7.761414524		Anxa1	annexin A1	phospholipase inhib	full-length
10466659	1.039093665	2.367084033	0.153630164	-5.947712245	1.752882487	7.73923103	8.279388205		Gda	guanine deaminase	zinc ion binding ///	full-length
10466938	1.234924516	7.454948	0.484304433	-1.15410145	1.209748799	6.783236747	5.987491074		5033414D02Rik	RIKEN cDNA 5033	membrane /// integr	full-length
10467136	2.23139962	4.464153385	-0.181187222	-6.189017938	3.193009273	8.131547955	5.842932533		Ch25h	cholesterol 25-hydr	cholesterol 25-hydr	full-length
10467162	-0.485973925	-1.878965891	-0.057457006	-6.279743793	-1.085659013	5.465672875	11.72353271		Pank1	pantothenate kinas	nucleotide binding /	full-length
10467258	1.743792282	8.304126921	-0.034522795	-6.36784749	2.16151098	10.42488712	6.773575795		Myof	myoferlin	protein binding /// n	full-length
10467380	-1.227459889	4.630282756	-0.203845706	-5.559771897	-1.534317983	6.727543129	11.11372254	Cluster IX	Cyp2c67	cytochrome P450, f	---	full-length
10467390	-0.679323982	0.318456085	-0.081922589	-6.194780819	-1.017023863	3.974182851	11.78690644	Cluster X	Cyp2c40 /// Cyp2c6	cytochrome P450, f	monooxygenase ac	full-length
10467470	1.314609753	3.088273489	-0.034192431	-6.375454433	1.417669415	3.478550281	6.273448877		Aldh18a1	aldehyde dehydrog	catalytic activity ///	full-length
10467578	0.586541882	-0.449422514	0.104218207	-6.036816321	1.011810868	4.573310485	9.749611344		Pik3ap1	phosphoinositide-3-	transmembrane rec	full-length
10467637	1.281091776	6.161719347	0.200794235	-5.428309076	0.936677504	2.340316923	5.487164912		Arhgap19	Rho GTPase activa	molecular_function	full-length
10467784	-0.666140936	-0.651284599	-0.108035018	-6.108207919	-1.496857138	7.313804516	6.937847078	Cluster X	4833409A17Rik	RIKEN cDNA 4833	electron carrier acti	full-length
10467897	-1.098497015	-3.519599384	-0.103969431	-6.347909421	-1.871648582	0.123379608	11.70373801	Cluster X	Cyp2c44	cytochrome P450, f	molecular_function	full-length
10467979	-1.299861662	-6.223951391	0.064296005	-6.389060274	-4.964946688	0.730997934	11.72412214	Cluster IX	Scd1	stearoyl-Coenzyme	stearoyl-CoA 9-des	full-length
10468239	1.628226296	-2.491945685	0.181851542	-6.307403634	1.876323788	-1.769586517	8.201952358		Cyp17a1	cytochrome P450, f	monooxygenase ac	full-length
10468487	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10468893	0.821631407	2.505914089	0.236738381	-4.809370592	1.045313051	4.666078602	7.679715771		Csf2ra	colony stimulating f	receptor activity ///	full-length
10468898	1.355226248	3.363232707	0.096979944	-6.262641606	1.41530759	3.414444433	5.403412983	Cluster I	Lax1	lymphocyte transm	plasma membrane	full-length
10469127	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est

10469151	-1.09904051	3.683538683	-0.358697252	-4.011651557	-1.84718356	9.185510864	6.211024708		Itih5	inter-alpha (globulir	endopeptidase inhil	full-length
10469255	1.043544068	5.214728599	-0.114549611	-5.974501882	0.863400911	2.750628656	5.998005878	Cluster III	Prkcq	protein kinase C, th	nucleotide binding /	full-length
10469322	2.502514974	15.4271181	-0.208275089	-5.111702718	2.610121959	15.54949623	10.17853404		Vim	vimentin	structural molecule	full-length
10469358	-0.334914628	-5.778514205	0.004215786	-6.391530788	-1.191121203	1.910282519	8.790619309		Mrc1	mannose receptor,	receptor activity /// t	full-length
10469559	-0.553455971	-1.947956292	0.036076356	-6.358158882	-1.237654348	5.371693234	7.279968357	Cluster X	Msrb2	methionine sulfoxid	protein-methionine-	full-length
10469695	1.515625389	10.31404439	0.069668518	-6.212716695	1.554868245	10.19164936	6.152865308		Apbb1ip	amyloid beta (A4) p	cytoplasm /// cytosk	full-length
10469786	0.164780482	-6.74866932	-0.063986309	-6.310895518	1.147040946	3.095557268	4.385367898	Cluster IV	Il1f9	interleukin 1 family,	cytokine activity /// i	full-length
10469816	1.162612069	4.476102537	0.083360068	-6.232796699	2.104332738	10.94604248	6.901085021	Cluster II	Il1rn	interleukin 1 recept	receptor activity /// i	full-length
10470175	-1.151736031	0.248149205	0.19826752	-6.002416157	-0.969368416	-1.542616087	4.642760215		Lcn13	lipocalin 13	transporter activity /	full-length
10470555	1.351323335	2.125680621	0.508036617	-4.044562247	1.057040467	-0.539325351	6.21651426		Gbgt1	globoside alpha-1,3	Golgi apparatus ///	full-length
10471555	-0.320794681	-5.196116014	-0.215564303	-5.396313475	-1.110891505	3.567156219	6.960526538		Angptl2	angiopoietin-like 2	receptor binding ///	full-length
10471929	1.471319367	6.2574927	0.216651746	-5.520648774	1.355851953	4.90748036	5.271438072		Arhgap15	Rho GTPase activa	GTPase activator a	full-length
10472162	-0.354201633	-6.229096622	-0.035024645	-6.380942152	-1.023118894	-1.677103861	8.278362786	Cluster X	Gpd2	glycerol phosphate	glycerol-3-phospha	full-length
10472501	1.386446546	2.792861378	0.062918096	-6.344909272	1.908121919	5.862240339	8.272018868		Lass6	LAG1 homolog, cer	DNA binding /// trar	full-length
10472782	0.962237676	5.638324812	-0.070126044	-6.190085999	1.07699999	6.49487946	8.604974033		Hat1	histone aminotrans	histone acetyltransf	full-length
10472820	1.67427159	2.524216297	-0.348339332	-5.515396952	1.718186251	2.390939912	6.683535679	Cluster I	Itga6	integrin alpha 6	receptor activity /// i	full-length
10473022	1.840878591	9.516247438	-0.215327435	-5.437928037	1.762595863	8.568949184	7.444680794		Plp2	proteolipid protein 2	membrane /// integr	full-length
10473125	3.040177509	14.96289202	0.082566369	-6.254106968	3.15719443	15.02883799	7.736763775		Itga4	integrin alpha 4	fibronectin binding /	full-length
10473356	0.889473419	2.783997756	0.603111285	-0.212655311	1.195175187	5.5804509	9.298366494		Ube2l6	ubiquitin-conjugatin	ubiquitin-protein liga	full-length

Affymetrix ID	BS/Non Inf.		LS/Non Inf.		ReINF/Non Inf.		Average	Cluster	Gene	Gene	Gene Ontology (GC	Transcript
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10473809	2.276347359	13.17978987	0.156697321	-5.763880538	2.333451637	13.07123598	6.887271262	Cluster VI	Sfpi1	SFFV proviral integ	DNA binding /// trar	full-length
10474223	-0.653317953	-1.906825879	-0.048673356	-6.347400731	-1.00339428	1.451262269	5.983055728	Cluster X	Cd59b	CD59b antigen	negative regulation	full-length
10474700	1.429393917	4.546001536	0.003900972	-6.391554785	2.114859009	8.614663777	6.760881527	Cluster II	Thbs1	thrombospondin 1	structural molecule	full-length
10474769	1.694252799	4.254073872	-0.098473107	-6.29101682	1.274127459	0.934172217	5.8795331		Bub1b	budding uninhibitec	nucleotide binding /	full-length
10474825	1.348332924	3.233275253	0.359960564	-4.827029422	0.961176156	-0.414379405	5.259583211		D2Ertd750e	DNA segment, Chr	protein binding /// c	full-length
10474875	2.069323413	4.951738572	0.277640499	-5.80497004	1.502060139	1.2016752	4.718535857		Casc5	cancer susceptibilit	nucleus	full-length
10474984	1.2537303	1.476734591	0.180259208	-6.038038947	0.727392292	-3.223205407	4.684452844	Cluster III	Nusap1	nucleolar and spinc	mitotic sister chrom	full-length
10475378	-0.758797377	-0.851628764	-0.417484698	-3.809338771	-1.031414275	1.574031397	5.976881303		Casc4	cancer susceptibilit	membrane /// integr	full-length
10475487	1.968727263	6.901889108	0.045331301	-6.366327642	2.488236245	9.22045879	5.869697832		Slc28a2	solute carrier family	nucleoside binding	full-length
10475517	0.768308943	-3.806840117	0.073828972	-6.350962746	1.990038234	3.7825673	4.850709738		AA467197	expressed sequenc	nucleus	full-length
10475866	0.993393233	1.646458463	-0.21287927	-5.605477779	1.411874532	4.946074487	6.546310036	Cluster IV	Bcl2l11	BCL2-like 11 (apop	peripheral to memb	full-length
10475990	1.321651003	-0.222691502	0.063259436	-6.363944852	1.824248664	2.472712141	8.843556456		Slc20a1	solute carrier family	receptor activity /// i	full-length
10476021	2.609838095	14.0693225	0.222477963	-5.311369005	2.451237167	12.92864886	8.821230176	Cluster VI	Sirpa	signal-regulatory pr	protein binding /// ir	full-length
10476395	-1.466583564	3.417241497	-0.080949703	-6.313858329	-2.024070395	6.576874324	6.897514685	Cluster IX	Bmp2	bone morphogeneti	ossification /// ostec	full-length
10476399	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10(	---	est
10476590	-0.80652864	-3.250836903	-0.479307348	-4.726232494	-1.094123552	-1.417422763	5.756261639		Macrod2	MACRO domain co	---	full-length
10476945	1.612151193	9.761750156	0.076682808	-6.216996184	1.845031353	10.9457588	5.580810296		Cst7	cystatin F (leukocys	endopeptidase inhil	full-length
10477187	2.287114466	5.354366738	0.230379833	-6.029966973	1.792698443	2.322244512	5.948502264		Tpx2	TPX2, microtubule-	nucleus /// aster ///	full-length
10477250	2.337438242	13.59489776	0.14689577	-5.82747763	2.58673914	14.39972479	7.648146316		Hck	hemopoietic cell kir	nucleotide binding /	full-length
10477717	1.653046945	5.644478407	-0.172927881	-5.982425501	2.180939091	8.424264226	6.496627531	Cluster VI	Procr	protein C receptor,	receptor activity /// (	full-length
10478048	0.910169562	1.570409737	0.154463421	-5.894999431	1.806274412	8.716186554	11.83996246	Cluster IV	Lbp	lipopolysaccharide	lipopolysaccharide	full-length
10478326	-1.08985098	0.287600729	-0.155512263	-6.119442073	-1.514611201	3.141173401	9.253589467		Sgk2	serum/glucocorticoi	nucleotide binding /	full-length
10478572	1.009483165	2.70305541	-0.075123091	-6.268622741	0.73987763	-0.611736451	5.26826722	Cluster III	Ube2c	ubiquitin-conjugatin	ubiquitin-protein liga	full-length
10478746	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10(	---	est
10478897	1.545188129	11.84018457	-0.054856567	-6.253329124	1.830065027	13.44745795	8.576595502		Ptpn1	protein tyrosine pho	phosphoprotein pho	full-length
10479154	1.127171583	2.725645939	0.080661788	-6.277319369	1.395153147	4.598200105	6.209895047		Tubb1	tubulin, beta 1	nucleotide binding /	full-length
10479811	-1.156750889	0.163185123	-0.034842992	-6.379743713	-1.229963918	0.357956207	6.78419562		Mcm10	minichromosome m	nucleus /// DNA rep	full-length
10479950	0.986305057	6.708816978	-0.095438479	-5.970120481	1.089400784	7.430600981	7.407963305		Cugbp2	CUG triplet repeat,	nucleotide binding /	full-length
10479979	1.003945769	-1.348297151	0.010880811	-6.39069996	0.755072263	-3.579009726	5.958785638		---	---	---	est
10480090	-1.059367462	1.903077506	-0.329063689	-4.76536529	-1.724280797	6.784493083	6.294424228	Cluster IX	Itga8	integrin alpha 8	metanephros devel	full-length
10480347	1.783493623	9.407880442	0.082159487	-6.237088808	1.741157007	8.690982313	7.739346798		Pip4k2a	phosphatidylinosito	nucleotide binding /	full-length
10480432	1.007256885	1.945022711	-0.115663072	-6.141665516	0.571942453	-3.061366811	3.970897341	Cluster III	Mastl	microtubule associa	nucleotide binding /	full-length
10480714	0.745906467	-0.495507262	-0.06252931	-6.311930644	1.10793801	2.905329345	7.444314595		Uap1l1	UDP-N-acteylgluco	metabolic process /	full-length
10480725	-0.62017123	-2.226247105	0.05694818	-6.330124557	-1.28025693	4.058936142	7.975430416		BC029214	cDNA sequence BC	---	full-length
10480751	-0.812513081	-2.822787455	0.008191352	-6.391164137	-1.372146758	1.095958329	11.33875798	Cluster X	C8g	complement compo	transporter activity /	full-length

10481164	1.499911038	8.188441124	0.351713205	-3.730003063	1.742438361	9.531294595	6.712015649		Slc2a6	solute carrier family	sugar:hydrogen syr	full-length
10481278	-4.618514149	0.287678602	-3.508298616	-1.267319969	-4.5741576	-0.156064067	5.646560443		Cel	carboxyl ester lipas	carboxylesterase a	full-length
10481435	-0.452658511	-2.880627858	0.080315205	-6.203816408	-1.830777349	10.73973843	10.25468932		Ccbl1	cysteine conjugate-	catalytic activity ///	full-length
10481627	5.422026923	16.25269912	0.280252088	-5.789664209	6.199083402	17.43109168	10.24787587	Cluster VIII	Lcn2	lipocalin 2	transporter activity	full-length
10481634	-1.394724484	10.51124781	-0.812888691	4.498990842	-1.003010376	6.20383801	9.762130228		Slc25a25	solute carrier family	binding /// calcium i	full-length
10482059	1.297382784	4.655290928	-0.141591016	-6.017572196	1.349124346	4.666306011	6.611375033		Ggta1	glycoprotein galact	Golgi apparatus ///	full-length
10482517	0.789310287	5.266841605	0.738696992	4.726737769	1.119984884	8.889017575	8.655197278		Nmi	N-myc (and STAT)	cytoplasm	full-length
10482802	3.133753561	14.05353684	-0.110863888	-6.192840249	3.30678609	14.2982301	5.945448866		Cytip	cytohesin 1 interact	protein binding /// c	full-length
10482929	1.213924445	8.128884811	0.196392235	-4.999120725	1.953828402	13.37519537	6.740579655		Ly75	lymphocyte antigen	receptor activity ///	full-length
10483110	0.651924901	2.049059179	1.159482111	8.031769564	0.689270922	2.21736966	8.971028461	Cluster V	Ifih1	interferon induced	nucleotide binding	full-length
10483161	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10483249	0.969727763	-1.539572481	0.142184462	-6.204401998	1.34629822	0.946266159	5.693007346		Galnt3	UDP-N-acetyl-alph	polypeptide N-acet	full-length
10483381	1.14346345	3.620088485	0.117881209	-6.113738456	1.306362724	4.652829378	6.686791978		Stk39	serine/threonine kir	nucleotide binding	full-length
10483698	1.036669508	1.720432057	0.146225288	-6.034092405	1.002733837	1.015235206	6.286672412		Wipf1	WAS/WASL interac	actin binding /// cyt	full-length
10484261	0.22264535	-6.629486176	0.088032791	-6.288362416	1.042231506	0.231202691	5.663838342		Cerkl /// Itga4	ceramide kinase-lik	kinase activity /// fi	full-length
10484307	1.042377068	2.290352498	-0.288250174	-4.975611444	1.097056524	2.414553571	5.909022108		Frzb	frizzled-related prot	protein binding /// e	full-length
10484355	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10485355	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	predicted
10485405	2.19778607	12.63192896	0.1808263	-5.585504399	2.198175872	12.22320785	7.166124152		Cd44	CD44 antigen	ureteric bud branch	full-length
10485963	1.579041319	1.859263967	0.091158953	-6.328738677	1.314221035	-0.232820621	6.046620223		Arhgap11a	Rho GTPase activa	molecular_function	full-length
10486061	1.636580761	6.955332487	0.021141737	-6.383690769	1.653159083	6.640092414	6.740774706		Rasgrp1	RAS guanyl releasi	guanyl-nucleotide e	full-length
10486396	1.544583646	7.535214006	0.055232564	-6.323524553	1.517356346	6.895712777	7.53213852		Ehd4	EH-domain contain	nucleotide binding	full-length
10487208	2.132013634	6.930580439	0.175232161	-6.073086876	2.564921095	8.663711398	5.431067874		Atp8b4	ATPase, class I, ty	molecular_function	full-length
10487238	1.075451275	3.878158087	0.291828522	-4.600700831	1.250490616	5.116706739	7.029848773		Hdc	histidine decarboxy	catalytic activity ///	full-length
10487340	1.346288104	0.60358664	-0.02421615	-6.38705662	0.958127153	-2.488644529	5.605997001	Cluster III	Ncaph	non-SMC condensi	mitotic cell cycle ///	full-length
10487480	1.85170374	0.410289633	0.076209028	-6.368060649	1.421994546	-2.09797532	4.969871344		Bub1	budding uninhibite	nucleotide binding	full-length
10487577	1.470184246	2.880917356	0.239751447	-5.801636967	0.857762945	-2.261287653	5.496666163		Ckap2l	cytoskeleton assoc	---	full-length
10487588	1.487458904	5.010420229	-0.269352787	-5.34984473	1.200556517	2.307039784	6.472466881	Cluster I	Il1a	interleukin 1 alpha	fever /// cytokine ac	full-length
10487823	0.937000816	2.825210048	0.596289547	-0.666297485	1.030714293	3.421336319	7.743666614		Siglec1	sialic acid binding I	protein binding /// s	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GO**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10487894	0.902658979	-1.604711239	-0.076041071	-6.330375242	1.023294616	-0.931563301	6.155330075		Rassf2	Ras association (R	protein binding /// c	full-length
10488010	-0.985082535	7.929494214	-0.045525343	-6.270308424	-1.17629024	9.596205036	11.02519548	Cluster X	Hao1	hydroxyacid oxidas	catalytic activity ///	full-length
10488378	0.820779523	-2.828105627	-0.015823979	-6.389502661	1.16943537	-0.459226653	7.368731101		Thbd	thrombomodulin	receptor activity ///	full-length
10488382	2.196648792	10.05072932	-0.000321767	-6.391789206	2.338103101	10.36782719	7.864071105		Cd93	CD93 antigen	receptor activity ///	full-length
10488797	-1.046676771	7.314904487	-0.061737616	-6.21445487	-1.313048792	9.55646174	10.10297225		Pxmp4	peroxisomal memb	molecular_function	full-length
10489107	2.190013447	17.10455946	0.694088519	4.071162841	2.58830289	18.63870009	9.489867642		Samhd1	SAM domain and H	catalytic activity	full-length
10489127	1.72691417	7.035595823	0.140457505	-6.073955682	1.661165552	6.157245534	6.766258985		Rbl1	retinoblastoma-like	negative regulation	full-length
10489204	1.210349338	7.898924156	-0.114845951	-5.896990548	1.73056493	11.72345347	10.21912957		Tgm2	transglutaminase 2	protein-glutamine g	full-length
10489343	-1.020362697	4.925927418	-0.49598417	-1.204491305	-0.961320444	3.8534758	6.188048357		---	---	---	full-length
10489705	0.893820493	2.197492168	0.173000991	-5.671609089	1.653667376	8.631553115	8.015016919		Slc13a3	solute carrier family	transporter activity	full-length
10489721	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10489784	1.129847105	4.776458203	0.000922482	-6.391768928	0.921190013	2.195474417	6.89857238		Prex1	phosphatidylinosito	guanyl-nucleotide e	full-length
10489850	0.781538063	1.524650904	0.870342109	2.999385161	1.204230603	5.715675467	8.090565356		Znfx1	zinc finger, NFX1-t	transcription factor	full-length
10490104	1.11031877	4.199328841	0.182073611	-5.637317234	0.875473487	1.340698654	6.092918514	Cluster III	Aurka	aurora kinase A	nucleotide binding	full-length
10490150	2.167278677	11.68300406	1.565366321	7.543765647	3.203619306	15.90162988	8.144558527		Zbp1	Z-DNA binding prot	DNA binding /// left-	full-length
10490302	-1.099140789	-3.03707422	-0.66495656	-4.566146086	-1.038667667	-3.635738217	5.113174204		2810021G02Rik	RIKEN cDNA 2810	nucleus /// zinc ion	partial
10490736	1.05939643	2.203802441	-0.10776939	-6.184421694	0.954374037	0.799740609	6.492394904		Rgs19	regulator of G-prote	signal transducer a	full-length
10490815	0.626273718	-5.384865984	0.444880703	-5.394918177	1.58816708	-0.04577535	3.719220959		EG545500	predicted gene, EG	---	predicted
10490838	-0.090906679	-7.264961319	-0.366572097	-6.157150685	-1.853971946	-3.124483211	7.159613852		Fabp5	fatty acid binding p	transporter activity	full-length
10490903	1.594708433	8.007296943	-0.071260628	-6.276639307	1.723753448	8.490839003	5.829475019		Car13	carbonic anhydrase	carbonate dehydrat	full-length
10490913	-1.427361545	-4.399947827	-0.038265739	-6.389270431	-2.21013299	-2.039857731	12.88593209		Car3	carbonic anhydrase	carbonate dehydrat	full-length
10491171	-0.126651563	-6.914563058	-0.004285614	-6.391371083	-1.157099333	3.935191732	11.46663293		Slc2a2	solute carrier family	transporter activity	full-length
10491820	-0.881621768	-1.342150972	-0.16465323	-6.075180347	-1.215368197	1.120574566	7.371326175		---	---	---	partial
10491825	-1.023493694	-0.755477346	-0.289789207	-5.582842608	-1.457525049	2.154534068	8.294847327		3110057O12Rik	RIKEN cDNA 3110	extracellular region	full-length
10492091	-1.406083063	1.778749749	-0.339470485	-5.384489922	-0.920394222	-2.214397792	6.991975435		Smad9	MAD homolog 9 (D	transcription factor	full-length

10492306	-1.538005023	5.152888223	-0.369577344	-4.617708703	-2.525921069	10.51328669	8.146746129		Sucnr1	succinate receptor	signal transducer a	full-length
10492330	-0.987700718	0.727339732	-0.066443367	-6.324116146	-1.1803411	2.076567839	7.270819935		P2ry1	purinergic receptor	signal transducer a	full-length
10492335	1.390197359	5.989864168	0.064238671	-6.304739568	1.428579417	5.87115285	6.825175127		Rap2b	RAP2B, member of	nucleotide binding /	full-length
10492355	-1.972058483	-2.398509281	-0.019475285	-6.391108652	-2.555377739	-0.723329521	7.707558343		Mme	membrane metallo	metalloendopeptida	full-length
10492709	-1.10420078	4.755080807	0.102439929	-6.114352213	-0.547543446	-2.176818813	6.746506592		Accn5	amiloride-sensitive	ion channel activity	full-length
10492964	2.054120144	8.480746272	0.32839555	-4.953293619	1.955428375	7.46931784	10.52916924		Cd5l	CD5 antigen-like	scavenger receptor	full-length
10493267	1.379408241	6.291817394	0.108063175	-6.131506904	1.310039654	5.278431511	6.586090015	Cluster III	Arhgef2	rho/rac guanine nu	cell morphogenesis	full-length
10493382	-0.214911884	-6.658169959	0.010809969	-6.39018176	-1.72812515	5.573660868	10.44931984		Pklr	pyruvate kinase live	magnesium ion bin	full-length
10493494	-0.376055168	-5.598076293	0.34861437	-4.960545672	-1.063046077	0.32077515	5.781147173		OTTMUSG000000	predicted gene, OT	---	est
10493565	0.549360285	-2.203700476	1.17638093	5.065378109	0.959920239	2.332170282	7.961050431	Cluster V	Adar	adenosine deamina	DNA binding /// left-	full-length
10493812	0.999658342	-1.20553094	-0.086885369	-6.319455893	1.225937422	0.190172335	4.931077818		S100a4	S100 calcium bindi	calcium ion binding	full-length
10493820	2.296802396	6.484542299	-0.079777326	-6.338016921	2.390666549	6.514419374	6.401541876		S100a6	S100 calcium bindi	calcium ion binding	full-length
10493831	1.758579557	-2.514106685	0.147641968	-6.344279803	2.93520884	1.430012164	5.334916203		S100a8	S100 calcium bindi	calcium ion binding	full-length
10493990	1.777697873	11.85901845	-0.070688835	-6.218009453	1.746375887	11.22758032	8.438467007		S100a11	S100 calcium bindi	calcium ion binding	full-length
10494085	-1.504956893	5.847725171	0.013048054	-6.388782566	-1.838775915	7.730653007	11.44435794		Selenbp2	selenium binding p	nucleus /// cytoplas	full-length
10494200	0.905656274	5.004684097	-0.062057027	-6.232017507	1.023967446	5.962479367	7.887207167		Cdc42se1	CDC42 small effect	molecular_function	full-length
10494271	1.805060349	14.41137887	0.31312555	-2.607897327	1.846231506	14.29088649	10.85415198		Ctss	cathepsin S	cysteine-type endo	full-length
10494402	2.39627033	9.825098051	0.148761463	-6.093725107	2.03263627	7.448767931	9.772640277		Hist2h3c1 /// Hist1h	histone cluster 2, H	nucleosome /// DN	full-length
10494405	2.652913096	10.42586529	0.201708481	-5.904442389	2.316343401	8.383221114	10.25997666	Cluster VI	Hist1h3i /// Hist2h3	histone cluster 1, H	nucleosome /// DN	full-length
10494407	1.226955146	3.266511383	-0.032853118	-6.373882845	1.167441713	2.347156158	5.686962689		Hist2h2bb	histone cluster 2, H	nucleosome /// DN	full-length
10494428	-1.194767303	5.006952945	-0.505645951	-2.07561042	-1.658245952	8.351119618	10.42168866		Txnip	thioredoxin interact	enzyme inhibitor ac	full-length
10494978	2.203143558	13.42807981	0.264158951	-4.584654698	2.342397764	13.75701655	5.656789039	Cluster VI	Ptpn22	protein tyrosine pho	phosphoprotein pho	full-length
10495054	0.976844801	3.873447258	-0.06495891	-6.269029634	1.311118981	6.747761519	7.902039064		Rhoc	ras homolog gene f	nucleotide binding /	full-length
10495186	0.824301174	-0.711695591	-0.115664347	-6.181346497	1.107906276	1.628782911	4.109839783		AI504432	expressed sequen	---	full-length
10495405	1.453969597	7.105962576	-0.085669757	-6.221004679	1.456067497	6.690657404	6.478906338		Slc25a24	solute carrier family	binding /// calcium i	full-length
10495518	-0.693274171	-1.359419813	-0.218146885	-5.534314175	-1.184343633	3.268898491	5.681527449		Olfm3	olfactomedin 3	protein binding /// e	full-length
10495896	0.913129916	3.2571604	-0.041265788	-6.340999143	1.002827644	3.846864386	6.846953768	Cluster III	Camk2d	calcium/calmodulin	G1/S transition of m	full-length
10495967	1.354234742	0.827011826	0.124588025	-6.263104704	2.381974553	6.396731559	9.040940457		Tifa	TRAF-interacting p	protein binding /// c	full-length
10495993	0.07569608	-7.261208423	-0.183283114	-6.284979671	-1.709707887	-1.633310084	9.219813751	Cluster X	Elovl6	ELOVL family mem	mitochondrion /// er	full-length
10496077	-0.67019505	-3.573502718	-0.106317566	-6.271527148	-1.062430195	-0.590630599	10.90189143		Agxt2l1	alanine-glyoxylate a	molecular_function	full-length
10496167	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10496204	1.695650222	6.139390726	0.185005073	-5.908723217	1.361047196	3.291607718	4.443752023		Cenpe	centromere protein	nucleotide binding /	full-length
10496251	-0.964290777	0.643438373	-0.040767926	-6.365454611	-1.248245797	2.803508045	8.534815189	Cluster X	Bdh2	3-hydroxybutyrate	molecular_function	full-length
10496336	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10496462	-2.21497949	6.256828344	-0.345880155	-5.420028583	-3.223494496	10.2348597	7.204933661		Adh6-ps1	alcohol dehydroger	---	est
10496466	-0.759348365	-2.771787547	-0.068934639	-6.340368337	-1.321410999	1.461886207	11.20726209	Cluster X	Adh4	alcohol dehydroger	NADPH:quinone re	full-length
10496539	2.854213321	11.02144562	0.816850256	-1.248233075	3.400255208	12.69614175	6.761024783	Cluster VI	Gbp5	guanylate binding p	nucleotide binding /	full-length
10496555	2.232860934	4.746793524	0.547898981	-4.665511057	1.816516982	2.146092557	7.126066346	Cluster I	Gbp5 /// Gbp1	guanylate binding p	nucleotide binding /	full-length
10496569	2.50615924	12.81241891	1.39531857	5.93746963	3.280003354	15.59183685	9.502672628		Gbp6	guanylate binding p	---	full-length

Affymetrix ID Transcript Cluster	BS/Non Inf. logFC	B	LS/Non Inf. logFC	B	ReINF/Non Inf. logFC	B	Average expression	Cluster Number	Gene Symbol	Gene Title	Gene Ontology (G Description	Transcript Classification
10496580	2.963882834	14.66561321	1.709195653	7.808379768	3.884613508	17.41547932	8.949500648	Cluster VI	Gbp3	guanylate binding p	nucleotide binding /	full-length
10496592	4.090107564	18.46460104	0.80005463	0.810977844	5.239747688	20.78971155	9.041489013		Gbp2	guanylate binding p	nucleotide binding /	full-length
10496771	0.848295535	2.894500613	-0.439878336	-2.029693971	1.082847048	5.122465238	5.288206063		Mcoln2	mucolipin 2	ion channel activity	full-length
10496872	0.105441508	-7.212869645	-0.204146665	-6.14943201	-1.106771509	-2.561390092	8.108222395		Eltd1	EGF, latrophilin sev	signal transducer a	full-length
10497265	1.602293919	5.711770862	-0.267726559	-5.383800038	0.494901118	-4.472099734	7.062811718		Fabp4	fatty acid binding p	cytokine production	full-length
10497327	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10497337	-0.909425065	-2.044823179	0.003249056	-6.391692323	-1.295446196	0.554801464	8.53776767		Car1	carbonic anhydrase	carbonate dehydrat	full-length
10497349	3.177987358	16.22771721	0.122437546	-6.051802313	3.061177538	15.43834905	6.195426107	Cluster VI	Sirpb1	signal-regulatory pr	plasma membrane	full-length
10497356	3.011856328	11.32795434	0.121350449	-6.228470576	2.885852617	10.39333336	5.796150474	Cluster VI	Sirpb1	signal-regulatory pr	plasma membrane	full-length
10497358	3.492406805	18.42353986	0.105331108	-6.081046627	3.489397154	18.11994854	6.414803454	Cluster VIII	Sirpb1	signal-regulatory pr	plasma membrane	full-length
10497364	3.115699732	15.50284029	0.150886028	-5.923354235	3.061396461	14.92783868	6.01226361	Cluster VI	Sirpb1	signal-regulatory pr	plasma membrane	full-length
10497372	1.89567073	4.12352216	0.049689596	-6.371655078	1.749368544	2.857209446	5.741104927		381484	predicted gene, 38	---	full-length
10497381	-2.114348761	5.626499526	-0.093957814	-6.316215326	-1.434157113	1.128976174	10.75370078	Cluster IX	Cyp7b1	cytochrome P450, f	monooxygenase ac	full-length
10497463	-5.918705204	0.641683144	-4.25687709	-1.378526399	-6.077101567	0.518385455	6.084062008		Cpb1	carboxypeptidase E	carboxypeptidase a	full-length
10497548	0.686323484	-2.357796721	0.022018952	-6.384508938	1.022029263	0.559279836	8.355804269		Fndc3b	fibronectin type III c	molecular_function	full-length

10497831	2.804679494	7.016382663	0.18197643	-6.188390261	2.297682686	4.335728394	6.331291008		Ccna2	cyclin A2	female pronucleus	full-length
10498273	0.869754459	2.314938236	0.050207653	-6.322796602	1.30343628	6.303905314	8.183470017		Tm4sf1	transmembrane 4 s	membrane /// integ	full-length
10498345	1.066422262	4.229505024	0.272322896	-4.687337086	0.97528667	2.864787964	4.774033721		Gpr171	G protein-coupled r	signal transducer a	full-length
10498350	1.131973359	5.387571302	0.211953089	-5.212993655	1.429854563	7.642674968	6.095436896		P2ry14	purinergic receptor	signal transducer a	full-length
10498367	2.132316749	13.66321598	0.364085565	-3.041337603	2.140804027	13.3120143	7.910850404		P2ry13	purinergic receptor	signal transducer a	full-length
10498802	0.669237012	-1.206828645	0.033740049	-6.367370069	1.118959786	3.244980393	7.92779443		Rapgef2	Rap guanine nucle	guanyl-nucleotide e	full-length
10498871	-0.605416875	-3.802506755	-0.06519525	-6.340476276	-1.342345369	2.163252426	7.266984278		Tmem144	transmembrane pr	membrane /// integ	full-length
10498992	1.583734252	-0.268014801	0.125626294	-6.316382077	2.732048746	4.806417864	7.358903429	Cluster VI	Tlr2	toll-like receptor 2	response to molecu	full-length
10499639	1.148444861	9.917073815	0.270258628	-3.013270299	0.864936844	6.160745658	6.857180033	Cluster III	Cks1b	CDC28 protein kin	cell cycle /// cyclin-	full-length
10499811	-0.749912186	2.62979437	-0.057855458	-6.26135351	-1.425125635	9.45449093	6.81371053		Npr1	natriuretic peptide r	guanylate cyclase	full-length
10499861	0.868392203	-4.938878727	-0.27630983	-6.120893481	1.434833506	-2.467125706	5.006318676	Cluster IV	S100a9	S100 calcium bindi	calcium ion binding	full-length
10500021	-0.598605127	-3.71104111	-0.116727782	-6.21945157	-1.130448477	0.758197305	7.36619145		Cgn	cingulin	molecular_function	full-length
10500276	1.057230924	0.318808766	0.085514942	-6.302409849	0.930891964	-1.12261383	5.871618035		BC028528	cDNA sequence B	extracellular region	full-length
10500283	-0.907628246	-4.034302332	0.079343894	-6.360762027	-1.294123849	-2.099228282	8.846132989		Car14	carbonic anhydras	carbonate dehydra	full-length
10500333	1.030054002	2.660153709	0.093375732	-6.21134251	0.814047726	0.008541734	8.643694391	Cluster III	Hist2h4	histone cluster 2, H	nucleosome /// DN	full-length
10500335	1.965315954	12.35784153	0.413768311	-2.495672213	2.240771132	13.51299659	7.979055521	Cluster VI	Fcgr1	Fc receptor, IgG, hi	antibody-dependen	full-length
10500360	-1.885245988	8.309156029	-0.743437323	-0.580718924	-1.816723786	7.441634124	4.675005969		---	---	---	partial
10500527	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10500529	0.592712485	-4.913433487	0.485607835	-4.759637517	1.026958256	-2.083890297	5.754704695		Phgdh	3-phosphoglycerat	catalytic activity ///	full-length
10500534	-1.831290894	9.614677766	-0.187486015	-5.636986015	-2.109315358	10.87414346	5.600527943	Cluster IX	Hsd3b4	hydroxy-delta-5-ste	catalytic activity ///	full-length
10500539	-1.831290894	9.614677766	-0.187486015	-5.636986015	-2.109315358	10.87414346	5.600527943	Cluster IX	Hsd3b4	hydroxy-delta-5-ste	catalytic activity ///	full-length
10500545	-4.466250581	3.95255621	-0.253834241	-6.300573029	-7.01891522	8.684451519	7.804054556	Cluster IX	Hsd3b5	hydroxy-delta-5-ste	catalytic activity ///	full-length
10500547	-0.95787231	-0.844089045	0.031123829	-6.380689317	-1.959163729	5.960366863	7.922376311	Cluster X	Hsd3b2	hydroxy-delta-5-ste	catalytic activity ///	full-length
10500555	-0.562984572	0.220804405	-0.060260284	-6.239372205	-1.209782032	7.962405831	10.16184924	Cluster X	Hsd3b3	hydroxy-delta-5-ste	catalytic activity ///	full-length
10500677	2.090561007	8.903773752	-0.225180639	-5.650019446	2.13372695	8.7132887	6.463473438		Cd2	CD2 antigen	protein binding /// e	full-length
10501020	3.521425603	-1.533829062	-0.041952741	-6.390533951	5.760785238	2.581837839	5.868352879		Chi3l3	chitinase 3-like 3	catalytic activity ///	full-length
10501063	2.419626469	17.92752791	0.102709477	-5.840760185	2.700752331	18.82987692	9.652832945		Cd53	CD53 antigen	membrane /// integ	full-length
10501199	-0.452464254	-4.72662594	-0.089243804	-6.274955869	-1.248243828	2.441176362	9.638588832		Gstm7	glutathione S-trans	glutathione transfer	full-length
10501456	1.003786545	7.133918013	-0.052857943	-6.254365475	1.113846405	7.916344738	6.437975495		---	---	---	partial
10501494	-7.078706891	0.898707182	-5.408247963	-0.750617638	-7.182894401	0.664028756	6.181829707		Amy2 /// Amy2-1 ///	amylase 2, pancre	extracellular space	full-length
10501500	-5.513863339	0.455552363	-4.040526292	-1.388772766	-5.519387062	0.102692609	7.891640469		Amy2 /// Amy2-1 ///	amylase 2, pancre	extracellular space	full-length
10501511	-5.513863339	0.455552363	-4.040526292	-1.388772766	-5.519387062	0.102692609	7.891640469		Amy2 /// Amy2-1 ///	amylase 2, pancre	extracellular space	full-length
10501522	-5.513863339	0.455552363	-4.040526292	-1.388772766	-5.519387062	0.102692609	7.891640469		Amy2 /// Amy2-1 ///	amylase 2, pancre	extracellular space	full-length
10501533	-5.513863339	0.455552363	-4.040526292	-1.388772766	-5.519387062	0.102692609	7.891640469		Amy2 /// Amy2-1 ///	amylase 2, pancre	extracellular space	full-length
10501608	2.4940662	19.29720036	0.433103612	0.477316281	3.028660203	21.04402626	9.103576726		Vcam1	vascular cell adhes	protein binding /// p	full-length
10501832	-0.703728821	0.564580179	-0.051410778	-6.314784419	-1.169113603	5.424733821	11.62599751		Abcd3	ATP-binding casse	nucleotide binding	full-length
10502042	1.158938931	-0.961024221	0.282475121	-5.811032686	2.272198614	5.319585729	5.743961452		Alpk1	alpha-kinase 1	protein serine/thre	partial
10502050	1.264153495	1.019324424	0.163111565	-6.130843877	2.508329387	8.03877974	6.481018994		Alpk1	alpha-kinase 1	protein serine/thre	partial
10502052	1.217642889	1.649460101	0.357928319	-4.983309158	2.229917526	7.862130479	5.809516172		Alpk1	alpha-kinase 1	protein serine/thre	partial
10502214	-1.441490785	5.831756425	0.018890704	-6.384939041	-1.955023762	8.947756	7.63025315	Cluster IX	Cyp2u1	cytochrome P450,	monooxygenase a	full-length
10502359	1.047123585	2.10660925	-0.17456406	-5.859242112	1.165342151	2.803463997	5.329258129		Dapp1	dual adaptor for ph	protein binding /// c	full-length
10502791	1.72980546	6.460096346	2.451059069	9.703244267	2.538556691	10.54772542	8.922873303		Ifi44	interferon-induced	cytoplasm	full-length
10503098	1.12087455	9.16649602	0.22657926	-4.002854203	1.267462966	10.2001285	8.740269781	Cluster IV	Lyn	Yamaguchi sarcom	nucleotide binding	full-length
10503107	1.210883621	-1.479176424	0.441200848	-5.297594013	1.123371753	-2.34224208	5.745856049		6330407A03Rik	RIKEN cDNA 6330	---	est
10503259	0.71075106	-3.502199062	0.833572592	-1.766163267	1.74806222	3.810376611	11.11612948		Trp53inp1	transformation rela	nucleus /// nucleolu	full-length
10503264	0.80018273	-0.546093189	0.085283575	-6.264695021	1.145722462	2.463499391	4.370066467	Cluster III	Ccne2	cyclin E2	nucleus /// DNA rep	full-length
10504132	1.154501975	7.682119763	0.190441677	-5.045321599	1.457848711	10.01149842	7.441514734	Cluster IV	Ccl19	chemokine (C-C m	cytokine activity ///	full-length
10504159	1.263902377	8.541210455	0.179068296	-5.22511788	1.620040715	11.0681254	7.744442309	Cluster I	Ccl19	chemokine (C-C m	cytokine activity ///	full-length
10504188	1.247460392	8.028118294	0.208877483	-4.933193894	1.606075678	10.59785731	7.671031933	Cluster I	Ccl19	chemokine (C-C m	cytokine activity ///	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**ene Ontology (G**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10504450	1.374237537	4.30695401	0.163359013	-5.97646688	1.727983013	6.45557898	7.325054622		Glipr2	GLI pathogenesis-r	extracellular region	full-length
10504470	1.036813654	1.216806165	0.070051692	-6.316137341	0.934969897	-0.105357499	5.18571552		Melk	maternal embryoni	nucleotide binding	full-length
10504755	1.104173149	4.215796045	0.068890641	-6.276610206	0.987961819	2.624518467	5.731324865		---	---	---	full-length
10504957	1.659106466	2.727341358	0.058664783	-6.363646175	1.356978648	0.377861056	5.874075936		Smc2	structural maintena	nucleotide binding	full-length
10505237	-1.835456143	4.209594875	-0.020626952	-6.388025909	-2.309321443	6.359789196	5.641677358		---	---	---	partial

10505240	-1.824042215	5.875474533	-0.041646578	-6.37085449	-2.241176931	7.825299864	9.654945202		---	---	---	partial
10505246	-1.078396876	4.186598597	0.104751531	-6.117513776	-1.433196039	6.968534361	8.770093611		---	---	---	partial
10505249	-1.549320269	9.311143631	-0.03645657	-6.351725658	-1.691131542	9.92352641	5.308936508		---	---	---	partial
10505252	-2.094043322	5.89526118	-0.448497692	-4.764433154	-1.594250883	2.514799143	3.537291186		---	---	---	partial
10505254	-1.059310095	3.931112576	0.056436624	-6.31188146	-1.465305959	7.159891437	9.178442497		---	---	---	partial
10505258	-1.078396876	4.186598597	0.104751531	-6.117513776	-1.433196039	6.968534361	8.770093611		---	---	---	partial
10505261	-1.79069742	2.923489377	-0.042707013	-6.378478522	-2.502056727	6.178757378	7.536035166		---	---	---	partial
10505266	-3.260832218	10.46882506	0.268415779	-5.820240386	-3.300730203	10.1868863	5.050715117		---	---	---	est
10505268	-3.327199141	7.375661503	-0.048566695	-6.380674121	-5.272031533	12.41781227	8.809710765		---	---	---	partial
10505445	3.697345251	9.006854527	0.309899347	-5.92472881	4.563266905	11.08752886	7.292208797	Cluster VIII	Orm3	orosomucoid 3	regulation of immur	full-length
10505451	4.048123888	15.39771843	1.293573101	2.72557464	4.248471717	15.59205888	10.43849224	Cluster VIII	Orm2	orosomucoid 2	regulation of immur	full-length
10505465	1.552349619	7.385950892	0.272769147	-4.950720894	1.492149387	6.49569411	7.211583109		6330416G13Rik	RIKEN cDNA 6330	membrane /// integr	full-length
10505517	1.392360012	6.537298422	-0.100535701	-6.160479341	1.426285119	6.383264745	6.489037468	Cluster I	Tlr4	toll-like receptor 4	production of nitric	full-length
10505954	-0.743684646	-2.765931967	-0.140287766	-6.172245692	-1.749566145	4.627333442	7.457666882		Tek	endothelial-specific	nucleotide binding	full-length
10506301	-0.551928794	-4.927852319	-0.671589256	-3.242641346	-1.197141023	-0.313610272	5.054139309		Lepr	leptin receptor	receptor activity ///	full-length
10506424	1.722933002	13.56979114	0.048152883	-6.276686095	1.90506514	14.3644255	11.58666251		Actg1	actin, gamma, cyto	nucleotide binding	full-length
10506470	0.514724911	-4.544929581	-0.090965599	-6.28975042	1.208573121	1.248189754	6.842369458		1700024P16Rik	RIKEN cDNA 1700	---	full-length
10507112	1.21282565	0.449480157	-0.200612267	-6.015644977	0.979151645	-1.692920505	4.433124852		Stil	Scl/Tal1 interruptin	cytoplasm /// multic	full-length
10507143	-1.749302798	2.676270202	-0.086035231	-6.337981857	-1.199526858	-1.184359761	11.48058243	Cluster IX	Cyp4a12a	cytochrome P450,	monooxygenase ac	full-length
10507152	-1.745882186	1.760001157	-0.03744113	-6.383226571	-1.029173176	-2.94100677	11.35715876	Cluster IX	Cyp4a12b	cytochrome P450,	---	full-length
10507163	-1.586173566	3.300594136	-0.293690082	-5.581814352	-1.754581961	3.969444523	10.53782732	Cluster IX	Cyp4a10 /// Cyp4a	cytochrome P450,	monooxygenase ac	full-length
10507171	-1.600555938	3.737808648	-0.374337247	-5.047580779	-2.050260901	6.065245149	9.30165601		---	---	---	full-length
10507177	-1.399312885	3.408950784	-0.305666633	-5.269435753	-1.905806228	6.415111324	11.10098751		---	---	---	full-length
10507551	-0.40913542	-5.92499634	-0.305761199	-5.621297102	-1.479917185	1.513741854	6.674353081		2610528J11Rik	RIKEN cDNA 2610	membrane /// integr	full-length
10507594	0.786247657	0.275984507	0.038333276	-6.359479728	1.126266754	3.448712353	8.348748867		Slc2a1	solute carrier family	transporter activity	full-length
10508074	1.224172216	6.893819036	-0.020582181	-6.378220938	1.49815728	8.829003226	5.43016219	Cluster I	Csf3r	colony stimulating f	receptor activity ///	full-length
10508392	0.604579188	-2.876945203	-0.021402613	-6.384193892	1.219722557	2.792559373	8.305394404	Cluster IV	Rnf19b	ring finger protein 1	protein binding /// u	partial
10508465	1.096159238	4.341455092	-0.232706909	-5.144035353	1.054121205	3.503736076	8.892038057		Marcksl1	MARCKS-like 1	calmodulin binding	full-length
10508651	1.428246488	3.639934544	0.235488087	-5.700699127	1.350735328	2.645887997	9.082184175		Sdc3	syndecan 3	cytoskeletal protein	full-length
10508663	2.131432829	12.71215782	0.105314161	-6.085221306	2.134207432	12.31774639	9.94727218		Laptm5	lysosomal-associat	lysosome /// transp	full-length
10508686	-0.665065811	1.579804889	-0.168309635	-5.333158024	-1.172566728	7.333785404	7.831642648	Cluster X	Mecr	mitochondrial trans	catalytic activity ///	full-length
10508734	1.227089815	0.659518197	-0.232228884	-5.881836148	1.771007031	3.979533479	5.783498594		Ptafr	platelet-activating f	lipopolysaccharide	full-length
10508772	2.069788983	9.938298853	0.238854654	-5.398122014	2.214170121	10.31473025	7.027859568		Fgr	Gardner-Rasheed f	nucleotide binding	full-length
10508800	0.598241802	-6.186061261	0.814571297	-4.537040434	1.471048151	-2.678610145	11.35434024		LOC433762	hypothetical gene L	---	full-length
10508992	-0.759562274	-1.346786733	-0.091376155	-6.258688238	-1.029124337	0.949563308	7.571644761		Paqr7	progestin and adipo	receptor activity ///	full-length
10509063	0.724057015	-2.401637236	0.367700106	-4.802581025	2.273292831	8.570711406	7.107333145		Il22ra1	interleukin 22 recep	receptor activity ///	full-length
10509071	0.21334721	-6.73984086	0.012148726	-6.390010416	1.676198354	4.493302054	6.851812466		9130219A07Rik	RIKEN cDNA 9130	---	est
10509122	-0.909022103	3.927889361	-0.277369326	-4.183375808	-1.164514333	6.26844788	5.384640604		Cnr2	cannabinoid recept	signal transducer a	full-length
10510172	2.229784039	9.906739667	0.087552928	-6.269238428	2.028331702	8.351731187	7.271841256		Hmgb2	high mobility group	DNA binding /// nuc	full-length
10510221	0.485100034	-6.389974587	0.883388894	-3.875778153	1.46718775	-2.00126656	8.886326633		LOC433762	hypothetical gene L	---	full-length
10510580	0.931184299	3.274063665	-0.216429932	-5.163590948	1.324086867	6.765598218	5.815692187		Tnfrsf9	tumor necrosis fact	receptor activity ///	full-length
10511703	0.842047827	-4.430517514	-0.003120657	-6.391743419	2.072713533	1.95990597	8.18134533	Cluster II	Ripk2	receptor (TNFRSF)	nucleotide binding	full-length
10511779	1.265676598	0.112535437	0.049124964	-6.372024497	1.00674632	-2.081660998	5.780640819		Atp6v0d2	ATPase, H+ transp	transport /// ion trar	full-length
10512067	0.676696165	1.73026268	1.371760957	8.96247481	0.718724378	1.940262323	8.862401896	Cluster V	Ddx58	DEAD (Asp-Glu-Ala	nucleotide binding	full-length
10512322	1.263902377	8.541210455	0.179068296	-5.22511788	1.620040715	11.0681254	7.744442309	Cluster I	Ccl19	chemokine (C-C m	cytokine activity ///	full-length
10512372	1.291507809	7.537817358	0.193786292	-5.283885262	1.664054368	10.10468174	7.658796508	Cluster I	Ccl19	chemokine (C-C m	cytokine activity ///	full-length
10512463	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10512774	1.182610633	8.414833724	0.033051201	-6.34326183	1.370280674	9.730311245	5.985724094		Coro2a	coronin, actin bindi	actin binding	full-length
10512886	1.173904512	-1.050748677	0.197090762	-6.11571038	2.207433522	4.729970638	7.992343589		Acnat2	acyl-coenzyme A a	peroxisome /// lipid	full-length
10513512	-0.844587145	-0.920512729	-0.110923385	-6.216009249	-1.048139723	0.621945711	12.84287633		Apobec3 /// 261001	apolipoprotein B m	nucleus /// cytoplas	full-length
10513514	-1.147172821	2.711931858	-0.005847025	-6.39120667	-1.206132765	2.829548276	4.692947639		Mup5	major urinary protei	transporter activity	full-length
10513529	-1.469449186	3.032749596	0.030041371	-6.3817994	-1.926975685	5.575148705	12.2411669		Mup3	major urinary protei	transporter activity	full-length
10513538	-2.889917101	5.623844043	-0.048292435	-6.38105518	-3.246053694	6.520896268	8.974474653		OTTMUSG000000	predicted gene, OT	extracellular region	full-length
10513884	-0.62443526	-2.965486101	0.344831351	-4.805185009	-1.097474683	1.267175796	7.723190895		Tle1	transducin-like enh	negative regulation	full-length
10514763	-1.037911163	-0.634430218	0.01096071	-6.390556991	-1.181121869	0.142731399	11.5893039	Cluster X	C8a	complement comp	molecular_function	full-length
10514912	-1.315696234	-4.81168371	0.016194844	-6.391350085	-1.800609574	-3.472423852	8.863544694	Cluster IX	Dio1	deiodinase, iodothy	thyroxine 5'-deiodin	full-length

10515187	-1.240374971	-2.380161726	-0.301128197	-5.990012881	-0.958789494	-4.181687463	12.02813561	Cluster X	Cyp4a14	cytochrome P450, f	monooxygenase ac	full-length
10515201	-0.996936139	4.826747692	-0.180027879	-5.386393476	-1.081831399	5.315395436	7.389424209	Cluster X	Cyp4b1	cytochrome P450, f	monooxygenase ac	full-length
10515257	1.119811724	2.298966831	0.212421331	-5.685271006	0.99340464	0.74349973	5.418414643		Rad54l	RAD54 like (S. cere	nucleotide binding /	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10515431	1.465222473	2.740900943	-0.015062334	-6.389401103	0.957056365	-1.519888442	5.34577183		Kif2c	kinesin family mem	nucleotide binding /	full-length
10515836	2.379249664	6.022861486	-0.29400008	-5.790342268	2.251547677	4.974301413	5.796594912		Ccnb1	cyclin B1	in utero embryonic	full-length
10515943	0.864970913	0.44763327	-0.124975421	-6.102940461	1.106779099	2.464167249	5.713036622		Ctps	cytidine 5'-triphosp	catalytic activity ///	full-length
10516620	1.694389687	10.30249984	0.17363347	-5.548707385	1.631536235	9.42277261	6.394918544	Cluster I	Lck	lymphocyte protein	nucleotide binding /	full-length
10516735	0.844041879	2.642137936	-0.178133083	-5.47222708	1.037530701	4.432913267	9.019065674		Tinagl1	tubulointerstitial ne	cysteine-type endo	full-length
10516956	1.858736245	6.418412888	-0.107797797	-6.244664402	2.006934796	6.87173106	6.090713256		Smpdl3b	sphingomyelin pho	sphingomyelin pho	full-length
10516966	2.588968761	13.53671939	0.652643701	-0.632349967	2.54579908	12.93558707	8.051175654		BC013712	cDNA sequence B	---	full-length
10517141	1.23425791	5.998878361	0.175339373	-5.611325978	0.999460328	3.254150911	9.388291567		Hmgn2	high mobility group	chromatin /// DNA	full-length
10517165	2.787284002	18.36674901	0.219309129	-4.541756331	2.738496887	17.87476476	8.028379154		Cd52	CD52 antigen	plasma membrane	full-length
10517169	2.193709969	13.20535468	0.046292769	-6.329843826	2.018337369	11.80268499	8.758177898		Sh3bgrl3	SH3 domain bindin	nucleus /// cytoplas	full-length
10517508	1.651673624	8.970014699	0.235731943	-5.128491345	1.432561982	6.867746858	9.798965194	Cluster I	C1qb	complement comp	extracellular region	full-length
10517513	1.507213702	8.506541118	0.052136359	-6.316437191	1.292978497	6.287599556	9.943914586	Cluster I	C1qc	complement comp	extracellular region	full-length
10517517	1.212081704	7.093635038	0.222952128	-4.896702241	1.022916741	4.737124599	9.768256547		C1qa	complement comp	extracellular region	full-length
10517573	-4.020076475	1.066526237	-2.973625016	-0.858394294	-4.008993513	0.667138621	6.621416685		Ela3	elastase 3, pancre	---	full-length
10518050	-3.462694365	0.080181744	-2.766466163	-1.073853751	-3.639056473	0.167433849	7.239245988		RP23-395H4.4	elastase 2A	serine-type endope	full-length
10518069	1.032631446	2.817935154	0.124612889	-6.065833001	1.781728953	8.522600898	9.351403993		Efhd2	EF hand domain c	calcium ion binding	full-length
10518350	2.266408038	10.83301824	0.066612813	-6.311296172	2.108056996	9.541218936	7.879824932		Hmgb2	high mobility group	DNA binding /// nuc	full-length
10518352	2.305347254	11.33655404	0.088733747	-6.242364556	2.129224781	9.96217178	7.783047024		Hmgb2	high mobility group	DNA binding /// nuc	full-length
10518455	1.149284052	10.08963719	0.158852677	-4.978083181	1.141937937	9.583810891	7.168895658		Agtrap	angiotensin II, type	receptor activity ///	full-length
10518570	1.019036746	10.22361508	0.043540111	-6.23909302	0.934764796	8.766580599	9.276692013		Pgd	phosphogluconate	catalytic activity ///	full-length
10518686	1.598758802	6.732289463	0.157290799	-5.954639732	1.637992202	6.580544325	6.972624099	Cluster I	Pik3cd	phosphatidylinosito	B cell homeostasis	full-length
10518927	1.400873284	8.28010289	-0.141049576	-5.801686501	1.594007211	9.377134244	6.135767054		Kcnab2	potassium voltage-	ion channel activity	full-length
10519060	1.280019499	5.704153807	0.276476088	-4.788489348	1.509543732	7.168188277	7.730143514	Cluster I	Tnfrsf14	tumor necrosis fact	receptor activity ///	full-length
10519497	1.612248779	4.610940813	0.158806933	-6.087735569	2.742829652	10.35014798	11.48310367		Steap4	STEAP family mem	catalytic activity ///	full-length
10519527	0.730722662	-1.602351296	-0.143838886	-6.063157346	1.033933813	1.049471296	6.373375195		Abcb1a	ATP-binding casse	nucleotide binding /	full-length
10519717	0.37182779	-4.442789469	0.000194516	-6.391790027	1.04205853	3.272067154	4.362042281		Sema3a	sema domain, imm	regulation of heart	full-length
10519983	2.559961142	14.76732355	0.181043256	-5.538450955	2.834605182	15.58208948	7.423864822		Fgl2	fibrinogen-like prot	receptor binding ///	full-length
10520483	-0.719422639	0.989909267	-0.012106436	-6.38729102	-1.070196998	4.697527603	9.704759092		D5Wsu178e	DNA segment, Chr	magnesium ion bin	full-length
10521090	1.149787559	1.430180708	-0.200974652	-5.880304315	1.006486824	-0.172834659	6.16234815		Tacc3	transforming, acidi	microtubule cytosk	full-length
10521337	1.03364227	0.883496568	0.129384459	-6.152746917	1.417694582	3.687566613	6.22716218		Rgs12	regulator of G-prot	---	full-length
10521667	1.72978259	1.622385566	0.034205403	-6.384708897	2.722079638	6.069471593	5.474908448		Bst1	bone marrow strom	catalytic activity ///	full-length
10521678	1.204890737	9.303623405	-0.140772408	-5.471227047	1.437007397	10.97736657	9.432181133	Cluster I	Cd38	CD38 antigen	catalytic activity ///	full-length
10521731	1.842467326	3.565849461	0.071592056	-6.351957807	1.413759053	0.524882839	4.927158736		Ncapg	on-SMC condensin	molecular_function	full-length
10521984	1.306492635	6.084672192	0.085704366	-6.214648796	1.238071405	5.050327263	6.284279642		G6pd2	glucose-6-phospha	catalytic activity ///	full-length
10522182	0.965086759	1.910631568	0.145967491	-5.966689617	1.208073108	3.844019491	5.991735453		Rhoh	ras homolog gene f	nucleotide binding /	full-length
10522368	1.902127558	3.048195535	0.267211383	-5.934821793	1.476881222	0.185042244	7.547637514		Npal1	NIPA-like domain c	---	full-length
10522742	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10522788	1.096315453	1.15583001	0.018632389	-6.38703845	0.779611118	-2.077684168	4.170000416		Stap1	signal transducing	SH3/SH2 adaptor a	full-length
10523095	-0.699819598	-3.66432302	-0.083681321	-6.325346272	-1.27783002	0.522530708	10.19779127		Afm	afamin	molecular_function	full-length
10523111	-0.68798233	2.864128156	-0.177800734	-5.005357588	-1.168898563	8.392738412	9.124755368		---	---	---	partial
10523128	2.353735697	11.28112705	-0.085021066	-6.261217696	2.727384639	12.62536763	6.480180031		Ppbp	pro-platelet basic p	extracellular region	full-length
10523134	1.130537193	3.025673457	-0.068952728	-6.303520605	1.234365862	3.547113811	5.506924025	Cluster I	Pf4	platelet factor 4	cytokine activity ///	full-length
10523151	1.082928599	-4.536493553	0.103410703	-6.361719771	1.603644197	-2.56625509	7.962662087	Cluster IV	Cxcl1	chemokine (C-X-C	cytokine activity ///	full-length
10523156	0.445510488	-5.259017323	0.139755294	-6.169261462	1.208245062	0.911598792	4.36961213	Cluster IV	Cxcl2	chemokine (C-X-C	cytokine activity ///	full-length
10523245	-0.869709305	0.940314761	-0.139619593	-5.998605986	-1.313227857	4.80516275	7.063521405		Gm1381	gene model 1381, (	---	full-length
10523451	1.259124401	1.277238776	-0.03563931	-6.378280844	0.982456416	-1.271665933	7.232306715		Anxa3	annexin A3	phospholipase inhi	full-length
10523468	1.036774594	3.116865653	-0.084789021	-6.231203812	0.936646446	1.682861701	6.677464425	Cluster III	Bmp2k	BMP2 inducible kin	nucleotide binding /	full-length
10523766	1.120194244	5.999778219	0.182684333	-5.381709458	1.126915596	5.639521387	8.080128587		Lrrc8c	leucine rich repeat	protein binding /// m	full-length
10524169	1.134241686	1.327770778	0.153076663	-6.088332218	0.619546808	-3.669983154	5.088754071		Pole	polymerase (DNA d	nucleotide binding /	full-length
10524460	-0.042359731	-7.274444876	0.147026509	-6.326833914	-1.682937912	-1.977483509	8.085762867	Cluster X	Acacb	acetyl-Coenzyme A	---	full-length
10524621	1.64443359	9.983793594	1.402923774	7.772469496	2.492736703	14.52549431	8.316851404	Cluster VI	Oasl2	2'-5' oligoadenylate	2'-5'-oligoadenylate	full-length

10524631	1.271140494	-0.051774318	2.041081748	4.881689944	1.824955646	3.084365489	8.774205986		Oasl1	2'-5' oligoadenylate	transferase activity	full-length
10524698	-2.604987434	-0.190074515	-1.911155236	-1.861118206	-2.565794715	-0.666942502	5.713268427		Pla2g1b	phospholipase A2,	phospholipase A2 a	full-length
10525158	0.259411308	-6.429619395	1.291466177	2.979334035	0.260451854	-6.531576988	4.836230779	Cluster V	Oas1b	2'-5' oligoadenylate	RNA binding /// ATI	full-length
10525591	1.131437489	-0.668457903	0.002403372	-6.391741441	0.633610339	-4.653466407	4.412665271	Cluster III	Kntc1	kinetochore associa	nucleus /// cytoplas	full-length
10526277	-0.567420247	-6.278300017	0.309217192	-6.085983944	-1.314966798	-3.358485219	8.797389512	Cluster X	Mlxipl	MLX interacting pro	negative regulation	full-length
10526459	1.117017361	9.325944193	0.401653873	-0.627230216	1.118510335	8.909997343	6.120885384		Rasa4	RAS p21 protein ac	GTPase activator a	full-length
10526783	1.39751038	1.903074128	0.252567471	-5.793929465	1.636013896	3.120635891	4.399725004		BC055004	cDNA sequence BC	---	full-length
10527012	1.20701124	4.307187051	0.10906417	-6.148555619	1.169268777	3.548658099	7.039741206	Cluster X	Lfng	LFNG O-fucosylpep	ovarian follicle deve	full-length
10527425	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10527441	1.327024459	7.971451129	0.034531634	-6.352750331	1.360513138	7.83070935	9.890346488		Arpc1b	actin related protein	actin binding /// cyto	full-length
10527638	1.935186461	6.057292723	0.00074991	-6.391784733	2.034933053	6.202042595	7.912935821		Alox5ap	arachidonate 5-lipo	leukotriene metabo	full-length
10527940	1.607056921	9.894421419	-0.140605516	-5.806170852	1.39390809	7.778445317	6.259755396		Pftk1	PFTAIRE protein ki	nucleotide binding /	full-length
10528102	-0.838941192	-1.718208883	-0.108900387	-6.251119721	-1.42968	2.755096583	12.28757905		Crot	carnitine O-octanoy	peroxisome /// lipid	full-length

Affymetrix ID Transcript Cluster	BS/Non Inf. logFC	B	LS/Non Inf. logFC	B	ReINF/Non Inf. logFC	B	Average expression	Cluster Number	Gene Symbol	Gene Title	Gene Ontology (GC Description	Transcript Classification
10528165	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10528205	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10(	---	est
10528207	1.199865519	3.122942178	-0.124069006	-6.136657803	1.145415435	2.241629194	9.935285488	Cluster I	Cd36	CD36 antigen	receptor activity ///	full-length
10528480	2.297230659	13.35734635	0.134572421	-5.917481776	2.472209076	13.82980929	9.26226561		EG625174	predicted gene, EG	---	predicted
10529264	-0.656355279	-3.56120771	-0.202113835	-5.948032636	-1.677421809	4.115313893	7.174509154		Spon2	spondin 2, extracell	protein binding /// e	full-length
10529689	0.961939528	8.121719782	-0.076697433	-6.025217488	1.024087467	8.426305883	9.664797798		Wdr1	WD repeat domain	actin binding /// cyto	full-length
10530059	-0.797257189	-2.590421481	-0.299741634	-5.518635894	-1.037694172	-0.919880198	6.49544829		2310045A20Rik	RIKEN cDNA 2310	binding /// membran	full-length
10530145	2.138883209	12.69568451	-0.216623487	-5.194784516	2.260975394	12.94993209	5.812565331	Cluster VI	Tlr1	toll-like receptor 1	receptor activity ///	full-length
10530319	1.505208549	2.838926792	0.119000901	-6.249295992	1.669163969	3.521566452	7.123079465		Atp8a1	ATPase, aminopho	nucleotide binding /	full-length
10530615	-0.702213504	0.105841257	-0.208181113	-5.330869611	-1.189715885	5.078107354	8.948758429		Ociad2	OCIA domain conta	mitochondrion /// m	full-length
10530692	-0.732808555	-5.338901469	-0.125577288	-6.327619373	-2.089464883	1.167683614	8.556329294		Kdr	kinase insert domai	nucleotide binding /	full-length
10531041	-1.404877858	-0.54126263	-0.045070416	-6.380158629	-1.605974095	0.283412934	11.71327095		Ugt2b1	UDP glucuronosyltr	transferase activity	full-length
10531061	-1.258891651	4.644726328	-0.726748129	-0.111938819	-1.499099422	6.183889502	6.53193895		Ugt2b37	UDP glucuronosyltr	mitochondrial inner	full-length
10531073	-1.470261681	8.067553359	-0.456169947	-2.341268608	-1.366076756	6.777528605	9.469183318		Ugt2b38	UDP glucuronosyltr	transferase activity	full-length
10531111	2.542718608	-6.095023149	-0.037514606	-6.391515629	6.912661483	-1.642527878	5.737288701		Sult1e1	sulfotransferase far	estrone sulfotransfe	full-length
10531126	4.331377006	11.78363841	-0.554428007	-4.80297856	3.942546604	10.23702165	6.407936852		Igj	immunoglobulin joir	antigen binding /// h	full-length
10531370	2.187735235	14.86611267	0.023616533	-6.370204362	2.509249521	16.08938075	8.100304438		Naaa	N-acylethanolamine	molecular_function	full-length
10531407	4.230603993	13.3164919	0.558497386	-4.29308072	4.796607967	14.40701864	9.559737964		Cxcl9	chemokine (C-X-C	cytokine activity ///	full-length
10531415	3.284129055	5.845560629	1.275170985	-2.147104625	4.005126507	7.706551685	9.175392777	Cluster VI	Cxcl10	chemokine (C-X-C	cytokine activity ///	full-length
10531610	0.98385874	-0.57829419	0.380557814	-4.900875215	1.247119593	1.21164673	7.826576476		Rasgef1b	RasGEF domain fa	molecular_function	full-length
10531724	3.319720646	14.79925329	0.970168557	1.452632206	3.657079648	15.55435614	7.425699956		Plac8	placenta-specific 8	molecular_function	full-length
10531737	0.984070218	4.771663021	0.101573771	-6.049083512	1.175057297	6.34732289	7.263779614		Hpse	heparanase	magnesium ion bin	full-length
10531919	-0.631746848	1.954017921	-0.152766819	-5.348052982	-1.011321636	6.651337276	10.49195738	Cluster X	Hsd17b11	hydroxysteroid (17-	catalytic activity ///	full-length
10531952	1.37351566	-2.54142828	-0.064450839	-6.377030186	0.769732376	-5.571127626	5.61889919		Abcg3	ATP-binding casset	ATP binding /// tran	full-length
10531972	2.349572989	9.844674668	0.607825287	-2.525618466	2.931001638	12.0634303	7.959047606		5830443L24Rik	RIKEN cDNA 5830	---	full-length
10531980	2.245776889	7.377351891	1.013104077	-0.159453106	3.321957416	11.59482549	8.008903549		BC057170	cDNA sequence BC	---	full-length
10531987	3.001872053	15.28462841	1.531899181	7.144571613	3.583991093	16.96410638	8.549475557		Gbp4	guanylate binding p	molecular_function	full-length
10531994	2.58480368	9.202894426	2.083055304	6.584028558	3.330253664	11.80189986	10.81659213		Mpa2l /// Gbp10 ///	macrophage activa	molecular_function	full-length
10532019	2.299860249	5.418681624	0.698528732	-3.649504623	3.045127192	8.229421318	8.974694434		EG634650 /// Mpa2	predicted gene, EG	---	full-length
10532711	1.367416175	5.33692343	0.148763246	-5.97291717	1.355700108	4.816796094	6.539748262		Cmklr1	chemokine-like rec	signal transducer a	full-length
10532744	1.956270544	13.1953109	0.021228792	-6.375379787	1.787402847	11.70904145	7.154404705	Cluster I	Selplg	selectin, platelet (p-	protein binding /// s	full-length
10532857	1.078725368	5.566797827	0.106280071	-6.032250173	1.018985849	4.507585858	7.832323581		Gltp	glycolipid transfer p	cytoplasm /// transp	full-length
10532896	1.310288639	8.811469981	0.099528839	-6.017946032	1.097963601	6.314889252	5.337949623		2610524H06Rik	RIKEN cDNA 2610	---	full-length
10533213	0.718674826	-2.156746735	0.552797754	-3.024190516	1.557288695	4.698343648	5.978388153		Oas3 /// Oit3	2'-5' oligoadenylate	calcium ion binding	full-length
10533246	1.620768242	11.31870212	1.277637728	8.088600327	1.959525872	13.17069218	7.334970652		Oas1a /// Oas1g	2'-5' oligoadenylate	2'-5'-oligoadenylate	full-length
10533256	0.979266296	-0.309686024	0.682697834	-2.265786012	1.350371736	2.36042009	6.862800256		Oas1a	2'-5' oligoadenylate	2'-5'-oligoadenylate	full-length
10533304	0.898563536	3.861867055	0.87661583	3.894930495	1.237655444	7.035459343	9.482743221		Trafd1	TRAF type zinc fing	molecular_function	full-length
10533720	0.847900592	-3.293404715	0.359663356	-5.501237865	1.155932277	-1.434072446	5.068292115		Gpr109a	G protein-coupled r	purinergic nucleotic	full-length
10534202	1.497221117	8.562128128	0.159620749	-5.703104428	1.637319588	9.189512321	7.310640225	Cluster I	Ncf1	neutrophil cytosolic	leukocyte mediated	full-length
10534303	0.837551527	1.353029814	-0.198276659	-5.496011516	1.117886985	3.924167835	5.509498245	Cluster IV	Lat2	linker for activation	plasma membrane	full-length
10534456	1.030326699	5.922588357	0.114693982	-5.907766368	1.031717746	5.510187318	6.781889841		Hip1	huntingtin interactir	protein binding /// cy	full-length

10534667	1.711306691	-5.047851074	0.255508404	-6.33445769	3.460607591	-1.161170389	6.658070615		Serpine1	serine (or cysteine)	serine-type endope	full-length
10534909	1.367097702	11.01569862	0.297753313	-2.934592916	1.512096737	11.80063875	6.816630375		---	---	---	partial
10534927	1.79706072	7.910552567	-0.107863203	-6.188827792	1.727961831	7.019979011	7.540054851		Pilra	paired immunoglob	receptor activity ///	full-length
10534935	1.116518393	-0.737309763	0.009959055	-6.390931916	1.063662256	-1.459862694	7.080462816		Pilrb1	paired immunoglob	molecular_function	full-length
10535065	1.112697062	2.638786069	0.131079012	-6.091150333	1.31405468	3.991355168	5.800175541		Adap1	ArfGAP with dual P	---	full-length
10535331	-0.288362471	-5.687197354	-0.011275371	-6.389109456	-1.205415178	3.942936602	6.194322943	Cluster X	Mmd2	monocyte to macro	receptor activity ///	full-length
10535669	-0.608036357	-2.903560265	-0.407347783	-4.138117913	-1.381125838	4.010612152	9.169198597	Cluster X	Cyp3a41a /// Cyp3a	cytochrome P450, f	monooxygenase ac	full-length
10535683	-0.632854784	-2.475649941	-0.413194425	-3.987630172	-1.419620522	4.578521391	9.095289311	Cluster X	Cyp3a41a /// Cyp3a	cytochrome P450, f	monooxygenase ac	full-length
10535698	-0.717689038	-3.602766572	-0.668484276	-3.198004033	-1.694113113	3.184049697	7.28328377	Cluster X	Cyp3a44	cytochrome P450, f	molecular_function	full-length
10535704	-0.474377149	-3.845469686	-0.316725946	-4.689234303	-1.302848347	4.342360616	12.01243072	Cluster X	Cyp3a11	cytochrome P450, f	monooxygenase ac	full-length
10536908	-0.987355742	4.198048371	-0.233094982	-4.916189967	-1.200393353	5.954835806	7.309902618		Tspan33	tetraspanin 33	membrane /// integ	full-length
10537014	-4.267138497	0.23996627	-3.169580791	-1.458238224	-4.468419067	0.296300514	5.496844338		Cpa2	carboxypeptidase A	carboxypeptidase a	full-length
10537051	-5.125330544	0.707598472	-3.680291178	-1.340797733	-5.183349316	0.443975037	6.939805354		Cpa1	carboxypeptidase A	carboxypeptidase a	full-length
10537146	1.301238411	-0.188406708	-0.411773695	-5.266625185	0.642846731	-4.946503886	6.151940185		Akr1b8	aldo-keto reductase	aldehyde reductase	full-length
10537318	0.805299667	-3.050053128	-0.04989012	-6.369779401	1.410595253	1.105937084	7.940098086		Trim24	tripartite motif-conta	DNA binding /// pro	full-length
10537410	1.564634357	5.185007785	0.171468505	-5.977959798	1.55295223	4.678547621	6.604190282		Tbxas1	thromboxane A syn	prostaglandin biosy	full-length
10537627	-2.497038611	-1.033031987	-1.631618451	-3.108408462	-2.599142403	-1.038058382	5.773280136	Cluster IX	Prss2	protease, serine, 2	serine-type endope	full-length
10537634	-2.131670239	-2.310482206	-1.809623313	-2.604242905	-2.350799642	-1.903448881	4.452451047		Try4	trypsin 4	molecular_function	full-length
10537638	-3.204437387	-3.002784426	-2.299598663	-3.928435871	-3.397947448	-2.90033889	5.589625497		Try10	trypsin 10	---	full-length
10537645	-1.518424462	-1.715262595	-1.201381581	-2.540331568	-1.599057217	-1.634943686	4.756948756		EG386551	predicted gene, EG	---	full-length
10537650	-2.628866431	2.045346863	-1.910450754	-0.236794553	-2.590407041	1.510460278	5.796098436		Prss1 /// EG43652	protease, serine, 1	---	full-length
10538126	1.302693065	5.979621458	0.030313669	-6.36964317	1.318089389	5.684835714	8.709321434		Gimap4	GTPase, IMAP fam	nucleotide binding /	full-length
10538135	1.493718804	5.135227609	0.058407606	-6.338087828	1.419631119	4.152539987	5.382631459		Gimap7	GTPase, IMAP fam	---	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10538150	0.891902187	4.426075359	0.064630248	-6.230894838	1.009913526	5.384984887	9.403364187		Tmem176a	transmembrane pro	membrane /// integ	full-length
10538187	1.757590118	1.924235445	-0.059336325	-6.369875724	2.2816099	4.254548426	5.536182891		Gpnmb	glycoprotein (trans	integrin binding /// i	full-length
10538290	1.230180721	0.792611219	0.18076346	-6.070752888	2.035729863	5.657787245	9.046165486		Snx10	sorting nexin 10	protein binding /// tr	full-length
10538459	-0.490805719	-0.175182728	-0.178178144	-4.944530153	-1.159475539	8.55508039	9.383372307		Aqp1	aquaporin 1	transporter activity /	full-length
10538590	1.227329012	6.210918115	1.272159264	6.537075251	2.133543007	12.31792119	8.770870552		---	---	---	partial
10538753	1.183873423	0.463386368	0.174701207	-6.089758324	2.05540792	5.799515633	7.979313772		---	---	---	predicted
10538791	1.348206365	0.482216258	0.000702213	-6.391787102	1.613719912	1.826959842	4.748716527		Tnip3	TNFAIP3 interactin	---	full-length
10538832	1.344891412	2.195535295	-0.014109919	-6.389553538	1.147378575	0.287996827	7.095652374		Mad2l1	MAD2 mitotic arres	mitotic sister chrom	full-length
10538868	1.867623301	5.382874151	0.120156856	-6.240972118	1.558145676	2.994215302	6.736994596		---	---	---	partial
10538871	5.180824847	12.3400242	-0.722970889	-4.387550686	5.024076841	11.55768214	6.993904357		---	---	---	full-length
10538880	5.465986878	11.21222467	0.200778498	-6.258348998	5.009546027	9.745014202	5.388562803		---	---	---	full-length
10538882	3.988322749	11.17756693	-0.316665081	-5.794057073	3.651164433	9.696808996	5.779626007		---	---	---	partial
10538887	1.626032565	3.617536967	0.281128253	-5.638770491	1.383600257	1.558271453	5.188283669		---	---	---	partial
10538903	3.639446982	12.77814982	0.037286782	-6.378155642	3.693791535	12.54637505	6.017442376		Igk /// Igk-V28	immunoglobulin ka	---	full-length
10538921	5.269700073	15.59175001	-0.27031826	-5.860634049	5.083949316	14.80356768	6.848396715		---	---	---	full-length
10538924	2.549728485	6.651355601	0.189171847	-6.143014222	2.516680072	6.071233287	5.567036555		---	---	---	full-length
10538929	3.110082959	10.52112339	0.314539229	-5.540449177	2.87837111	9.169452172	5.505147768		---	---	---	partial
10538936	1.19400107	0.82780394	0.198078472	-5.982348674	1.513947047	2.79369738	5.022714438		---	---	---	partial
10538965	-1.079913289	-5.033685353	-0.12306488	-6.35808042	-2.406340289	-0.315421076	12.48429525		Fabp1	fatty acid binding p	chromatin binding /	full-length
10538979	1.884386723	9.972051814	-0.121350677	-6.063792712	1.839722786	9.25627372	6.290456288	Cluster I	Cd8b1	CD8 antigen, beta	protein binding /// p	full-length
10538993	2.435200159	13.96637883	0.175840779	-5.611633089	2.683781324	14.72361739	6.704989056	Cluster VI	Cd8a	CD8 antigen, alpha	T cell mediated imn	full-length
10539135	2.400092038	11.15146765	0.17657177	-5.87748213	2.67392062	12.02407116	6.904038347	Cluster VI	Capg	capping protein (ac	actin binding /// ext	full-length
10539143	-1.340049279	2.087067645	-0.262969315	-5.6677477	-1.118071821	-0.009589508	10.96438438	Cluster X	Retsat	retinol saturase (all	nuclear outer mem	full-length
10539194	-2.284685173	-3.42404642	-1.659263665	-4.152818098	-2.407475335	-3.370867754	3.852161108		Reg2	regenerating islet-d	binding /// sugar bir	full-length
10539200	-4.303455637	1.600038646	-3.009234867	-0.866034307	-4.353565683	1.329317359	5.49493167		Reg1	regenerating islet-d	binding /// sugar bir	full-length
10539739	0.392861777	-6.614629902	0.004629884	-6.391696126	1.091395763	-3.570269893	5.757768105		Asprv1	aspartic peptidase,	aspartic-type endo	full-length
10539894	-0.650547635	-0.798878414	-0.107371017	-6.108277628	-1.427635017	6.833139186	8.810296483		Mgll	monoglyceride lipa	catalytic activity ///	full-length
10540531	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10541129	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10541301	0.961304696	-2.19626656	-0.132619405	-6.252270477	1.730598394	2.64949218	7.714486184		Tuba8	tubulin, alpha 8	nucleotide binding /	full-length
10541307	1.467594006	-0.214646847	2.673612272	5.932332763	2.212753053	3.406596545	8.88341955	Cluster VII	Usp18	ubiquitin specific pe	ubiquitin thiolestera	full-length

10541555	2.499316029	10.30599854	0.155515002	-6.067786757	2.647846219	10.56891475	7.575845904		Clec4a1	C-type lectin domai	receptor activity ///	full-length
10541564	2.181030312	9.109689713	0.1864162	-5.898599431	2.215501568	8.863505426	6.366280056		Clec4a3	C-type lectin domai	receptor activity ///	full-length
10541587	1.444384594	1.635042984	-0.133708857	-6.237945857	1.777871	3.365023917	5.251275153	Cluster I	Clec4a2	C-type lectin domai	binding /// sugar bir	full-length
10541605	3.189066798	15.81100189	-0.078259397	-6.261469908	3.51025235	16.55909848	7.65980052	Cluster VI	Clec4n	C-type lectin domai	binding /// sugar bir	full-length
10541614	1.109455582	-5.10538896	0.041497601	-6.388286718	2.278539289	-1.159767644	4.781095005		Clec4d	C-type lectin domai	receptor activity ///	full-length
10542040	0.901244144	3.338800073	0.38183743	-2.954799517	1.049267358	4.56925432	6.417619661		Parp11	poly (ADP-ribose) p	NAD+ ADP-ribosylt	full-length
10542112	-2.07804802	4.645552	-0.203021174	-6.090713373	-2.180427736	4.756135804	7.128489478		Clec2h	C-type lectin domai	receptor activity ///	full-length
10542120	1.120788223	4.433712224	-0.091156361	-6.189470102	1.052270773	3.338048578	5.933644672		Clec2i	C-type lectin domai	receptor activity ///	full-length
10542164	2.35175771	14.82393968	0.264471009	-4.40401917	2.337216866	14.36964127	7.545243188	Cluster VI	Clec12a	C-type lectin domai	receptor activity ///	full-length
10542214	1.516059884	10.06961699	-0.124661121	-5.856932687	1.117500275	6.061358825	4.557232756		Klrd1	killer cell lectin-like	receptor activity ///	full-length
10542340	0.565619751	-4.624754503	-0.027730843	-6.384159308	1.035620454	-1.128372678	8.44670565		8430419L09Rik	RIKEN cDNA 8430	membrane /// integr	full-length
10542355	1.003654338	1.919552154	-0.099480336	-6.205455339	1.348751322	4.630097236	6.521056009		Emp1	epithelial membran	membrane /// integr	full-length
10542691	1.025578115	2.207117181	0.098672132	-6.205868442	0.893499504	0.490746467	6.072193196		Lrmp	lymphoid-restricted	cytoplasm /// endop	full-length
10542714	-0.53528605	-3.27098776	-0.089568939	-6.243781831	-1.054075729	1.901768801	8.168015426		Lyrm5	LYR motif containin	---	full-length
10542738	-0.890912817	1.703082563	-0.139112812	-5.95759342	-1.14581209	3.91033086	7.204707642		Rassf8	Ras association (R	signal transduction	full-length
10542880	-1.375223082	4.267789579	-0.338205364	-4.786839349	-0.66782887	-2.632884327	9.964710237		4833442J19Rik	RIKEN cDNA 4833	cytoplasm /// protei	full-length
10542911	1.079647187	2.472015403	1.608997563	6.728283017	1.44022008	5.157220072	7.052902858		Samd9l	sterile alpha motif d	---	partial
10542981	1.238308257	10.29823471	0.058069712	-6.206008381	1.220068834	9.692568448	8.15037344		Gmfg	glia maturation fact	actin binding /// intr	full-length
10543017	-1.285060644	3.216926915	-0.320377271	-5.01097749	-1.544289163	4.79244192	7.211177926		Pdk4	pyruvate dehydroge	two-component ser	full-length
10543029	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10543239	1.307003194	7.071950037	0.315425551	-4.008410902	1.056870174	4.245455478	6.238678328		Tcfec	transcription factor	DNA binding /// nuc	full-length
10543253	-0.957457964	1.351978779	-0.329854988	-4.62396308	-1.412002318	5.02157503	6.002353325		Wnt2	wingless-related MI	signal transducer a	full-length
10543859	1.06808906	3.594018587	0.093379958	-6.191578884	0.780765571	0.106582191	8.015701646		Akr1b3	aldo-keto reductase	aldehyde reductase	full-length
10544133	0.860848168	5.293252462	0.984498908	6.705128829	1.207183487	8.777079634	9.529086139		Parp12	poly (ADP-ribose) p	nucleic acid binding	full-length
10544273	1.467855131	-2.781289098	0.097065519	-6.364533782	2.251458378	0.256643696	4.744979894		Clec5a	C-type lectin domai	binding /// sugar bir	full-length
10544326	-5.217479134	0.318080899	-3.889176018	-1.374968279	-5.415118037	0.293705121	5.941530118		2210010C04Rik	RIKEN cDNA 2210	---	full-length
10544333	-4.878951629	0.972249168	-3.47444622	-1.202145618	-4.722345848	0.300049573	6.493015577		1810049H19Rik	RIKEN cDNA 1810	---	full-length
10544342	-1.38815449	-1.72743561	-0.728523783	-4.411818003	-1.35057967	-2.234486931	4.815866665		Prss1 /// EG43652	protease, serine, 1	molecular_function	full-length
10544588	1.731553396	4.693833281	0.230709479	-5.837980586	1.850440197	5.008816977	5.495834857		Gimap3	GTPase, IMAP fam	nucleotide binding /	full-length
10544596	0.968846906	8.1034998	0.089860184	-5.90203911	1.195967696	10.17072248	11.70921069		Tmem176b	transmembrane pro	nucleus /// membra	full-length
10544687	-0.604483826	-5.406329366	-0.538575583	-4.903868304	-1.593278246	0.242569203	5.002401673	Cluster X	Cycs	cytochrome c, som	iron ion binding /// s	full-length
10544891	1.025416337	4.637222806	0.009665117	-6.388927238	1.22465331	6.209636014	6.968012409	Cluster IV	Nod1	nucleotide-binding	nucleotide binding /	full-length
10544932	-0.653466925	-5.158829795	-0.071934036	-6.362366881	-1.170351566	-2.308200474	12.68889334		Inmt	indolethylamine N-r	cytoplasm /// methy	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10545009	-0.617852807	0.277821372	-0.171312774	-5.420694359	-1.038331881	5.201375074	6.597642054		Pigy	phosphatidylinosito	glycosylphosphatid	full-length
10545135	0.84733356	0.736241415	0.02925264	-6.37386436	1.035456607	2.31267373	4.458958344	Cluster III	Il12rb2	interleukin 12 recep	receptor activity ///	full-length
10545173	3.947470398	7.801508509	-0.557541792	-5.358604934	3.720881824	6.681115109	6.432806415		Igk	immunoglobulin ka	---	full-length
10545175	3.620822916	8.241599792	-0.308968869	-5.965273281	3.281235567	6.659968092	6.231359876		Igk	immunoglobulin ka	---	full-length
10545177	4.879720774	10.83500356	0.119157671	-6.336102844	4.709271098	9.983840733	7.217148335		---	---	---	partial
10545180	1.074493296	-2.877055952	-0.297561424	-5.942624841	1.349984679	-1.550618893	4.450322808		---	---	---	partial
10545184	4.191205765	8.606774533	-0.123172733	-6.336381583	4.075828648	7.844903835	6.884540295		---	---	---	full-length
10545187	3.745234598	8.964745556	-0.002711172	-6.391755095	3.757547634	8.571050279	6.15812255		Gm1502	gene model 1502, (	---	full-length
10545190	1.771286472	0.467813679	-0.442069489	-5.562220678	2.09947135	1.714082791	3.456652557		---	---	---	partial
10545194	3.867655173	10.72826563	0.095303268	-6.336092389	3.719663176	9.835291039	6.023863757		---	---	---	partial
10545196	4.160253065	10.36000369	-0.363278562	-5.763098015	3.976279146	9.391801095	7.375811418		Igk-C	immunoglobulin ka	---	full-length
10545198	4.551976092	10.88341315	-0.39911229	-5.702970414	4.540179008	10.42712775	7.399256472		EG667683	predicted gene, EG	---	full-length
10545202	2.20524159	2.627054912	-0.297440105	-6.001326385	2.270085476	2.525371094	4.78550929		---	---	---	partial
10545205	2.555751768	7.184218082	-0.299616722	-5.732270449	2.92231295	8.32118	5.109260646		---	---	---	partial
10545208	4.683603411	12.78002111	-0.269056119	-5.976175647	4.45067736	11.75915313	7.10385586		---	---	---	partial
10545210	1.712350878	2.991919333	0.151545569	-6.208487051	1.709491429	2.571970291	5.931006451		---	---	---	partial
10545212	1.863756755	4.62818496	-0.33032819	-5.452527459	1.982773015	4.892185849	4.683602111		---	---	---	partial
10545215	3.244106044	10.38276562	0.009459353	-6.391051874	3.194680603	9.771288313	4.792748626		Igk /// Igk-V28	immunoglobulin ka	---	full-length
10545220	3.027746412	4.491449461	0.042847291	-6.385506023	3.204628174	4.697114334	5.141271856		Igk	immunoglobulin ka	---	full-length
10545231	3.897572662	9.962044365	-0.247288641	-6.073699401	3.422563822	7.990392171	5.820163332		---	---	---	partial
10545233	1.092155898	-2.803208422	0.15332421	-6.270647235	1.619744565	-0.075596745	4.946801393		---	---	---	partial

10545235	1.939304416	3.215096736	0.407074977	-5.383556219	1.626172128	1.048579795	4.300834653		---	---	---	partial
10545237	2.288284333	1.719962738	0.053323282	-6.381761579	1.961022612	-0.099138606	3.962047183		---	---	---	partial
10545239	4.170547499	5.23678536	-0.281548291	-6.230142657	3.683430676	3.459091894	5.823827454		---	---	---	partial
10545242	1.509432217	-0.047831693	0.188549028	-6.196971991	1.434633628	-0.830530102	4.436658207		---	---	---	full-length
10545247	3.880419068	7.368772861	0.00822767	-6.391556488	3.840305739	6.81570426	6.248249711		---	---	---	partial
10545249	1.638620534	2.99591071	-0.031258189	-6.383152041	1.841074001	3.824357974	3.952005986		---	---	---	partial
10545436	-1.020814267	6.472473968	-0.308102506	-3.24258128	-1.141375519	7.33312383	7.592659834		Elmod3	ELMO/CED-12 don	cytoskeleton /// pha	full-length
10545479	2.138600799	11.17809679	0.058970851	-6.316682596	2.272557253	11.48366456	8.999598868	Cluster VI	Tmsb10	thymosin, beta 10	actin binding /// acti	full-length
10545588	1.801270758	8.571242381	0.111060397	-6.152802051	2.172406423	10.36842405	6.76182383		Hk2	hexokinase 2	nucleotide binding /	full-length
10545623	0.865563697	-1.422367337	-0.131906242	-6.183498324	1.001157838	-0.565173289	6.128726582		Dok1	docking protein 1	MAPKKK cascade /	full-length
10545742	-1.262267066	6.295356771	-0.151973174	-5.792769671	-1.47294725	7.652241658	5.716105068		Cd207	CD207 antigen	binding /// sugar bir	full-length
10545771	-1.015849432	1.948688093	-0.14610234	-6.003346222	-0.945650414	0.869556877	6.269596666		Cyp26b1	cytochrome P450, f	cell fate determinat	full-length
10545874	-1.574658459	3.619608938	-0.142176525	-6.17746049	-2.143981708	6.639828486	7.877041429		Cml5	camello-like 5	gastrulation with mo	full-length
10545877	-1.086524626	1.891220449	0.185996876	-5.854124247	-0.70464353	-2.199757932	6.35389523		Cml4	camello-like 4	gastrulation with mo	full-length
10545891	-0.978154133	-1.635021031	-0.023643906	-6.386752383	-1.843285697	3.939729123	8.452101051		Cml1	camello-like 1	gastrulation with mo	full-length
10546010	1.635190038	8.144417129	-0.068944804	-6.286765593	1.684284427	8.059143678	6.707468188		Arhgap25	Rho GTPase activa	molecular_function	full-length
10546163	1.288021587	2.258804717	-0.119583093	-6.216734934	1.043585432	-0.119013389	6.699560963	Cluster III	Mcm2	minichromosome m	nucleotide binding /	full-length
10546450	1.065107497	-0.771954957	0.085123692	-6.323751221	1.065189689	-1.10545746	6.447167751		Adamts9	a disintegrin-like an	endopeptidase activ	full-length
10546685	1.433205157	12.14808823	-0.150233284	-5.220133995	2.160202195	16.57691024	7.646366775		Eif4e3	eukaryotic translatio	RNA binding /// tran	full-length
10547177	1.743317735	10.51655172	0.033728367	-6.358595718	1.53666394	8.585771749	7.000275126		Rassf4	Ras association (Ra	protein binding /// c	full-length
10547641	1.178969056	6.847315807	-0.135551767	-5.790542253	1.353094389	8.021651358	5.643649959		Slc2a3	solute carrier family	transporter activity /	full-length
10547657	1.158355624	1.025588383	0.089549919	-6.296772474	1.01208364	-0.553993921	7.087393376		C3ar1	complement compo	signal transducer a	full-length
10547664	2.488361682	-1.858207141	-0.1142466	-6.374674161	3.589701885	0.91120557	4.753343963	Cluster VI	Clec4e	C-type lectin domai	binding /// sugar bir	full-length
10547769	1.113049516	6.395094568	-0.043980596	-6.323354762	1.196052103	6.792625377	8.685361709	Cluster I	Ptpn6	protein tyrosine pho	phosphotyrosine bi	full-length
10547943	1.454027551	2.297393466	-0.093718068	-6.306184191	0.919697143	-2.088356342	6.472423361	Cluster III	Ncapd2	non-SMC condensi	condensed chromo	full-length
10547976	0.993934567	3.160914864	0.201633614	-5.454445162	1.513566669	7.438343214	8.050597381	Cluster IV	Tapbpl	TAP binding proteir	endoplasmic reticul	full-length
10547985	1.016971327	2.270108072	-0.083415872	-6.254448167	0.933686289	1.041672949	4.92446595		Cd27	CD27 antigen	receptor activity /// t	full-length
10548105	0.884921887	2.260098887	-0.091799574	-6.173910438	1.152650781	4.659582653	8.904855359		Ccnd2	cyclin D2	protein binding /// n	full-length
10548333	1.081289891	1.478771999	0.058296918	-6.340841512	1.324606035	3.145379991	4.718214576		Cd69	CD69 antigen	binding /// sugar bir	full-length
10548345	1.113955594	9.336334446	0.231152774	-3.836939526	0.88228811	6.177127447	4.607908797		Klrk1	killer cell lectin-like	stimulatory C-type l	full-length
10548375	1.933835241	10.19085679	-0.287587648	-4.756791274	2.229314335	11.46596917	6.920833395	Cluster VI	Clec7a	C-type lectin domai	opsonin binding /// :	full-length
10548385	0.329061223	-6.25747062	-0.015525362	-6.38939143	1.112665967	-0.519086245	3.836599121	Cluster IV	Olr1	oxidized low density	receptor activity /// l	full-length
10548409	1.209790687	2.98417177	0.133889943	-6.10780664	0.922783042	-0.029248186	4.454207527		Klrc1	killer cell lectin-like	receptor activity /// c	full-length
10548552	1.704290842	5.400526595	0.254376487	-5.616474318	1.692015875	4.895178356	6.089857864		Klra2	killer cell lectin-like	receptor activity /// l	full-length
10548563	0.203174376	-6.786084379	-0.023791213	-6.384932638	1.002515371	-0.568825628	10.90138827		Ptp4a1	protein tyrosine pho	phosphoprotein pho	full-length
10548892	2.376679407	13.06583452	-0.129994987	-5.995776758	2.571755739	13.60155074	8.391525411		Arhgdib	Rho, GDP dissocia	Rho GDP-dissociat	full-length
10548931	-0.928498126	1.814184681	0.130000611	-6.032653398	-1.102888231	3.179813467	5.992259881		Slc15a5	solute carrier family	transporter activity /	full-length
10548978	-3.253879463	-2.716360147	-0.069520509	-6.388883525	-5.712868154	1.631655564	9.441043394		Slco1a1	solute carrier organ	transporter activity /	full-length
10549079	-0.327349507	-2.842953112	-0.138947076	-5.372483723	-1.112731197	8.733601432	11.10601146		Gys2	glycogen synthase	catalytic activity /// g	full-length
10549842	-0.56813921	-4.512811354	-0.11814695	-6.248933813	-1.01888337	-1.093179714	5.358407993		Zfp667	zinc finger protein 6	nucleic acid binding	full-length
10550102	1.272753686	2.731013103	-0.012670289	-6.389554025	0.938080243	-0.540920962	6.371335232	Cluster III	Lig1	ligase I, DNA, ATP-	nucleotide binding /	full-length
10550332	1.456915823	10.57295684	-0.276091475	-3.78048223	1.600253118	11.27102857	6.554242928		Slc1a5	solute carrier family	transport /// dicarbo	full-length
10550509	1.40668621	4.023298817	0.034538332	-6.374443301	1.776642398	6.206743046	6.613428384	Cluster I	Pglyrp1	peptidoglycan reco	cytokine activity /// p	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**ene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10550574	1.011821926	0.986606585	0.166845321	-5.973699243	0.648851727	-2.91261629	8.536770809		Dmpk	dystrophia myotonic	nucleotide binding /	full-length
10550877	1.154006695	6.61333711	-0.054370879	-6.290974995	1.314843607	7.697330521	6.257940699		Kcnn4	potassium intermed	ion channel activity	full-length
10550906	1.423959823	2.284566113	-0.16407417	-6.12276362	1.996032658	5.508024134	6.352374772		Plaur	plasminogen activa	receptor activity /// c	full-length
10551009	2.152247786	11.29932053	0.06618156	-6.296615201	2.327133813	11.81417332	8.970687919	Cluster VI	Tmsb10	thymosin, beta 10	actin binding /// acti	full-length
10551185	1.525739803	9.086396447	-0.037132841	-6.350530888	1.521563027	8.621544912	7.811191209	Cluster I	Tgfb1	transforming growth	skeletal developme	full-length
10551197	1.995448437	-1.745835255	-0.000722319	-6.391789872	1.265578975	-4.70000345	6.721180265		Cyp2b10	cytochrome P450, f	monooxygenase ac	full-length
10551218	5.094542089	9.700679465	0.004543228	-6.391729327	4.788458311	8.533791914	6.912699648		Cyp2b9	cytochrome P450, f	monooxygenase ac	full-length
10551226	1.338785124	-1.004945906	-0.272812694	-5.984675181	2.229569033	3.468696504	11.50531954		Cyp2a4 /// Cyp2a5	cytochrome P450, f	monooxygenase ac	full-length
10551282	0.984463127	-0.341392145	-0.18194532	-5.999130654	1.560037462	3.783532525	11.23443618		LOC100047728	similar to Cytochror	---	predicted
10551531	-3.482734292	1.798098074	-2.474934989	-0.597595526	-3.384344021	1.134666603	6.484586453		Sycn	syncollin	exocytosis /// meml	full-length
10551666	1.063651251	3.704322634	-0.091060417	-6.195746577	1.151246088	4.145266506	6.094338234	Cluster III	Map4k1	mitogen-activated p	nucleotide binding /	full-length

10551836	-1.079398091	1.737468547	-0.136579557	-6.101425793	-1.374376285	3.839536377	6.174343215		Cox7a1	cytochrome c oxida	cytochrome-c oxida	full-length
10551883	2.082306122	11.63513967	0.096046518	-6.167482684	1.867245844	9.908789997	8.116751475		Tyrobp	TYRO protein tyros	protein binding /// m	full-length
10552406	3.605802648	16.36720527	-0.028292351	-6.376967424	3.835114939	16.72594633	7.137538368		Nkg7	natural killer cell gr	membrane /// integr	full-length
10552546	-2.132805047	0.290142955	-1.223982521	-2.983733431	-2.867613478	2.797506766	5.835915508		Klk1b5 /// Klk1	kallikrein 1-related	serine-type endope	full-length
10552587	-0.693389413	-1.609011899	-0.363548055	-4.36158272	-1.005078555	1.273315084	5.152680447		Klk1b21 /// Klk1b11	kallikrein 1-related	serine-type endope	full-length
10552613	-1.075721965	-4.656093775	-0.090825569	-6.369504832	-2.766459413	1.896174721	6.697389197		Klk1b4	kallikrein 1-related	serine-type endope	full-length
10552672	-0.569360621	-0.202201149	-0.027033339	-6.364260018	-1.063185731	5.782636617	9.587106689	Cluster X	0610012D14Rik	RIKEN cDNA 0610	catalytic activity ///	full-length
10552697	1.147404179	4.083421498	-0.066036355	-6.295995792	1.508764369	6.735004348	6.218809944		Napsa	napsin A aspartic p	aspartic-type endop	full-length
10553274	4.231593123	13.79603473	1.644106897	3.267471496	4.826383706	14.95683786	10.89707688	Cluster VIII	Saa2	serum amyloid A 2	lipid transporter act	full-length
10553324	1.44739001	10.40683442	0.214947019	-4.707807574	1.344638146	9.100266006	7.837450989		Tmem86a	transmembrane prc	membrane /// integr	full-length
10553521	-0.651089912	-2.780971932	0.071244537	-6.317421422	-1.12518984	1.380540731	8.112004398		Gas2	growth arrest speci	cytoplasm /// cytosk	full-length
10554269	0.989542952	2.409342316	-0.182421479	-5.708627637	1.440710909	6.078915615	9.287571596		Abhd2	abhydrolase domai	carboxylesterase ac	full-length
10554445	2.126659625	1.305808035	-0.183271077	-6.266894329	1.48416195	-2.100941116	5.587346463		Prc1	protein regulator of	cytokinesis /// nucle	full-length
10554574	1.473720448	6.217605425	0.152003768	-5.952613654	1.42197675	5.383846925	8.031510374		Tm6sf1	transmembrane 6 s	membrane /// integr	full-length
10554667	1.995925785	9.722000893	-0.094785121	-6.218695357	1.700754938	7.400410652	5.529158116		Tmc3	transmembrane cha	membrane /// integr	full-length
10554752	-1.521891648	13.59095004	-0.111325866	-5.639038417	-1.565327165	13.52693787	8.212983056	Cluster IX	Nox4	NADPH oxidase 4	cell morphogenesis	full-length
10554789	1.477290767	7.004389845	0.097815822	-6.180534884	1.531562769	6.990565117	11.65407239		Ctsc	cathepsin C	cysteine-type endop	full-length
10554938	-1.427258619	7.568391889	-0.717048873	0.851460429	-0.73273188	0.109889385	7.236328263		Rab30	RAB30, member R	nucleotide binding /	full-length
10555297	1.020711768	-0.690698792	-0.012246979	-6.390219234	0.41184225	-5.818791331	5.231612306		Kcne3	potassium voltage-	ion channel activity	full-length
10555389	1.422158403	8.165149409	-0.144747098	-5.800543804	1.251518363	6.247067877	9.020985141		Ucp2	uncoupling protein	transporter activity /	full-length
10555695	1.185301859	-0.195874552	-0.151502415	-6.194600494	0.66700294	-4.377226874	7.942038136		Rrm1	ribonucleotide redu	nucleotide binding /	full-length
10556076	-0.082431454	-7.128672087	0.006296502	-6.390919007	-1.216702095	4.271852027	7.480336181		Olfml1	olfactomedin-like 1	---	full-length
10556113	1.870826501	1.923754905	0.024549358	-6.388475562	2.156432708	2.979553764	10.31657437		Rbm3	RNA binding motif	nucleotide binding /	full-length
10556266	0.976488054	-0.831164458	-0.207286714	-5.932782303	1.233556491	0.890500461	6.618218245		Wee1	WEE 1 homolog (S	nucleotide binding /	full-length
10556297	1.422324293	0.480335542	0.027788845	-6.38635303	1.756048809	2.136278228	6.971825707		Adm	adrenomedullin	hormone activity ///	full-length
10556463	-0.533290905	-4.460906832	0.061729221	-6.34617116	-1.002127656	-0.610427559	7.729134391		Arntl	aryl hydrocarbon re	protein import into r	full-length
10556491	1.367068804	4.757496088	-0.110235936	-6.181007357	1.294420151	3.743401298	6.035223049		Far1	fatty acyl CoA redu	catalytic activity ///	full-length
10556718	-0.94454829	5.222880281	-0.18888513	-5.098173173	-1.060518968	6.106292125	4.198809029	Cluster X	Acsm2	acyl-CoA synthetas	nucleotide binding /	full-length
10557156	1.596533156	4.900610636	-0.231587245	-5.71687089	1.23407194	1.772270399	6.111169413		Plk1	polo-like kinase 1 (I	nucleotide binding /	full-length
10557177	1.456905662	3.603600124	0.229483816	-5.762277206	1.194176888	1.181546842	6.865538424		Prkcb	protein kinase C, be	nucleotide binding /	full-length
10557300	-0.451514055	-6.883706377	0.200074203	-6.313992841	-1.698664839	-3.369918685	10.16455178		Aqp8	aquaporin 8	transporter activity /	full-length
10557342	1.709032774	6.46979585	-0.066305321	-6.324941081	2.084829622	8.354575214	5.500078996		Il21r	interleukin 21 recep	receptor activity ///	full-length
10557591	2.264311061	6.947032734	0.20401139	-6.0096209	2.373930848	7.063120002	8.022686726	Cluster VI	Itgal	integrin alpha L	magnesium ion bin	full-length
10557862	2.902894071	8.77960763	-0.017250545	-6.389448449	3.707068077	11.2660564	6.611231517	Cluster VI	Itgam	integrin alpha M	opsonin binding ///	full-length
10557895	1.988131165	5.96098942	-0.228548999	-5.873503408	1.755887189	4.15183735	5.605603664	Cluster I	Itgax	integrin alpha X	magnesium ion bin	full-length
10558159	-1.734631321	-0.308581976	-0.918384221	-3.698450692	-1.584966198	-1.391899799	7.52125894		Dmbt1	deleted in malignar	blastocyst developr	full-length
10558769	1.102944728	7.420735129	0.293431153	-3.455853204	1.534709747	10.90592798	9.193924249		Ifitm1	interferon induced t	somitogenesis /// ar	full-length
10558961	0.649858755	-2.72707557	-0.136054216	-6.119287897	1.253185665	2.562208838	9.546806135		Tspan4	tetraspanin 4	protein binding /// m	full-length
10559207	2.629630822	12.50528627	-0.302338275	-4.929534021	2.443469467	11.21230507	7.780481748		Lsp1	lymphocyte specific	actin binding /// sigr	full-length
10559446	1.519439627	6.594175256	-0.349609597	-4.34155494	1.842959652	8.414895062	7.118440949	Cluster I	Lilrb3	leukocyte immunog	B cell homeostasis	full-length
10559454	1.954483762	9.770911013	-0.047270742	-6.346073036	1.885174336	8.910691498	7.616675208		Pira6 /// Pira11 /// F	paired-Ig-like recep	receptor activity	full-length
10559467	2.26042485	10.20783018	0.018338144	-6.386237448	2.405262108	10.5224867	7.167265355		Lilrb3 /// Pira11 /// F	leukocyte immunog	B cell homeostasis	full-length
10559478	0.962402552	-2.541971057	0.082366752	-6.342825483	1.038680081	-2.303792674	4.641826028		Pira11 /// Pira3 /// F	paired-Ig-like recep	receptor activity	full-length
10559486	2.074623104	10.24418575	0.157433037	-5.920343057	2.298638164	11.04398681	6.891761136		Lair1	leukocyte-associate	receptor activity ///	full-length
10560131	-1.210852231	-2.234522053	-0.00930185	-6.391358341	-2.007000473	1.756988801	11.11210444		2810007J24Rik	RIKEN cDNA 2810	transferase activity	full-length
10560242	1.553544974	2.05719126	-0.24522134	-5.916881493	2.450593209	6.600151566	6.340460568		C5ar1	complement compc	signal transducer a	full-length
10561104	1.090845657	2.145105046	0.065273864	-6.320118777	1.159256242	2.366831714	7.993092339		Axl	AXL receptor tyrosi	nucleotide binding /	full-length
10561212	-1.359348463	2.282731428	-0.121882688	-6.227609699	-1.756596636	4.59635977	6.869244968	Cluster IX	Ltbp4	latent transforming	binding /// calcium i	full-length
10562096	-0.676901261	-0.031191382	-0.074230389	-6.240564116	-1.112077297	4.564742589	8.790791689		Tmem147	transmembrane prc	membrane /// integr	full-length
10562169	0.752259566	-2.266763285	0.052136435	-6.356989548	1.427399868	3.094905248	12.07359576		Hamp	hepcidin antimicrob	hormone activity ///	full-length
10562192	2.431143474	14.04423238	-0.072748699	-6.249054763	2.378242355	13.38892215	8.511915673		Fxyd5	FXYD domain-cont	ion channel activity	full-length
10562563	0.910785281	4.067807565	0.021390963	-6.375785285	1.009882233	4.782340146	6.152697254	Cluster III	Ccne1	cyclin E1	cyclin-dependent pr	full-length
10562637	2.746447753	7.836127016	-0.063204719	-6.36193252	2.419523639	5.93823877	6.150578498		Ccnb1	cyclin B1	in utero embryonic	full-length

Affymetrix ID	BS/Non Inf.		LS/Non Inf.		ReINF/Non Inf.		Average	Cluster	Gene	Gene	Gene Ontology (GC	Transcript
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10562720	2.046875368	9.740517083	0.46950103	-3.22013828	2.30809334	10.74657569	8.050192967		Siglece	sialic acid binding I	receptor activity ///	full-length

10563178	1.173121541	8.287286764	-0.060305149	-6.232503048	1.16029006	7.724832677	6.558505195	Cluster I	Cd37	CD37 antigen	positive regulation	full-length
10563441	1.772961735	8.852920249	0.010213921	-6.389561909	2.183331887	10.90463498	7.849129923		Emp3	epithelial membran	membrane /// integ	full-length
10563597	4.007478807	11.80545596	0.847655806	-2.73308582	5.205372499	14.50838653	9.567851952	Cluster VIII	Saa3	serum amyloid A 3	lipid transporter act	full-length
10563602	0.383073325	-3.86605996	0.196204279	-5.343552436	1.255272175	6.284731258	11.45169954		Saa4	serum amyloid A 4	lipid transporter act	full-length
10563611	3.799359435	8.139212188	1.884045371	1.156400555	4.635045588	10.06601669	9.443243247	Cluster VIII	Saa1 /// Saa2	serum amyloid A 1	lipid transporter act	full-length
10563766	1.188174559	1.214464212	0.378376891	-4.891419197	0.946957862	-1.15373998	5.648022165		EG639116	predicted gene, EG	---	predicted
10564631	1.064097142	2.206766916	0.109202709	-6.180683712	1.647755488	6.557961765	7.442117782		Slco3a1	solute carrier organ	transporter activity	full-length
10565018	2.042997062	13.48671116	0.023514217	-6.372399432	2.191080163	13.9193052	8.155987333		Iqgap1	IQ motif containing	GTPase activator a	full-length
10565598	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10565609	0.666624543	-4.701266542	0.401022074	-5.367815831	-1.401322398	-0.106790866	9.432551632		Thrsp	thyroid hormone re	nucleus	full-length
10565727	0.096649126	-7.263946294	0.135581025	-6.360989645	2.287224356	-1.877639108	8.210278955		Tsku	tsukushin	protein binding /// e	full-length
10565815	-0.79017821	2.605171744	-0.043826816	-6.324367663	-1.012834563	4.856357004	7.460872958		---	---	---	partial
10565910	-1.058232268	0.78108637	-0.09980445	-6.257923222	-0.587393088	-3.898346854	7.035716077		Plekhb1	pleckstrin homolog	Golgi membrane ///	full-length
10565958	1.181014202	7.953311355	-0.049832356	-6.289956736	1.568587761	10.89447534	6.13666484		P2ry6	pyrimidinergic rece	signal transducer a	full-length
10565994	1.703157686	-2.276138611	0.777455738	-5.035495268	1.343662017	-4.000121975	6.265680221		Art2b	ADP-ribosyltransfe	NAD(P)+-protein-a	full-length
10566050	2.039599425	16.2300615	0.507635237	1.139335763	2.098140795	16.20395601	8.29913843		Il18bp	interleukin 18 bindi	extracellular region	full-length
10566205	-1.02628318	-3.33211446	-1.022875925	-2.585612338	-1.537553549	-0.718804323	9.290583912		Dub2a	deubiquitinating en	ubiquitin thiolestera	full-length
10566326	1.27047279	4.335815651	1.525684589	6.338196343	1.445346288	5.344975495	8.234077767		Trim12	tripartite motif-cont	protein binding /// i	full-length
10566333	0.925378923	5.322879603	1.047902123	6.634719537	1.124458778	7.122328659	7.643176504		9230105E10Rik ///	RIKEN cDNA 9230	zinc ion binding ///	full-length
10566346	1.164459081	-0.086963458	1.260653278	1.183493086	1.341955519	0.845040549	6.354233761		9230105E10Rik	RIKEN cDNA 9230	zinc ion binding ///	full-length
10566358	1.672719508	9.953264368	1.573616131	8.675752337	1.956450413	11.40013736	8.880907825		Trim30	tripartite motif-cont	DNA binding /// pro	full-length
10566366	0.862117914	-1.086470961	1.848450782	6.510871502	1.499344747	3.826346219	6.954639752		AI451617	expressed sequen	zinc ion binding ///	full-length
10566571	2.015762239	8.177826088	1.177736938	2.653028045	2.394134934	9.78497485	7.150740907		---	---	---	partial
10566574	2.573775802	14.78012787	1.58528115	8.527865073	3.002805171	16.20088858	8.837129981		Gvin1	GTPase, very large	nucleotide binding	full-length
10566578	2.320623234	11.95029597	1.411432527	6.091811646	2.689087005	13.29741414	7.907652068		---	---	---	partial
10566583	1.962889178	10.10431478	0.544400366	-1.971505706	2.239474659	11.25430137	6.811766162		EG668139	predicted gene, EG	---	est
10566585	2.216831725	12.61924638	1.19873079	5.493181613	2.700311575	14.55843689	6.465554543		---	---	---	partial
10566934	0.927594691	-0.464337125	-0.167316469	-6.027507661	1.0269406	0.075466825	8.595759076		Lyve1	lymphatic vessel e	receptor activity ///	full-length
10567355	0.723097802	-1.958132564	0.21275853	-5.740641734	1.191278829	2.079137564	5.31099488		Gprc5b	G protein-coupled	signal transducer a	full-length
10567366	-2.756771512	-1.481551733	-1.645878884	-3.795966311	-2.761773629	-1.783168099	4.698983407		Gp2	glycoprotein 2 (zym	extracellular region	full-length
10567394	-1.466515558	5.457974812	-0.143275415	-6.044682836	-1.969461384	8.438314365	6.107730106		---	---	---	partial
10567580	2.334282223	11.10716057	0.189490087	-5.775230493	2.268863418	10.34270665	8.155888604		Igsf6	immunoglobulin su	membrane /// integ	full-length
10567825	1.697079536	12.12660444	-0.082721721	-6.120708313	2.029589093	13.84965263	6.37311917	Cluster VI	Lat	linker for activation	immunological syn	full-length
10568024	2.936625877	16.99416919	-0.081623491	-6.186863521	3.026322846	17.00194338	7.666034216	Cluster VI	Coro1a	coronin, actin bindi	immunological syn	full-length
10568050	0.964348837	7.280129971	-0.093918315	-5.922078594	1.130249648	8.711626208	10.57895066		Aldoa	aldolase A, fructos	catalytic activity ///	full-length
10568115	0.727738642	2.835747443	-0.143170365	-5.556668118	1.286146669	8.827448242	8.519490787		Mvp	major vault protein	cytoplasm /// ribonu	full-length
10568150	1.31910702	3.477877554	0.323563955	-4.989977385	1.003227782	0.367157237	5.361638752		Kif22	kinesin family mem	nucleotide binding	full-length
10568165	-3.579254408	1.394986327	-2.71492353	-0.414696414	-3.468951207	0.719661611	5.119558762		1810010M01Rik	RIKEN cDNA 1810	sugar binding /// ex	full-length
10568174	1.057084388	3.615748265	-0.139492564	-5.942634714	1.410682199	6.40422423	5.941662575	Cluster IV	Spn	sialophorin	response to protoz	full-length
10568202	1.202205635	3.25106577	0.073495508	-6.299249768	1.26703111	3.398794236	6.39487364	Cluster III	Sep-01	septin 1	nucleotide binding	full-length
10568355	0.81762988	1.04699209	-0.088090936	-6.20768866	1.248278417	5.053513414	5.689599012		Pycard	PYD and CARD do	cysteine-type endo	full-length
10568502	-1.377804224	-1.367528615	-0.907143772	-3.280314894	-1.323270595	-1.989328488	4.58460422		Cuzd1	CUB and zona pell	protein binding /// c	full-length
10568534	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10568714	2.305490808	6.229562359	0.103140737	-6.306677397	1.917213703	3.75452049	6.288998887		Mki67	antigen identified b	chromosome, centr	full-length
10568731	-1.157134337	-2.549366519	-1.79257992	1.564200412	-0.389999925	-6.644170383	4.061080795		---	---	---	---
10569020	2.295357295	7.338453665	0.199108027	-6.01271929	2.225064418	6.546045977	6.391430144		Ifitm6	interferon induced t	integral to membra	full-length
10569102	1.630031385	8.700835618	1.618719345	8.188775075	2.121904933	11.41614346	9.761425048	Cluster VI	Irf7	interferon regulator	DNA binding /// tra	full-length
10569168	-0.27608831	-6.649786554	0.097613414	-6.31164991	-1.134287641	-1.038163273	9.713838521		Slc25a22	solute carrier family	transporter activity	full-length
10569504	1.320110788	5.201303899	-0.058829001	-6.321300138	1.190022039	3.644137964	5.49246579		Tnfrsf23	tumor necrosis fac	receptor activity ///	full-length
10569646	1.315356324	-1.72792574	0.03072577	-6.387199047	0.778407193	-4.978915833	8.65021619	Cluster III	Ccnd1	cyclin D1	cyclin-dependent p	full-length
10569656	0.948502913	4.987700059	0.107697182	-5.963490092	1.017441076	5.348458066	6.858076398		Tpcn2	two pore segment	ion channel activity	full-length
10569707	1.097125844	7.604693653	-0.172097962	-5.177398293	1.041336698	6.566480025	8.098896359		Myadm	myeloid-associated	membrane /// integ	full-length
10569823	-0.500664845	-5.333765492	0.143744417	-6.212716093	-1.310729239	0.379730915	6.002014582		C330021F23Rik	RIKEN cDNA C330	---	full-length
10569877	1.363851524	-1.534171492	-0.134805541	-6.30583988	1.877324041	0.871720013	5.427011323		1810033B17Rik	RIKEN cDNA 1810	---	full-length
10569890	1.229114054	9.690567487	0.421153749	-0.757421906	1.393553842	10.76156788	8.186660791		Aida	axin interactor, dor	protein binding ///	full-length
10570201	1.415147689	4.184122329	0.202489355	-5.81103585	2.159936578	8.591274577	7.103869424		Atp11a	ATPase, class VI, t	nucleotide binding	full-length

10570434	1.288892481	8.700405724	0.010303883	-6.387608637	1.701830707	11.58616462	8.009019487		Ifitm1	interferon induced t	somitogenesis /// a	full-length
10570516	1.055426457	2.531663204	-0.034572065	-6.368529115	1.393865867	5.1101362	5.345884845		Kbtbd11	kelch repeat and B	protein binding	full-length
10570741	0.82074073	-4.755559576	-0.279885532	-6.053187767	1.197062342	-2.999170265	5.698761457	Cluster IV	Defb1	defensin beta 1	extracellular region	full-length
10571353	-0.786875151	-1.800032056	-0.046168078	-6.36342326	-1.108540972	0.760941782	6.44495606		6430573F11Rik	RIKEN cDNA 6430	metabolic process /	full-length
10571467	-0.851288191	-2.934068636	-0.107692629	-6.297124774	-1.0050332	-2.085521085	5.135357867		Pdgfrl	platelet-derived gro	extracellular region	full-length
10571560	-0.820605476	-0.861132884	-0.20605097	-5.762673116	-1.045951751	0.940980823	4.766269446		Mtnr1a	melatonin receptor	signal transducer a	full-length
10571653	1.484903434	11.12355499	-0.067440408	-6.191838441	1.647874316	11.94917416	11.25135463		Actg1	actin, gamma, cyto	nucleotide binding /	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10571657	-0.898437649	3.774642629	-0.217125767	-4.957173292	-1.572468215	9.770228294	12.26350583		Acsl1	acyl-CoA synthetas	magnesium ion bin	full-length
10571870	2.1660213	10.56469354	-0.000878644	-6.391776221	1.944828899	8.852722552	7.816133841		Hmgb2	high mobility group	DNA binding /// nuc	full-length
10571891	-1.011472727	2.048971034	-0.136889676	-6.039866342	-1.16043877	3.061795481	9.276019657		Aadat	aminoadipate amin	catalytic activity ///	full-length
10571984	1.206350869	6.613270595	2.061132524	11.42846226	1.216813538	6.281791409	6.93792394		Ddx60	DEAD (Asp-Glu-Al	---	full-length
10572130	1.272495458	7.969791284	-0.315345704	-3.56679605	1.562378322	9.969947953	8.882638026	Cluster I	Lpl	lipoprotein lipase	catalytic activity ///	full-length
10572445	1.927095013	13.75689922	0.083724618	-6.108390781	1.840766804	12.81223116	6.176396948		Lrrc25	leucine rich repeat	molecular_function	full-length
10572747	1.361457919	6.914622087	-0.018454617	-6.382935596	1.35718919	6.44694994	9.158382093		Tpm4	tropomyosin 4	podosome /// actin	full-length
10572897	3.036385549	10.56187205	0.181931781	-6.077909688	3.771312644	12.73340048	9.916885271		Hmox1	heme oxygenase (	heme oxygenase (	full-length
10572906	1.40915828	1.353655958	0.094768544	-6.314687073	1.305920204	0.266896996	6.735054999	Cluster III	Mcm5	minichromosome m	nucleotide binding /	full-length
10573261	2.023993028	6.493652228	0.049562639	-6.364965465	1.782584126	4.63361828	6.487735301		Asf1b	ASF1 anti-silencing	chromatin /// nucle	full-length
10573747	1.072119104	3.038392793	0.118845734	-6.104001343	1.011865488	2.044673282	6.637704975		Adcy7	adenylate cyclase	magnesium ion bin	full-length
10573865	0.598241802	-6.186061261	0.814571297	-4.537040434	1.471048151	-2.678610145	11.35434024		LOC433762	hypothetical gene L	---	full-length
10573939	1.669668792	7.661391044	0.20954169	-5.581158576	1.486922888	5.891162953	6.762544118		Lpcat2	lysophosphatidylch	calcium ion binding	full-length
10574023	3.230663828	5.277827034	1.56538796	-1.002613442	4.399314522	8.412765748	11.06260202		Mt2	metallothionein 2	cellular zinc ion hor	full-length
10574027	2.177833598	1.877305594	0.937955367	-3.574091649	3.273161254	5.83903369	11.47718211		Mt1	metallothionein 1	copper ion binding	full-length
10574098	1.405643455	5.120012094	1.027576558	2.266919856	1.598108131	6.144212318	7.536384407		---	---	---	predicted
10574102	1.131814074	4.396099723	0.976087739	3.191274672	1.399812503	6.359044025	8.077742135		---	---	---	predicted
10574104	1.623911316	7.431082697	1.206804933	4.326201891	1.825704851	8.372477306	7.179411789		Nlrc5	NLR family, CARD	---	partial
10574133	0.808193905	-0.12334535	0.631819291	-1.387184456	1.090495398	2.356378041	6.643898551		---	---	---	predicted
10574135	1.597083603	4.158338918	1.190551163	1.658516751	1.922102983	5.797794345	6.264940751		---	---	---	predicted
10574137	1.353420921	5.541135783	0.998203614	2.693046624	1.513226287	6.383392515	7.34922217		---	---	---	predicted
10574139	1.326458199	4.961181163	0.830920005	0.786073881	1.356789862	4.789746181	6.678549157		---	---	---	predicted
10574141	1.218715219	5.653507891	0.766855346	1.353592975	1.182768309	4.892365848	7.082576626		---	---	---	predicted
10574143	1.156878964	1.694146524	0.552884607	-3.163188726	1.206426522	1.721163796	5.737667443		---	---	---	predicted
10574145	1.695629671	4.603911797	1.033255947	0.290666544	1.796824611	4.82386263	6.577996629		---	---	---	---
10574149	1.953811894	7.796369561	1.474958954	4.781401289	2.166848881	8.581612859	8.43450932		---	---	---	predicted
10574151	1.145269654	1.79117031	0.770040946	-1.009889521	1.386446307	3.3564062	7.164818717		---	---	---	---
10574157	1.518835677	6.859488335	1.199876876	4.440605206	1.740651185	8.017124287	7.861920593		---	---	---	---
10574159	1.394070924	5.488908497	1.165908873	3.833393085	1.771116714	7.816273045	7.806328846		---	---	---	predicted
10574161	0.825130519	3.172802917	0.623777015	0.979911837	1.034954352	5.223927408	7.872669586		---	---	---	predicted
10574163	1.219108958	4.78896865	0.755728311	0.568989492	1.385664549	5.801148202	6.334122499		---	---	---	partial
10574350	-0.806377793	1.175036659	-0.064162026	-6.288003502	-1.305911366	5.871005272	7.111573176		Mmp15	matrix metallopepti	metalloendopeptida	full-length
10574432	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	predicted
10574434	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10574471	1.112040662	4.882303381	-0.03435892	-6.359697017	0.975437572	3.049439322	8.386159746		Cmtm3	CKLF-like MARVEL	cytokine activity ///	full-length
10574488	-0.861275668	-0.109750158	-0.191176235	-5.803602389	-1.276013733	3.347399122	6.663429754		4833426J09Rik	RIKEN cDNA 4833	magnesium ion bin	full-length
10574498	-0.7737782	-1.941909866	-0.36267449	-4.846787778	-1.65748767	4.898805968	10.97506209		Ces6	carboxylesterase 6	---	full-length
10574511	-0.917963404	-1.253970713	-0.336821874	-5.223667478	-1.237247507	1.011362901	4.828648789		BC015286	cDNA sequence B	---	partial
10574524	-1.172249139	0.312160015	-0.444225429	-4.671334223	-1.742967382	3.892166062	8.040426254		Ces2	carboxylesterase 2	---	full-length
10574532	-0.950006372	-1.189546979	-0.208400083	-5.942559926	-1.425663356	2.14745542	10.55367563		Ces2	carboxylesterase 2	---	full-length
10574545	-0.90557559	2.127845151	-0.009239098	-6.389703303	-1.575531229	7.824288339	10.93279401		Ces5	carboxylesterase 5	---	full-length
10574607	-1.158294348	2.20157457	0.018261248	-6.386733625	-1.57375082	5.064847167	11.99954944		EG13909	predicted gene, EG	carboxylesterase a	full-length
10574617	-1.834191613	5.237764299	-0.355856574	-5.16438228	-2.135989514	6.54126211	6.242408521		BC026374	cDNA sequence B	carboxylesterase a	full-length
10574976	1.000579753	3.35146952	0.020942815	-6.380665243	0.691225186	-0.587720547	7.407612094		Pla2g15	phospholipase A2,	phosphatidylcholine	full-length
10574985	0.895817867	2.791983347	0.253398291	-4.783041984	1.344614463	6.858705973	5.175531643		Slc7a6	solute carrier family	plasma membrane	full-length
10575052	-0.680392424	-3.791011825	-0.044788904	-6.372486717	-1.393293487	1.394009511	8.404381915		Cdh1	cadherin 1	trophectodermal ce	full-length
10575153	-0.748635678	1.407162055	-0.113659168	-6.0039872	-1.120603407	5.25221234	11.05118996	Cluster X	Cyb5b	cytochrome b5 type	iron ion binding /// r	full-length

10575249	-0.827200011	1.126185817	-0.150209376	-5.873764582	-1.193859429	4.521324665	6.607033861		Txnl4b	thioredoxin-like 4B	nucleus /// spliceos	full-length
10575685	-1.529206522	-1.807930684	-0.145557737	-6.3175522	-3.476618305	5.77224222	10.69239738		Nudt7	nudix (nucleoside d	magnesium ion bin	full-length
10575799	1.477968765	3.270583137	-0.026214354	-6.383920973	1.618546016	3.8299015	6.765863962	Cluster I	Plcg2	phospholipase C, g	follicular B cell diffe	full-length
10575833	-0.585077318	-0.048675578	-0.0271899	-6.364478337	-1.210969997	7.169440538	10.94267882	Cluster X	Hsd17b2	hydroxysteroid (17-	catalytic activity ///	full-length
10576034	2.145282996	12.66443503	0.037610855	-6.352698196	2.494087842	14.05168067	7.82006381	Cluster VI	Irf8	interferon regulator	DNA binding /// trar	full-length
10576332	0.29651147	-5.708458601	-0.26411089	-5.148870551	1.15831078	3.137749244	4.689227248		Tubb3	tubulin, beta 3	nucleotide binding /	full-length
10576774	-2.026572183	-0.612608243	0.058255737	-6.382605896	-2.254701884	-0.036315876	10.23722857		Clec4g	C-type lectin domai	binding /// sugar bir	full-length
10576883	1.445690953	0.899673806	-0.369975509	-5.443662341	1.127321275	-1.587692279	4.813250483		Shcbp1	Shc SH2-domain bi	protein binding /// S	full-length
10577190	1.375382906	2.66326166	-0.144045693	-6.151902225	1.190870074	0.850201802	7.359067777		Rasa3	RAS p21 protein ac	GTPase activator a	full-length
10577315	1.341175455	5.591540818	0.187664054	-5.6831357	2.414387567	12.08294063	6.001770719	Cluster II	Angpt2	angiopoietin 2	angiogenesis /// rec	full-length
10577641	-0.87177066	-3.072014003	0.146976607	-6.231639326	-1.178893724	-1.211726616	8.670180353		1810011O10Rik	RIKEN cDNA 1810	apoptosis	full-length
10577792	1.654872847	11.60916901	0.204477768	-4.938230095	1.758395223	11.91699234	7.15828819		Plekha2	pleckstrin homolog	phosphatidylinosito	full-length
10578222	-0.470616275	-5.382448721	-0.293487924	-5.609147228	-1.222282078	0.174799384	7.796455455		Dlc1	deleted in liver canc	neural tube closure	full-length
10578264	1.640294037	11.3524916	0.130249039	-5.776948067	1.892815275	12.64741578	8.633579254	Cluster I	Msr1	macrophage scave	receptor activity ///	full-length
10578352	1.066303587	4.224903579	0.107239801	-6.096187866	1.378102438	6.685645578	12.39986284		Fgl1	fibrinogen-like prote	receptor binding ///	full-length
10578539	1.230504724	2.700802037	-0.042114779	-6.365553167	1.126221196	1.418055363	8.035927094		Slc25a4	solute carrier family	transporter activity	full-length
10578690	1.055850881	-0.218172613	0.128460762	-6.213770044	0.612179691	-4.244010128	4.799082738		Neil3	nei like 3 (E. coli)	DNA binding /// dar	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**RelNF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10579199	-0.750218242	-2.578682891	-0.033584736	-6.378501512	-1.160097033	0.610910369	7.968760882		Slc25a42	solute carrier family	binding /// mitochor	full-length
10579347	2.679637727	15.98076274	0.211547155	-5.122072756	2.639602338	15.44635457	10.04021138	Cluster VI	Ifi30	interferon gamma i	lysosome /// disulfic	full-length
10579636	1.201350066	0.803016747	0.060442383	-6.353231916	1.147061348	0.015198705	5.402361328		Cyp4f18	cytochrome P450, f	monooxygenase ac	full-length
10579649	-1.464044998	8.590614004	-0.223768842	-5.04255229	-1.74453969	10.24371234	5.408798782		Cib3	calcium and integri	molecular_function	full-length
10579659	1.23702252	5.694064821	0.173979203	-5.663833666	0.986115368	2.80713826	9.376018221		Hmgn2	high mobility group	chromatin /// DNA b	full-length
10579812	0.926110624	3.013489897	-0.104846457	-6.093290438	1.266082515	6.027715515	7.390672217		Ednra	endothelin receptor	patterning of blood	full-length
10580033	1.20634148	3.404173199	0.075020409	-6.29326352	1.075030286	1.81732981	8.99859634		Cd97	CD97 antigen	signal transducer a	full-length
10580457	0.733519296	0.218247683	0.228778529	-5.200343868	1.22761383	5.080994497	8.691842419		N4bp1	NEDD4 binding pro	nucleus	full-length
10580649	-1.539150481	5.885981728	-0.018761119	-6.385805794	-2.080518735	8.964902167	10.119366		Es22	esterase 22	carboxylesterase a	full-length
10580663	-1.073190656	-1.144066149	-0.007423292	-6.391323154	-1.351097767	0.500043682	11.33425658		AU018778	expressed sequenc	carboxylesterase a	full-length
10580875	-0.580841635	1.078252732	-0.277353799	-3.476290254	-1.076809651	7.314405415	8.091762939		Gtl3	gene trap locus 3	---	full-length
10581009	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10581355	-4.542293816	-0.495573668	-3.525998106	-1.723803267	-4.658286126	-0.624479278	6.929591845		Ctrl	chymotrypsin-like	protein binding /// p	full-length
10581378	1.493759605	11.3400529	0.232306775	-4.302426109	1.61370749	11.84456263	8.846517091		Psmb10	proteasome (proso	endopeptidase activ	full-length
10581479	1.085082778	-1.390837056	0.206308541	-6.067875962	1.244635495	-0.601934228	5.694608326		Smpd3	sphingomyelin phos	Golgi cis cisterna //	full-length
10581538	1.494678423	-2.871036386	-0.219909863	-6.261570901	2.299000145	0.157159792	7.064339982		Nqo1	NAD(P)H dehydrog	NAD(P)H dehydrog	full-length
10581813	2.237409527	12.97783522	0.920882873	3.157367477	2.550343665	14.13122199	7.21010936		Mlkl	mixed lineage kinas	protein kinase activ	full-length
10581882	-5.004382372	0.674203021	-3.970793859	-0.647615756	-5.612058432	1.389447816	7.502971004	Cluster IX	Ctrb1	chymotrypsinogen	serine-type endope	full-length
10582162	1.295477601	6.024127081	-0.20239225	-5.455354505	1.308548533	5.70982988	7.437038421		Cotl1	coactosin-like 1 (Di	actin binding /// pro	full-length
10582275	0.68315794	1.362832746	0.081367546	-6.152528269	1.085227754	5.873296254	6.896369202		Slc7a5	solute carrier family	cytoplasm /// plasm	full-length
10582303	2.285554665	17.11726658	-0.019714681	-6.371322717	2.271416644	16.71428779	8.843436086		Cyba	cytochrome b-245,	iron ion binding /// c	full-length
10582337	1.020307857	1.65438095	0.262316316	-5.286635379	1.004171351	1.117039186	6.36809758		Fam38a	family with sequenc	---	partial
10582464	1.199615142	-3.390475435	1.755185887	-0.025388451	1.413787051	-2.619564211	5.005265228		---	---	---	est
10582626	-0.676574658	1.172751357	-0.228418314	-4.740456248	-1.002560291	4.867458052	7.493270746		Abcb10	ATP-binding casset	nucleotide binding /	full-length
10582862	1.222470381	2.24033804	-0.267919357	-5.474982597	1.655054482	5.067971887	6.311637224		Sp140	Sp140 nuclear body	zinc ion binding /// r	full-length
10582868	0.804972257	5.516120857	0.181768883	-4.707994889	1.03585264	7.995200852	6.321503972		---	---	---	partial
10582874	1.356642952	7.36001555	0.234880094	-4.994067087	1.407440196	7.355674074	5.476680342		---	---	---	partial
10582983	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10582985	1.83640695	8.497859179	0.265975955	-5.185358347	1.99554366	9.049086232	6.589406381		Casp1	caspase 1	response to hypoxi	full-length
10582997	1.46415344	5.130505833	-0.011850775	-6.389482726	1.75225527	6.745887094	6.092347803		Casp4	caspase 4, apoptos	cysteine-type endo	full-length
10583044	0.203809229	-6.754921395	0.002935269	-6.391680363	1.240774804	1.663332639	5.622822041		Mmp13	matrix metallopepti	metalloendopeptida	full-length
10583056	0.530989199	-2.407817915	0.145362625	-5.888961031	1.43600108	6.809808106	5.511252115		Mmp12	matrix metallopepti	metalloendopeptida	full-length
10583100	1.247746673	-5.001454639	0.05705446	-6.38625962	1.904813075	-3.096011019	4.376221325		Mmp8	matrix metallopepti	metalloendopeptida	full-length
10583112	1.258192923	-1.520867517	0.263929517	-6.012121355	0.890001159	-4.036879745	5.324367202		Mmp27	matrix metallopepti	---	partial
10583519	1.851682626	3.89999952	-0.098407512	-6.31272847	2.39341564	6.341427781	7.677904151	Cluster VI	Icam1	intercellular adhesi	immunological syna	full-length
10583669	2.151568257	12.70687032	0.128441279	-5.949412856	2.207489168	12.60412595	7.791693047		AB124611	cDNA sequence AE	membrane /// integ	full-length
10583870	1.330915761	-4.440336891	0.013796504	-6.391420524	2.681825352	0.037288177	6.258045271		Bmper	BMP-binding endot	protein binding /// e	full-length

10584271	-0.589085755	-5.281902793	0.019358883	-6.38933924	-1.462556703	0.036875979	6.966441469		Tmem218	transmembrane pr	membrane /// integr	full-length
10584628	1.520712284	3.806357442	0.382696148	-4.841564515	1.61002456	4.008474308	6.698572593	Cluster I	Thy1	thymus cell antigen	angiogenesis /// pla	full-length
10584634	0.485342848	-6.746328365	0.092083336	-6.372297993	1.982067339	-1.768627673	7.158435914		Usp2	ubiquitin specific p	ubiquitin thiolestera	full-length
10584674	1.221922053	5.19540903	-0.153054869	-5.85535902	1.181556338	4.400808769	7.547774796		Mcam	melanoma cell adh	protein binding /// p	full-length
10584787	0.904677482	-5.817492058	0.166290952	-6.33813466	1.705408089	-3.356615122	5.59374359		Treh	trehalase (brush-b	alpha,alpha-trehala	full-length
10584821	1.443063802	2.867208652	0.003480746	-6.391656128	1.590938443	3.488283413	5.454738536	Cluster I	Cd3d	CD3 antigen, delta	receptor activity ///	full-length
10585276	1.46357122	6.525526381	0.003646418	-6.391511158	1.642884787	7.433198817	6.177629544		Pou2af1	POU domain, class	DNA binding /// pro	full-length
10585331	-0.664898554	-1.739176038	-0.327581749	-4.622016821	-1.228916275	3.582868655	5.508108427		Exph5	exophilin 5	protein binding /// c	full-length
10585467	-0.631083144	-3.232791509	-0.230129491	-5.709152998	-1.649581456	4.978295451	8.586940969		C630028N24Rik	RIKEN cDNA C630	cytoplasm /// kinase	full-length
10585555	1.065143891	3.719904493	-0.045379804	-6.342539867	0.974896806	2.385931335	5.726911091	Cluster III	Pstpip1	proline-serine-thre	cytokinesis /// stres	full-length
10585699	-0.015406095	-7.279563877	-0.286137044	-6.249445561	-1.760242463	-3.474400242	7.313333192		Fabp5	fatty acid binding p	transporter activity /	full-length
10585932	2.11538302	11.25623822	0.171432219	-5.762362661	2.266552922	11.66160735	8.401558094		Pkm2	pyruvate kinase, m	magnesium ion bin	full-length
10585956	1.62005939	0.80805939	-0.247381889	-6.04466064	1.264457099	-1.655579774	5.997082669		---	---	---	partial
10585970	1.6398608	3.084281195	0.325493824	-5.503952756	1.555845978	2.141892749	7.198381975		---	---	---	partial
10585972	1.408902632	-0.075941997	0.000699054	-6.391787869	1.388663586	-0.550693098	5.683544686		---	---	---	partial
10585974	1.768309339	2.407438962	0.491673121	-4.931884511	1.874293025	2.605759066	5.514269818		---	---	---	partial
10585976	1.476646777	0.589578284	0.082792926	-6.346075173	1.334115339	-0.6645658	5.982576166		---	---	---	partial
10585978	1.15660176	-1.162714526	0.252165925	-5.944981638	0.974799579	-2.726063407	5.441697123		---	---	---	partial
10585980	1.178632391	0.391971766	-0.105991278	-6.279718113	1.036783586	-1.065134839	4.939331813		---	---	---	partial
10585982	1.767472613	1.817051336	0.461710107	-5.219018557	1.743954683	1.300412082	6.724500364		---	---	---	partial
10585986	1.663494069	2.93374179	0.172558536	-6.144004239	1.436132852	1.070486461	6.695883966		---	---	---	partial
10585988	1.460649028	2.597696769	0.049954082	-6.366110446	1.315756934	1.166878296	6.476252894		---	---	---	partial
10585990	1.328506137	1.457195247	-0.06986571	-6.343518407	1.136434334	-0.350058304	6.739393638		---	---	---	---
10585992	1.550959979	1.826181674	0.038216283	-6.380335099	1.499847097	1.115253644	6.257063528		Myo9a	myosin IXa	nucleotide binding /	partial
10586448	3.20401101	6.613024551	0.59256279	-4.990493443	2.903237993	5.065572295	6.232502426		2810417H13Rik	RIKEN cDNA 2810	nucleus /// mitocho	full-length
10586744	1.816520889	10.68801248	-0.042204085	-6.342583063	1.757269528	9.864861444	7.855565497		Anxa2	annexin A2	angiogenesis /// str	full-length
10586863	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**RelNF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**ene Ontology (G**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10587077	-1.857341369	4.227483312	-0.628483225	-3.647475521	-2.345978358	6.423511955	6.717095775	Cluster IX	Onecut1	one cut domain, fa	liver development /	full-length
10587082	-2.086301328	-0.444605055	-1.265734776	-3.127503402	-1.552078566	-2.97658102	7.460401236	Cluster IX	Onecut1	one cut domain, fa	liver development /	full-length
10587107	0.958353112	2.636334161	0.06733435	-6.283286413	1.313783841	5.645483336	5.094367196		Myo5a	myosin Va	microfilament moto	full-length
10587284	-0.193755905	-7.110517737	0.075143704	-6.366629432	-1.747058466	-0.082110897	11.81302491	Cluster X	Elovl5	ELOVL family mem	endoplasmic reticul	full-length
10587323	0.560706733	-2.168773762	-0.199769468	-5.507404468	1.160016816	4.170450425	10.55981074		Gsta1 /// Gsta2 ///	glutathione S-trans	glutathione transfer	full-length
10587331	0.564292247	-2.094186866	-0.183814667	-5.629660793	1.151686627	4.1353949	10.50164458		Gsta1 /// Gsta2 ///	glutathione S-trans	glutathione transfer	full-length
10587339	0.470591597	-3.784622356	-0.181016217	-5.761893042	1.087496305	2.620335511	10.23057276		Gsta1 /// Gsta2 ///	glutathione S-trans	glutathione transfer	full-length
10587683	2.113804778	11.96069987	0.202084703	-5.431345705	2.579828647	13.92517008	5.847751887	Cluster VI	Bcl2a1a /// Bcl2a1b	B-cell leukemia/lym	B cell homeostasis	full-length
10587690	1.693747441	10.56698699	0.093438521	-6.124508871	2.224635615	13.40609814	5.860841243		Bcl2a1a /// Bcl2a1b	B-cell leukemia/lym	B cell homeostasis	full-length
10587792	0.587952065	-0.730558264	-0.132895302	-5.861615827	1.01181343	4.182024136	9.303039621	Cluster IV	Plscr1	phospholipid scram	calcium ion binding	full-length
10587871	-0.601586956	-4.197567195	-0.032147527	-6.38090548	-1.236609233	0.68311506	10.27198573		Paqr9	progestin and adip	receptor activity ///	full-length
10588479	0.872329847	2.464739828	0.266863299	-4.645705145	1.011245986	3.608013346	5.845226262	Cluster II	Tlr9	toll-like receptor 9	receptor activity ///	full-length
10588577	-1.104097352	-0.897488473	-0.960635901	-1.275700278	-0.312196457	-6.583992686	7.097158297		Cish	cytokine inducible	regulation of cell gr	full-length
10588691	-0.60355476	-2.673100803	0.210482693	-5.651064739	-1.006267549	1.19076628	8.536694605		Hyal1	hyaluronoglucosam	catalytic activity ///	full-length
10588883	-0.717394298	3.834761337	-0.120684815	-5.648804359	-1.189243277	9.189144141	9.623753513	Cluster X	Amt	aminomethyltransf	aminomethyltransf	full-length
10589350	1.011792171	9.355506537	0.621217154	4.063258276	1.088344429	9.793164094	9.250151899		Shisa5	shisa homolog 5 (X	nucleus /// nuclear	full-length
10589511	-0.355154471	-3.882172103	0.045332332	-6.321899272	-1.019988257	4.760066063	9.265309811	Cluster X	Scap	SREBF chaperone	protein binding /// p	full-length
10589535	1.096511574	6.964250895	0.126979899	-5.770363446	0.559308871	-0.405660184	4.385120426		Ngp	neutrophilic granul	molecular_function	full-length
10589884	1.504106887	1.715153024	0.187280086	-6.111669164	1.505568063	1.339914705	4.892258091		Bcl2a1c	B-cell leukemia/lym	apoptosis	full-length
10589974	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10590365	-1.112052635	6.956953342	-0.292259408	-3.693227733	-1.610874853	10.90884318	7.11945231		Vipr1	vasoactive intestin	signal transducer a	full-length
10590381	-0.815495504	2.730762244	-0.196894068	-5.194362567	-1.050333028	5.045949646	6.805033857		Vipr1	vasoactive intestin	signal transducer a	full-length
10590438	-1.309109412	0.459072038	-0.181870862	-6.123635421	-2.091103501	4.856158601	6.056554873		C730027P07Rik	RIKEN cDNA C730	extracellular region	full-length
10590494	1.460783429	3.428239502	0.056091493	-6.353879394	0.98866721	-0.700054324	5.024740685		Kif15	kinesin family mem	nucleotide binding /	full-length
10590631	2.555080759	10.22388559	-0.227377469	-5.754057726	2.350490552	8.800780332	5.939069689	Cluster VI	Ccr2	chemokine (C-C m	signal transducer a	full-length
10590635	1.9159098	10.11404502	-0.278271725	-4.841580237	1.941415595	9.842923739	7.409304466		Ccr5	chemokine (C-C m	signal transducer a	full-length
10590844	-0.904960351	3.772062842	-0.238041793	-4.724810176	-1.038283567	4.857407495	9.378083354		9030420J04Rik	RIKEN cDNA 9030	---	full-length

10590860	-0.864870202	2.443384819	-0.060733054	-6.28737327	-1.005998032	3.621912266	8.465370604		9030420J04Rik	RIKEN cDNA 9030	---	full-length
10591773	1.239993481	6.103303693	0.158689824	-5.740079088	1.002234508	3.331654332	9.406909534		Hmgn2	high mobility group	chromatin /// DNA b	full-length
10591781	1.866435709	2.332913984	0.054320821	-6.374120949	0.771347804	-4.573352898	5.06924241	Cluster III	Anln	anillin, actin binding	cytokinesis /// actin	full-length
10592067	1.144100049	0.986816435	-0.084938827	-6.304820975	0.706985295	-3.148222273	7.472838342		Fli1	Friend leukemia int	DNA binding /// trar	full-length
10592201	0.949853886	-0.309837415	-0.129334847	-6.174142216	1.168349401	1.223832557	5.093078598		Chek1	checkpoint kinase 1	DNA damage checl	full-length
10592515	1.07161533	2.833704008	-0.275143323	-5.028764409	1.189275012	3.524586088	6.086010422		Ubash3b	ubiquitin associatec	nucleus /// cytoplas	full-length
10592535	1.017370632	5.635823152	0.011872693	-6.386541775	1.321741263	8.233092608	6.17404018		Sorl1	sortilin-related rece	receptor activity /// l	full-length
10592734	1.153962071	3.426954201	0.317298224	-4.689205932	1.297221529	4.275219372	7.170514512		Cbl	Casitas B-lineage ly	signal transducer a	full-length
10593015	3.014608224	15.62493976	0.257166531	-5.011064887	3.054704404	15.41322081	6.740589291		Cd3g	CD3 antigen, gamn	receptor activity /// t	full-length
10593024	1.662642464	10.40307918	0.337998876	-3.531891228	1.631219098	9.747135514	6.406061801	Cluster I	Cd3e	CD3 antigen, epsilo	immunological syna	full-length
10593050	1.560310176	9.482709168	-0.019791665	-6.379780658	1.470962961	8.35189499	6.431904833		Il10ra	interleukin 10 recep	receptor activity /// r	full-length
10593123	1.11296738	-0.125857871	-0.046221357	-6.370347832	0.931744765	-1.902624577	7.076061326		Tagln	transgelin	cytoplasm /// cytosk	full-length
10593198	-1.00211678	0.276048855	-0.178470018	-5.973424221	-1.102954644	0.794434027	7.819183718		Fam55b	family with sequenc	---	full-length
10593219	0.666527554	-5.629420569	0.023533454	-6.389515081	1.319612949	-2.609377186	9.593443895		Nnmt	nicotinamide N-met	cytoplasm /// nicotir	full-length
10593332	-0.63607921	-0.513362526	-0.008947177	-6.389538422	-1.510326579	8.152316221	8.24546996	Cluster X	Bco2	beta-carotene oxyg	iron ion binding /// ir	full-length
10593776	1.333150064	-4.680644435	0.09516658	-6.376032097	2.872558823	0.156877688	6.80627797		Nrg4	neuregulin 4	extracellular region	full-length
10594251	2.073804861	3.679913011	0.291994411	-5.876923031	1.550656314	0.385059722	5.952961445		Kif23	kinesin family mem	nucleotide binding /	full-length
10594426	1.125948016	2.021160026	0.065956951	-6.324752013	0.96114853	0.136310047	4.701121671	Cluster III	Zwilch	Zwilch, kinetochore	kinetochore /// mole	full-length
10594540	1.524446666	10.5511892	-0.15063484	-5.572880243	1.771546028	11.92552771	7.107017195		Plekho2	pleckstrin homology	---	full-length
10594645	1.582848021	9.279665923	0.008206193	-6.389850625	1.602785643	8.996489915	8.323701767		Rab8b	RAB8B, member R	nucleotide binding /	full-length
10594774	1.466087193	5.663956329	-0.078514389	-6.281595826	0.734888916	-1.485122457	6.203055383	Cluster III	Ccnb2	cyclin B2	in utero embryonic	full-length
10594798	1.352648817	-0.825177368	1.4836631	0.564021425	0.707374995	-5.017369709	4.265582919		---	---	---	est
10595148	0.448038371	-4.191597849	-0.225160449	-5.491783568	1.122470639	2.646722838	10.34448914		Gsta1 /// Gsta2 /// E	glutathione S-transf	glutathione transfer	full-length
10595480	-0.732382103	-3.155815129	-0.0428403	-6.372819131	-1.343804567	1.390286124	11.19179137	Cluster X	Me1	malic enzyme 1, NA	catalytic activity /// r	full-length
10595633	1.826881323	10.77219643	0.154169072	-5.762541958	2.348422238	13.35501925	6.628729039		Bcl2a1a /// Bcl2a1b	B-cell leukemia/lym	B cell homeostasis	full-length
10597239	-0.5838209	-5.213036196	-0.067480123	-6.360318669	-1.101684094	-2.040243395	7.108688951		Pth1r	parathyroid hormor	skeletal developme	full-length
10597258	-0.238565645	-5.260245793	0.06337906	-6.231524825	-1.120080883	6.769709548	7.348380142		Tmie	transmembrane inn	sensory perception	full-length
10597279	0.875481751	-1.930433223	0.180340355	-6.062010866	1.035350108	-0.940104584	6.636806527		Ccrl2	chemokine (C-C mo	signal transducer a	full-length
10597461	1.273547417	9.427617421	0.103761688	-5.918210871	1.365242481	9.825119252	6.417640539		Cmtm7	CKLF-like MARVEL	cytokine activity /// (	full-length
10597592	-1.794214656	-3.534871712	-0.082467267	-6.381470342	-3.036118043	0.037979568	10.22115761		Acaa1b	acetyl-Coenzyme A	---	full-length
10597648	0.562269729	-1.734812423	0.098631588	-6.138261639	1.009189258	3.276376293	8.832675135	Cluster IV	Myd88	myeloid differentiati	response to molecu	full-length
10597743	1.146003705	-0.230650522	-0.136783048	-6.220858457	0.869636254	-2.683689674	6.298475147		Cx3cr1	chemokine (C-X3-C	signal transducer a	full-length
10598004	1.140055244	-1.658488077	0.337932586	-5.67929761	1.47575061	0.154090193	3.605482505	Cluster IV	Ccr1	chemokine (C-C mo	signal transducer a	full-length
10598013	1.9159098	10.11404502	-0.278271725	-4.841580237	1.941415595	9.842923739	7.409304466		Ccr5	chemokine (C-C mo	signal transducer a	full-length
10598057	-1.599678722	3.16099454	-0.27873557	-5.687349679	-1.077285705	-0.952417706	6.584171712		---	---	---	full-length
10598175	1.84724539	6.089206942	-0.009494922	-6.39068755	1.639207706	4.326945456	6.166346746		Ear2 /// Ear1 /// Ear	eosinophil-associat	nucleic acid binding	full-length
10598612	-0.755430343	1.492499399	-0.113009677	-6.008477602	-1.194278095	5.970543829	10.93510976	Cluster X	Otc	ornithine transcarba	urea cycle /// ornith	full-length
Affymetrix ID	**BS/Non Inf.**		**LS/Non Inf.**		**ReINF/Non Inf.**		**Average**	**Cluster**	**Gene**	**Gene**	**Gene Ontology (GC**	**Transcript**
Transcript Cluster	logFC	B	logFC	B	logFC	B	expression	Number	Symbol	Title	Description	Classification
10598863	-0.620642586	-5.107383221	0.003554391	-6.391708884	-1.010671297	-2.86101392	11.80786913		Rgn	regucalcin	calcium ion binding	full-length
10599120	1.941700448	10.24234074	0.15949635	-5.842908838	2.058497896	10.51298076	6.429167252		Dock11	dedicator of cytokin	guanyl-nucleotide e	full-length
10599487	1.140980011	7.301257995	0.042383631	-6.321039046	0.986487009	5.206794859	6.140603316		Sash3	SAM and SH3 dom	positive regulation (	full-length
10600122	-1.433929497	1.63614647	-0.442214999	-4.86095387	-0.825105621	-3.173530517	4.639575726		Xlr3b /// Xlr3a /// Xlr	X-linked lymphocyte	---	full-length
10600836	2.136234111	12.59448237	0.138642485	-5.881471936	2.332296741	13.23373327	9.421055792		Msn	moesin	uropod /// binding //	full-length
10600852	1.442165658	5.794775752	0.395830323	-3.939065263	1.539670331	6.110978795	5.544133758		---	---	---	full-length
10601011	1.346304961	3.363619533	-0.196105956	-5.872700832	0.923780892	-0.635525602	4.186452861		Kif4	kinesin family mem	nucleotide binding /	full-length
10601303	-0.442696009	-5.05645191	-0.319724382	-5.17330785	-1.130519668	0.869003	4.980927194		Chic1	cysteine-rich hydro	molecular_function	full-length
10601312	-0.407471925	-6.206780863	0.154067342	-6.23139807	-1.469494271	0.280799559	6.190381414		ENSMUSG0000007	predicted gene, EN	---	est
10601385	2.694283129	11.03530586	0.071150649	-6.324494055	2.806677906	11.10123819	7.145522504		Tlr13	toll-like receptor 13	receptor activity /// t	full-length
10601421	1.799506357	5.993778379	0.018485336	-6.387458198	1.849144787	5.874800985	5.263667464		A630033H20Rik	RIKEN cDNA A630	signal transducer a	full-length
10601581	0.802288959	3.558902322	1.051126547	6.486161121	1.096507068	6.61792581	7.464083813		EG245575	predicted gene, EG	---	est
10601705	1.086159009	2.742681497	0.205352506	-5.629835031	0.719584968	-1.407555969	4.282998783		Cenpi	centromere protein	chromosome, centr	full-length
10601878	-0.709635844	-2.549617074	-0.353856984	-4.911205941	-1.076736512	0.475026556	4.664689074		Tceal1	transcription elonga	translation elongati	full-length
10602372	-1.90465327	3.104168308	-0.055860154	-6.370963753	-2.861078779	7.215786728	9.087483377		Alas2	aminolevulinic acid	catalytic activity /// 5	full-length
10602739	1.268880384	8.739230733	-0.00244091	-6.391547131	1.340352794	8.955886174	7.546610259		Acot9	acyl-CoA thioestera	carboxylesterase a	full-length
10602840	1.415497323	8.07369547	-0.296345381	-4.223525112	1.48752649	8.224603928	6.538639347		Sh3kbp1	SH3-domain kinase	protein binding /// cy	full-length

10603023	1.057906314	1.700075709	0.061298604	-6.330275379	1.227667931	2.814427958	6.284787024		---	---	---	est
10603051	2.10574055	7.274987604	0.150832869	-6.133690305	2.003895529	6.270591571	5.839276754		Ap1s2	adaptor-related pro	protein binding /// G	full-length
10603182	-0.626070906	-2.979360399	-0.189427885	-5.875210866	-1.005667151	0.398140376	5.556964725		Arhgap6	Rho GTPase activa	GTPase activator a	full-length
10603346	1.640935018	6.844658767	0.034848028	-6.370337649	1.662839771	6.566217795	7.047096878		Plp2	proteolipid protein 2	membrane /// integr	full-length
10603469	1.75129656	1.447138507	0.049058673	-6.378086038	2.027444229	2.522249632	10.09729143		Rbm3	RNA binding motif	nucleotide binding /	full-length
10603549	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		100043821 /// 1000	predicted gene, 10	---	est
10603551	2.348410859	15.4206588	0.313929435	-3.503557037	2.644555768	16.43050597	9.96949981		Cybb	cytochrome b-245,	ion channel activity	full-length
10603803	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10603860	1.572862994	9.656322094	0.201149425	-5.24243163	1.463783018	8.372273592	9.327615765	Cluster I	Cfp	complement factor	extracellular region	full-length
10604393	1.606692364	5.730692578	-0.152180488	-6.049258987	1.642357438	5.551785659	5.86890507		ENSMUSG000000	predicted gene, EN	---	full-length
10604713	1.241563186	3.506204625	-0.035081777	-6.370930816	1.050292755	1.398835748	5.87872755		Arhgef6	Rac/Cdc42 guanine	molecular_function	full-length
10604763	1.348731927	8.787998136	0.036211512	-6.34407391	1.307431851	7.988151547	9.612194625		Arpc1b	actin related protei	actin binding /// cyt	full-length
10604922	0.385023417	-3.821399984	-0.089895268	-6.155659675	1.005127728	3.83829998	9.092456637		BC023829	cDNA sequence B	---	full-length
10604996	-1.590028689	1.215820492	-0.501952069	-4.914214493	-0.913800389	-3.443114576	4.93450208		Xlr3a /// Xlr3b /// Xl	X-linked lymphocyt	---	full-length
10605007	-1.351500699	0.938373702	-0.545731625	-4.234562836	-0.74137891	-3.871771558	4.788588524		Xlr3b /// Xlr3a /// Xl	X-linked lymphocyt	---	full-length
10605256	1.967516635	10.18583129	-0.298403805	-4.700466366	2.116546905	10.63107294	8.841183335		Flna	filamin, alpha	actin binding /// pro	full-length
10605338	2.151634022	11.68565898	-0.00315093	-6.391558935	2.091145993	10.92398439	8.250294662	Cluster I	G6pdx	glucose-6-phospha	cytokine production	full-length
10605392	-0.9406814	-1.447558895	0.168971364	-6.105996026	-1.231568053	0.507698279	7.95645788	Cluster X	F8	coagulation factor	copper ion binding	full-length
10605465	0.766916155	1.073383087	-0.048400134	-6.327675598	1.092092932	4.312824434	7.419095524		Prkx	protein kinase, X-li	nucleotide binding /	full-length
10605711	1.358617225	4.318155759	-0.221156598	-5.632267613	1.522300563	5.155943257	5.349618038		Pdk3	pyruvate dehydrog	two-component ser	full-length
10606016	3.007203022	15.68104904	-0.048056134	-6.337447836	3.151624743	15.86242894	8.451119842	Cluster VI	Il2rg	interleukin 2 recept	receptor activity ///	full-length
10606058	1.829297628	10.41515309	0.00704491	-6.390494702	1.82537758	9.961725969	6.904253681		Cxcr3	chemokine (C-X-C	signal transducer a	full-length
10606389	1.29246205	-1.715605831	0.325276788	-5.877856046	1.070140116	-3.291557057	6.547321226		Gm379	gene model 379, (	---	predicted
10606609	1.094145054	-2.640633085	-0.271722069	-6.001873049	0.542342422	-5.954910103	5.147382982		Tspan6	tetraspanin 6	membrane /// integr	full-length
10606694	1.353600518	7.960271777	-0.135923326	-5.834549067	1.406457587	7.976947413	5.619798995		Btk	Bruton agammaglo	nucleotide binding /	full-length
10606714	0.870023297	1.879252839	0.139390648	-5.919537435	1.04836931	3.401492535	7.600325744		Gla	galactosidase, alph	catalytic activity ///	full-length
10607429	-0.488662795	-6.097090524	-0.825587163	-3.532697959	-1.076411999	-3.117384936	6.217143022		LOC280487	pol polyprotein	---	partial
10607865	2.261002621	10.69651563	0.099544895	-6.216558988	2.110968857	9.449428899	10.05651212		Tmsb4x	thymosin, beta 4, X	actin binding /// pro	full-length
10607868	1.467902197	8.79670545	0.305383041	-4.012898471	1.142536438	5.459812405	5.577972487		Tlr8	toll-like receptor 8	receptor activity ///	full-length
10607870	1.249120355	5.951246017	0.265667492	-4.770377685	1.397622577	6.810227315	5.68741911	Cluster IV	Tlr7	toll-like receptor 7	single-stranded RN	full-length