

Supplementary Material

Targeting macrophage circadian rhythms with microcurrent stimulation to activate cancer immunity through phagocytic defense

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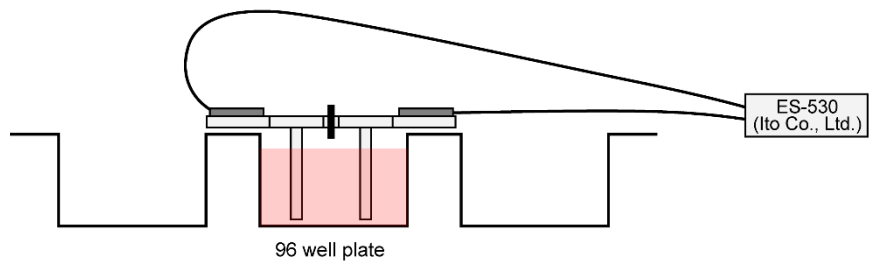
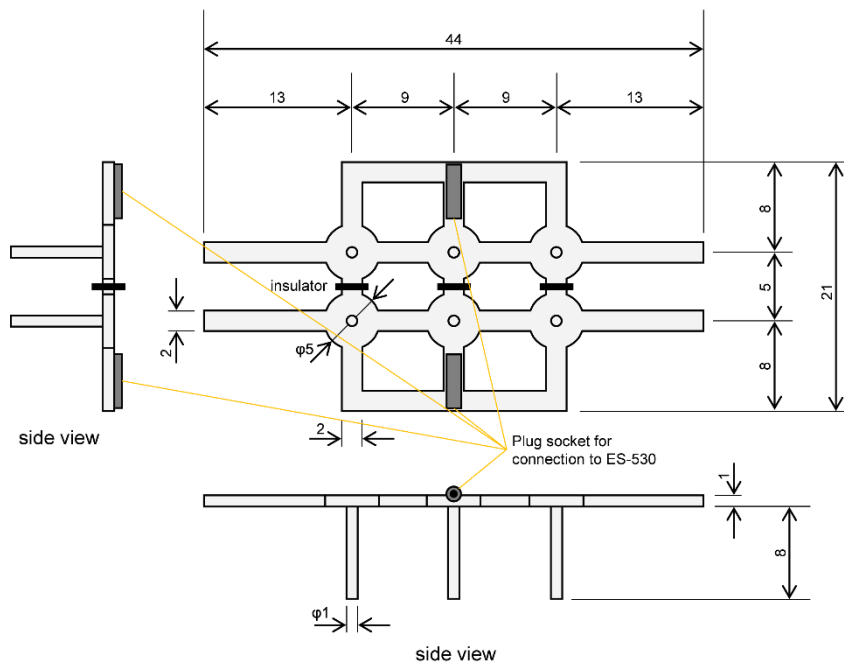


Figure S1. Design of platinum electrodes used for microcurrent stimulation (MCS) in RAW264.7 and PMA-treated THP-1 cells.

All parts were fabricated with platinum except for the insulator part. Platinum with a purity of at least 99.95% was used in the fabrication of the electrodes. MCS: microcurrent stimulation.

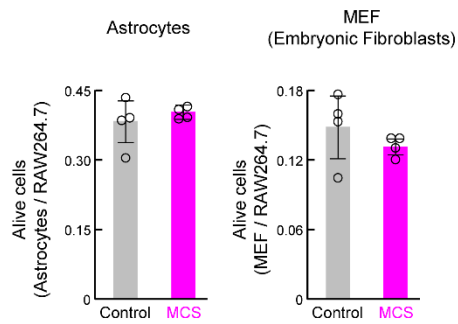


Figure S2. The number of living mouse embryonic fibroblasts (MEF) and mouse astrocytes after co-cultured with RAW264.7 cells. The number of living cells was determined immediately after the addition of MEF and astrocytes 12 h after microcurrent stimulation (MCS) for RAW264.7 cells, and co-incubated for another 3 h. Data are presented as the mean \pm S.D. (n = 4).

Term (GO molecular function)	%	P-Value
protein binding	26.2	<0.01
identical protein binding	11.6	<0.01
RNA polymerase II core promoter proximal region sequence-specific DNA binding	5.9	0.043
calcium ion binding	4.3	0.011
transcription factor activity, sequence-specific DNA binding	3.9	0.014
transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	3.6	<0.01
receptor binding	3.5	<0.01
sequence-specific DNA binding	3.1	0.014
peptidase activity	3	0.043
actin binding	2.6	0.019
transmembrane signaling receptor activity	1.9	<0.01
serine-type endopeptidase activity	1.8	<0.01
microtubule binding	1.8	0.037
transcription regulatory region sequence-specific DNA binding	1.8	0.044
cytokine activity	1.7	0.026
extracellular matrix structural constituent	1.5	<0.01
integrin binding	1.5	<0.01
serine-type peptidase activity	1.5	<0.01
heme binding	1.5	0.021
lyase activity	1.4	0.014
G-protein coupled receptor binding	1.2	<0.01
protein tyrosine kinase activity	1.1	0.045
collagen binding	1	<0.01
transmembrane receptor protein tyrosine kinase activity	0.8	0.011
cadherin binding	0.8	0.044
oxygen binding	0.6	<0.01
extracellular matrix structural constituent conferring tensile strength	0.6	0.023
ionotropic glutamate receptor binding	0.6	0.034
alpha-tubulin binding	0.6	0.034
microtubule motor activity	0.6	0.042
RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding	0.6	0.042
haptoglobin binding	0.5	<0.01
oxygen transporter activity	0.5	<0.01
hydro-lyase activity	0.5	<0.01
tumor necrosis factor receptor binding	0.5	0.034
calcium-activated potassium channel activity	0.4	<0.01
platelet-derived growth factor binding	0.4	<0.01
organic acid binding	0.4	0.01
carbonate dehydratase activity	0.4	0.022
inward rectifier potassium channel activity	0.4	0.049
hemoglobin beta binding	0.3	0.012
kinetochore binding	0.3	0.018
hemoglobin alpha binding	0.3	0.032
hyaluronoglucosaminidase activity	0.3	0.04
hemoglobin binding	0.3	0.049

Figure S3. Gene Ontology analysis of genes exhibiting MCS-dependent expression variation, based on RNA-seq results obtained from RNA extracted from intraperitoneal macrophages collected 12 h post-MCS.

All terms with $P < 0.05$ are shown. The hierarchy of parent-child terms targeting the top 25 match rates is shown in **Figure 2D**. The analysis includes genes with a Control-to-MCS ratio > 2 . The gene list is provided in **Table S1**.

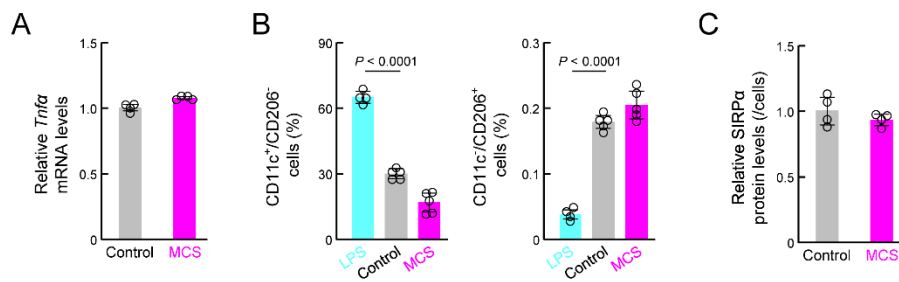


Figure S4. Influence of microcurrent stimulation (MCS) on cytokine, M1/M2 differentiation, and SIRP α expression.

(A) mRNA expression levels of *Tnfa* in control and MCS-treated RAW264.7 cells. (B) Left: variation in the ratio of CD11c⁺ CD206⁻ RAW264.7 cells among all cells. Right: Variation in the ratio of CD11c⁻ CD206⁺ RAW264.7 cells among all cells. (C) SIRP α expression of RAW264.7 per cell assessed using flow cytometry. The control value is normalized to 1.0. All values were measured 12 h after MCS. Data are expressed as the mean \pm S.D. (n = 4).

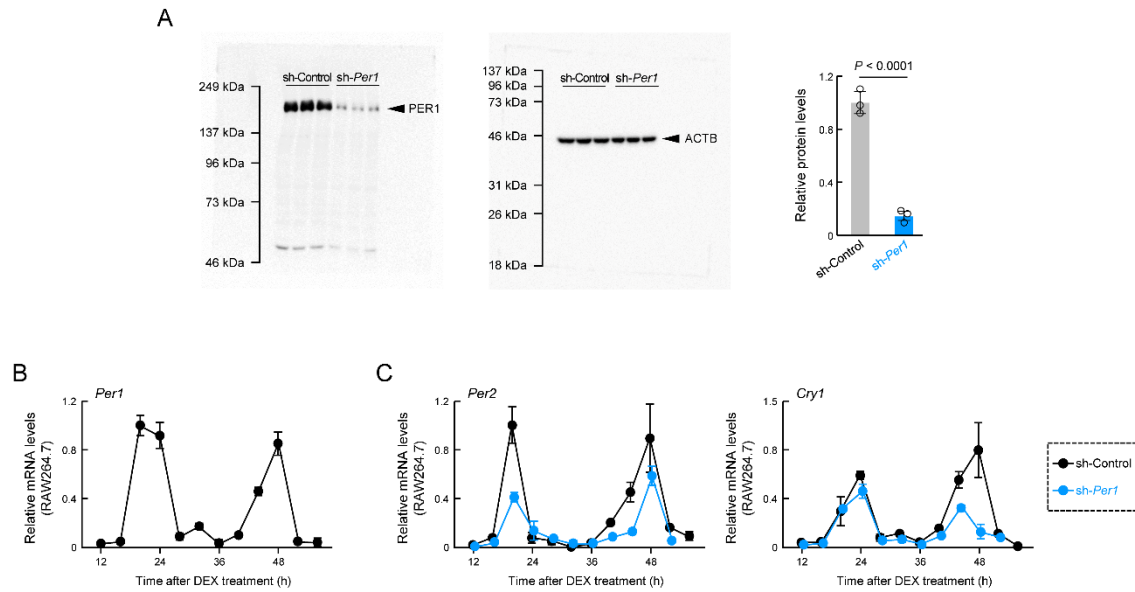


Figure S5. Effect of dexamethasone and sh-Per1 on the circadian rhythm of clock genes expression in RAW264.7.

(A) Protein expression of PER1 and ACTB in RAW264.7 transduced sh-Control or sh-Per1 lentivirus used in **Figures 3G, 4D, and S14E**. Left panels indicate uncropped western blot images. (B) Temporal expression profiles of *Per1* mRNA in RAW264.7 cells following synchronization of the circadian clock. Cells were treated with 100 nM dexamethasone for 2 h to synchronize the circadian clock, and the mRNA levels of *Per1* were assessed at the indicated time points. A significant time-dependent variation in the mRNA levels of *Per1* ($P < 0.05$; one-way ANOVA) was observed. (C) Temporal expression profiles of *Per2* and *Cry1* mRNA in RAW264.7 cells with sh-Control and sh-Per1 following synchronization of the circadian clock. Cells were treated with 100 nM dexamethasone for 2 h to synchronize the circadian clock, and the mRNA levels of *Per2* and *Cry1* were assessed at the indicated time points. A significant time-dependent variation in the mRNA levels of *Per2* and *Cry1* ($P < 0.05$; one-way ANOVA) was observed. Data are expressed as the mean with S.D. ($n = 4$). sh-Per1, *Per1* small hairpin RNA.

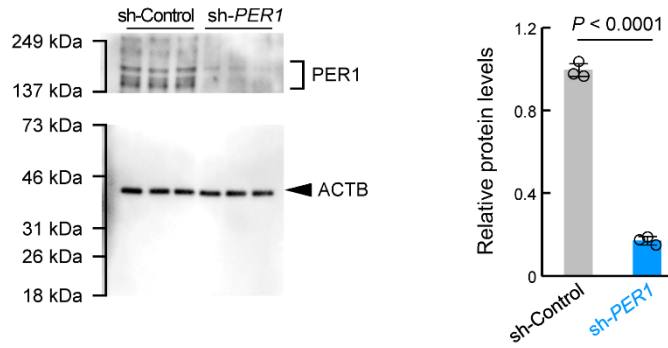


Figure S6. Effect of sh-*PER1* on THP-1.

Protein expression of PER1 and ACTB in THP-1 transduced sh-Control or sh-*PER1* lentivirus used in **Figure 3H**. Left panels indicate uncropped western blot images. sh-*PER1*, *PER1* small hairpin RNA.

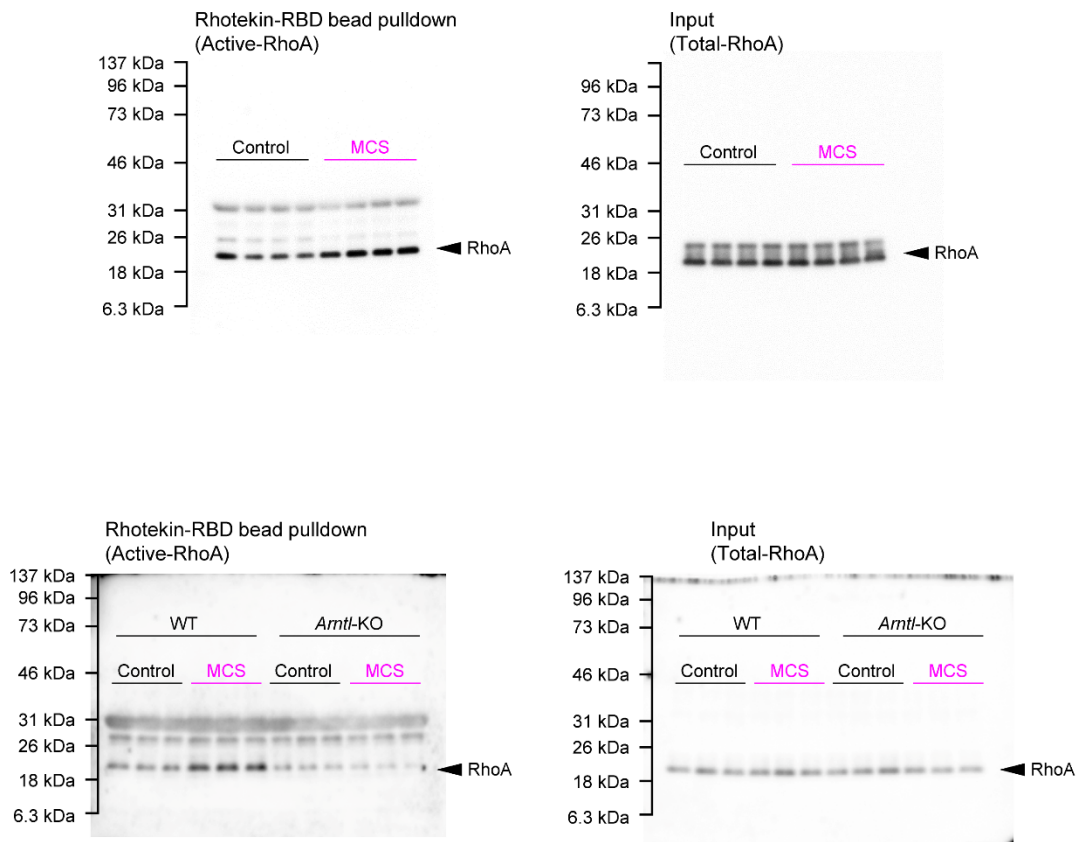


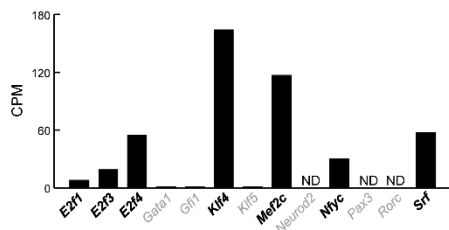
Figure S7. Uncropped western blot images using Figure 5.

A

ChIP-Atlas, $P < 0.01$ and Fold Enrichment > 4

ID	Antigen	Log P-value	Log Q-value	Fold Enrichment
SRX1532691	E2f4	-11.8	-7.8	6.58
SRX1532694	E2f4	-10.6	-6.7	6.47
SRX1532692	E2f4	-10.2	-6.5	6.16
SRX122394	E2f4	-14.3	-9.9	11.45
SRX122397	E2f4	-7.8	-4.3	7.72
SRX344966	Epitope tags	-4.5	-1.4	4.18
SRX1120754	E2f3	-4.1	-1.1	4.49
SRX122396	E2f4	-4	-1	6.67
SRX118005	Gata1	-3.1	-0.4	4.75
SRX1120752	E2f1	-2.8	-0.3	4.93
SRX8713937	Klf4	-2.5	-0.1	4.31
SRX1547317	Srf	-2.5	-0.1	4.15
SRX495627	Rorc	-3	-0.4	6.84
SRX1035395	Gfi1	-2.8	-0.3	6.12
SRX13554160	Mef2c	-2.6	-0.1	5.43
SRX1979970	Neurod2	-2.6	-0.1	5.36
SRX10157960	Klf5	-2.4	-0.1	4.96
SRX5358289	Pax3	-2.3	-0.1	4.47
SRX22006953	Nfyc	-2.2	-0.1	4.34

B



C

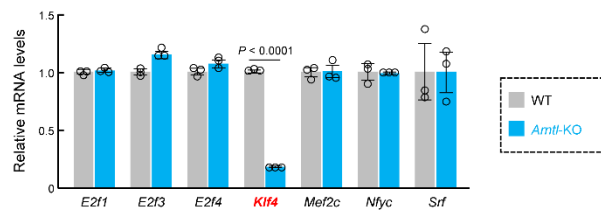


Figure S8. Screening for a transcription factor (TF) that mediates the effects of MCS on genes whose expression levels are time dependent.

(A) ChIP-Atlas enrichment analysis using genes whose expression differed between ZT2 and ZT14 in control mice and increased by MCS in ZT14. The threshold values were set at $P < 0.01$ and Fold Enrichment > 4 . Gene lists are shown in **Table S4**. (B) Comparison of mRNA expression levels of candidate transcription factors in mouse peritoneal macrophages using RNA-seq results. Genes with CPM values < 1 are shown in gray; these were excluded from the candidate transcription factors. (C) Expression levels of candidate transcription factors in wild-type and *Arntl*-KO RAW264.7 cells. For panel C, data are expressed as the mean \pm S.D. ($n = 3$). Statistical significance was determined using two-tailed Student's *t*-tests. *P*-values are shown in each graph. MCS: microcurrent stimulation; S.D.: standard deviation; MCS: microcurrent stimulation.

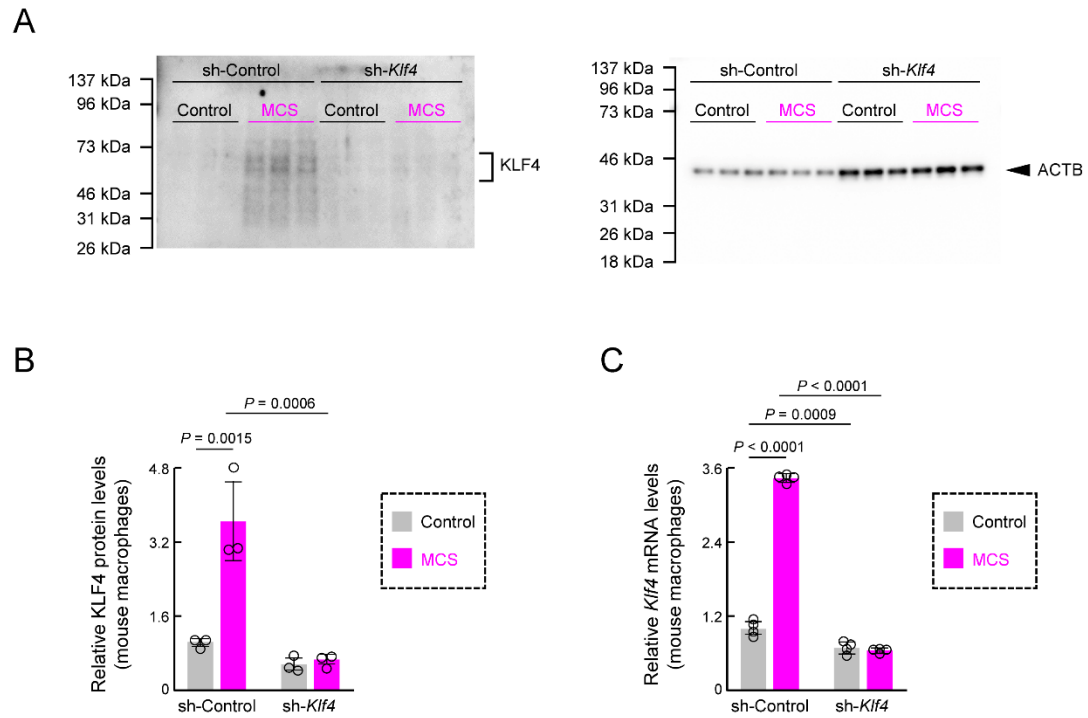


Figure S9. Effect of sh-*Klf4* and MCS on mouse peritoneal macrophages.

(A-C) Protein expression of KLF4 and ACTB (A,B) and mRNA expression of *Klf4* (C) in MCS-treated cultured mouse peritoneal macrophages transduced sh-Control or sh-*Klf4* lentivirus used in **Figure 5I-K**. All values were measured 12 h following MCS. Panel A shows uncropped western blot images. Data are expressed as the mean \pm S.D. ($n = 3-4$). Statistical significance was determined using two-way ANOVA with Tukey–Kramer post-hoc tests. P -values are shown in each graph. ANOVA: analysis of variance; sh-*Klf4*, *Klf4* small hairpin RNA; MCS: microcurrent stimulation.

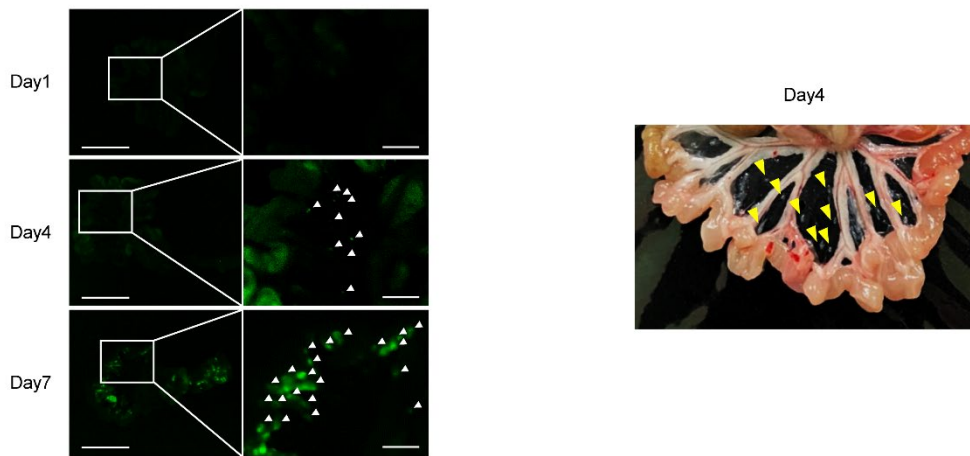


Figure S10. Tumor growth following intraperitoneal implantation of 4T1.

Female BALB/c mice were injected i.p. 5.0×10^5 GFP-expressing 4T1 cells/500 μ L PBS/mouse. The left panel shows GFP fluorescence around the small intestine at 1, 4, and 7 days after transplantation; weak GFP fluorescence from the nodular tumor was observed from day 4. The right panel shows brightfield images of the small intestine and periportal area on day 4. Arrows indicate nodular tumors. GFP: green fluorescent protein; i.p.: intraperitoneal; PBS: phosphate-buffered saline.

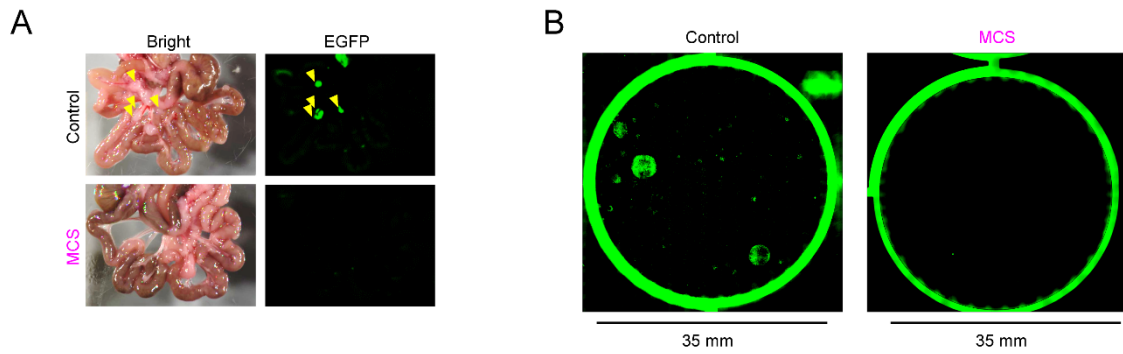


Figure S11. Effect of microcurrent stimulation on the metastatic potential of 4T1 cells.

(A) Photographic and GFP-fluorescence images of the removed small intestine prepared from control and MCS-treated mice injected with 4T1 via the tail vein. Yellow arrows indicate nodular tumors formed around the portal vein. The comparison of the quantified GFP-positive area is shown in **Figure 8M**. (B) GFP-fluorescence image of metastatic colonies isolated from tumor-bearing mice femora bone marrow. Cells were cultured in a 35 mm dish with 60 μM of 6-thioguanine. Two weeks after culture, colonies derived from metastatic 4T1 cells were stained using Cell Counting Kit-8 for quantification. The comparison of the quantified colonies area is shown in **Figure 8O**. GFP: green fluorescent protein; MCS: microcurrent stimulation.

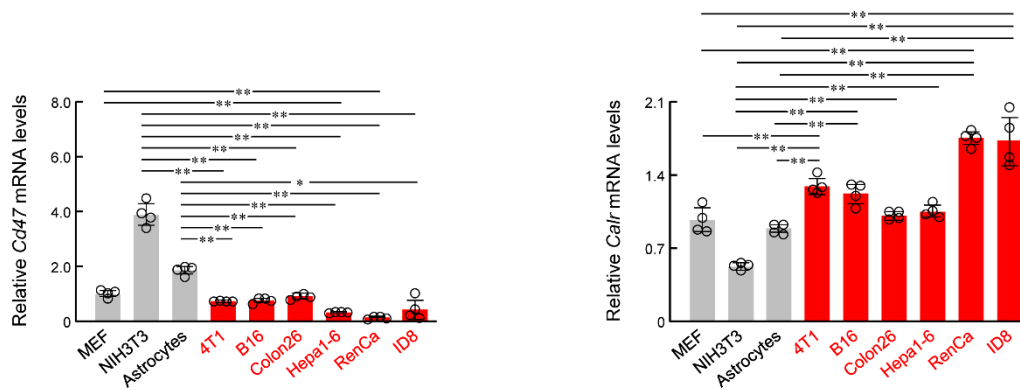


Figure S12. Expression of eat-me and don't-eat-me signaling receptors in cancer cells.

mRNA expression of *Cd47* and *Calr* in tumor-derived (4T1, B16, Hepa1-6, Colon26, RenCa, ID8) and non-tumor-derived (MEF, NIH3T3, Astrocyte) cancer cell lines in mice. Data are shown as the mean \pm S.D. (n = 4). The value of 4T1 is set at 1.0. ** $P < 0.01$, * $P < 0.05$; significant difference from each group (one-way ANOVA with Tukey–Kramer post-hoc test). ANOVA: analysis of variance; MEFs: mouse embryonic fibroblasts; S.D.: standard deviation.

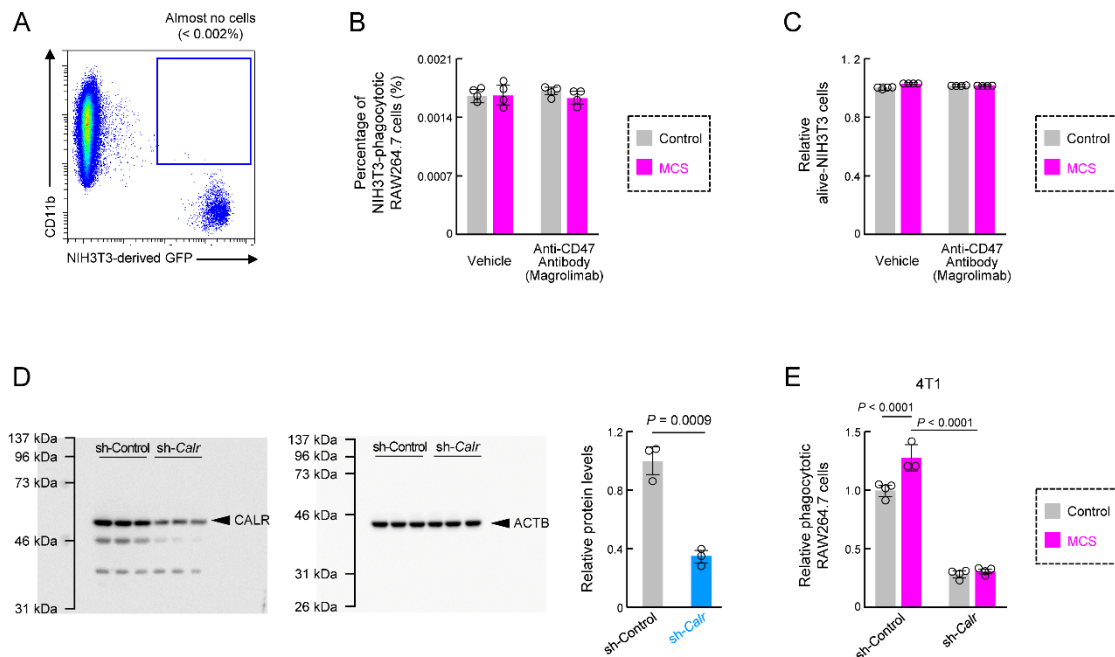


Figure S13. Effect of sh-*Calr* transduction into 4T1 on the activation of RAW264.7 phagocytosis by MCS.

(A) Representative flow cytometry panel of RAW264.7 cells and NIH3T3 cells co-cultured for 3 h. The CD11b⁺ cell population in the upper left is RAW264.7 cells, and the GFP⁺ cell population in the lower right is NIH3T3 cells. There were negligible CD11b⁺/GFP⁺ cells, which are macrophages that have engulfed NIH3T3 cells (<0.002%). (B,C) Effects of CD47 inhibitor (magrolimab; 10 µg/mL) exposure of the phagocytic activity (B) and number of surviving NIH3T3 cells (C) measured using NIH3T3 cells of RAW264.7 cells under MCS. Magrolimab was added 11 h and 30 m post-MCS, and 30 m later of the addition of magrolimab, NIH3T3 cells was added. The phagocytic activity and number of surviving NIH3T3 cells were measured immediately 3 h after the addition of NIH3T3 cells. The percentage of RAW264.7 cells that showed phagocytic activity was 0.002% or less in all groups, and neither magrolimab nor MCS affected. (D) Protein expression of CALR and ACTB in GFP-4T1 cells transduced sh-Control or sh- *Calr* lentivirus. Left panels indicate uncropped western blot images. (E) Relative number of RAW264.7 cells phagocytosing sh-Control or sh-*Calr* transduced GFP-4T1 cells. The phagocytic activity was measured immediately after the addition of each cancer cell 12 h after MCS and co-incubated for another 3 h. Data are expressed as the mean ± S.D (n = 3-5). Statistical significance was determined two-tailed Student's *t*-tests (D) and two-way ANOVA with Tukey–Kramer post-hoc tests (B,C, and E). *P*-values are shown in each graph. ANOVA: analysis of variance; sh-*Calr*, *Calr* small hairpin RNA.

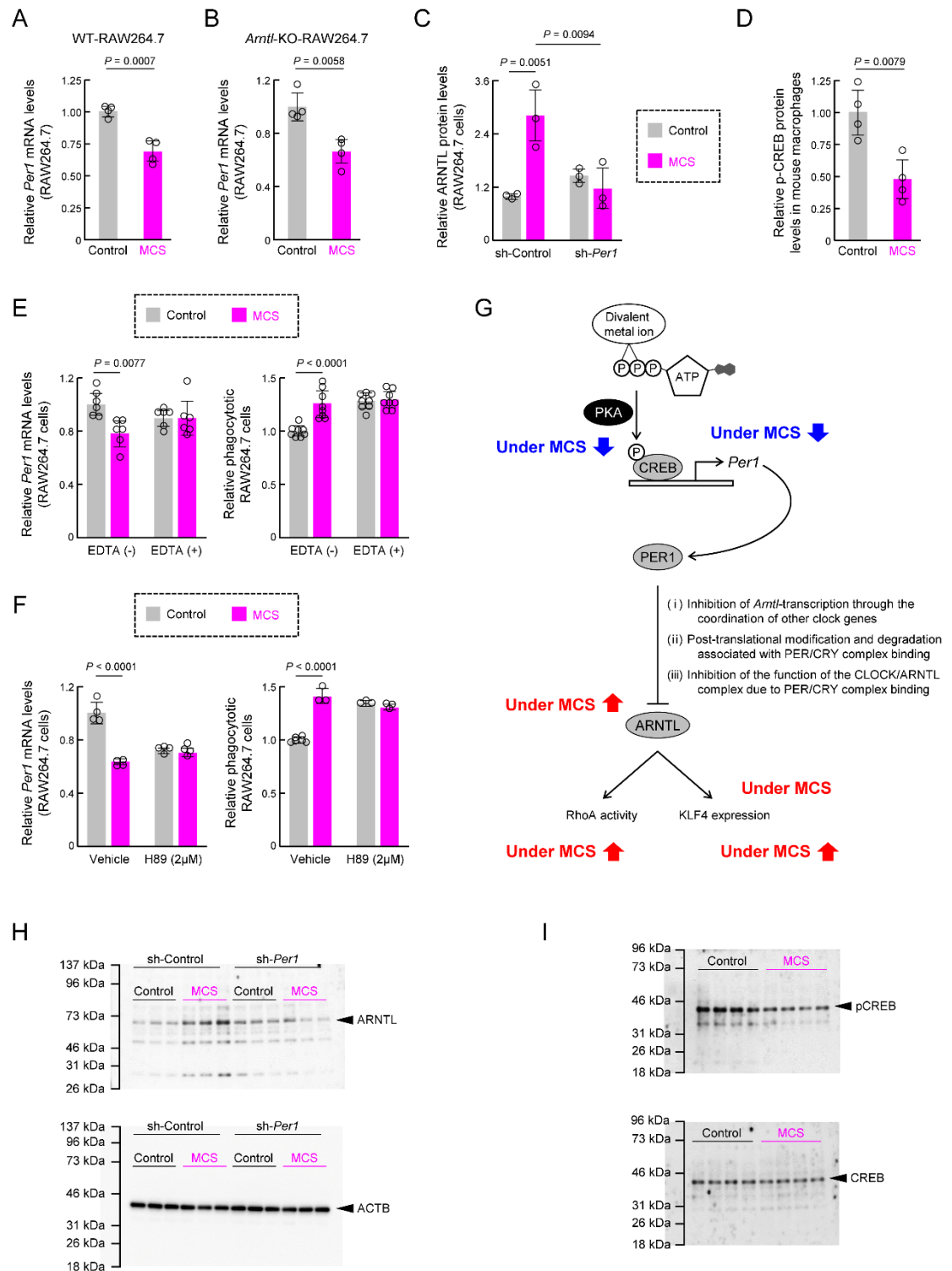


Figure S14. Mechanism underlying *Per1* downregulation by microcurrent stimulation.

(A,B) Effect of MCS on the expression level of *Per1* mRNA in WT (A) and *Arntl*-KO (B) RAW264.7 cells. *Per1* mRNA was measured 15 m post-MCS. MCS decreased *Per1* expression in both cell lines. (C) Protein expression of ARNTL in RAW264.7 cells transduced sh-Control or sh-*Per1* lentivirus. The

protein levels were measured 12 h after MCS. **(D)** The expression levels of p-CREB protein in intraperitoneal macrophages from Control or MCS-treated female BALB/c mice. Macrophages were collected 15 m post-MCS. **(E)** Effects of PKA inhibitor (H89; 2 μ M) exposure on the expression of *Per1* mRNA (left) and phagocytic activity measured using opsonized bead (right) of RAW264.7 cells under MCS. H89 was added to the medium 30 m before MCS. *Per1* mRNA was measured 15 m post-MCS. Beads were added 12 h post-MCS and co-incubated for another 3 h. The phagocytic activity was measured immediately after the addition of beads. **(F)** Effects of EDTA (1mM) exposure on the expression of *Per1* mRNA (left) and phagocytic activity measured using opsonized bead (right) of RAW264.7 cells under MCS. EDTA was added to the medium 30 m before the start of MCS. *Per1* mRNA was measured 15 m post-MCS. Beads were added 12 h post-MCS and co-incubated for another 3 h. The phagocytic activity was measured immediately after the addition of beads. **(G)** The pathway by which MCS acts on the ARNTL protein via *Per1*. **(H,I)** Uncropped western blot images using panel C (H) and D (I). Data are expressed as the mean \pm S.D (n =3-6). Statistical significance was determined using two-way ANOVA with Tukey–Kramer post-hoc tests. P-CREB: phospho-CREB; sh-*Per1*, *Per1* small hairpin; MCS: microcurrent stimulation; PKA: protein kinase A; EDTA: ethylenediaminetetraacetic acid; WT: Wild-type.

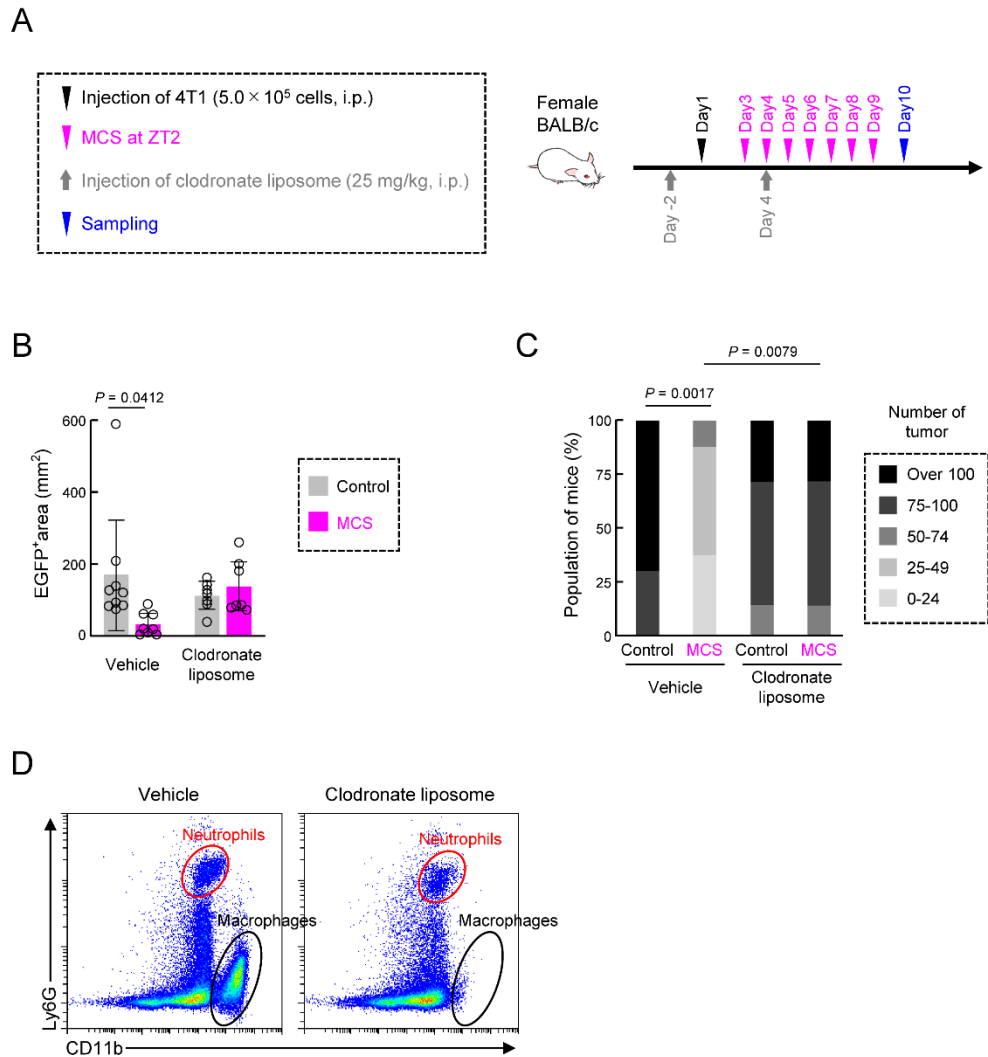


Figure S15. Effect of macrophage depletion on the antitumor effect of microcurrent stimulation.

(A) Protocol of macrophage removal by clodronate liposome, MCS treatment, and 4T1 cell injection. (B) The 4T1-derived GFP-positive area around the portal vein. (C) The number of nodular tumors formed in the abdominal cavity. Each mouse was ranked based on tumor count; the percentage of mice in each rank is presented for each group. (D) Representative flow cytometry images of CD11b and Ly6G expression in mice administered and not administered clodronate liposomes. CD11b is expressed in macrophages and neutrophils, whereas Ly6G is expressed only in neutrophils. The population of CD11b-positive, Ly6G-negative cells, including macrophages, disappeared as a result of the addition of clodronate liposomes; however, the population of CD11b-positive, Ly6G-positive cells, which are neutrophils, did not disappear. Data are expressed as mean \pm S.D. ($n = 4-10$). Statistical significance was determined using two-way ANOVA with Tukey–Kramer post-hoc tests. P -values are shown in each graph. ANOVA: analysis of variance; GFP: green fluorescent protein; MCS: microcurrent stimulation; S.D.: standard deviation.

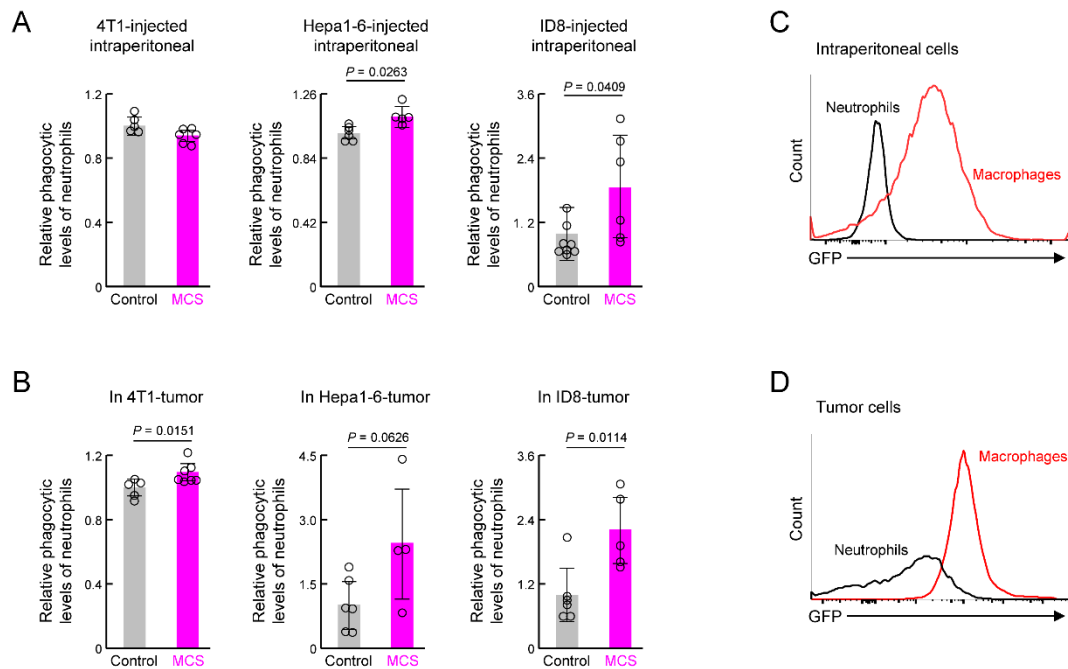
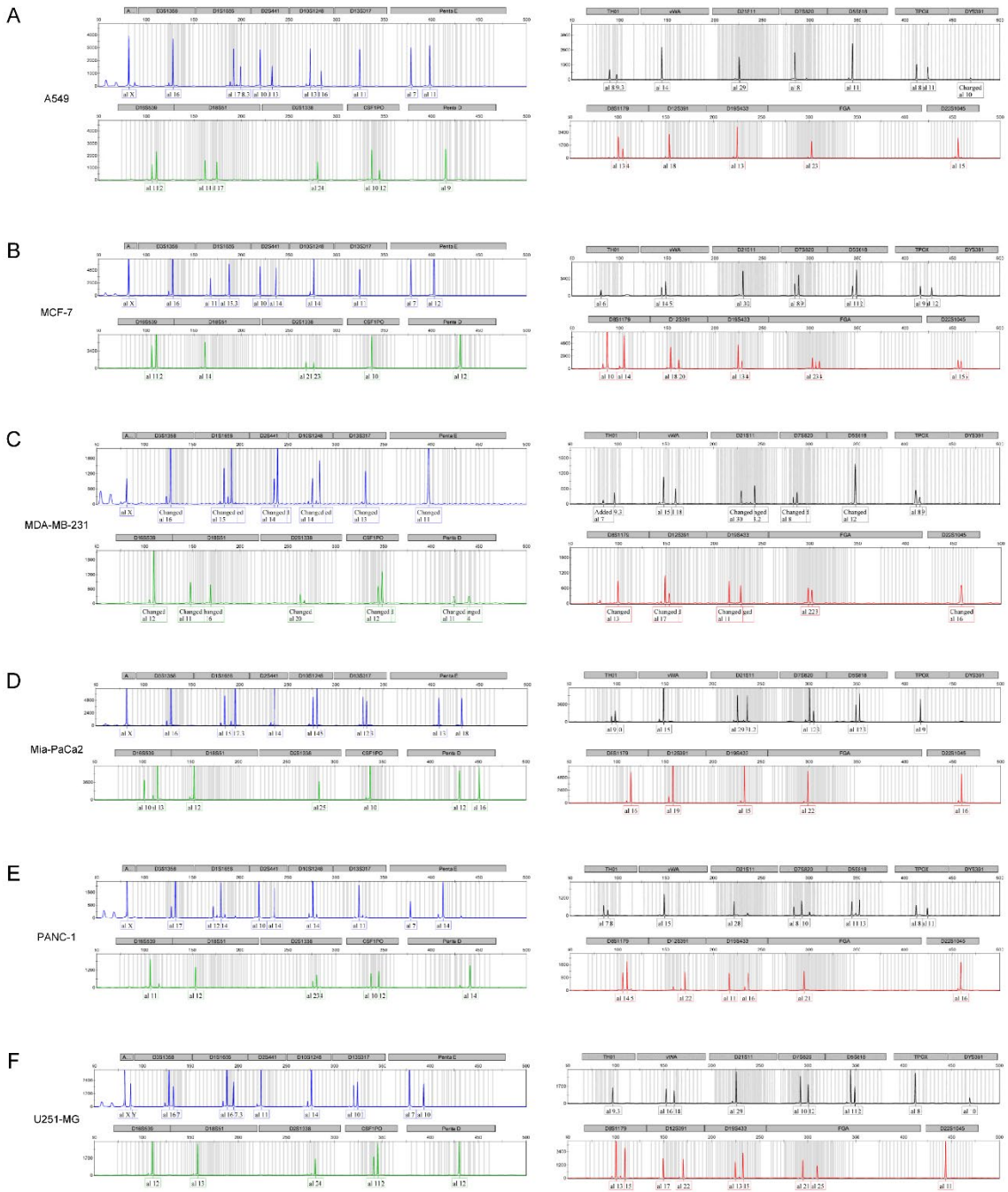
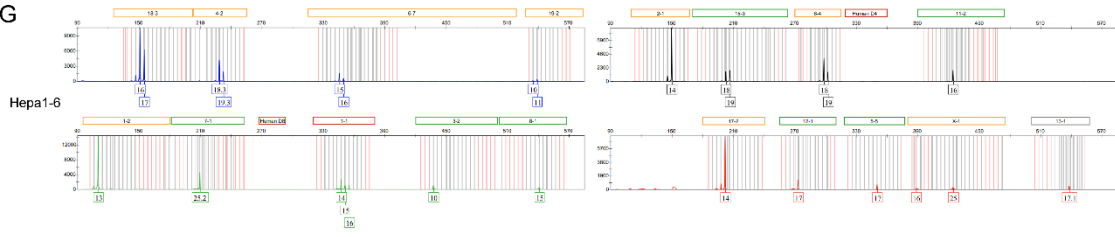


Figure S16. Phagocytic activity of neutrophils in mice transplanted with cancer cells.

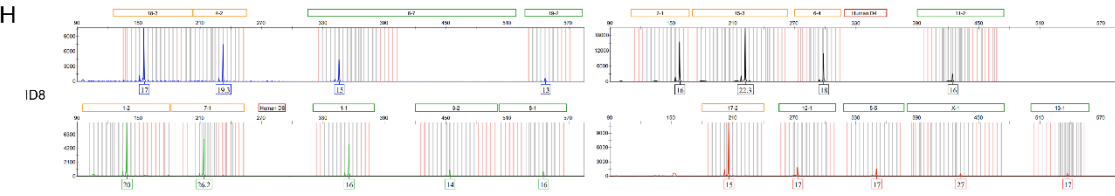
(A) The number of GFP-positive neutrophils derived from cancer cells in the abdominal cavity of mice transplanted with 4T, Hepa1-6, and ID8. The schedule for the transplantation of cancer cells and MCS for each mouse is shown in **Figures 6A and 7A,I**. (B) The number of GFP-positive neutrophils derived from cancer cells in the tumor of mice transplanted with 4T, Hepa1-6, and ID8. The schedule for the transplantation of cancer cells and MCS for each mouse is shown in **Figures 6G and 7D,L**. (C,D) Comparison of GFP fluorescence intensity derived from 4T1 in macrophages and neutrophils prepared from the abdominal cavity and tumors of MCS-treated mice transplanted with 4T1. Data are expressed as the mean \pm S.D. ($n = 4-10$). Statistical significance was determined using two-tailed Student's *t*-tests. *P*-values are shown in each graph. ANOVA: analysis of variance; GFP: green fluorescent protein; MCS: microcurrent stimulation; S.D.: standard deviation.



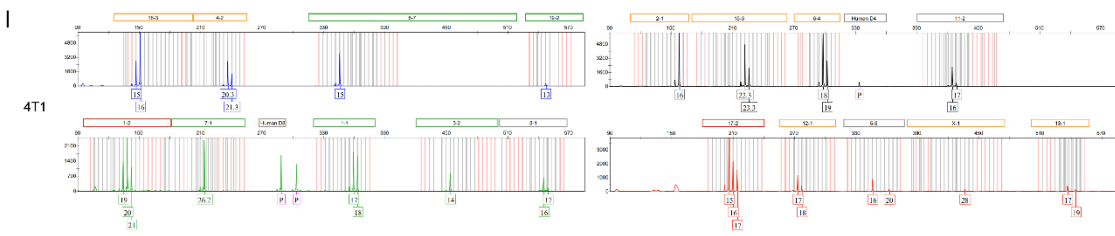
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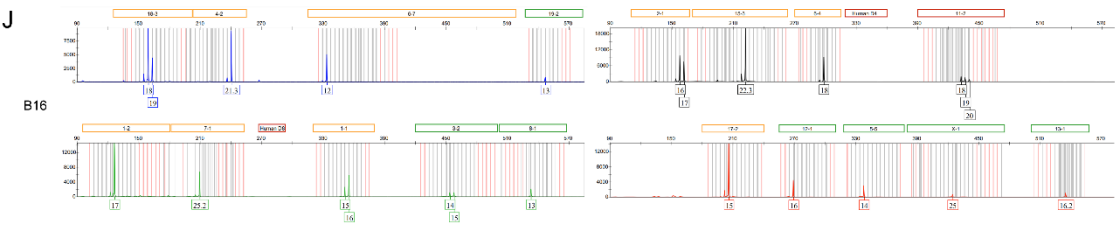
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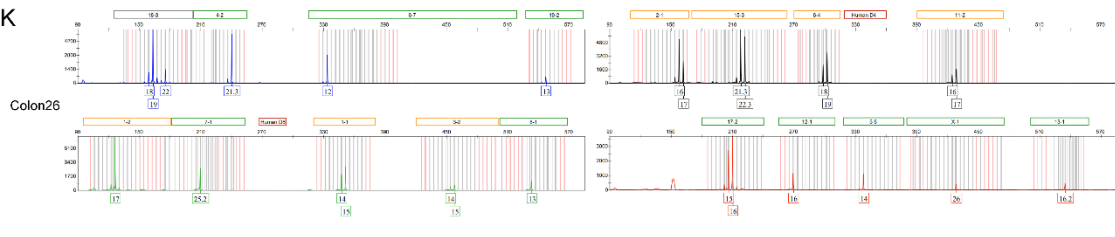
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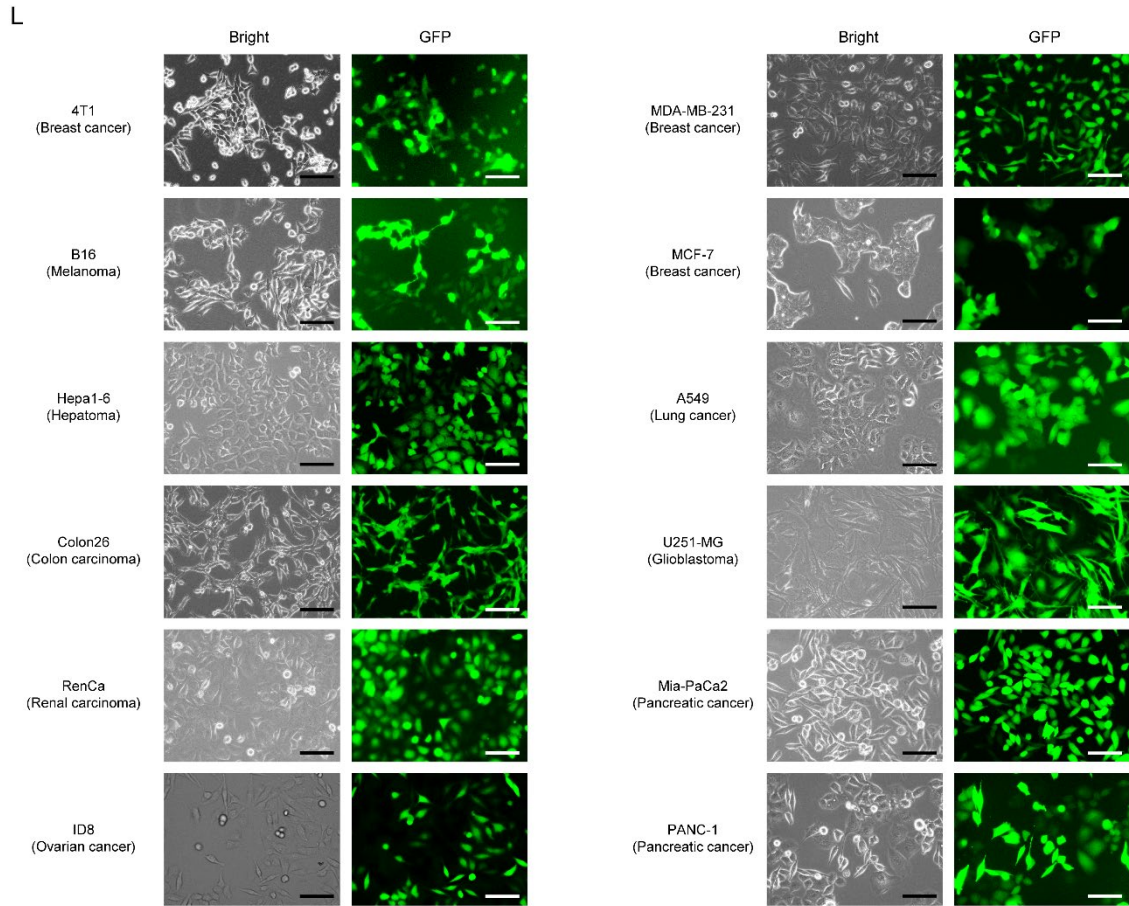


Figure S17. Status of GFP-positive cancer cell lines.

Results of STR analysis of GFP-positive A549 (A), MCF-7 (B), MDA-MB-231 (C), Mia-PaCa2 (D), PANC-1 (E), U251-MG (F), Hepa1-6 (G), ID8 (H), B16 (I), 4T1 (J), and Colon26 (K). STR of all GFP-positive cell lines matched the ATCC and JCRB database. (L) Fluorescence and corresponding bright-field microscope photos of all GFP-expressing cancer cell lines. Scale bar: 50 µm. GFP: green fluorescent protein; STR: The short tandem repeat; JCRB: Japanese Collection of Research Bioresources Cell Bank.

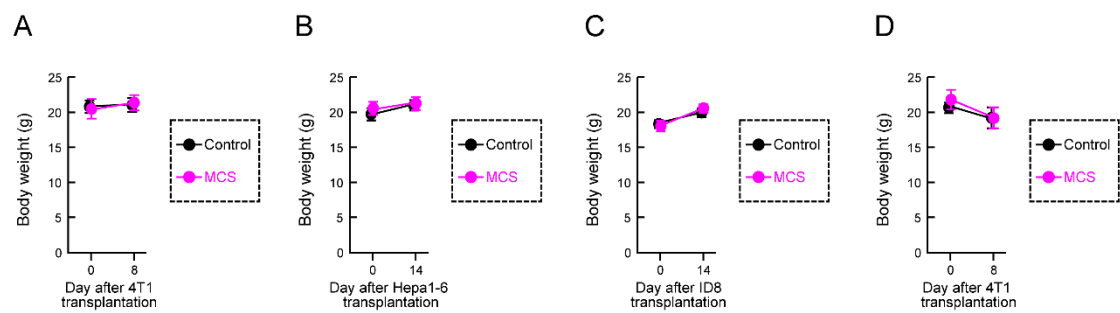


Figure S18. Body weight of mice following transplantation.

Body weight of mice described in **Figure 6 (A)**, **Figure 7 (B, C)**, and **Figure 8 (D)**. Data are presented as the mean \pm S.D. (n = 6–8). MCS: microcurrent stimulation.

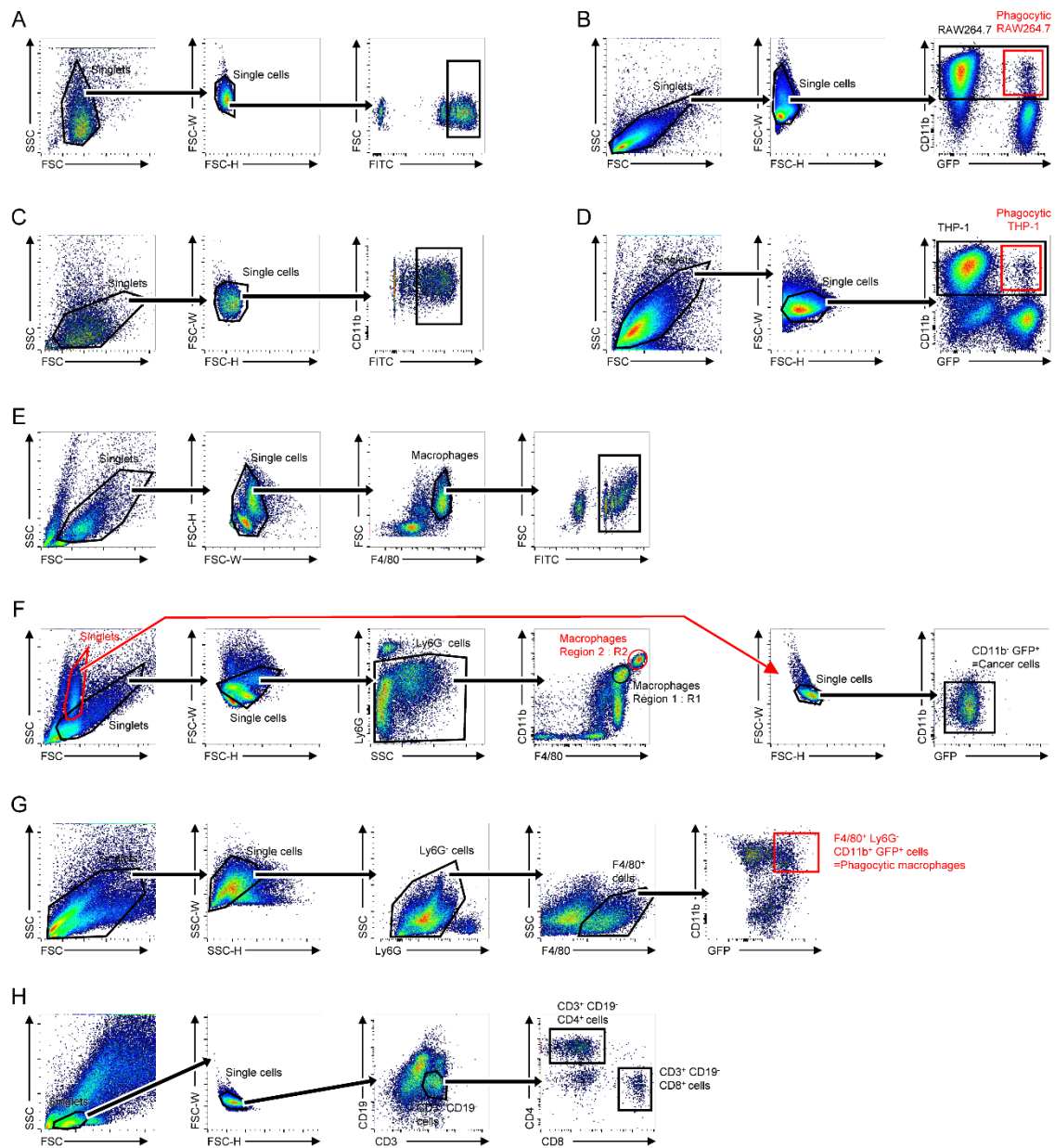


Figure S19. Gating strategies used for flow cytometry analysis.

Gating strategies of (A) RAW254.7 phagocytosed opsonized beads, (B) RAW254.7 phagocytosed GFP-expressing cancer cells, (C) PMA-treated THP-1 phagocytosed opsonized beads, (D) PMA-treated THP-1 phagocytosed GFP-expressing cancer cells, (E) intraperitoneal macrophages cultured with opsonized beads, (F) intraperitoneal $F4/80^+$ $CD11b^+$ $Ly6G^-$ cells and cancer cells of mice implanted with cancer cells in the abdominal cavity, (G) $F4/80^+$ $CD11b^+$ $Ly6G^-$ GFP^+ cells in tumors collected from the periportal area, and (H) $CD3^+$ $CD19^-$ $CD8^+$ cells and $CD3^+$ $CD19^-$ $CD4^+$ cells in tumors collected from the periportal area. GFP: green fluorescent protein; PMA: phorbol 12-myristate 13-acetate.

Table S1. Gene list using GO analysis in Figure S3 and Figure 2D

Gene Symbol	Genbank accession	Description	Control / MCS	
			log2FC	log2CPM
1110065P20Rik	NM_001142727	RIKEN cDNA 1110065P20 gene	1.920	1.536423
1300017J02Rik	NM_027918	RIKEN cDNA 1300017J02 gene	-1.056	-0.916557
1500011K16Rik	NM_175125	RIKEN cDNA 1500011K16 gene	1.206	3.336269
1600002K03Rik	NM_027207	RIKEN cDNA 1600002K03 gene	1.063	2.113538
1600029I14Rik	NR_028123	RIKEN cDNA 1600029I14 gene	1.171	-0.780272
1700003M07Rik	NR_040647	RIKEN cDNA 1700003M07 gene	1.171	-0.780272
1700007L15Rik	NR_045709	RIKEN cDNA 1700007L15 gene	2.174	0.217760
1700008C04Rik	NR_126468	RIKEN cDNA 1700008C04 gene	-1.188	0.463420
1700019D03Rik	NM_144953	RIKEN cDNA 1700019D03 gene	2.091	-0.918034
1700027J07Rik	NR_040581	RIKEN cDNA 1700027J07 gene	-1.564	0.286776
1700028E10Rik	NR_045699	RIKEN cDNA 1700028E10 gene	-1.600	0.718293
1700028J19Rik	NR_029436	RIKEN cDNA 1700028J19 gene	-1.056	-0.916557
1700034J05Rik	NM_001164236	RIKEN cDNA 1700034J05 gene	1.135	2.599731
1700056E22Rik	NM_028516	RIKEN cDNA 1700056E22 gene	1.141	0.151793
1700066B19Rik	NM_001033168	RIKEN cDNA 1700066B19 gene	-2.202	-0.330362
1700071M16Rik	NR_045444	RIKEN cDNA 1700071M16 gene	1.163	3.879029
1700084J12Rik	NM_028551	ribosomal protein L7-like 1 pseudogene	-1.071	-0.537785
1700099I09Rik	NR_130171	RIKEN cDNA 1700099I09 gene	-1.737	0.808924
1700109K24Rik	NR_108037	RIKEN cDNA 1700109K24 gene	-5.666	-0.915573
1700110C19Rik	NR_045461	RIKEN cDNA 1700110C19 gene	-1.289	-0.430623
2410018L13Rik	NM_028362	RIKEN cDNA 2410018L13 gene	-2.488	-0.149312
2510003B16Rik	NR_131048	RIKEN cDNA 2510003B16 gene	-3.267	-0.329881
2610027K06Rik	NR_077059	RIKEN cDNA 2610027K06 gene	1.044	-0.152647
2610206C17Rik	NR_038175	RIKEN cDNA 2610206C17 gene	-6.074	-0.652047
2610306M01Rik	NR_028298	RIKEN cDNA 2610306M01 gene	1.295	0.459304
2700099C18Rik	NR_024720	NDC80 homolog, kinetochore complex component pseudogene	1.255	0.218690
2900026A02Rik	NM_001347397	RIKEN cDNA 2900026A02 gene	-1.220	0.084442
2900057B20Rik	NR_045365	RIKEN cDNA 2900057B20 gene	-1.976	0.287240
2900076A07Rik	NR_045299	RIKEN cDNA 2900076A07 gene	2.153	-0.240841
3110021A11Rik	NR_030776	RIKEN cDNA 3110021A11 gene	-1.479	-0.330843
3110056K07Rik	NR_045055	RIKEN cDNA 3110056K07 gene	-1.101	3.063772
3110070M22Rik	NM_026084	RIKEN cDNA 3110070M22 gene	-1.533	0.010676
3300005D01Rik	NR_045079	RIKEN cDNA 3300005D01 gene	1.330	0.007372
3830403N18Rik	NM_027510	RIKEN cDNA 3830403N18 gene	-1.955	0.764761
3830432H09Rik	NR_126486	RIKEN cDNA 3830432H09 gene	5.783	-0.781251
4631405J19Rik	NM_001002794	RIKEN cDNA 4631405J19 gene	-1.071	-0.537785
4632428C04Rik	NR_033631	RIKEN cDNA 4632428C04 gene	-1.738	2.565174
4732491K20Rik	NR_045290	RIKEN cDNA 4732491K20 gene	-1.397	-0.067564
4833422M21Rik	NR_130160	RIKEN cDNA 4833422M21 gene	-1.087	0.221948
4921507P07Rik	NM_027564	RIKEN cDNA 4921507P07 gene	-1.369	-0.778803
4921515E04Rik	NR_045711	RIKEN cDNA 4921515E04 gene	1.194	-0.070409
4930405O22Rik	NR_130176	RIKEN cDNA 4930405O22 gene	-1.011	0.669868
4930412C18Rik	NR_030693	RIKEN cDNA 4930412C18 gene	1.855	0.006901
4930417O13Rik	NR_015527	RIKEN cDNA 4930417O13 gene	-1.056	-0.916557
4930486L24Rik	NM_178098	RIKEN cDNA 4930486L24 gene	1.330	0.007372
4930512B01Rik	NR_033573	RIKEN cDNA 4930512B01 gene	-1.079	-0.237971
4930512J16Rik	NR_131021	RIKEN cDNA 4930512J16 gene	-1.369	-0.778803
4930525G20Rik	NR_045194	RIKEN cDNA 4930525G20 gene	-1.845	-0.537299
4930550L24Rik	NM_023774	RIKEN cDNA 4930550L24 gene	1.835	-0.433038
4930562C15Rik	NM_001252142	RIKEN cDNA 4930562C15 gene	-1.458	0.222414
4930564C03Rik	NM_029257	RIKEN cDNA 4930564C03 gene	-2.277	0.156003
4930579K19Rik	NM_175227	RIKEN cDNA 4930579K19 gene	-1.220	0.084442
4931408C20Rik	NM_001033764	RIKEN cDNA 4931408C20 gene	-5.666	-0.915573
4933404K13Rik	NR_131055	RIKEN cDNA 4933404K13 gene	2.091	-0.918034
4933406J10Rik	NR_046004	RIKEN cDNA 4933406J10 gene	2.153	-0.240841
4933416M07Rik	NR_045840	RIKEN cDNA 4933416M07 gene	-2.284	-0.916065
4933417E11Rik	NR_040454	RIKEN cDNA 4933417E11 gene	1.143	1.342511
4933424G05Rik	NR_045372	RIKEN cDNA 4933424G05 gene	1.428	-0.654973
4933433H22Rik	NR_045458	RIKEN cDNA 4933433H22 gene	-1.627	-0.653023
5031425F14Rik	NR_015558	RIKEN cDNA 5031425F14 gene	1.173	3.118620
5031434O11Rik	NR_033624	RIKEN cDNA 5031434O11 gene	-2.202	-0.330362
5430431A17Rik	NR_131001	RIKEN cDNA 5430431A17 gene	1.428	-0.654973
5730405O15Rik	NR_038158	RIKEN cDNA 5730405O15 gene	-2.727	0.011621
5730460C07Rik	NR_045801	RIKEN cDNA 5730460C07 gene	2.091	-0.918034
6330415G19Rik	NR_126484	RIKEN cDNA 6330415G19 gene	-2.171	0.085383
6330418K02Rik	NR_045821	RIKEN cDNA 6330418K02 gene	1.076	0.513996
6430550D23Rik	NM_001145351	RIKEN cDNA 6430550D23 gene	-1.079	-0.237971
9130019P16Rik	NM_198118	RIKEN cDNA 9130019P16 gene	-1.087	0.221948
9230116L04Rik	NR_110486	RIKEN cDNA 9230116L04 gene	1.445	-0.240363
9230116N13Rik	NR_024328	RIKEN cDNA 9230116N13 gene	1.343	0.845579
9330159M07Rik	NR_037982	RIKEN cDNA 9330159M07 gene	-1.260	0.670318
9630028B13Rik	NM_176943	RIKEN cDNA 9630028B13 gene	1.194	-0.070409
9830107B12Rik	NM_001177896	RIKEN cDNA 9830107B12 gene	1.111	1.217317
A630019I02Rik	NR_046182	RIKEN cDNA A630019I02 gene	-1.587	1.289054
A930007I19Rik	NR_015567	RIKEN cDNA A930007I19 gene	-1.344	0.155067
A930019D19Rik	NR_040619	RIKEN cDNA A930019D19 gene	-1.071	-0.537785
AA413626	NR_102683	ribosomal protein L17 pseudogene	-1.056	-0.916557

AA986860	NM_177604	expressed sequence AA986860	1.773	0.282141
AI661453	NM_145489	expressed sequence AI661453	-1.079	-0.237971
AW551984	NM_001199556	expressed sequence AW551984	2.091	-0.918034
Aanat	NM_009591	arylalkylamine N-acetyltransferase	1.639	0.458847
Abca13	NM_178259	ATP-binding cassette, sub-family A (ABC1), member 13	5.783	-0.781251
Abcb4	NM_008830	ATP-binding cassette, sub-family B (MDR/TAP), member 4	-1.087	0.221948
Acer1	NM_175731	alkaline ceramidase 1	-1.056	-0.916557
Acnat1	NM_001164565	acyl-coenzyme A amino acid N-acyltransferase 1	1.171	-0.780272
Acpp	NM_019807	acid phosphatase, prostate	1.183	1.150163
Acr	NM_001205049	acrosin prepropeptide	-6.074	-0.652047
Acrbp	NM_001127340	proacrosin binding protein	-1.019	3.090596
Acyp1	NM_025421	acylphosphatase 1, erythrocyte (common) type	1.189	2.636477
Adamts3	NM_001081401	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 3	2.091	-0.918034
Adgrd1	NM_001081342	adhesion G protein-coupled receptor D1	1.428	-0.654973
Adgrf3	NM_001014394	adhesion G protein-coupled receptor F3	2.091	-0.918034
Adgrg5	NM_001033468	adhesion G protein-coupled receptor G5	1.350	3.537420
Adm	NM_009627	adrenomedullin	-1.897	1.381209
Agbl1	NM_001199224	ATP/GTP binding protein-like 1	-1.278	3.154374
Ager	NM_001271422	advanced glycosylation end product-specific receptor	1.044	-0.152647
Airm	NR_002853	antisense Igf2r RNA	-1.627	-0.653023
Akap14	NM_001033785	A kinase (PRKA) anchor protein 14	-1.056	-0.916557
Akap5	NM_0011101471	A kinase (PRKA) anchor protein 5	-1.457	3.000019
Alyref2	NM_019484	Aly/REF export factor 2	-1.096	1.190298
Amacr	NM_008537	alpha-methylacyl-CoA racemase	1.135	2.599731
Angptl2	NM_011923	angiopoietin-like 2	-1.184	1.519887
Angptl4	NM_020581	angiopoietin-like 4	2.112	0.512632
Angptl7	NM_001039554	angiopoietin-like 7	-1.679	1.573956
Ank3	NM_009670	ankyrin 3, epithelial	2.091	-0.918034
Ankle1	NM_001310502	ankyrin repeat and LEM domain containing 1	1.044	-0.152647
Ankmy1	NM_001347091	ankyrin repeat and MYND domain containing 1	2.348	-0.780762
Ankrd34b	NM_175455	ankyrin repeat domain 34B	-1.369	-0.778803
Ankrd66	NM_001254953	ankyrin repeat domain 66	1.381	0.513541
Apbb2	NM_001201413	amyloid beta (A4) precursor protein-binding, family B, member 2	-1.797	-0.149789
Apcs	NM_011318	serum amyloid P-component	-1.056	-0.916557
Apof	NM_133997	apolipoprotein F	1.171	-0.780272
Apoh	NM_013475	apolipoprotein H	1.017	0.081623
Apol10b	NM_177820	apolipoprotein L 10B	-1.089	0.406607
Apol7c	NM_175391	apolipoprotein L 7c	-5.666	-0.915573
Ar	NM_013476	androgen receptor	1.518	1.248706
Arap3	NM_001205336	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	1.267	4.579340
Arhgap19	NM_001163495	Rho GTPase activating protein 19	1.104	0.344252
Arhgap8	NM_001164627	Rho GTPase activating protein 8	-1.234	1.465457
Asap3	NM_001008232	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	-1.056	-0.916557
Asb14	NM_001170748	ankyrin repeat and SOCS box-containing 14	-1.201	0.286312
Asgr2	NM_001313925	asialoglycoprotein receptor 2	-2.284	-0.916065
Ass1	NM_007494	argininosuccinate synthetase 1	1.133	4.666438
Atad3aos	NM_175157	ATPase family, AAA domain containing 3A, opposite strand	1.089	-0.432555
Atg16l2	NM_001111111	autophagy related 16-like 2 (S. cerevisiae)	-1.010	3.161139
Atp1a2	NM_178405	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide	-1.369	-0.778803
Atp1b1	NM_009721	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	-1.522	1.743977
Atp1b4	NM_001290389	ATPase, (Na ⁺)/K ⁺ transporting, beta 4 polypeptide	1.171	-0.780272
Atp5e	NM_025983	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit	1.349	5.509464
Atp6v0c-ps2	NR_037854	ATPase, H ⁺ transporting, lysosomal V0 subunit C, pseudogene 2	11.405	4.201016
Atp6v1c2	NM_001159632	ATPase, H ⁺ transporting, lysosomal V1 subunit C2	-1.289	-0.430623
Atp6v1g2	NM_001347351	ATPase, H ⁺ transporting, lysosomal V1 subunit G2	-1.039	1.156142
Auts2	NM_177047	autism susceptibility candidate 2	-2.337	0.809813
Axin2	NM_015732	axin 2	1.361	2.623357
B230216N24Rik	NR_037993	RIKEN cDNA B230216N24 gene	-1.845	-0.537299
B230217O12Rik	NR_040316	RIKEN cDNA B230217O12 gene	-1.150	1.223672
B3gnt4	NM_198611	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	2.091	-0.918034
B3gnt6	NM_001081167	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase)	-1.479	-0.330843
B430212C06Rik	NR_033214	RIKEN cDNA B430212C06 gene	1.552	0.402473
B4galnt4	NM_177897	beta-1,4-N-acetyl-galactosaminyl transferase 4	-1.369	-0.778803
B9d1	NM_001330780	B9 protein domain 1	-5.666	-0.915573
BC002163	NR_002445	NADH dehydrogenase Fe-S protein 5 pseudogene	3.350	1.480885
BC025920	NM_001033363	zinc finger protein pseudogene	-1.280	0.518095
BC030867	NM_153544	cDNA sequence BC030867	1.171	-0.780272
BC037032	NR_028266	cDNA Sequence BC037032	-2.034	-0.430140
BC051226	NR_045146	cDNA sequence BC051226	-1.089	0.406607
BC052688	NR_028430	cDNA sequence BC052688	1.171	-0.780272
Bag2	NM_145392	BCL2-associated athanogene 2	-1.369	-0.778803
Bard1	NM_007525	BRCA1 associated RING domain 1	1.053	2.413427
Bcl2l15	NM_001142959	BCL2-like 15	-1.056	-0.916557
Best1	NM_011913	bestrophin 1	1.428	-0.654973
Boll	NM_001113367	boule homolog, RNA binding protein	-1.056	-0.916557
Brdt	NM_001079873	bromodomain, testis-specific	1.428	-0.654973
Brsk2	NM_001009929	BR serine/threonine kinase 2	-1.198	1.895304
Btbd11	NM_001017525	BTB (POZ) domain containing 11	-1.079	-0.237971
Bub1b	NM_009773	BUB1B, mitotic checkpoint serine/threonine kinase	1.545	1.613734
C1qtnf5	NM_001040631	C1q and tumor necrosis factor related protein 5	1.460	0.343791
C1rb	NM_001113356	complement component 1, r subcomponent B	-2.284	-0.916065
C1rl	NM_181344	complement component 1, r subcomponent-like	1.386	3.808859
C1s1	NM_001097617	complement component 1, s subcomponent 1	1.017	0.081623

<i>C330013E15Rik</i>	NR_045701	RIKEN cDNA C330013E15 gene	1.044	-0.152647
<i>C430049B03Rik</i>	NR_038184	RIKEN cDNA C430049B03 gene	1.361	0.282604
<i>C4bp</i>	NM_007576	complement component 4 binding protein	1.171	-0.780272
<i>C5ar2</i>	NM_001146005	complement component 5a receptor 2	-1.163	0.892917
<i>Cacna1f</i>	NM_019582	calcium channel, voltage-dependent, alpha 1F subunit	1.646	-0.539725
<i>Cacna1i</i>	NM_001044308	calcium channel, voltage-dependent, alpha 1I subunit	-1.042	6.867565
<i>Cacnb2</i>	NM_001252533	calcium channel, voltage-dependent, beta 2 subunit	1.171	-0.780272
<i>Cacnb3</i>	NM_001044741	calcium channel, voltage-dependent, beta 3 subunit	2.075	0.150859
<i>Capn12</i>	NM_001110807	calpain 12	2.566	-0.655460
<i>Capn3</i>	NM_001109761	calpain 3	-2.202	-0.330362
<i>Car12</i>	NM_001306148	carbonic anhydrase 12	1.044	-0.152647
<i>Car2</i>	NM_001357334	carbonic anhydrase 2	-1.657	0.084912
<i>Car3</i>	NM_007606	carbonic anhydrase 3	-1.397	-0.067564
<i>Car9</i>	NM_139305	carbonic anhydrase 9	1.773	0.282141
<i>Casc1</i>	NM_177222	cancer susceptibility candidate 1	1.445	-0.240363
<i>Caskin1</i>	NM_027937	CASK interacting protein 1	1.343	0.845579
<i>Cbln3</i>	NM_019820	cerebellin 3 precursor protein	-1.369	-0.778803
<i>Ccdc116</i>	NM_001164606	coiled-coil domain containing 116	-1.084	0.010204
<i>Ccdc146</i>	NM_029195	coiled-coil domain containing 146	2.091	-0.918034
<i>Ccdc155</i>	NM_201374	coiled-coil domain containing 155	2.091	-0.918034
<i>Ccdc169</i>	NM_001290138	coiled-coil domain containing 169	1.835	-0.433038
<i>Ccdc18</i>	NM_028481	coiled-coil domain containing 18	2.003	-0.333727
<i>Ccdc28b</i>	NM_025455	coiled coil domain containing 28B	1.019	2.523262
<i>Ccdc80</i>	NM_026439	coiled-coil domain containing 80	1.710	1.924143
<i>Ccdc89</i>	NM_027298	coiled-coil domain containing 89	2.348	-0.780762
<i>Ccl4</i>	NM_013652	chemokine (C-C motif) ligand 4	-3.267	-0.329881
<i>Ccnb2</i>	NM_007630	cyclin B2	1.139	1.614933
<i>Ccpg1os</i>	NM_001198789	cell cycle progression 1, opposite strand	1.295	0.459304
<i>Ccr3</i>	NM_009914	chemokine (C-C motif) receptor 3	4.668	4.170687
<i>Ccs</i>	NM_016892	copper chaperone for superoxide dismutase	1.173	3.313859
<i>Cd163l1</i>	NM_172909	CD163 molecule-like 1	-2.171	0.085383
<i>Cd207</i>	NM_144943	CD207 antigen	-1.071	-0.537785
<i>Cd209g</i>	NM_027343	CD209g antigen	-1.369	-0.778803
<i>Cd3d</i>	NM_013487	CD3 antigen, delta polypeptide	1.014	1.043833
<i>Cd46</i>	NM_010778	CD46 antigen, complement regulatory protein	1.646	-0.539725
<i>Cd8b1</i>	NM_009858	CD8 antigen, beta chain 1	1.133	0.712922
<i>Cdc42ep1</i>	NM_027219	CDC42 effector protein (Rho GTPase binding) 1	1.428	-0.654973
<i>Cdca5</i>	NM_026410	cell division cycle associated 5	2.112	0.512632
<i>Cdh22</i>	NM_174988	cadherin 22	-5.885	-0.777822
<i>Cdh3</i>	NM_001037809	cadherin 3	-1.369	-0.778803
<i>Cdk1</i>	NM_007659	cyclin-dependent kinase 1	1.235	1.183918
<i>Cdk5l1</i>	NM_009871	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	1.235	1.183918
<i>Ceacam2</i>	NM_001113368	carcinoembryonic antigen-related cell adhesion molecule 2	-2.727	0.011621
<i>Cebpe</i>	NM_207131	CCAAT/enhancer binding protein (C/EBP), epsilon	1.227	2.040919
<i>Celf4</i>	NM_001146292	CUGBP, Elav-like family member 4	-1.416	1.286633
<i>Centpe</i>	NM_173762	centromere protein E	1.069	2.469222
<i>Centph</i>	NM_021886	centromere protein H	1.835	-0.433038
<i>Centpm</i>	NM_001080158	centromere protein M	1.171	-0.780272
<i>Cep55</i>	NM_001164362	centrosomal protein 55	1.978	1.113878
<i>Cercam</i>	NM_207298	cerebral endothelial cell adhesion molecule	1.126	1.687559
<i>Ces1c</i>	NM_007954	carboxylesterase 1C	-1.087	0.221948
<i>Cetn4</i>	NM_145825	centrin 4	-1.071	-0.537785
<i>Cfap126</i>	NM_001081275	cilia and flagella associated protein 126	-1.369	-0.778803
<i>Cfhr1</i>	NM_015780	complement factor H-related 1	-2.034	-0.430140
<i>Cfi</i>	NM_001329552	complement component factor i	-2.949	-0.536813
<i>Cgn</i>	NM_001037711	cingulin	1.044	-0.152647
<i>Cgref1</i>	NM_001160149	cell growth regulator with EF hand domain 1	-1.289	-0.430623
<i>Chac1</i>	NM_026929	ChaC, cation transport regulator 1	-1.056	-0.916557
<i>Chadl</i>	NM_001164320	chondroadherin-like	-1.627	-0.653023
<i>Chaf1a</i>	NM_013733	chromatin assembly factor 1, subunit A (p150)	1.530	2.597764
<i>Chaf1b</i>	NM_028083	chromatin assembly factor 1, subunit B (p60)	1.468	0.927644
<i>Chil1</i>	NM_007695	chitinase-like 1	-1.089	0.406607
<i>Chrm4</i>	NM_007699	cholinergic receptor, muscarinic 4	2.091	-0.918034
<i>Chst1</i>	NM_001356552	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	-1.269	2.337535
<i>Chst13</i>	NM_027928	carbohydrate (chondroitin 4) sulfotransferase 13	3.263	1.940487
<i>Chsy3</i>	NM_001081328	chondroitin sulfate synthase 3	1.245	0.616671
<i>Ckap2l</i>	NM_181589	cytoskeleton associated protein 2-like	1.276	1.864373
<i>Cks1b</i>	NM_016904	CDC28 protein kinase 1b	1.193	1.564262
<i>Cldn22</i>	NM_029383	claudin 22	-1.479	-0.330843
<i>Cldn3</i>	NM_009902	claudin 3	2.566	-0.655460
<i>Clec2g</i>	NM_001168223	C-type lectin domain family 2, member g	-3.024	0.223813
<i>Clec4g</i>	NM_029465	C-type lectin domain family 4, member g	-2.612	-0.066614
<i>Clnk</i>	NM_013748	cytokine-dependent hematopoietic cell linker	-1.056	-0.916557
<i>Clrn1</i>	NM_153384	clarin 1	-1.369	-0.778803
<i>Clu</i>	NM_013492	clusterin	1.025	0.928519
<i>Cmtm1</i>	NM_181990	CKLF-like MARVEL transmembrane domain containing 1	5.565	-0.918525
<i>Col1a1</i>	NM_007742	collagen, type I, alpha 1	1.569	0.151326
<i>Col1a2</i>	NM_007743	collagen, type I, alpha 2	2.353	0.342870
<i>Col3a1</i>	NM_009930	collagen, type III, alpha 1	2.616	0.885444
<i>Col4a4</i>	NM_007735	collagen, type IV, alpha 4	1.171	-0.780272
<i>Col4a5</i>	NM_001163155	collagen, type IV, alpha 5	1.654	1.883820
<i>Col6a1</i>	NM_009933	collagen, type VI, alpha 1	-1.079	-0.237971
<i>Coro2b</i>	NM_175484	coronin, actin binding protein, 2B	-1.397	-0.067564

<i>Cox7a2</i>	NM_009945	cytochrome c oxidase subunit VIIa 2	1.082	4.756301
<i>Cpe</i>	NM_013494	carboxypeptidase E	-1.056	-0.916557
<i>Cpne5</i>	NM_153166	copine V	-1.479	-0.330843
<i>Cpne7</i>	NM_170684	copine VII	-1.369	-0.778803
<i>Cpne9</i>	NM_170673	copine family member IX	-1.627	-0.653023
<i>Crmp1</i>	NM_001136058	collapsin response mediator protein 1	-1.230	3.064642
<i>Cryab</i>	NM_001289782	crystallin, alpha B	1.454	0.081154
<i>Ctsk</i>	NM_007802	cathepsin K	-2.352	-0.237013
<i>Ctsw</i>	NM_009985	cathepsin W	1.111	1.217317
<i>Ctxn1</i>	NM_183315	cortexin 1	-1.369	-0.778803
<i>Cx3cl1</i>	NM_009142	chemokine (C-X3-C motif) ligand 1	1.171	-0.780272
<i>Cxcl1</i>	NM_008176	chemokine (C-X-C motif) ligand 1	-1.140	2.600769
<i>Cxcl13</i>	NM_018866	chemokine (C-X-C motif) ligand 13	-2.047	8.084261
<i>Cxcl3</i>	NM_203320	chemokine (C-X-C motif) ligand 3	-2.715	0.465252
<i>Cyb5r2</i>	NM_001205227	cytochrome b5 reductase 2	-2.034	-0.430140
<i>Cyb5rl</i>	NM_001346552	cytochrome b5 reductase-like	1.212	1.663491
<i>Cyp2c67</i>	NM_001024719	cytochrome P450, family 2, subfamily c, polypeptide 67	2.348	-0.780762
<i>Cyp2d9</i>	NM_010006	cytochrome P450, family 2, subfamily d, polypeptide 9	-1.369	-0.778803
<i>Cyp2j9</i>	NM_028979	cytochrome P450, family 2, subfamily j, polypeptide 9	-2.488	-0.149312
<i>Cyp39a1</i>	NM_001285947	cytochrome P450, family 39, subfamily a, polypeptide 1	-1.309	1.832340
<i>D130040H23Rik</i>	NM_172491	RIKEN cDNA D130040H23 gene	-1.004	3.564427
<i>D5Erd605e</i>	NR_033625	DNA segment, Chr 5, ERATO Doi 605, expressed	2.348	-0.780762
<i>D630045J12Rik</i>	NM_194061	RIKEN cDNA D630045J12 gene	-1.369	-0.778803
<i>D7Erd143e</i>	NR_028425	DNA segment, Chr 7, ERATO Doi 143, expressed	-1.056	-0.916557
<i>Dach1</i>	NM_001038610	dachshund family transcription factor 1	3.574	0.800056
<i>Dapk2</i>	NM_010019	death-associated protein kinase 2	2.731	0.150392
<i>Dbp</i>	NM_016974	D site albumin promoter binding protein	-1.600	3.711966
<i>Ddr2</i>	NM_022563	discoidin domain receptor family, member 2	1.646	-0.539725
<i>Depdc1b</i>	NM_178683	DEP domain containing 1B	1.175	0.887639
<i>Dlec1</i>	NM_177117	deleted in lung and esophageal cancer 1	-1.845	-0.537299
<i>Dlg5</i>	NM_001163513	discs large MAGUK scaffold protein 5	-1.359	1.546960
<i>Dnaaf1</i>	NM_026648	dynein, axonemal assembly factor 1	1.171	-0.780272
<i>Dnah5</i>	NM_133365	dynein, axonemal, heavy chain 5	-3.403	-0.236534
<i>Dnah6</i>	NM_001164669	dynein, axonemal, heavy chain 6	-2.284	-0.916065
<i>Dnm3</i>	NM_001038619	dynamamin 3	-1.220	0.084442
<i>Dpp6</i>	NM_001136060	dipeptidylpeptidase 6	-1.344	0.155067
<i>Dsg2</i>	NM_007883	desmoglein 2	-2.284	-0.916065
<i>Dsp</i>	NM_023842	desmoplakin	-1.527	0.670768
<i>Dtl</i>	NM_001305233	denticleless E3 ubiquitin protein ligase	1.499	2.230
<i>Dtx1</i>	NM_008052	deltex 1, E3 ubiquitin ligase	-1.487	5.211
<i>Dusp14</i>	NM_019819	dual specificity phosphatase 14	-1.071	-0.538
<i>Dusp19</i>	NM_024438	dual specificity phosphatase 19	1.257	1.312
<i>Dusp8</i>	NM_008748	dual specificity phosphatase 8	-1.247	-0.150
<i>Dynl1b</i>	NM_009342	dynein light chain Tctex-type 1B	1.007	5.267
<i>Dynl1f</i>	NM_001166627	dynein light chain Tctex-type 1F	2.592	1.586
<i>E130008D07Rik</i>	NR_045153	RIKEN cDNA E130008D07 gene	-5.666	-0.916
<i>E130311K13Rik</i>	NM_177856	RIKEN cDNA E130311K13 gene	-1.243	1.380
<i>E230029C05Rik</i>	NR_015614	RIKEN cDNA E230029C05 gene	-1.397	-0.068
<i>E330023G01Rik</i>	NR_045332	RIKEN cDNA E330023G01 gene	-1.056	-0.917
<i>Echdc3</i>	NM_024208	enoyl Coenzyme A hydratase domain containing 3	-1.254	1.995
<i>Efhc1</i>	NM_027974	EF-hand domain (C-terminal) containing 1	1.044	-0.153
<i>Efnb3</i>	NM_007911	ephrin B3	1.171	-0.780
<i>Efs</i>	NM_010112	embryonal Fyn-associated substrate	1.447	1.905
<i>Egfl8</i>	NM_152922	EGF-like domain 8	1.646	-0.540
<i>Egr1</i>	NM_007913	early growth response 1	-1.274	4.524
<i>Egr2</i>	NM_001347458	early growth response 2	-1.152	2.824
<i>Egr3</i>	NM_001289925	early growth response 3	-2.217	2.763
<i>Ehf</i>	NM_007914	ets homologous factor	-1.845	-0.537
<i>Eil3</i>	NM_145973	elongation factor RNA polymerase II-like 3	-1.142	2.523
<i>Elovl6</i>	NM_130450	ELOVL family member 6, elongation of long chain fatty acids (yeast)	1.059	1.184
<i>Emid1</i>	NM_080595	EMI domain containing 1	1.171	-0.780
<i>Emp2</i>	NM_007929	epithelial membrane protein 2	1.171	-0.780
<i>Endou</i>	NM_001168693	endonuclease, polyU-specific	-2.202	-0.330
<i>Enpp2</i>	NM_001136077	ectonucleotide pyrophosphatase/phosphodiesterase 2	1.835	-0.433
<i>Entpd2</i>	NM_009849	ectonucleoside triphosphate diphosphohydrolase 2	2.091	-0.918
<i>Epdr1</i>	NM_134065	ependymin related protein 1 (zebrafish)	-1.627	-0.653
<i>Epor</i>	NM_010149	erythropoietin receptor	2.348	-0.781
<i>Eps8l1</i>	NM_001290416	EPS8-like 1	1.044	-0.153
<i>ErbB2</i>	NM_001003817	erb-b2 receptor tyrosine kinase 2	1.039	0.803
<i>Ercc8</i>	NM_028042	excision repair cross-complementing rodent repair deficiency, complementation group 8	1.021	2.248
<i>Esam</i>	NM_027102	endothelial cell-specific adhesion molecule	2.091	-0.918
<i>Esm1</i>	NM_023612	endothelial cell-specific molecule 1	2.348	-0.781
<i>Etv4</i>	NM_001316365	ets variant 4	1.835	-0.433
<i>Evc2</i>	NM_145920	EvC ciliary complex subunit 2	-1.056	-0.917
<i>Evgl</i>	NM_025276	envoplakin	1.171	-0.780
<i>Eya1</i>	NM_001252192	EYA transcriptional coactivator and phosphatase 1	-1.093	0.851
<i>F2r</i>	NM_010169	coagulation factor II (thrombin) receptor	1.507	1.686
<i>F630042J09Rik</i>	NR_033540	RIKEN cDNA F630042J09 gene	1.361	0.283
<i>F730043M19Rik</i>	NR_015602	RIKEN cDNA F730043M19 gene	1.428	-0.655
<i>F9</i>	NM_001305797	coagulation factor IX	-1.056	-0.917
<i>Fabp5</i>	NM_001272097	fatty acid binding protein 5, epidermal	1.694	1.613
<i>Fabp7</i>	NM_021272	fatty acid binding protein 7, brain	1.416	5.659
<i>Fads6</i>	NM_178035	fatty acid desaturase domain family, member 6	1.171	-0.780

<i>Fam124a</i>	NM_001243857	family with sequence similarity 124, member A	-1.369	-0.779
<i>Fam160a1</i>	NM_172682	family with sequence similarity 160, member A1	-1.236	1.854
<i>Fam166b</i>	NM_001162381	family with sequence similarity 166, member B	-1.289	-0.431
<i>Fam198a</i>	NM_001199927	family with sequence similarity 198, member A	-3.403	-0.237
<i>Fam92b</i>	NM_001033980	family with sequence similarity 92, member B	1.428	-0.655
<i>Fbxl15</i>	NM_133694	F-box and leucine-rich repeat protein 15	1.210	1.281
<i>Fbxo36</i>	NM_025386	F-box protein 36	-1.056	-0.917
<i>Fbxw13</i>	NM_177598	F-box and WD-40 domain protein 13	-1.417	1.494
<i>Fcgr4</i>	NM_144559	Fc receptor, IgG, low affinity IV	1.127	5.855
<i>Fcmr</i>	NM_026976	Fc fragment of IgM receptor	-1.416	6.130
<i>Fcrlb</i>	NM_001029984	Fc receptor-like B	2.566	-0.655
<i>Fdx1l</i>	NM_001039824	ferredoxin 1-like	1.227	2.041
<i>Fer1l5</i>	NM_001277076	fer-1-like 5 (C. elegans)	-1.289	-0.431
<i>Fetub</i>	NM_001083904	fetuin beta	1.428	-0.655
<i>Ffar1</i>	NM_194057	free fatty acid receptor 1	-1.416	1.289
<i>Fgf1</i>	NM_010197	fibroblast growth factor 1	-1.247	-0.150
<i>Fgf11</i>	NM_001291104	fibroblast growth factor 11	-1.614	1.721
<i>Fgfr3</i>	NM_001163215	fibroblast growth factor receptor 3	-1.247	-0.150
<i>Fgl1</i>	NM_145594	fibrinogen-like protein 1	1.445	-0.240
<i>Fhit</i>	NM_001308285	fragile histidine triad gene	-1.289	-0.431
<i>Fibcd1</i>	NM_178887	fibrinogen C domain containing 1	-1.845	-0.537
<i>Flt4</i>	NM_008029	FMS-like tyrosine kinase 4	-1.028	0.933
<i>Foxc1</i>	NM_008592	forkhead box C1	1.428	-0.655
<i>Foxc2</i>	NM_013519	forkhead box C2	-1.845	-0.537
<i>Foxd2</i>	NM_008593	forkhead box D2	-1.397	-0.068
<i>Foxd2os</i>	NR_030721	forkhead box D2, opposite strand	1.171	-0.780
<i>Fmpd4</i>	NM_001033330	FERM and PDZ domain containing 4	-1.797	-0.150
<i>Fsbp</i>	NM_001256142	fibrinogen silencer binding protein	5.972	-0.656
<i>Fsd2</i>	NM_172904	fibronectin type III and SPRY domain containing 2	-1.845	-0.537
<i>Fxyd6</i>	NM_022004	FXYD domain-containing ion transport regulator 6	2.008	0.712
<i>G0s2</i>	NM_008059	G0/G1 switch gene 2	2.003	-0.334
<i>G730013B05Rik</i>	NR_040379	RIKEN cDNA G730013B05 gene	1.278	-0.333
<i>Gabbr2</i>	NM_001081141	gamma-aminobutyric acid (GABA) B receptor, 2	-1.620	1.050
<i>Gad2</i>	NM_008078	glutamic acid decarboxylase 2	-1.369	-0.779
<i>Gadd45g</i>	NM_011817	growth arrest and DNA-damage-inducible 45 gamma	1.089	0.968
<i>Gal3st3</i>	NM_001024717	galactose-3-O-sulfotransferase 3	-1.188	0.463
<i>Galr2</i>	NM_010254	galanin receptor 2	2.091	-0.918
<i>Gas6</i>	NM_019521	growth arrest specific 6	-1.620	1.050
<i>Gdpd3</i>	NM_024228	glycerophosphodiester phosphodiesterase domain containing 3	1.445	-0.240
<i>Gdpd5</i>	NM_201352	glycerophosphodiester phosphodiesterase domain containing 5	1.460	0.344
<i>Ggn</i>	NM_182694	gametogenetin	1.466	0.758
<i>Ggnbp2os</i>	NR_131197	gametogenetin binding protein 2, opposite strand	-1.280	0.518
<i>Gh</i>	NM_008117	growth hormone	-2.034	-0.430
<i>Gins1</i>	NM_001163476	GINS complex subunit 1 (Psf1 homolog)	1.731	-0.071
<i>Gins2</i>	NM_178856	GINS complex subunit 2 (Psf2 homolog)	1.526	0.967
<i>Gja1</i>	NM_010288	gap junction protein, alpha 1	1.445	-0.240
<i>Gjb1</i>	NM_001302496	gap junction protein, beta 1	-1.056	-0.917
<i>Gli1</i>	NM_010296	GLI-Kruppel family member GLI1	1.014	1.044
<i>Glis3</i>	NM_001305671	GLIS family zinc finger 3	-1.479	-0.331
<i>Gm10046</i>	NR_033484	predicted gene 10046	1.646	-0.540
<i>Gm10638</i>	NR_027829	predicted gene 10638	2.091	-0.918
<i>Gm10677</i>	NR_046048	predicted gene 10677	-2.284	-0.916
<i>Gm10768</i>	NR_033472	predicted gene 10768	2.091	-0.918
<i>Gm11346</i>	NR_024599	X-linked lymphocyte-regulated 5 pseudogene	-1.067	1.936
<i>Gm11545</i>	NM_001105561	predicted gene 11545	-1.079	-0.238
<i>Gm11944</i>	NR_045708	predicted gene 11944	-2.171	0.085
<i>Gm12159</i>	NR_045100	predicted gene 12159	2.091	-0.918
<i>Gm12505</i>	NR_040674	predicted gene 12505	1.171	-0.780
<i>Gm12522</i>	NR_040560	predicted gene 12522	2.091	-0.918
<i>Gm128</i>	NM_001024841	predicted gene 128	1.381	0.514
<i>Gm13830</i>	NR_131932	predicted gene 13830	-1.369	-0.779
<i>Gm13889</i>	NM_001145034	predicted gene 13889	-1.369	-0.779
<i>Gm13986</i>	NR_126479	predicted gene 13986	1.865	0.343
<i>Gm14308</i>	NM_001099349	predicted gene 14308	-1.644	4.434
<i>Gm14327</i>	NR_038101	predicted gene 14327	-1.316	1.224
<i>Gm14405</i>	NR_040256	predicted gene 14405	-1.369	-0.779
<i>Gm14430</i>	NM_001100415	predicted gene 14430	5.725	3.654
<i>Gm14434</i>	NM_001101804	predicted gene 14434	7.542	0.563
<i>Gm15441</i>	NR_040409	predicted gene 15441	2.266	0.282
<i>Gm15612</i>	NR_045880	predicted gene 15612	-1.498	0.464
<i>Gm15708</i>	NR_040432	predicted gene 15708	-2.193	2.055
<i>Gm16062</i>	NR_045686	predicted gene 16062	1.017	0.082
<i>Gm16223</i>	NR_131130	predicted gene 16223	1.104	0.344
<i>Gm16367</i>	NM_001031622	predicted gene 16367	-1.627	-0.653
<i>Gm16386</i>	NR_030709	zinc finger protein 946 pseudogene	-1.152	2.824
<i>Gm1653</i>	NR_040591	predicted gene 1653	-3.117	-0.430
<i>Gm16701</i>	NR_037988	predicted gene, 16701	3.073	-0.334
<i>Gm16712</i>	NR_108021	predicted gene, 16712	-1.797	-0.150
<i>Gm16845</i>	NR_040406	predicted gene, 16845	-1.243	1.380
<i>Gm16998</i>	NR_038016	predicted gene, 16998	-1.369	-0.779
<i>Gm17757</i>	NR_040453	GTPase, very large interferon inducible 1 pseudogene	2.239	5.903
<i>Gm17769</i>	NR_027377	predicted gene, 17769	-1.369	-0.779
<i>Gm18853</i>	NR_040456	GTPase, very large interferon inducible 1 pseudogene	-12.831	5.589

<i>Gm19345</i>	NM_001270489	predicted gene, 19345	-1.071	-0.538
<i>Gm20187</i>	NR_045052	predicted gene, 20187	-2.202	-0.330
<i>Gm20324</i>	NR_045068	predicted gene, 20324	-1.797	-0.150
<i>Gm20337</i>	NR_045057	predicted gene, 20337	-1.627	-0.653
<i>Gm21992</i>	NM_001290127	predicted gene 21992	-5.666	-0.916
<i>Gm2848</i>	NR_046069	predicted gene 2848	-1.035	1.915
<i>Gm30505</i>	NR_110508	predicted gene, 30505	1.089	-0.433
<i>Gm3704</i>	NR_131166	predicted gene 3704	-1.289	-0.431
<i>Gm38426</i>	NR_103491	predicted gene, 38426	-1.089	0.407
<i>Gm4371</i>	NR_028311	eukaryotic translation initiation factor 3, subunit I pseudogene	-1.289	-0.431
<i>Gm4532</i>	NR_030674	predicted gene 4532	-3.267	-0.330
<i>Gm4791</i>	NM_001243258	predicted gene 4791	-1.056	-0.917
<i>Gm5088</i>	NR_002862	poly(A)-binding protein, cytoplasmic pseudogene	-1.010	2.014
<i>Gm5424</i>	NR_002687	argininosuccinate synthase pseudogene	-1.564	4.677
<i>Gm5434</i>	NM_001014396	ubiquitin-conjugating enzyme E2F (putative) pseudogene	1.044	-0.153
<i>Gm5464</i>	NM_001034881	predicted gene 5464	-1.585	0.519
<i>Gm5512</i>	NR_002891	required for meiotic nuclear division 1 pseudogene	-2.034	-0.430
<i>Gm5523</i>	NR_004447	glyceraldehyde-3-phosphate dehydrogenase pseudogene	-2.277	0.156
<i>Gm6093</i>	NR_131140	predicted gene 6093	3.333	-0.154
<i>Gm6377</i>	NM_001037917	predicted gene 6377	-1.726	1.123
<i>Gm6644</i>	NR_028277	Akr1b3 pseudogene	12.240	5.022
<i>Gm8221</i>	NR_033577	apolipoprotein L 7c pseudogene	-2.113	2.618
<i>Gm8369</i>	NM_001164202	predicted gene 8369	-1.066	1.874
<i>Gm9054</i>	NR_045872	predicted gene 9054	2.185	0.565
<i>Gm9079</i>	NR_004052	transmembrane emp24 domain trafficking protein 2 pseudogene	-1.280	0.518
<i>Gm973</i>	NM_001013771	predicted gene 973	-1.845	-0.537
<i>Gm9733</i>	NM_001076679	predicted gene 9733	1.202	0.403
<i>Gm9958</i>	NR_045618	predicted gene 9958	-1.044	1.256
<i>Gnao1</i>	NM_001113384	guanine nucleotide binding protein, alpha O	-1.797	-0.150
<i>Gnat2</i>	NM_008141	guanine nucleotide binding protein, alpha transducing 2	1.445	-0.240
<i>Gnb5</i>	NM_010313	guanine nucleotide binding protein (G protein), beta 5	1.111	1.217
<i>Gng11</i>	NM_025331	guanine nucleotide binding protein (G protein), gamma 11	2.731	0.150
<i>Gpbar1</i>	NM_174985	G protein-coupled bile acid receptor 1	5.565	-0.919
<i>Gpc6</i>	NM_001079844	glypican 6	1.637	1.043
<i>Gpr1</i>	NM_001357045	G protein-coupled receptor 1	2.091	-0.918
<i>Gpr15</i>	NM_001162955	G protein-coupled receptor 15	1.428	-0.655
<i>Gpr152</i>	NM_206973	G protein-coupled receptor 152	-1.071	-0.538
<i>Gpr176</i>	NM_201367	G protein-coupled receptor 176	-1.479	-0.331
<i>Gpr182</i>	NM_007412	G protein-coupled receptor 182	-1.243	0.808
<i>Gpr52</i>	NM_001146330	G protein-coupled receptor 52	-1.468	1.789
<i>Gpx2-ps1</i>	NR_033563	glutathione peroxidase 2, pseudogene 1	-1.479	-0.331
<i>Grasp</i>	NM_019518	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	-1.397	-0.068
<i>Grhl1</i>	NM_001161406	grainyhead like transcription factor 1	-3.117	-0.430
<i>Grin3b</i>	NM_130455	glutamate receptor, ionotropic, NMDA3B	-1.079	-0.238
<i>Gsdmcl-ps</i>	NR_029414	gasdermin C-like, pseudogene	2.322	0.664
<i>Gsg1</i>	NM_001080552	germ cell associated 1	1.133	0.713
<i>Gstm4</i>	NM_001160411	glutathione S-transferase, mu 4	1.055	1.926
<i>Gucy2f</i>	NM_001007576	guanylate cyclase 2f	-2.034	-0.430
<i>Gvin1</i>	NM_001039160	GTPase, very large interferon inducible 1	-1.073	9.145
<i>H2-Q7</i>	NM_001198560	histocompatibility 2, Q region locus 7	2.491	1.981
<i>H2-T9</i>	NM_010399	histocompatibility 2, T region locus 9	1.158	3.767
<i>H2afy2</i>	NM_207000	H2A histone family, member Y2	-1.348	1.350
<i>Hal</i>	NM_010401	histidine ammonia lyase	-1.183	7.875
<i>Hap1</i>	NM_010404	huntingtin-associated protein 1	-1.487	2.090
<i>Hapln3</i>	NM_178255	hyaluronan and proteoglycan link protein 3	1.428	-0.655
<i>Haus8</i>	NM_001163042	4HAUS augmin-like complex, subunit 8	1.328	2.454
<i>Hba-a1</i>	NM_008218	hemoglobin alpha, adult chain 1	6.398	3.367
<i>Hba-a2</i>	NM_001083955	hemoglobin alpha, adult chain 2	11.868	4.656
<i>Hbb-b1</i>	NM_001278161	hemoglobin, beta adult major chain	7.328	4.268
<i>Hbb-b2</i>	NM_016956	hemoglobin, beta adult minor chain	7.048	0.149
<i>Hbb-bt</i>	NM_008220	hemoglobin, beta adult t chain	7.048	0.149
<i>Hcn3</i>	NM_008227	hyperpolarization-activated, cyclic nucleotide-gated K+ 3	-2.202	-0.330
<i>Hcst</i>	NM_011827	hematopoietic cell signal transducer	1.047	3.229
<i>Hddc2</i>	NM_027168	HD domain containing 2	1.079	1.734
<i>Hddc3</i>	NM_026812	HD domain containing 3	1.017	2.295
<i>Hgf</i>	NM_001289458	hepatocyte growth factor	1.567	3.719
<i>Hic1</i>	NM_001098203	hypermethylated in cancer 1	-1.163	0.893
<i>Hid1</i>	NM_001346774	HID1 domain containing	1.171	-0.780
<i>Hist1h1b</i>	NM_020034	histone cluster 1, H1b	1.056	2.743
<i>Hist1h1c</i>	NM_015786	histone cluster 1, H1c	1.115	6.451
<i>Hist1h1d</i>	NM_145713	histone cluster 1, H1d	1.049	4.610
<i>Hist1h2ah</i>	NM_175659	histone cluster 1, H2ah	1.336	1.905
<i>Hist1h2an</i>	NM_178184	histone cluster 1, H2an	1.626	1.863
<i>Hist1h2ao</i>	NM_001177544	histone cluster 1, H2ao	1.069	3.900
<i>Hist1h2ap</i>	NM_178185	histone cluster 1, H2ap	-1.434	1.917
<i>Hist1h2bh</i>	NM_178197	histone cluster 1, H2bh	1.842	1.341
<i>Hist1h3b</i>	NM_178203	histone cluster 1, H3b	1.000	2.182
<i>Hist1h4j</i>	NM_178210	histone cluster 1, H4j	1.637	1.043
<i>Hist2h2ab</i>	NM_178213	histone cluster 2, H2ab	-1.280	0.518
<i>Hist2h3c1</i>	NM_178216	histone cluster 2, H3c1	1.528	2.647
<i>Hnf1a</i>	NM_009327	HNF1 homeobox A	1.194	-0.070
<i>Hnf4a</i>	NM_001312906	hepatic nuclear factor 4, alpha	1.089	-0.433
<i>Hoxa5</i>	NM_010453	homeobox A5	5.783	-0.781

<i>Hoxb3</i>	NM_001079869	homeobox B3	-1.010	1.492
<i>Hrh4</i>	NM_153087	histamine receptor H4	1.089	-0.433
<i>Hsd17b1</i>	NM_010475	hydroxysteroid (17-beta) dehydrogenase 1	-2.284	-0.916
<i>Hsf3</i>	NM_001310754	heat shock transcription factor 3	-1.091	0.570
<i>Hsf5</i>	NM_001045527	heat shock transcription factor family member 5	1.428	-0.655
<i>Hspa12b</i>	NM_028306	heat shock protein 12B	-1.761	1.410
<i>Htr5b</i>	NM_010483	5-hydroxytryptamine (serotonin) receptor 5B	1.171	-0.780
<i>Hyal5</i>	NM_028957	hyaluronoglucosaminidase 5	1.295	0.459
<i>Hyal6</i>	NM_028920	hyaluronoglucosaminidase 6	1.278	-0.333
<i>Id1</i>	NM_001355113	inhibitor of DNA binding 1	1.039	3.300
<i>Ido1</i>	NM_001293690	indoleamine 2,3-dioxygenase 1	-2.284	-0.916
<i>Ido2</i>	NM_145949	indoleamine 2,3-dioxygenase 2	-5.666	-0.916
<i>Ifi27</i>	NM_026790	interferon, alpha-inducible protein 27	1.023	5.079
<i>Ifit1b12</i>	NM_053217	interferon induced protein with tetratricopeptide repeats 1B like 2	-2.949	-0.537
<i>Ifitm10</i>	NM_001347541	interferon induced transmembrane protein 10	-1.079	-0.238
<i>Igsf3</i>	NM_207205	immunoglobulin superfamily, member 3	1.031	2.148
<i>Igsf9b</i>	NM_001033323	immunoglobulin superfamily, member 9B	-2.237	0.465
<i>Il1r2</i>	NM_001356478	interleukin 1 receptor-like 2	2.756	-0.540
<i>Il23r</i>	NM_144548	interleukin 23 receptor	-1.627	-0.653
<i>Il4</i>	NM_021283	interleukin 4	1.855	0.007
<i>Il2r2</i>	NM_001164528	immunoglobulin-like domain containing receptor 2	-5.885	-0.778
<i>Impg2</i>	NM_174876	interphotoreceptor matrix proteoglycan 2	-1.202	1.256
<i>Ino80dos</i>	NR_045914	INO80 complex subunit D, opposite strand	-1.195	1.350
<i>Inpp5j</i>	NM_172439	inositol polyphosphate 5-phosphatase J	6.567	2.638
<i>Insl3</i>	NM_013564	insulin-like 3	-7.965	0.855
<i>Insm2</i>	NM_020287	insulinoma-associated 2	-1.479	-0.331
<i>Iqsec3</i>	NM_001033354	IQ motif and Sec7 domain 3	-1.737	0.809
<i>Isg15</i>	NM_015783	ISG15 ubiquitin-like modifier	1.039	0.803
<i>Islr2</i>	NM_001161535	immunoglobulin superfamily containing leucine-rich repeat 2	-3.117	-0.430
<i>Itgae</i>	NM_008399	integrin alpha E, epithelial-associated	-1.141	1.493
<i>Itih5</i>	NM_172471	inter-alpha (globulin) inhibitor H5	-1.548	0.852
<i>Itm2a</i>	NM_008409	integral membrane protein 2A	2.289	-0.154
<i>Jph3</i>	NM_020605	junctophilin 3	-1.220	0.084
<i>Kazn</i>	NM_001109684	kazrin, periplakin interacting protein	1.595	-0.153
<i>Kcnc1</i>	NM_001112739	potassium voltage gated channel, Shaw-related subfamily, member 1	-1.247	-0.150
<i>Kcnj1</i>	NM_001168354	potassium inwardly-rectifying channel, subfamily J, member 1	-2.034	-0.430
<i>Kcnj13</i>	NM_001110227	potassium inwardly-rectifying channel, subfamily J, member 13	1.800	1.311
<i>Kcnj5</i>	NM_010605	potassium inwardly-rectifying channel, subfamily J, member 5	-2.047	1.352
<i>Kcnmb1</i>	NM_031169	potassium large conductance calcium-activated channel, subfamily M, beta member 1	-1.458	0.222
<i>Kcnmb3</i>	NM_001195074	potassium large conductance calcium-activated channel, subfamily M, beta member 3	-1.647	-0.237
<i>Kcnn1</i>	NM_032397	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	3.333	-0.154
<i>Kcnt1</i>	NM_001145403	potassium channel, subfamily T, member 1	-1.056	-0.917
<i>Khdc3</i>	NM_001311106	KH domain containing 3, subcortical maternal complex member	1.162	1.250
<i>Kif14</i>	NM_001081258	kinesin family member 14	1.014	1.044
<i>Kif17</i>	NM_001190978	kinesin family member 17	5.565	-0.919
<i>Kif4</i>	NM_008446	kinesin family member 4	1.472	1.457
<i>Kirrel</i>	NM_001170985	kirre like nephrin family adhesion molecule 1	1.295	0.459
<i>Kiss1r</i>	NM_053244	KISS1 receptor	1.194	-0.070
<i>Klc3</i>	NM_001286038	kinesin light chain 3	-2.284	-0.916
<i>Klf11</i>	NM_178357	Kruppel-like factor 11	1.447	3.631
<i>Klf5</i>	NM_009769	Kruppel-like factor 5	1.171	-0.780
<i>Klhl14</i>	NM_001081403	kelch-like 14	-1.063	3.196
<i>Klk13</i>	NM_001039042	kallikrein related-peptidase 13	-1.071	-0.538
<i>Klk4</i>	NM_019928	kallikrein related-peptidase 4 (prostase, enamel matrix, prostate)	2.348	-0.781
<i>Klrd1</i>	NM_010654	killer cell lectin-like receptor, subfamily D, member 1	2.034	0.458
<i>Krt8</i>	NM_031170	keratin 8	-1.091	0.570
<i>LOC106740</i>	NR_027905	uncharacterized LOC106740	-1.147	1.319
<i>Lag3</i>	NM_008479	lymphocyte-activation gene 3	1.202	0.403
<i>Lamb1</i>	NM_008482	laminin B1	-2.057	0.011
<i>Lamb2</i>	NM_008483	laminin, beta 2	1.062	3.212
<i>Lbx2</i>	NM_010692	ladybird homeobox 2	1.428	-0.655
<i>Lepr</i>	NM_001122899	leptin receptor	-1.280	0.518
<i>Lhfp</i>	NM_175386	lipoma HMGIC fusion partner	-2.468	0.288
<i>Liph</i>	NM_001083894	lipase, member H	1.773	0.282
<i>Lnx1</i>	NM_001159577	ligand of numb-protein X 1	-2.506	0.936
<i>Lox</i>	NM_001286181	lysyl oxidase	-1.289	-0.431
<i>Lrrc19</i>	NM_001356281	leucine rich repeat containing 19	1.171	-0.780
<i>Lrrc27</i>	NM_001143755	leucine rich repeat containing 27	3.447	-0.072
<i>Lta</i>	NM_010735	lymphotoxin A	-1.498	0.464
<i>Ltk</i>	NM_008523	leukocyte tyrosine kinase	-1.458	0.222
<i>Ly6c1</i>	NM_001252055	lymphocyte antigen 6 complex, locus C1	1.194	-0.070
<i>Ly6c2</i>	NM_001099217	lymphocyte antigen 6 complex, locus C2	-1.479	-0.331
<i>Lym7</i>	NM_029327	LYR motif containing 7	-1.458	0.222
<i>Lyve1</i>	NM_053247	lymphatic vessel endothelial hyaluronan receptor 1	-1.306	4.445
<i>Maged2</i>	NM_001199246	melanoma antigen, family D, 2	1.026	2.199
<i>Mak</i>	NM_001145802	male germ cell-associated kinase	-5.666	-0.916
<i>Mamdc4</i>	NM_001081199	MAM domain containing 4	2.008	0.712
<i>Mansc4</i>	NM_001034903	MANSC domain containing 4	1.445	-0.240
<i>Masp2</i>	NM_001003893	mannan-binding lectin serine peptidase 2	-1.158	1.012
<i>Mboat1</i>	NM_153546	membrane bound O-acyltransferase domain containing 1	1.450	2.058
<i>Mcm6</i>	NM_001313695	minichromosome maintenance complex component 6	1.042	4.138
<i>Mcoln3</i>	NM_134160	mucopolip 3	-1.344	0.155
<i>Mctp1</i>	NM_030174	multiple C2 domains, transmembrane 1	1.542	4.059

<i>Mefv</i>	NM_001161790	Mediterranean fever	-1.842	0.464
<i>Meik</i>	NM_010790	maternal embryonic leucine zipper kinase	1.463	0.566
<i>Meox1</i>	NM_010791	mesenchyme homeobox 1	1.428	-0.655
<i>Met</i>	NM_008591	met proto-oncogene	1.044	-0.153
<i>Mfrp</i>	NM_001190314	membrane frizzled-related protein	1.089	-0.433
<i>Mgll</i>	NM_001166249	monoglyceride lipase	3.902	1.585
<i>Mgmt</i>	NM_008598	O-6-methylguanine-DNA methyltransferase	1.020	1.539
<i>Mid1</i>	NM_001290504	midline 1	-1.145	2.440
<i>Mkx</i>	NM_177595	mohawk homeobox	7.207	0.280
<i>Mmp12</i>	NM_001320076	matrix metalloproteinase 12	-1.369	-0.779
<i>Mmp14</i>	NM_008608	matrix metalloproteinase 14 (membrane-inserted)	-1.647	-0.237
<i>Mmp24</i>	NM_010808	matrix metalloproteinase 24	1.005	1.151
<i>Mmp25</i>	NM_001033339	matrix metalloproteinase 25	2.528	1.535
<i>Mmp8</i>	NM_008611	matrix metalloproteinase 8	-1.188	0.463
<i>Mmrn2</i>	NM_153127	multimerin 2	5.783	-0.781
<i>Mogat1</i>	NM_026713	monoacylglycerol O-acyltransferase 1	1.127	1.430
<i>Morn4</i>	NM_198108	MORN repeat containing 4	-1.056	-0.917
<i>Mrgpra4</i>	NM_153524	MAS-related GPR, member A4	1.017	0.082
<i>Mrgprx1</i>	NM_207540	MAS-related GPR, member X1	-5.666	-0.916
<i>Mroh2a</i>	NM_001177364	maestro heat-like repeat family member 2A	2.756	-0.540
<i>Ms4a7</i>	NM_001025610	membrane-spanning 4-domains, subfamily A, member 7	-2.760	-0.653
<i>Msln</i>	NM_001356286	mesothelin	1.278	-0.333
<i>Msrb3</i>	NM_177092	methionine sulfoxide reductase B3	1.171	-0.780
<i>Mt2</i>	NM_008630	metallothionein 2	-1.955	0.765
<i>Mtcp1</i>	NM_001039373	mature T cell proliferation 1	-1.069	1.995
<i>Mtfn1</i>	NM_026443	mitochondrial fission process 1	1.533	0.802
<i>Mtfr</i>	NM_027930	mitochondrial fission regulator 2	2.566	-0.655
<i>Mtss1l</i>	NM_001310591	metastasis suppressor 1-like	-1.877	0.223
<i>Mtus2</i>	NM_029920	microtubule associated tumor suppressor candidate 2	1.739	1.114
<i>Mup19</i>	NM_001135127	major urinary protein 19	8.042	1.002
<i>Mup21</i>	NM_001009550	major urinary protein 21	-1.056	-0.917
<i>Mustn1</i>	NM_181390	musculoskeletal, embryonic nuclear protein 1	1.044	-0.153
<i>Mutyh</i>	NM_001159581	mutY DNA glycosylase	1.209	1.043
<i>Mybpc3</i>	NM_008653	myosin binding protein C, cardiac	-2.057	0.011
<i>Myh6</i>	NM_001164171	myosin, heavy polypeptide 6, cardiac muscle, alpha	2.091	-0.918
<i>Myh7</i>	NM_080728	myosin, heavy polypeptide 7, cardiac muscle, beta	2.184	2.749
<i>Mylk</i>	NM_139300	myosin, light polypeptide kinase	4.091	1.751
<i>Mylk3</i>	NM_001297612	myosin light chain kinase 3	1.952	0.402
<i>Myo5b</i>	NM_008661	myosin VB	-1.670	0.764
<i>Myzap</i>	NM_001033208	myocardial zonula adherens protein	-1.546	1.673
<i>Naalad1</i>	NM_001009546	N-acetylated alpha-linked acidic dipeptidase-like 1	6.770	-0.072
<i>Nanog</i>	NM_001289828	Nanog homeobox	-1.219	1.049
<i>Nap1l5</i>	NM_021432	nucleosome assembly protein 1-like 5	-1.057	1.598
<i>Nat14</i>	NM_201355	N-acetyltransferase 14	-1.071	-0.538
<i>Ncapg</i>	NM_019438	non-SMC condensin I complex, subunit G	1.607	1.311
<i>Ndufaf6</i>	NM_001085493	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	1.150	1.006
<i>Ndufb2</i>	NM_026612	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	1.272	2.561
<i>Neto2</i>	NM_001081324	neuropilin (NRP) and tolloid (TLL)-like 2	-1.842	0.464
<i>Neurod4</i>	NM_001329489	neurogenic differentiation 4	-1.454	1.697
<i>Ngp</i>	NM_008694	neutrophilic granule protein	-6.652	-0.236
<i>Nhsl1</i>	NM_001163592	NHS-like 1	-1.071	-0.538
<i>Nkapl</i>	NM_025719	NFKB activating protein-like	5.565	-0.919
<i>Nlrp4f</i>	NM_175290	NLR family, pyrin domain containing 4F	2.923	-0.434
<i>Nmral1</i>	NM_001290761	NmrA-like family domain containing 1	1.115	2.148
<i>Nphp1</i>	NM_001291012	nephronophthisis 1 (juvenile) homolog (human)	1.365	1.925
<i>Nptxr</i>	NM_030689	neuronal pentraxin receptor	-5.666	-0.916
<i>Nr1d1</i>	NM_145434	nuclear receptor subfamily 1, group D, member 1	-1.633	4.113
<i>Nr2f2</i>	NM_009697	nuclear receptor subfamily 2, group F, member 2	-1.055	1.519
<i>Nr4a2</i>	NM_001139509	nuclear receptor subfamily 4, group A, member 2	-1.288	1.409
<i>Nrap</i>	NM_001286552	nebulin-related anchoring protein	1.230	1.756
<i>Nrg2</i>	NM_001167891	neuregulin 2	-1.201	0.286
<i>Nsg1</i>	NM_010942	neuron specific gene family member 1	-1.280	0.518
<i>Ntmt1</i>	NM_001356433	N-terminal Xaa-Pro-Lys N-methyltransferase 1	1.074	2.427
<i>Ntn3</i>	NM_010947	netrin 3	-1.089	0.407
<i>Nubpl</i>	NM_029760	nucleotide binding protein-like	1.048	1.985
<i>Nudt12</i>	NM_026497	nudix (nucleoside diphosphate linked moiety X)-type motif 12	1.295	0.459
<i>Nxpe2</i>	NM_030069	neurexophilin and PC-esterase domain family, member 2	-1.220	0.084
<i>Nyap1</i>	NM_001347505	neuronal tyrosine-phosphorylated phosphoinositide 3-kinase adaptor 1	-1.260	0.670
<i>Olfml2b</i>	NM_177068	olfactomedin-like 2B	2.731	0.150
<i>Olf164</i>	NM_146451	olfactory receptor 164	-1.505	0.974
<i>Olf173</i>	NM_147000	olfactory receptor 173	2.348	-0.781
<i>Oosp2</i>	NM_001037634	oocyte secreted protein 2	-1.056	-0.917
<i>Ophn1</i>	NM_001313754	oligophrenin 1	-1.627	-0.653023
<i>Orc1</i>	NM_001014425	origin recognition complex, subunit 1	1.104	0.344252
<i>Osbpl6</i>	NM_001290733	oxysterol binding protein-like 6	-1.047	2.192468
<i>Pabpc1l</i>	NM_001114079	poly(A) binding protein, cytoplasmic 1-like	-1.056	-0.916557
<i>Pacsin3</i>	NM_001289677	protein kinase C and casein kinase substrate in neurons 3	1.855	0.006901
<i>Panct2</i>	NR_131964	pluripotency-associated noncoding transcript 2	-1.134	1.787863
<i>Paqr5</i>	NM_028748	progesterin and adipoQ receptor family member V	-3.267	-0.329881
<i>Paqr8</i>	NM_001355122	progesterin and adipoQ receptor family member VIII	-1.028	0.933337
<i>Pard6b</i>	NM_021409	par-6 family cell polarity regulator beta	-1.458	0.222414
<i>Pbk</i>	NM_023209	PDZ binding kinase	1.104	0.344252
<i>Pbld2</i>	NM_026085	phenazine biosynthesis-like protein domain containing 2	2.348	-0.780762

<i>Pcbd1</i>	NM_025273	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	2.153	-0.240841
<i>Pcdh1</i>	NM_029357	protocadherin 1	1.674	0.218224
<i>Pcdhac2</i>	NM_001003672	protocadherin alpha subfamily C, 2	-2.760	-0.652535
<i>Pcdhb16</i>	NM_053141	protocadherin beta 16	1.278	-0.333247
<i>Pcdhga6</i>	NM_033589	protocadherin gamma subfamily A, 6	-1.585	0.518551
<i>Pcdhga8</i>	NM_033591	protocadherin gamma subfamily A, 8	-1.123	2.381819
<i>Pcgf2</i>	NM_001163307	polycomb group ring finger 2	-1.089	0.406607
<i>Pcsk4</i>	NM_008793	proprotein convertase subtilisin/kexin type 4	-1.289	-0.430623
<i>Pcsk9</i>	NM_153565	proprotein convertase subtilisin/kexin type 9	2.153	-0.240841
<i>Pcyt1b</i>	NM_177546	phosphate cytidyltransferase 1, choline, beta isoform	-1.976	0.287240
<i>Pdk4</i>	NM_013743	pyruvate dehydrogenase kinase, isoenzyme 4	9.394	2.253892
<i>Peg10</i>	NM_001040611	paternally expressed 10	1.445	-0.240363
<i>Perm1</i>	NM_172417	PPARGC1 and ESRR induced regulator, muscle 1	-1.585	0.518551
<i>Pex11a</i>	NM_011068	peroxisomal biogenesis factor 11 alpha	1.692	1.370829
<i>Pfn4</i>	NM_028376	profilin family, member 4	-2.284	-0.916065
<i>Pgf</i>	NM_001271705	placental growth factor	5.972	-0.655947
<i>Pglyrp1</i>	NM_009402	peptidoglycan recognition protein 1	1.305	3.018613
<i>Phex</i>	NM_011077	phosphate regulating endopeptidase homolog, X-linked	1.835	-0.433038
<i>Piezo2</i>	NM_001039485	piezo-type mechanosensitive ion channel component 2	-2.760	-0.652535
<i>Pigr</i>	NM_011082	polymeric immunoglobulin receptor	-1.038	1.975049
<i>Pira1</i>	NM_011087	paired-Ig-like receptor A1	1.455	5.640761
<i>Pitpnm2os1</i>	NR_045369	phosphatidylinositol transfer protein, membrane-associated 2, opposite strand 1	-1.056	-0.916557
<i>Pkhd11</i>	NM_138674	polycystic kidney and hepatic disease 1-like 1	1.361	0.282604
<i>Pla2g3</i>	NM_172791	phospholipase A2, group III	7.207	0.280291
<i>Pla2r1</i>	NM_008867	phospholipase A2 receptor 1	1.428	-0.654973
<i>Plagl1</i>	NM_009538	pleiomorphic adenoma gene-like 1	-2.284	-0.916065
<i>Platr26</i>	NM_201366	pluripotency associated transcript 26	1.646	-0.539725
<i>Plat1</i>	NM_029639	placenta expressed transcript 1	1.428	-0.654973
<i>Plin2</i>	NM_007408	perilipin 2	1.572	7.557100
<i>Plvap</i>	NM_032398	plasmalemma vesicle associated protein	1.646	-0.539725
<i>Pmel</i>	NM_021882	premelanosome protein	1.044	-0.152647
<i>Pnpla1</i>	NM_001034885	patatin-like phospholipase domain containing 1	-1.202	1.256299
<i>Pnpla3</i>	NM_054088	patatin-like phospholipase domain containing 3	2.003	-0.333727
<i>Pon1</i>	NM_011134	paraoxonase 1	-2.284	-0.916065
<i>Postn</i>	NM_001198765	periostin, osteoblast specific factor	1.418	2.411712
<i>Pparg</i>	NM_001127330	peroxisome proliferator activated receptor gamma	-1.087	0.221948
<i>Ppic</i>	NM_008908	peptidylprolyl isomerase C	2.091	-0.918034
<i>Ppm1j</i>	NM_027982	protein phosphatase 1J	-1.307	0.347944
<i>Ppp1r26</i>	NM_001005420	protein phosphatase 1, regulatory subunit 26	1.143	1.342511
<i>Ppp1r32</i>	NM_133689	protein phosphatase 1, regulatory subunit 32	-2.034	-0.430140
<i>Prmel5</i>	NM_001085418	preferentially expressed antigen in melanoma like 5	-1.627	-0.653023
<i>Prc1</i>	NM_001285997	protein regulator of cytokinesis 1	1.093	2.294520
<i>Prdm1</i>	NM_007548	PR domain containing 1, with ZNF domain	-1.185	2.509293
<i>Prdm16</i>	NM_001177995	PR domain containing 16	-3.403	-0.236534
<i>Prickle4</i>	NM_001290337	prickle planar cell polarity protein 4	-1.056	-0.916557
<i>Prkag3</i>	NM_153744	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	1.171	-0.780272
<i>Prob1</i>	NM_001270646	proline rich basic protein 1	-1.709	1.957897
<i>Proser2</i>	NM_001159657	proline and serine rich 2	1.674	0.218224
<i>Prrg1</i>	NM_001164275	proline rich Gla (G-carboxyglutamic acid) 1	-2.488	-0.149312
<i>Prss23</i>	NM_029614	protease, serine 23	-2.760	-0.652535
<i>Prss30</i>	NM_013921	protease, serine 30	-1.056	-0.916557
<i>Prss35</i>	NM_178738	protease, serine 35	-1.099	2.013879
<i>Prtg</i>	NM_175485	protogenin	-1.289	-0.430623
<i>Prx</i>	NM_019412	periaxin	1.463	0.565801
<i>Psmb11</i>	NM_175204	proteasome (prosome, macropain) subunit, beta type, 11	2.091	-0.918034
<i>Psmc3ip</i>	NM_008949	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	-1.289	-0.430623
<i>Ptgdr2</i>	NM_009962	prostaglandin D2 receptor 2	1.194	-0.704009
<i>Ptk6</i>	NM_001356304	PTK6 protein tyrosine kinase 6	-1.071	-0.537785
<i>Ptpnd</i>	NM_001014288	protein tyrosine phosphatase, receptor type, D	-1.535	1.573551
<i>Ptpnu</i>	NM_001083119	protein tyrosine phosphatase, receptor type, U	-1.380	0.893358
<i>R74862</i>	NM_133790	expressed sequence R74862	-1.172	1.742795
<i>Rab20</i>	NM_011227	RAB20, member RAS oncogene family	-1.257	1.648200
<i>Rab30</i>	NM_029494	RAB30, member RAS oncogene family	-1.002	3.228400
<i>Rab34</i>	NM_001159482	RAB34, member RAS oncogene family	-1.444	0.934214
<i>Rab36</i>	NM_029781	RAB36, member RAS oncogene family	1.089	-0.432555
<i>Rab37</i>	NM_001163753	RAB37, member RAS oncogene family	1.006	2.427837
<i>Rab3b</i>	NM_023537	RAB3B, member RAS oncogene family	-2.715	0.465252
<i>Rab40b</i>	NM_139147	Rab40B, member RAS oncogene family	5.783	-0.781251
<i>Rab44</i>	NM_001002786	RAB44, member RAS oncogene family	1.085	4.311332
<i>Rab6b</i>	NM_173781	RAB6B, member RAS oncogene family	-1.479	-0.330843
<i>Rad51</i>	NM_011234	RAD51 recombinase	1.407	0.887200
<i>Rad54b</i>	NM_001039556	RAD54 homolog B (S. cerevisiae)	-1.079	-0.237971
<i>Radil</i>	NM_001289588	Ras association and DIL domains	-5.666	-0.915573
<i>Ramp1</i>	NM_001168392	receptor (calcitonin) activity modifying protein 1	-1.463	1.319860
<i>Rbfox3</i>	NM_001024931	RNA binding protein, fox-1 homolog (C. elegans) 3	2.149	2.846396
<i>Rcor2</i>	NM_001320554	REST corepressor 2	1.141	0.151793
<i>Rdh5</i>	NM_134006	retinol dehydrogenase 5	1.646	-0.539725
<i>Rdh7</i>	NM_001150749	retinol dehydrogenase 7	1.171	-0.780272
<i>Rec114</i>	NM_028598	REC114 meiotic recombination protein	1.595	-0.153123
<i>Reep1</i>	NM_178608	receptor accessory protein 1	-1.011	0.669868
<i>Reep2</i>	NM_001204914	receptor accessory protein 2	-1.188	0.463420
<i>Rel12</i>	NM_153793	RELT-like 2	-1.289	-0.430623
<i>Rem1</i>	NM_009047	rad and gem related GTP binding protein 1	-1.141	1.492724

<i>Retnlg</i>	NM_181596	resistin like gamma	1.427	2.112074
<i>Rfc4</i>	NM_145480	replication factor C (activator 1) 4	1.316	1.964864
<i>Rftn2</i>	NM_001356287	raftlin family member 2	-1.173	3.055008
<i>Rgcc</i>	NM_025427	regulator of cell cycle	1.639	0.458847
<i>Rgs13</i>	NM_153171	regulator of G-protein signaling 13	-1.406	0.407067
<i>Rgs7bp</i>	NM_029879	regulator of G-protein signalling 7 binding protein	2.091	-0.918034
<i>Rhbdd3</i>	NM_001290491	rhomboid domain containing 3	1.031	2.399218
<i>Rhebl1</i>	NM_026967	Ras homolog enriched in brain like 1	1.014	1.043833
<i>Rhobtb3</i>	NM_028493	Rho-related BTB domain containing 3	-1.056	-0.916557
<i>Rimbp3</i>	NM_001033338	RIMS binding protein 3	-1.056	-0.916557
<i>Rln3</i>	NM_173184	relaxin 3	-1.056	-0.916557
<i>Rmi2</i>	NM_001033278	RecQ mediated genome instability 2	1.150	1.006123
<i>Rmp</i>	NR_001460	RNA component of mitochondrial RNAase P	1.120	8.192853
<i>Rnaset2b</i>	NM_026611	ribonuclease T2B	-1.110	3.906453
<i>Rnf148</i>	NM_027754	ring finger protein 148	-2.541	-0.778313
<i>Rnf180</i>	NM_027934	ring finger protein 180	-1.011	0.669868
<i>Rnf39</i>	NM_001099632	ring finger protein 39	-1.220	0.084442
<i>Rnf43</i>	NM_172448	ring finger protein 43	-1.024	2.928075
<i>Ropn1l</i>	NM_145852	ropporin 1-like	1.194	-0.070409
<i>Ror1</i>	NM_001312690	receptor tyrosine kinase-like orphan receptor 1	-1.247	-0.150266
<i>Rpl14-ps1</i>	NR_110499	ribosomal protein L14, pseudogene 1	1.784	1.562650
<i>Rpl22l1</i>	NM_001347226	ribosomal protein L22 like 1	1.934	4.613764
<i>Rpl26</i>	NM_009080	ribosomal protein L26	1.679	3.677328
<i>Rpl39</i>	NM_026055	ribosomal protein L39	1.060	7.657849
<i>Rpl3</i>	NR_024198	ribonuclease P RNA-like 3	-1.330	8.980465
<i>Rps15a-ps4</i>	NR_036572	ribosomal protein S15A, pseudogene 4	1.309	3.152171
<i>Rragb</i>	NM_001004154	Ras-related GTP binding B	-1.158	1.011769
<i>Rsad2</i>	NM_021384	radical S-adenosyl methionine domain containing 2	1.454	0.081154
<i>Rsph3b</i>	NM_001083945	radial spoke 3B homolog (Chlamydomonas)	-1.028	1.787472
<i>Rwdd2a</i>	NM_001145968	RWD domain containing 2A	1.175	0.887639
<i>Rwdd3</i>	NM_025637	RWD domain containing 3	-1.092	0.717397
<i>S100a5</i>	NM_011312	S100 calcium binding protein A5	1.428	-0.654973
<i>S100a9</i>	NM_001281852	S100 calcium binding protein A9 (calgranulin B)	-2.897	2.417844
<i>S1pr3</i>	NM_010101	sphingosine-1-phosphate receptor 3	-1.793	1.548179
<i>Saa1</i>	NM_001357493	serum amyloid A 1	1.020	1.538851
<i>Sag</i>	NM_009118	S-antigen, retina and pineal gland (arrestin)	-1.670	0.764314
<i>Sall2</i>	NM_001244916	spalt like transcription factor 2	2.003	-0.333727
<i>Samd4</i>	NM_001037221	sterile alpha motif domain containing 4	-2.284	-0.916065
<i>Sapcd2</i>	NM_001081085	suppressor APC domain containing 2	1.171	-0.780272
<i>Scama6</i>	NR_028519	small Cajal body-specific RNA 6	2.371	1.586809
<i>Sccpdh</i>	NM_178653	saccharopine dehydrogenase (putative)	1.133	2.041290
<i>Scn3b</i>	NM_001083917	sodium channel, voltage-gated, type III, beta	-1.674	1.087055
<i>Scn4a</i>	NM_133199	sodium channel, voltage-gated, type IV, alpha	-1.324	3.762057
<i>Scnn1a</i>	NM_011324	sodium channel, nonvoltage-gated 1 alpha	-2.284	-0.916065
<i>Sdc2</i>	NM_008304	syndecan 2	2.091	-0.918034
<i>Sdk1</i>	NM_177879	sidekick cell adhesion molecule 1	1.141	0.151793
<i>Sdsl</i>	NM_133902	serine dehydratase-like	1.322	0.665374
<i>Sec16b</i>	NM_001159986	SEC16 homolog B (S. cerevisiae)	1.881	1.215626
<i>Sema3g</i>	NM_001025379	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	1.017	0.081623
<i>Sema4g</i>	NM_011976	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin)	-1.737	0.808924
<i>Serpina10</i>	NM_001301404	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 10	1.044	-0.152647
<i>Serpinb6b</i>	NM_011454	serine (or cysteine) peptidase inhibitor, clade B, member 6b	-1.087	0.221948
<i>Serpinb7</i>	NM_027548	serine (or cysteine) peptidase inhibitor, clade B, member 7	-1.056	-0.916557
<i>Serpinf1</i>	NM_011340	serine (or cysteine) peptidase inhibitor, clade F, member 1	-2.284	-0.916065
<i>Setd4</i>	NM_145482	SET domain containing 4	1.422	1.183493
<i>Sez6l2</i>	NM_001252566	seizure related 6 homolog like 2	-1.034	1.049023
<i>Sh2b2</i>	NM_001302938	SH2B adaptor protein 2	-1.048	3.435303
<i>Sh2d1a</i>	NM_001313688	SH2 domain containing 1A	1.428	-0.654973
<i>Shcgp1</i>	NM_011369	Shc SH2-domain binding protein 1	2.824	0.217295
<i>Shf</i>	NM_001013829	Src homology 2 domain containing F	-1.458	0.222414
<i>Shisa2</i>	NM_145463	shisa family member 2	6.140	-0.540695
<i>Shisa7</i>	NM_001290291	shisa family member 7	-3.024	0.223813
<i>Siglecf</i>	NM_001271019	sialic acid binding Ig-like lectin F	4.393	2.951597
<i>Skida1</i>	NM_028317	SKI/DACH domain containing 1	5.565	-0.918525
<i>Slain1os</i>	NR_045148	SLAIN motif family, member 1, opposite strand	-1.564	1.012639
<i>Slc16a8</i>	NM_020516	solute carrier family 16 (monocarboxylic acid transporters), member 8	2.348	-0.780762
<i>Slc18a1</i>	NM_153054	solute carrier family 18 (vesicular monoamine), member 1	2.348	-0.780762
<i>Slc22a4</i>	NM_001330304	solute carrier family 22 (organic cation transporter), member 4	1.460	0.343791
<i>Slc25a18</i>	NM_001081048	solute carrier family 25 (mitochondrial carrier), member 18	1.025	0.928519
<i>Slc25a31</i>	NM_178386	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	1.171	-0.780272
<i>Slc25a47</i>	NM_001012310	solute carrier family 25, member 47	-1.877	0.222881
<i>Slc27a5</i>	NM_009512	solute carrier family 27 (fatty acid transporter), member 5	1.835	-0.433038
<i>Slc29a4</i>	NM_146257	solute carrier family 29 (nucleoside transporters), member 4	-1.585	0.518551
<i>Slc2a10</i>	NM_130451	solute carrier family 2 (facilitated glucose transporter), member 10	1.445	-0.240363
<i>Slc2a5</i>	NM_019741	solute carrier family 2 (facilitated glucose transporter), member 5	2.153	-0.240841
<i>Slc39a12</i>	NM_001012305	solute carrier family 39 (zinc transporter), member 12	-1.627	-0.653023
<i>Slc43a3</i>	NM_021398	solute carrier family 43, member 3	1.059	1.184343
<i>Slc46a2</i>	NM_021053	solute carrier family 46, member 2	-1.056	-0.916557
<i>Slc4a10</i>	NM_001242378	solute carrier family 4, sodium bicarbonate cotransporter-like, member 10	-1.533	0.010676
<i>Slc6a9</i>	NM_001355175	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	1.089	-0.432555
<i>Slco1b2</i>	NM_020495	solute carrier organic anion transporter family, member 1b2	-1.056	-0.916557
<i>Slco4c1</i>	NM_172658	solute carrier organic anion transporter family, member 4C1	5.783	-0.781251
<i>Slfn1</i>	NM_177570	schlafen like 1	-1.056	-0.916557

<i>Slit2</i>	NM_001291227	slit guidance ligand 2	-2.949	-0.536813
<i>Smim5</i>	NM_183259	small integral membrane protein 5	-1.627	-0.653023
<i>Snap91</i>	NM_001277982	synaptosomal-associated protein 91	-2.541	-0.778313
<i>Snhg10</i>	NR_003145	small nucleolar RNA host gene 10	5.972	-0.655947
<i>Snhg18</i>	NR_038186	small nucleolar RNA host gene 18	-1.481	0.808480
<i>Snora23</i>	NR_033336	small nucleolar RNA, H/ACA box 23	3.209	-0.241319
<i>Snord15a</i>	NR_002172	small nucleolar RNA, C/D box 15A	1.428	-0.654973
<i>Snord15b</i>	NR_002173	small nucleolar RNA, C/D box 14B	-1.397	-0.067564
<i>Sorbs2</i>	NM_001205219	sorbin and SH3 domain containing 2	-2.155	0.407987
<i>Sox4</i>	NM_009238	SRY (sex determining region Y)-box 4	1.835	-0.433038
<i>Sox5os3</i>	NR_040519	SRY (sex determining region Y)-box 5, opposite strand 3	-1.470	1.086624
<i>Sox6</i>	NM_001025559	SRY (sex determining region Y)-box 6	-1.715	1.599678
<i>Sp3os</i>	NM_183265	trans-acting transcription factor 3, opposite strand	-1.873	1.225370
<i>Spag6</i>	NM_001001334	sperm associated antigen 6	-5.666	-0.915573
<i>Spam1</i>	NM_001079875	sperm adhesion molecule 1	1.835	-0.433038
<i>Sparc</i>	NM_001290817	secreted acidic cysteine rich glycoprotein	1.460	0.343791
<i>Spata7</i>	NM_001289572	spermatogenesis associated 7	-1.417	1.493543
<i>Spc25</i>	NM_001199123	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	1.109	0.846021
<i>Spp1</i>	NM_001204201	secreted phosphoprotein 1	1.391	3.770646
<i>Sptbn4</i>	NM_001199234	spectrin beta, non-erythrocytic 4	1.278	-0.333247
<i>Srd5a1</i>	NM_175283	steroid 5 alpha-reductase 1	2.266	0.281679
<i>Ssc4d</i>	NM_001160366	scavenger receptor cysteine rich family, 4 domains	1.541	0.616221
<i>Sstr4</i>	NM_009219	somatostatin receptor 4	-1.178	0.621185
<i>Stag3</i>	NM_016964	stromal antigen 3	1.270	3.028127
<i>Stard10</i>	NM_019990	START domain containing 10	-1.041	2.032539
<i>Stc1</i>	NM_009285	stanniocalcin 1	1.428	-0.654973
<i>Stc2</i>	NM_011491	stanniocalcin 2	-1.369	-0.778803
<i>Steap4</i>	NM_054098	STEAP family member 4	-3.219	1.747918
<i>Stil</i>	NM_001304551	Scf/Tal1 interrupting locus	1.463	0.565801
<i>Stmn1</i>	NM_019641	stathmin 1	1.647	3.044369
<i>Sult4a1</i>	NM_001356515	sulfotransferase family 4A, member 1	2.153	-0.240841
<i>Syde1</i>	NM_027875	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	1.595	-0.153123
<i>Syne1</i>	NM_001079686	spectrin repeat containing, nuclear envelope 1	1.211	5.960392
<i>Syt12</i>	NM_134164	synaptotagmin XII	-2.541	-0.778313
<i>Syt11</i>	NM_031393	synaptotagmin-like 1	1.124	2.095628
<i>Syt14</i>	NM_001290717	synaptotagmin-like 4	1.646	-0.539725
<i>Tagln3</i>	NM_019754	transgelin 3	2.756	-0.540210
<i>Tarm1</i>	NM_177363	T cell-interacting, activating receptor on myeloid cells 1	-1.087	0.221948
<i>Tat</i>	NM_146214	tyrosine aminotransferase	-1.079	-0.237971
<i>Tbx2</i>	NM_009324	T-box 2	-1.056	-0.916557
<i>Tc2n</i>	NM_001082976	tandem C2 domains, nuclear	-1.071	-0.537785
<i>Tcaf2</i>	NM_146174	TRPM8 channel-associated factor 2	-1.220	0.084442
<i>Tceal1</i>	NM_001356367	transcription elongation factor A (SII)-like 1	2.091	-0.918034
<i>Tcerg1l</i>	NM_183289	transcription elongation regulator 1-like	1.646	-0.539725
<i>Tcf23</i>	NM_053085	transcription factor 23	1.751	0.757631
<i>Tdrkh</i>	NM_028307	tudor and KH domain containing protein	1.123	2.263104
<i>Tead1</i>	NM_001166584	TEA domain family member 1	-2.760	-0.652535
<i>Teddm1a</i>	NM_178244	transmembrane epididymal protein 1A	1.646	-0.539725
<i>Teddm1b</i>	NM_001008426	transmembrane epididymal protein 1B	-1.369	-0.778803
<i>Tesc</i>	NM_021344	tescalcin	1.055	0.665823
<i>Tex11</i>	NM_001167997	testis expressed gene 11	1.171	-0.780272
<i>Tex15</i>	NM_031374	testis expressed gene 15	-1.247	-0.150266
<i>Tex22</i>	NM_029381	testis expressed gene 22	2.923	-0.433520
<i>Tgfb3</i>	NM_009368	transforming growth factor, beta 3	1.194	-0.070409
<i>Thbs1</i>	NM_001313914	thrombospondin 1	1.438	7.101035
<i>Themis</i>	NM_001305663	thymocyte selection associated	1.126	1.687559
<i>Ticrr</i>	NM_029835	TOPBP1-interacting checkpoint and replication regulator	1.047	1.281488
<i>Tigd3</i>	NM_198634	tigger transposable element derived 3	1.017	0.081623
<i>Tigit</i>	NM_001146325	T cell immunoreceptor with Ig and ITIM domains	1.089	-0.432555
<i>Tlr5</i>	NM_016928	toll-like receptor 5	1.171	-0.780272
<i>Tm6sf2</i>	NM_001293795	transmembrane 6 superfamily member 2	1.445	-0.240363
<i>Tmc4</i>	NM_181820	transmembrane channel-like gene family 4	-1.097	1.379130
<i>Tmem117</i>	NM_178789	transmembrane protein 117	-1.627	-0.653023
<i>Tmem14a</i>	NM_001290679	transmembrane protein 14A	1.278	-0.333247
<i>Tmem160</i>	NM_026938	transmembrane protein 160	1.081	4.473179
<i>Tmem17</i>	NM_153596	transmembrane protein 17	-1.647	-0.237492
<i>Tmem200b</i>	NM_001201367	transmembrane protein 200B	1.089	-0.432555
<i>Tmem205</i>	NM_001253867	transmembrane protein 205	1.007	2.883393
<i>Tmem216</i>	NM_001277860	transmembrane protein 216	1.176	1.639419
<i>Tmem221</i>	NM_001100462	transmembrane protein 221	-1.071	-0.537785
<i>Tmem229a</i>	NM_177013	transmembrane protein 229A	2.011	2.738187
<i>Tmem240</i>	NM_001101506	transmembrane protein 240	-1.533	0.010676
<i>Tmem254a</i>	NM_025311	transmembrane protein 254a	6.426	-0.334687
<i>Tmem254b</i>	NM_001270495	transmembrane protein 254b	-8.305	1.161709
<i>Tmem254c</i>	NM_001270498	transmembrane protein 254c	9.018	1.898420
<i>Tmem38a</i>	NM_001357278	transmembrane protein 38A	-1.449	0.621637
<i>Tmem81</i>	NM_029025	transmembrane protein 81	1.056	2.742923
<i>Tmem91</i>	NM_001290497	transmembrane protein 91	-2.541	-0.778313
<i>Tmem98</i>	NM_029537	transmembrane protein 98	-1.056	-0.916557
<i>Tmod4</i>	NM_016712	tropomodulin 4	-1.020	0.807591
<i>Tmsb15b1</i>	NM_001081983	thymosin beta 15b1	1.428	-0.654973
<i>Tnf</i>	NM_001278601	tumor necrosis factor	-1.281	2.243155
<i>Tnfrsf19</i>	NM_001164155	tumor necrosis factor receptor superfamily, member 19	1.162	1.249548

<i>Tnfsf14</i>	NM_019418	tumor necrosis factor (ligand) superfamily, member 14	1.761	1.661904
<i>Tnfsf18</i>	NM_183391	tumor necrosis factor (ligand) superfamily, member 18	-1.289	-0.430623
<i>Tnfsf9</i>	NM_009404	tumor necrosis factor (ligand) superfamily, member 9	-1.071	-0.537785
<i>Tnni3</i>	NM_009406	troponin I, cardiac 3	-1.369	-0.778803
<i>Tnnt3</i>	NM_001163664	troponin T3, skeletal, fast	-1.079	-0.237971
<i>Tnr</i>	NM_022312	tenascin R	-1.139	1.572338
<i>Top2a</i>	NM_011623	topoisomerase (DNA) II alpha	1.311	4.504489
<i>Tpbp</i>	NM_001164792	trophoblast glycoprotein	-1.079	-0.237971
<i>Tpx2</i>	NM_001141975	TPX2, microtubule-associated	1.382	2.440062
<i>Trim12a</i>	NM_023835	tripartite motif-containing 12A	2.566	-0.655460
<i>Trim36</i>	NM_001170855	tripartite motif-containing 36	1.153	1.538446
<i>Trim43b</i>	NM_001170884	tripartite motif-containing 43B	-1.056	-0.916557
<i>Trim6</i>	NM_001013616	tripartite motif-containing 6	5.565	-0.918525
<i>Trim72</i>	NM_001079932	tripartite motif-containing 72	1.475	2.002644
<i>Troap</i>	NM_001162506	trophinin associated protein	1.454	0.081154
<i>Trp53cor1</i>	NR_036469	tumor protein p53 pathway corepressor 1	1.044	-0.152647
<i>Trpc2</i>	NM_001109897	transient receptor potential cation channel, subfamily C, member 2	6.961	0.079277
<i>Trpm3</i>	NM_001035239	transient receptor potential cation channel, subfamily M, member 3	2.348	-0.780762
<i>Trpt1</i>	NM_153597	tRNA phosphotransferase 1	-1.657	0.084912
<i>Tspan33</i>	NM_001301407	tetraspanin 33	3.073	-0.334207
<i>Tspo</i>	NM_009775	translocator protein	1.089	6.158546
<i>Tssk4</i>	NM_001253888	testis-specific serine kinase 4	-1.071	-0.537785
<i>Tst</i>	NM_009437	thiosulfate sulfurtransferase, mitochondrial	2.112	0.512632
<i>Ttc39a</i>	NM_001145948	tetratricopeptide repeat domain 39A	1.330	0.007372
<i>Ttc9</i>	NM_001033149	tetratricopeptide repeat domain 9	-2.284	-0.916065
<i>Ttk</i>	NM_001110265	Ttk protein kinase	1.276	0.802712
<i>Tll11</i>	NM_028921	tubulin tyrosine ligase-like family, member 11	1.595	-0.153123
<i>Tll7</i>	NM_001302957	tubulin tyrosine ligase-like family, member 7	-2.541	-0.778313
<i>Tyh1</i>	NM_001001454	tweety family member 1	-1.289	-0.430623
<i>Tub</i>	NM_021885	tubby bipartite transcription factor	-1.141	2.562177
<i>Tubb3</i>	NM_023279	tubulin, beta 3 class III	1.133	0.713
<i>Tube1</i>	NM_028006	epsilon-tubulin 1	1.129	1.116
<i>Ubap1l</i>	NM_001111145	ubiquitin-associated protein 1-like	1.089	-0.433
<i>Ube2c</i>	NM_026785	ubiquitin-conjugating enzyme E2C	1.276	1.429
<i>Ube4bos3</i>	NR_131918	ubiquitination factor E4B, opposite strand 3	1.055	0.666
<i>Ugt1a9</i>	NM_201644	UDP glucuronosyltransferase 1 family, polypeptide A9	-6.392	-0.429
<i>Ugt2b5</i>	NM_009467	UDP glucuronosyltransferase 2 family, polypeptide B5	2.091	-0.918
<i>Uox</i>	NM_009474	urate oxidase	2.566	-0.655
<i>Vangl2</i>	NM_033509	VANGL planar cell polarity 2	1.569	0.151
<i>Vmn2r-ps129</i>	NR_033648	vomer nasal 2, receptor, pseudogene 129	-1.247	-0.150
<i>Vmn2r26</i>	NM_019917	vomer nasal 2, receptor 26	1.291	4.694
<i>Vmn2r84</i>	NM_001081448	vomer nasal 2, receptor 84	-2.637	0.408
<i>Whrn</i>	NM_001008791	whirlin	-1.021	3.332
<i>Wipf3</i>	NM_001167860	WAS/WASL interacting protein family, member 3	-1.481	0.808
<i>Wnt16</i>	NM_053116	wingless-type MMTV integration site family, member 16	-1.079	-0.238
<i>Wnt8b</i>	NM_011720	wingless-type MMTV integration site family, member 8B	-5.666	-0.916
<i>Wtip</i>	NM_207212	WT1-interacting protein	1.064	2.820
<i>Wwc1</i>	NM_170779	WW, C2 and coiled-coil domain containing 1	-1.369	-0.779
<i>Xkrr</i>	NM_183319	X-linked Kx blood group related, X-linked	1.461	3.490
<i>Xlr3b</i>	NM_001081643	X-linked lymphocyte-regulated 3B	-1.071	-0.538
<i>Xlr4a</i>	NM_001081642	X-linked lymphocyte-regulated 4A	-1.845	-0.537
<i>Xlr4b</i>	NM_001293676	X-linked lymphocyte-regulated 4B	-1.004	1.408
<i>Xlr4c</i>	NM_183094	X-linked lymphocyte-regulated 4C	-2.555	0.349
<i>Xpnpep2</i>	NM_001289729	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	1.017	0.082
<i>Xrra1</i>	NM_001164258	X-ray radiation resistance associated 1	1.428	-0.655
<i>Zbtb16</i>	NM_001033324	zinc finger and BTB domain containing 16	1.365	5.059
<i>Zdhhc2</i>	NM_001357249	zinc finger, DHHC domain containing 2	1.176	2.131
<i>Zfa-ps</i>	NM_009540	zinc finger protein, autosomal, pseudogene	1.731	-0.071
<i>Zfx2os</i>	NR_004444	zinc finger homeobox 2, opposite strand	-2.314	0.519
<i>Zfp30</i>	NM_013705	zinc finger protein 30	-1.170	0.763
<i>Zfp473</i>	NM_001289836	zinc finger protein 473	1.171	-0.780
<i>Zfp493</i>	NM_028402	zinc finger protein 493	-1.066	1.874
<i>Zfp503</i>	NM_145459	zinc finger protein 503	-1.600	0.718
<i>Zfp57</i>	NM_001013745	zinc finger protein 57	5.972	-0.656
<i>Zfp612</i>	NM_175480	zinc finger protein 612	-1.089	0.407
<i>Zfp72</i>	NM_001081680	zinc finger protein 72	-1.163	0.893
<i>Zfp827</i>	NM_001294279	zinc finger protein 827	-1.026	3.771
<i>Zfp867</i>	NM_178417	zinc finger protein 867	-1.149	2.888
<i>Zfp938</i>	NM_001105557	zinc finger protein 938	-1.156	2.106
<i>Zfp940</i>	NM_173738	zinc finger protein 940	-1.253	1.288
<i>Zfp941</i>	NM_001001180	zinc finger protein 941	2.153	-0.241
<i>Zfr2</i>	NM_001034895	zinc finger RNA binding protein 2	1.206	0.759
<i>Zkscan16</i>	NM_001099323	zinc finger with KRAB and SCAN domains 16	-1.071	-0.538
<i>Znhit3</i>	NM_001005223	zinc finger, HIT type 3	1.018	1.966

Table S2. Gene list using GO analysis in Figure 3A

Gene Symbol	Genbank accession	Description	Control / MCS	
			log2FC	log2CPM
<i>1500011K16Rik</i>	NM_175125	RIKEN cDNA 1500011K16 gene	1.206	3.336269
<i>1700071M16Rik</i>	NR_045444	RIKEN cDNA 1700071M16 gene	1.163	3.879029
<i>3110056K07Rik</i>	NR_045055	RIKEN cDNA 3110056K07 gene	-1.101	3.063772
<i>5031425F14Rik</i>	NR_015558	RIKEN cDNA 5031425F14 gene	1.173	3.118620
<i>Acrbp</i>	NM_001127340	proacrosin binding protein	-1.019	3.090596
<i>Adgrg5</i>	NM_001033468	adhesion G protein-coupled receptor G5	1.350	3.537420
<i>Agbl1</i>	NM_001199224	ATP/GTP binding protein-like 1	-1.278	3.154374
<i>Akap5</i>	NM_001101471	A kinase (PRKA) anchor protein 5	-1.457	3.000019
<i>Arap3</i>	NM_001205336	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	1.267	4.579340
<i>Ass1</i>	NM_007494	argininosuccinate synthetase 1	1.133	4.666438
<i>Atg16l2</i>	NM_001111111	autophagy related 16-like 2 (<i>S. cerevisiae</i>)	-1.010	3.161139
<i>Atp5e</i>	NM_025983	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	1.349	5.509464
<i>Atp6v0c-ps2</i>	NR_037854	ATPase, H+ transporting, lysosomal V0 subunit C, pseudogene 2	11.405	4.201016
<i>C1rl</i>	NM_181344	complement component 1, r subcomponent-like	1.386	3.808859
<i>Ca2ta1</i>	NM_001044308	calcium channel, voltage-dependent, alpha 1I subunit	-1.042	6.867565
<i>Ccr3</i>	NM_009914	chemokine (C-C motif) receptor 3	4.668	4.170687
<i>Ccs</i>	NM_016892	copper chaperone for superoxide dismutase	1.173	3.313859
<i>Cox7a2</i>	NM_009945	cytochrome c oxidase subunit VIIa 2	1.082	4.756301
<i>Cmp1</i>	NM_001136058	collapsin response mediator protein 1	-1.230	3.064642
<i>Cxcl13</i>	NM_018866	chemokine (C-X-C motif) ligand 13	-2.047	8.084261
<i>D130040H23Rik</i>	NM_172491	RIKEN cDNA D130040H23 gene	-1.004	3.564427
<i>Dbp</i>	NM_016974	D site albumin promoter binding protein	-1.600	3.711966
<i>Dtx1</i>	NM_008052	deltex 1, E3 ubiquitin ligase	-1.487	5.210563
<i>Dynl1b</i>	NM_009342	dynein light chain Tctex-type 1B	1.007	5.267176
<i>Egr1</i>	NM_007913	early growth response 1	-1.274	4.523850
<i>Fabp7</i>	NM_021272	fatty acid binding protein 7, brain	1.416	5.659176
<i>Fcgr4</i>	NM_144559	Fc receptor, IgG, low affinity IV	1.127	5.854742
<i>Fcmmr</i>	NM_026976	Fc fragment of IgM receptor	-1.416	6.130246
<i>Gm14308</i>	NM_001099349	predicted gene 14308	-1.644	4.433517
<i>Gm14430</i>	NM_001100415	predicted gene 14430	5.725	3.653902
<i>Gm17757</i>	NR_040453	GTPase, very large interferon inducible 1 pseudogene	2.239	5.902816
<i>Gm18853</i>	NR_040456	GTPase, very large interferon inducible 1 pseudogene	-12.831	5.588670
<i>Gm5424</i>	NR_002687	argininosuccinate synthase pseudogene	-1.564	4.676945
<i>Gm6644</i>	NR_028277	Akr1b3 pseudogene	12.240	5.022312
<i>Gvin1</i>	NM_001039160	GTPase, very large interferon inducible 1	-1.073	9.144623
<i>H2-T9</i>	NM_010399	histocompatibility 2, T region locus 9	1.158	3.766972
<i>Hal</i>	NM_010401	histidine ammonia lyase	-1.183	7.875363
<i>Hba-a1</i>	NM_008218	hemoglobin alpha, adult chain 1	6.398	3.366547
<i>Hba-a2</i>	NM_001083955	hemoglobin alpha, adult chain 2	11.868	4.656449
<i>Hbb-b1</i>	NM_001278161	hemoglobin, beta adult major chain	7.328	4.268307
<i>Hcst</i>	NM_011827	hematopoietic cell signal transducer	1.047	3.228529
<i>Hgf</i>	NM_001289458	hepatocyte growth factor	1.567	3.718730
<i>Hist1h1c</i>	NM_015786	histone cluster 1, H1c	1.115	6.450653
<i>Hist1h1d</i>	NM_145713	histone cluster 1, H1d	1.049	4.609709
<i>Hist1h2ao</i>	NM_001177544	histone cluster 1, H2ao	1.069	3.900243
<i>Id1</i>	NM_001355113	inhibitor of DNA binding 1	1.039	3.299522
<i>Ifi27</i>	NM_026790	interferon, alpha-inducible protein 27	1.023	5.078674
<i>Klf11</i>	NM_178357	Kruppel-like factor 11	1.447	3.631074
<i>Klhl14</i>	NM_001081403	kelch-like 14	-1.063	3.195577
<i>Lamb2</i>	NM_008483	laminin, beta 2	1.062	3.212174
<i>Lyve1</i>	NM_053247	lymphatic vessel endothelial hyaluronan receptor 1	-1.306	4.444605
<i>Mcm6</i>	NM_001313695	minichromosome maintenance complex component 6	1.042	4.138040
<i>Mctp1</i>	NM_030174	multiple C2 domains, transmembrane 1	1.542	4.058785
<i>Nr1d1</i>	NM_145434	nuclear receptor subfamily 1, group D, member 1	-1.633	4.112793
<i>Pglyrp1</i>	NM_009402	peptidoglycan recognition protein 1	1.305	3.018613
<i>Pira1</i>	NM_011087	paired-Ig-like receptor A1	1.455	5.640761
<i>Plin2</i>	NM_007408	perilipin 2	1.572	7.557100
<i>Rab30</i>	NM_029494	RAB30, member RAS oncogene family	-1.002	3.228400
<i>Rab44</i>	NM_001002786	RAB44, member RAS oncogene family	1.085	4.311332
<i>Rftn2</i>	NM_001356287	raftlin family member 2	-1.173	3.055008
<i>Rmrp</i>	NR_001460	RNA component of mitochondrial RNAase P	1.120	8.192853
<i>Rnaset2b</i>	NM_026611	ribonuclease T2B	-1.110	3.906453
<i>Rpl22l1</i>	NM_001347226	ribosomal protein L22 like 1	1.934	4.613764
<i>Rpl26</i>	NM_009080	ribosomal protein L26	1.679	3.677328
<i>Rpl39</i>	NM_026055	ribosomal protein L39	1.060	7.657849
<i>Rpl3</i>	NR_024198	ribonuclease P RNA-like 3	-1.330	8.980465
<i>Rps15a-ps4</i>	NR_036572	ribosomal protein S15A, pseudogene 4	1.309	3.152171
<i>Scn4a</i>	NM_133199	sodium channel, voltage-gated, type IV, alpha	-1.324	3.762057
<i>Sh2b2</i>	NM_001302938	SH2B adaptor protein 2	-1.048	3.435303
<i>Spp1</i>	NM_001204201	secreted phosphoprotein 1	1.391	3.770646
<i>Stag3</i>	NM_016964	stromal antigen 3	1.270	3.028127
<i>Stmn1</i>	NM_019641	stathmin 1	1.647	3.044369
<i>Syne1</i>	NM_001079686	spectrin repeat containing, nuclear envelope 1	1.211	5.960392
<i>Thbs1</i>	NM_001313914	thrombospondin 1	1.438	7.101035
<i>Tmem160</i>	NM_026938	transmembrane protein 160	1.081	4.473179
<i>Top2a</i>	NM_011623	topoisomerase (DNA) II alpha	1.311	4.504489
<i>Tspo</i>	NM_009775	translocator protein	1.089	6.158546

<i>Vmn2r26</i>	NM_019917	vomeronasal 2, receptor 26	1.291	4.694216
<i>Whrn</i>	NM_001008791	whirlin	-1.021	3.331669
<i>Xkrx</i>	NM_183319	X-linked Kx blood group related, X-linked	1.461	3.490385
<i>Zbtb16</i>	NM_001033324	zinc finger and BTB domain containing 16	1.365	5.059115
<i>Zfp827</i>	NM_001294279	zinc finger protein 827	-1.026	3.770834

Table S3. Phagocytosis-related gene expression shown in Figure 5E

Gene Symbol	Genbank accession	Description	log ₂ (ZT2/ZT14)	
			Control	MCS
<i>Actb</i>	NM_007393	actin, beta	0.071	0.115982
<i>Actg1</i>	NM_001313923	actin, gamma, cytoplasmic 1	0.228	0.012930
<i>Atp6ap1</i>	NM_018794	ATPase, H+ transporting, lysosomal accessory protein 1	0.128	0.025068
<i>Atp6v0a1</i>	NM_001243049	ATPase, H+ transporting, lysosomal V0 subunit A1	0.091	0.124081
<i>Atp6v0a2</i>	NM_011596	ATPase, H+ transporting, lysosomal V0 subunit A2	-0.201	0.216269
<i>Atp6v0b</i>	NM_033617	ATPase, H+ transporting, lysosomal V0 subunit B	-0.234	0.212740
<i>Atp6v0c</i>	NM_009729	ATPase, H+ transporting, lysosomal V0 subunit C	-0.053	-0.003881
<i>Atp6v0d1</i>	NM_013477	ATPase, H+ transporting, lysosomal V0 subunit D1	0.061	0.296234
<i>Atp6v0e</i>	NM_025272	ATPase, H+ transporting, lysosomal V0 subunit E	0.079	0.316161
<i>Atp6v0e2</i>	NM_001347164	ATPase, H+ transporting, lysosomal V0 subunit E2	-0.293	0.451371
<i>Atp6v1a</i>	NM_007508	ATPase, H+ transporting, lysosomal V1 subunit A	0.254	0.288856
<i>Atp6v1b2</i>	NM_007509	ATPase, H+ transporting, lysosomal V1 subunit B2	0.167	0.251854
<i>Atp6v1c1</i>	NM_025494	ATPase, H+ transporting, lysosomal V1 subunit C1	-0.105	-0.333098
<i>Atp6v1c2</i>	NM_001159632	ATPase, H+ transporting, lysosomal V1 subunit C2	-0.735	-0.919055
<i>Atp6v1d</i>	NM_023721	ATPase, H+ transporting, lysosomal V1 subunit D	-0.216	0.056981
<i>Atp6v1e1</i>	NM_007510	ATPase, H+ transporting, lysosomal V1 subunit E1	0.058	0.281697
<i>Atp6v1f</i>	NM_025381	ATPase, H+ transporting, lysosomal V1 subunit F	0.044	0.301869
<i>Atp6v1g1</i>	NM_024173	ATPase, H+ transporting, lysosomal V1 subunit G1	-0.002	0.392225
<i>Atp6v1g2</i>	NM_001347351	ATPase, H+ transporting, lysosomal V1 subunit G2	0.072	-1.435846
<i>Atp6v1h</i>	NM_001310442	ATPase, H+ transporting, lysosomal V1 subunit H	-0.036	0.393856
<i>C1ra</i>	NM_023143	complement component 1, r subcomponent A	0.019	0.784136
<i>C1rb</i>	NM_001113356	complement component 1, r subcomponent B	-0.250	-3.352015
<i>C3</i>	NM_009778	complement component 3	-0.032	0.000190
<i>Calr</i>	NM_007591	calreticulin	0.170	-0.224425
<i>Canx</i>	NM_001110499	calnexin	0.182	0.131213
<i>Cd14</i>	NM_009841	CD14 antigen	0.414	0.175229
<i>Cd209a</i>	NM_133238	CD209a antigen	0.539	-0.881988
<i>Cd209b</i>	NM_001037800	CD209b antigen	-0.447	-0.238992
<i>Cd209c</i>	NM_130903	CD209c antigen	0.213	-0.709337
<i>Cd209d</i>	NM_130904	CD209d antigen	0.072	-0.423098
<i>Cd209g</i>	NM_027343	CD209g antigen	-1.250	-1.182090
<i>Cd36</i>	NM_001159555	CD36 molecule	0.385	0.046878
<i>Clec7a</i>	NM_001309637	C-type lectin domain family 7, member a	-0.609	-0.429426
<i>Collec12</i>	NM_130449	collectin sub-family member 12	-0.008	-0.258131
<i>Comp</i>	NM_016685	cartilage oligomeric matrix protein	0.394	1.817910
<i>Coro1a</i>	NM_001301374	coronin, actin binding protein 1A	-0.088	0.584560
<i>Ctsl</i>	NM_009984	cathepsin L	1.025	-0.164970
<i>Ctss</i>	NM_001267695	cathepsin S	0.109	0.078287
<i>Cyba</i>	NM_001301284	cytochrome b-245, alpha polypeptide	0.060	0.490081
<i>Cybb</i>	NM_007807	cytochrome b-245, beta polypeptide	0.032	0.408418
<i>Dync1h1</i>	NM_030238	dynein cytoplasmic 1 heavy chain 1	-0.102	0.064359
<i>Dync1i2</i>	NM_001198872	dynein cytoplasmic 1 intermediate chain 2	0.081	-0.166915
<i>Dync1li1</i>	NM_146229	dynein cytoplasmic 1 light intermediate chain 1	-0.083	-0.162854
<i>Dync1li2</i>	NM_001013380	dynein, cytoplasmic 1 light intermediate chain 2	-0.325	0.076683
<i>Dync2h1</i>	NM_029851	dynein cytoplasmic 2 heavy chain 1	0.232	-0.502552
<i>Eea1</i>	NM_001001932	early endosome antigen 1	0.171	-0.460352
<i>Fcgr1</i>	NM_010186	Fc receptor, IgG, high affinity I	0.011	0.664105
<i>Fcgr2b</i>	NM_001077189	Fc receptor, IgG, low affinity IIb	-0.507	-0.032891
<i>Fcgr3</i>	NM_001356511	Fc receptor, IgG, low affinity III	0.132	0.021691
<i>Fcgr4</i>	NM_144559	Fc receptor, IgG, low affinity IV	0.230	0.979915
<i>H2-Aa</i>	NM_010378	histocompatibility 2, class II antigen A, alpha	0.019	-0.207204
<i>H2-Ab1</i>	NM_207105	histocompatibility 2, class II antigen A, beta 1	0.144	-0.430641
<i>H2-BI</i>	NM_008199	histocompatibility 2, blastocyst	0.563	0.579750
<i>H2-D1</i>	NM_010380	histocompatibility 2, D region locus 1	0.063	0.877035
<i>H2-DMa</i>	NM_010386	histocompatibility 2, class II, locus DMa	0.102	0.062918
<i>H2-DMb1</i>	NM_010387	histocompatibility 2, class II, locus Mb1	-0.029	-0.541305
<i>H2-DMb2</i>	NM_010388	histocompatibility 2, class II, locus Mb2	-0.095	-0.131516
<i>H2-Eb1</i>	NM_010382	histocompatibility 2, class II antigen E beta	0.129	-0.052332
<i>H2-Eb2</i>	NM_001033978	histocompatibility 2, class II antigen E beta2	-0.665	0.509788
<i>H2-K1</i>	NM_001001892	histocompatibility 2, K1, K region	-0.004	0.450812
<i>H2-L</i>	NM_001267808	histocompatibility 2, D region locus L	0.620	-0.182090
<i>H2-M3</i>	NM_013819	histocompatibility 2, M region locus 3	0.124	1.021002
<i>H2-Oa</i>	NM_008206	histocompatibility 2, O region alpha locus	0.424	-0.589265
<i>H2-Ob</i>	NM_010389	histocompatibility 2, O region beta locus	-0.031	-0.134261
<i>H2-Q1</i>	NM_010390	histocompatibility 2, Q region locus 1	0.182	0.414013
<i>H2-Q10</i>	NM_010391	histocompatibility 2, Q region locus 10	-0.099	0.760577
<i>H2-Q2</i>	NM_010392	histocompatibility 2, Q region locus 2	0.353	0.596620
<i>H2-Q4</i>	NM_001143689	histocompatibility 2, Q region locus 4	0.246	0.525274
<i>H2-Q7</i>	NM_001198560	histocompatibility 2, Q region locus 7	0.558	0.841757
<i>H2-Q9</i>	NM_001201460	histocompatibility 2, Q region locus 9	0.110	0.760408
<i>H2-T10</i>	NM_010395	histocompatibility 2, T region locus 10	-0.552	0.129371
<i>H2-T22</i>	NM_001347382	histocompatibility 2, T region locus 22	0.378	0.952889
<i>H2-T23</i>	NM_010398	histocompatibility 2, T region locus 23	0.152	0.632918
<i>H2-T24</i>	NM_008207	histocompatibility 2, T region locus 24	0.308	-0.136091
<i>Hgs</i>	NM_001159328	HGF-regulated tyrosine kinase substrate	-0.138	-0.186883
<i>Itga2</i>	NM_008396	integrin alpha 2	1.526	-1.691103
<i>Itga5</i>	NM_001314041	integrin alpha 5 (fibronectin receptor alpha)	-0.132	0.046936
<i>Itgam</i>	NM_001082960	integrin alpha M	0.293	0.021581

<i>Itgav</i>	NM_008402	integrin alpha V	-0.075	0.219202
<i>Itgb1</i>	NM_010578	integrin beta 1 (fibronectin receptor beta)	0.116	0.310404
<i>Itgb2</i>	NM_008404	integrin beta 2	0.133	0.249882
<i>Itgb3</i>	NM_016780	integrin beta 3	0.718	-0.386104
<i>Itgb5</i>	NM_001145884	integrin beta 5	0.394	-1.082554
<i>Lamp1</i>	NM_001317353	lysosomal-associated membrane protein 1	-0.021	0.108735
<i>Lamp2</i>	NM_001017959	lysosomal-associated membrane protein 2	0.089	0.194078
<i>M6pr</i>	NM_010749	mannose-6-phosphate receptor, cation dependent	0.081	0.141530
<i>Marco</i>	NM_010766	macrophage receptor with collagenous structure	-0.732	0.073749
<i>Mbl2</i>	NM_010776	mannose-binding lectin (protein C) 2	0.657	-1.182090
<i>Mrc1</i>	NM_008625	mannose receptor, C type 1	0.713	-0.666169
<i>Msr1</i>	NM_001113326	macrophage scavenger receptor 1	0.015	0.568547
<i>Ncf1</i>	NM_001286037	neutrophil cytosolic factor 1	-0.110	0.032240
<i>Ncf2</i>	NM_010877	neutrophil cytosolic factor 2	0.099	0.328914
<i>Ncf4</i>	NM_008677	neutrophil cytosolic factor 4	-0.140	0.274824
<i>Olr1</i>	NM_001301094	oxidized low density lipoprotein (lectin-like) receptor 1	0.417	0.545831
<i>Pik3c3</i>	NM_181414	phosphatidylinositol 3-kinase catalytic subunit type 3	-0.197	-0.134110
<i>Pikfyve</i>	NM_001310624	phosphoinositide kinase, FYVE type zinc finger containing	-0.273	0.128686
<i>Pla2r1</i>	NM_008867	phospholipase A2 receptor 1	1.072	0.817910
<i>Rab5a</i>	NM_025887	RAB5A, member RAS oncogene family	-0.147	-0.058971
<i>Rab5b</i>	NM_011229	RAB5B, member RAS oncogene family	-0.066	0.078798
<i>Rab5c</i>	NM_001305003	RAB5C, member RAS oncogene family	-0.036	0.080130
<i>Rab7</i>	NM_001293652	RAB7, member RAS oncogene family	0.021	-0.270604
<i>Rab7b</i>	NM_001311096	RAB7B, member RAS oncogene family	-0.275	0.197554
<i>Rac1</i>	NM_001347530	RAS-related C3 botulinum substrate 1	-0.066	0.083768
<i>Rilp</i>	NM_001029938	Rab interacting lysosomal protein	0.072	-0.120689
<i>Scarb1</i>	NM_001205082	scavenger receptor class B, member 1	-0.650	0.790016
<i>Sec22b</i>	NM_011342	SEC22 homolog B, vesicle trafficking protein	-0.008	0.472352
<i>Sec61a1</i>	NM_016906	Sec61 alpha 1 subunit (S. cerevisiae)	0.029	0.425560
<i>Sec61a2</i>	NM_001356411	Sec61, alpha subunit 2 (S. cerevisiae)	-0.452	-0.524482
<i>Sec61b</i>	NM_024171	Sec61 beta subunit	0.121	1.035008
<i>Sec61g</i>	NM_001109971	SEC61, gamma subunit	0.245	0.542946
<i>Stx12</i>	NM_133887	syntaxin 12	0.072	0.291207
<i>Stx18</i>	NM_001289535	syntaxin 18	0.304	0.104214
<i>Stx7</i>	NM_016797	syntaxin 7	0.174	-0.241796
<i>Tap1</i>	NM_001161730	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	0.220	0.134145
<i>Tap2</i>	NM_011530	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	0.056	0.591344
<i>Tcirg1</i>	NM_001136091	T cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	-0.458	0.370076
<i>Tfrc</i>	NM_001357298	transferrin receptor	-0.506	0.087999
<i>Thbs1</i>	NM_001313914	thrombospondin 1	4.220	-2.229074
<i>Thbs3</i>	NM_013691	thrombospondin 3	0.481	-0.221618
<i>Tlr2</i>	NM_011905	toll-like receptor 2	-0.420	0.337399
<i>Tlr4</i>	NM_021297	toll-like receptor 4	-0.022	0.413188
<i>Tlr6</i>	NM_011604	toll-like receptor 6	0.212	-0.163474
<i>Tuba1a</i>	NM_011653	tubulin, alpha 1A	-0.403	0.489584
<i>Tuba1b</i>	NM_011654	tubulin, alpha 1B	-0.399	0.610642
<i>Tuba1c</i>	NM_009448	tubulin, alpha 1C	-0.799	1.418716
<i>Tuba4a</i>	NM_001313723	tubulin, alpha 4A	-0.892	0.282360
<i>Tuba8</i>	NM_017379	tubulin, alpha 8	0.857	-0.597127
<i>Tubb2a</i>	NM_009450	tubulin, beta 2A class IIA	-0.492	0.827309
<i>Tubb2b</i>	NM_023716	tubulin, beta 2B class IIB	-0.013	0.501437
<i>Tubb3</i>	NM_023279	tubulin, beta 3 class III	0.979	0.895913
<i>Tubb4a</i>	NM_009451	tubulin, beta 4A class IVA	-0.080	-0.264552
<i>Tubb4b</i>	NM_146116	tubulin, beta 4B class IVB	-0.801	0.843197
<i>Tubb5</i>	NM_011655	tubulin, beta 5 class I	-0.449	0.418266
<i>Tubb6</i>	NM_026473	tubulin, beta 6 class V	-0.799	0.643286
<i>Vamp3</i>	NM_009498	vesicle-associated membrane protein 3	-0.109	0.485591

Table S4. Genes with more than 2-fold difference in expression between ZT2 and ZT14 in macrophages of control mice and more than 2-fold increase in expression by MCS in ZT14. Those genes were used Enrichment analysis of transcriptional factor using ChIP-Atlas in Figure S8A.

Gene Symbol	Genbank accession	Description	Control log ₂ (ZT2/ZT14)	ZT14 log ₂ (MCS/Control)
<i>1110065P20Rik</i>	NM_001142727	RIKEN cDNA 1110065P20 gene	-1.439	1.919500
<i>170007L15Rik</i>	NR_045709	RIKEN cDNA 170007L15 gene	-2.141	2.174114
<i>1700071M16Rik</i>	NR_045444	RIKEN cDNA 1700071M16 gene	-1.983	1.162904
<i>2610306M01Rik</i>	NR_028298	RIKEN cDNA 2610306M01 gene	-1.056	1.294584
<i>Acpp</i>	NM_019807	acid phosphatase, prostate	-1.357	1.183248
<i>Ankrd66</i>	NM_001254953	ankyrin repeat domain 66	-1.857	1.381365
<i>ApoH</i>	NM_013475	apolipoprotein H	-1.313	1.016634
<i>Ar</i>	NM_013476	androgen receptor	-1.324	1.517609
<i>B430212C06Rik</i>	NR_033214	RIKEN cDNA B430212C06 gene	-1.189	1.551948
<i>BC002163</i>	NR_002445	NADH dehydrogenase Fe-S protein 5 pseudogene	-4.239	3.349782
<i>Bub1b</i>	NM_009773	BUB1B, mitotic checkpoint serine/threonine kinase	-1.853	1.544959
<i>Ccdc80</i>	NM_026439	coiled-coil domain containing 80	-1.159	1.709616
<i>Ccnb2</i>	NM_007630	cyclin B2	-1.110	1.138619
<i>Ccpg1os</i>	NM_001198789	cell cycle progression 1, opposite strand	-1.171	1.294584
<i>Ccr3</i>	NM_009914	chemokine (C-C motif) receptor 3	-1.999	4.668483
<i>Cd3d</i>	NM_013487	CD3 antigen, delta polypeptide	-1.127	1.014183
<i>Cdca5</i>	NM_026410	cell division cycle associated 5	-2.206	2.111509
<i>Cdk1</i>	NM_007659	cyclin-dependent kinase 1	-1.509	1.235469
<i>Centp</i>	NM_173762	centromere protein E	-1.069	1.068766
<i>Chaf1a</i>	NM_013733	chromatin assembly factor 1, subunit A (p150)	-1.172	1.529838
<i>Chaf1b</i>	NM_028083	chromatin assembly factor 1, subunit B (p60)	-1.380	1.467763
<i>Chsy3</i>	NM_001081328	chondroitin sulfate synthase 3	-1.059	1.244893
<i>Clu</i>	NM_013492	clusterin	-1.063	1.025297
<i>Col1a1</i>	NM_007742	collagen, type I, alpha 1	-2.284	1.568521
<i>Col1a2</i>	NM_007743	collagen, type I, alpha 2	-2.894	2.353233
<i>Col3a1</i>	NM_009930	collagen, type III, alpha 1	-2.678	2.615573
<i>Cryab</i>	NM_001289782	crystallin, alpha B	-1.366	1.454229
<i>CtsW</i>	NM_009985	cathepsin W	-1.565	1.111242
<i>Depdc1b</i>	NM_178683	DEP domain containing 1B	-1.139	1.175392
<i>Dtl</i>	NM_001305233	denticleless E3 ubiquitin protein ligase	-1.068	1.498953
<i>Dynl1f</i>	NM_001166627	dynein light chain Tctex-type 1F	-2.635	2.592245
<i>Elovl6</i>	NM_130450	ELOVL family member 6, elongation of long chain fatty acids (yeast)	-1.179	1.059020
<i>ErbB2</i>	NM_001003817	erb-b2 receptor tyrosine kinase 2	-1.283	1.038732
<i>F630042J09Rik</i>	NR_033540	RIKEN cDNA F630042J09 gene	-1.313	1.360956
<i>Fabp7</i>	NM_021272	fatty acid binding protein 7, brain	-1.425	1.415953
<i>Gadd45g</i>	NM_011817	growth arrest and DNA-damage-inducible 45 gamma	-1.199	1.089060
<i>Gdpd5</i>	NM_201352	glycerophosphodiester phosphodiesterase domain containing 5	-1.313	1.459610
<i>Gins2</i>	NM_178856	GINS complex subunit 2 (Psf2 homolog)	-1.450	1.526347
<i>Gm13986</i>	NR_126479	predicted gene 13986	-2.494	1.865411
<i>Gm14434</i>	NM_001101804	predicted gene 14434	-10.481	7.541956
<i>Gm17757</i>	NR_040453	GTPase, very large interferon inducible 1 pseudogene	-2.603	2.239031
<i>Gm6644</i>	NR_028277	Akr1b3 pseudogene	-11.505	12.239549
<i>Gpc6</i>	NM_001079844	glypican 6	-1.700	1.636828
<i>Gstm4</i>	NM_001160411	glutathione S-transferase, mu 4	-1.033	1.054595
<i>Hba-a1</i>	NM_008218	hemoglobin alpha, adult chain 1	-2.803	6.398126
<i>Hgf</i>	NM_001289458	hepatocyte growth factor	-2.136	1.566606
<i>Hist1h1b</i>	NM_020034	histone cluster 1, H1b	-1.479	1.055702
<i>Hist1h1d</i>	NM_145713	histone cluster 1, H1d	-1.031	1.048995
<i>Hist1h2bh</i>	NM_178197	histone cluster 1, H2bh	-1.746	1.842105
<i>Hist1h3b</i>	NM_178203	histone cluster 1, H3b	-1.826	1.000186
<i>Hist1h4j</i>	NM_178210	histone cluster 1, H4j	-1.450	1.636828
<i>Inpp5j</i>	NM_172439	inositol polyphosphate 5-phosphatase J	-4.299	6.566967
<i>Kcnj13</i>	NM_001110227	potassium inwardly-rectifying channel, subfamily J, member 13	-1.589	1.800441
<i>Klf11</i>	NM_178357	Kruppel-like factor 11	-2.020	1.446732
<i>Klrd1</i>	NM_010654	killer cell lectin-like receptor, subfamily D, member 1	-2.038	2.034049
<i>Lag3</i>	NM_008479	lymphocyte-activation gene 3	-1.375	1.202246
<i>LipH</i>	NM_001083894	lipase, member H	-1.502	1.773074
<i>Mamdc4</i>	NM_001081199	MAM domain containing 4	-1.534	2.008217
<i>Melk</i>	NM_010790	maternal embryonic leucine zipper kinase	-1.171	1.463222
<i>Mup19</i>	NM_001135127	major urinary protein 19	-6.856	8.042178
<i>Myk</i>	NM_139300	myosin, light polypeptide kinase	-2.607	4.090987
<i>Ncapg</i>	NM_019438	non-SMC condensin I complex, subunit G	-1.383	1.607443
<i>Olfml2b</i>	NM_177068	olfactomedin-like 2B	-2.582	2.731481
<i>Orc1</i>	NM_001014425	origin recognition complex, subunit 1	-1.056	1.103592
<i>Pbk</i>	NM_023209	PDZ binding kinase	-1.375	1.103592
<i>Pcdh1</i>	NM_029357	protocadherin 1	-1.741	1.674420
<i>Pdk4</i>	NM_013743	pyruvate dehydrogenase kinase, isoenzyme 4	-9.653	9.394320
<i>Pira1</i>	NM_011087	paired-Ig-like receptor A1	-1.170	1.454939
<i>Pkhd11</i>	NM_138674	polycystic kidney and hepatic disease 1-like 1	-1.632	1.360956
<i>Plin2</i>	NM_007408	perilipin 2	-1.530	1.572348
<i>Proser2</i>	NM_001159657	proline and serine rich 2	-2.734	1.674420
<i>Rad51</i>	NM_011234	RAD51 recombinase	-1.517	1.406699
<i>Rcor2</i>	NM_001320554	REST corepressor 2	-1.053	1.140765
<i>Rgcc</i>	NM_025427	regulator of cell cycle	-1.632	1.638729
<i>Rmi2</i>	NM_001033278	RecQ mediated genome instability 2	-1.692	1.150124
<i>Rsad2</i>	NM_021384	radical S-adenosyl methionine domain containing 2	-1.366	1.454229
<i>Sccpdh</i>	NM_178653	saccharopine dehydrogenase (putative)	-1.001	1.133325
<i>Sds1</i>	NM_133902	serine dehydratase-like	-1.059	1.322353
<i>Setd4</i>	NM_145482	SET domain containing 4	-1.439	1.421807
<i>Slc22a4</i>	NM_001330304	solute carrier family 22 (organic cation transporter), member 4	-1.632	1.459610
<i>Sparc</i>	NM_001290817	secreted acidic cysteine rich glycoprotein	-2.889	1.459610
<i>Spc25</i>	NM_001199123	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-1.139	1.108680
<i>Stil</i>	NM_001304551	Scf/Tal1 interrupting locus	-1.636	1.463222

<i>Stmn1</i>	NM_019641	stathmin 1	-1.694	1.646594
<i>Tcf23</i>	NM_053085	transcription factor 23	-1.857	1.750854
<i>Tdrkh</i>	NM_028307	tudor and KH domain containing protein	-1.012	1.123296
<i>Thbs1</i>	NM_001313914	thrombospondin 1	-4.220	1.437821
<i>Themis</i>	NM_001305663	thymocyte selection associated	-1.024	1.125547
<i>Tnfrsf14</i>	NM_019418	tumor necrosis factor (ligand) superfamily, member 14	-2.061	1.760902
<i>Top2a</i>	NM_011623	topoisomerase (DNA) II alpha	-1.218	1.310762
<i>Tpx2</i>	NM_001141975	TPX2, microtubule-associated	-1.742	1.381880
<i>Trim72</i>	NM_001079932	tripartite motif-containing 72	-1.961	1.475401
<i>Ube2c</i>	NM_026785	ubiquitin-conjugating enzyme E2C	-1.270	1.275804
<i>Zbtb16</i>	NM_001033324	zinc finger and BTB domain containing 16	-2.258	1.364748
<i>Zdhhc2</i>	NM_001357249	zinc finger, DHHC domain containing 2	-1.004	1.176196
<i>Zfr2</i>	NM_001034895	zinc finger RNA binding protein 2	-1.450	1.206276

Table S5. Primer sets for PCR analysis of gene expression

Gene	Primers
Mouse <i>Per1</i>	
Forward	5'-CCAGATTGGTGGAGGTACTGAGT-3'
Reverse	5'-GCGAGAGTCTTCTTGGAGCAGTAG-3'
Mouse <i>Per2</i>	
Forward	5'-GACTGCGACGACAATGGGAA-3'
Reverse	5'-TTTGGCAGACTGCTCACTACT-3'
Mouse <i>Cry1</i>	
Forward	5'-AAGTCATCGTGCGCATTTC-3'
Reverse	5'-TCATCATGGTCATCAGACAGA-3'
Mouse <i>Cry2</i>	
Forward	5'-CACTGGTCCGCAAAGGACTA-3'
Reverse	5'-CCACGGGTCGAGGATGTAGA-3'
Mouse <i>Clock</i>	
Forward	5'-TTGCTCCACGGGAATCCTT-3'
Reverse	5'-GGAGGGAAAGTGCTCTGTGTAG-3'
Mouse <i>Arntl</i>	
Forward	5'-GGACTTCGCCTTACCTGTTC-3'
Reverse	5'-AACCATGTGCGAGTGCAGGCGC-3'
Mouse <i>Calr</i>	
Forward	5'-AAGATGCCCGATTTACGCAC-3'
Reverse	5'-CCCACAGTCGATATTCTGCTC-3'
Mouse <i>Cd47</i>	
Forward	5'-CACGGCCTCAACACTGAC-3'
Reverse	5'-ACAGGAGTATAGCCAAAATTGGG-3'
Mouse <i>Klf4</i>	
Forward	5'-GGCGAGTCTGACATGGCTG-3'
Reverse	5'-GCTGGACGACAGTCTTCTC-3'
Mouse <i>Tgfβ</i>	
Forward	5'-CTCAATACGTCAGACATTCGGG-3'
Reverse	5'-GTAACGCCAGGAATTGTGCTA-3'
Mouse <i>Tnfr</i>	
Forward	5'-CTGAACCTGGGGGTGATCGG-3'
Reverse	5'-GGCTTGCTACTCGAATTTGAG-3'
Mouse <i>Mki67</i>	
Forward	5'-GCGATCCCAGGATCCCTG-3'
Reverse	5'-GCTGCCTCTGCTGCCAGTT-3'
Mouse <i>Gapdh</i>	
Forward	5'-AAGAGGGATGCTGCCCTTAC-3'
Reverse	5'-CGGGACGAGGAAACACTCTC-3'
Mouse <i>E2f1</i>	
Forward	5'-TGCAGAAACGGCGCATCTAT-3'
Reverse	5'-CCGCTTACCAATCCCACC-3'
Mouse <i>E2f3</i>	
Forward	5'-CACTACGGAGTCCCAGATGTC-3'
Reverse	5'-GCTGCCTTGTTCAGATCCAGG-3'
Mouse <i>E2f4</i>	
Forward	5'-CTCACCACAAGTTCGTGTC-3'
Reverse	5'-TCTCGATCAGACCGATGCCTT-3'
Mouse <i>Gata1</i>	
Forward	5'-TGTCTCACCATCAGATTCCA-3'
Reverse	5'-TCCCTCCATAGTTGAGCAG-3'
Mouse <i>Gfi1</i>	
Forward	5'-AGAAGGCGCACAGCTATCAC-3'
Reverse	5'-GGCTCCATTTGACTCGC-3'
Mouse <i>Klf5</i>	
Forward	5'-GGCTCTCCCGAGTTCATA-3'
Reverse	5'-ATTACTGCCGTCTGGTTTGTG-3'
Mouse <i>Mef2c</i>	
Forward	5'-ACGAGGATAATGGATGAGCGT-3'
Reverse	5'-ATCAGTGCAATCTCACAGTCG-3'
Mouse <i>Neurod2</i>	
Forward	5'-AAGCCAGTGTCTTTCGTGG-3'
Reverse	5'-GCCTTGGTCATCTTGCGTTT-3'
Mouse <i>Nfyc</i>	
Forward	5'-GGATAACAAGCGTCTACTCTTC-3'
Reverse	5'-GTGGTCGTAGAACTGGTGGT-3'
Mouse <i>Pax3</i>	
Forward	5'-CATCCGACCTGGTGCCATC-3'
Reverse	5'-ATTTCAGCTAAACATGCC-3'
Mouse <i>Rorc</i>	
Forward	5'-CGCGGAGCAGACACACTTA-3'
Reverse	5'-CCCTGGACCTCTGTTTGGC-3'
Mouse <i>Srf</i>	
Forward	5'-CCAGGTGTCGGAATCTGACAG-3'
Reverse	5'-GCTGACTTGCAATGGGTAGA-3'
Mouse <i>Gba</i>	
Forward	5'-GCCAGGCTCATCGATTCTTC-3'
Reverse	5'-GAGTGCTCTGTAACGGCT-3'
Mouse <i>Rab3d</i>	
Forward	5'-GTCAGACGGTCTACCGACAT-3'
Reverse	5'-CATAGCTCCCGATAGTAGGC-3'