SUPPLEMENTAL MATERIAL

Conti et al., http://www.jem.org/cgi/content/full/jem.20081463/DC1

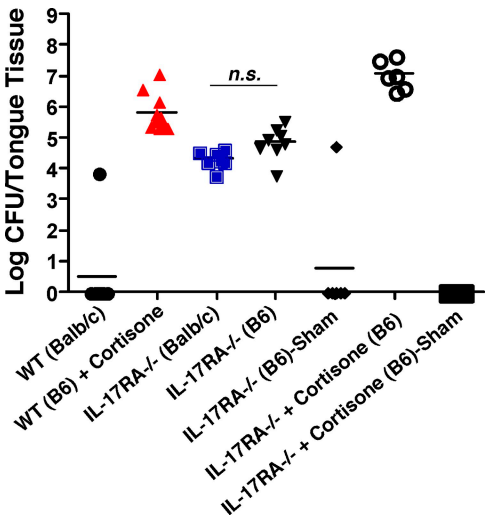

Figure S1. Similar levels of *C. albicans* infection are found in C57BL/6 versus BALB/c IL-17RA^{KO} mice. The indicated mice were infected with *C. albicans* per the standard protocol and CFU/g tongue tissue assessed after 5 d. Geometric means are indicated by horizontal bars. Experiment with the BALB/c IL-17RA^{KO} mice was performed once.

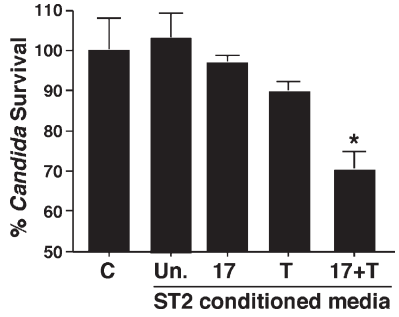

Figure S2. IL-17 stimulates nonimmune cells to secrete factors with fungicidal capacity. ST2 stromal cells were treated for 24 h with IL-17 (100 ng/ml) and/or TNF-α (2 ng/ml). Supernatants were concentrated and desalted, and incubated with 10^6 *Candida albicans* cells for 1.5 h at 37°C. Data are presented as percent of colonies compared with the average of untreated by unpaired Student's *t* test. *, $P < 0.001$ compared with untreated control. Experiment was performed twice with similar results.

WT Day 0 vs WT Day 1 (GCRMA > 2 Fold Changes 05-20-08 Both Experiments) Mouse 430_2 Arrays

Up Regulated Genes

Probeset ID	Fold Change	Gene Title	Gene Symbol	Chromosomal Location	Gene Ontology Biological Process	Gene Ontology Cellular Component	Gene Ontology Molecular Function
1450085_at	25.33	angiopoietin-like 2	Angptl2	chr2 B	[illegible]	[illegible]	[illegible]
1425631_at	25.23	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	chr19 C3	[illegible]	[illegible]	[illegible]
1453511_at	23.36	RIKEN cDNA 2310007B03 gene	2310007B03Rik	chr1 D	[illegible]	[illegible]	[illegible]
1420924_at	23.26	tissue inhibitor of metalloproteinase 2	Timp2	chr11 E2|11 72.0 cM	[illegible]	[illegible]	[illegible]
1421289_at	23.09	heat shock protein family, member 7 (cardiovascular)	Hspb7	chr4 E1	[illegible]	[illegible]	[illegible]
1421002_at	19.63	angiopoietin-like 2	Angptl2	chr2 B	[illegible]	[illegible]	[illegible]
1415959_at	19.25	solute carrier family 2 (facilitated glucose transporter), member 4	Slc2a4	chr11 C-E1|11 40.0 cM	[illegible]	[illegible]	[illegible]
1429496_x_at	18.95	RIKEN cDNA 2300002M23 gene	2300002M23Rik	chr17 B1	[illegible]	[illegible]	[illegible]
1440435_at	17.00	kyphoscoliosis peptidase	Ky	chr9 F1|9 56.0 cM	[illegible]	[illegible]	[illegible]
1458624_at	16.06	similar to RNA binding motif protein 24 /// RNA binding motif protein 24	LOC380843 /// Rbm24	chr13 A5	[illegible]	[illegible]	[illegible]
1460336_at	14.62	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	chr5 C1	[illegible]	[illegible]	[illegible]
1421421_at	14.22	angiopoietin-like 1	Angptl1	chr1 H1	[illegible]	[illegible]	[illegible]
1422017_s_at	13.54	RIKEN cDNA 4833439L19 gene	4833439L19Rik	chr13 B1	[illegible]	[illegible]	[illegible]
1417808_at	12.77	RIKEN cDNA 2310050C09 gene	2310050C09Rik	chr3 F2.1	[illegible]	[illegible]	[illegible]
1425329_a_at	12.29	cytochrome b5 reductase 3	Cyb5r3	chr15 45.2 cM	[illegible]	[illegible]	[illegible]
1425382_a_at	12.24	aquaporin 4	Aqp4	chr18 A1|18 6.0 cM	[illegible]	[illegible]	[illegible]
1417164_at	11.90	dual specificity phosphatase 10	Dusp10	chr1 H5	[illegible]	[illegible]	[illegible]
1432646_a_at	11.81	predicted gene, EG667653	EG667653	chr15 E3	[illegible]	[illegible]	[illegible]
1439675_at	11.80	RIKEN cDNA 4933429D07 gene	4933429D07Rik	---	[illegible]	[illegible]	[illegible]
1450311_at	11.68	solute carrier family 8 (sodium/calcium exchanger), member 3	Slc8a3	chr12 D1|12 41.0 cM	[illegible]	[illegible]	[illegible]
1443866_at	11.48	leucine-rich repeats and transmembrane domains 1	Lrtm1	chr14 A3	[illegible]	[illegible]	[illegible]
1451961_a_at	11.01	myelin basic protein	Mbp	chr18 E2-E4|18 55.0 cM	[illegible]	[illegible]	[illegible]
1451707_s_at	11.01	solute carrier family 41, member 3	Slc41a3	chr6 D2	[illegible]	[illegible]	[illegible]
1418450_at	10.98	immunoglobulin superfamily containing leucine-rich repeat	Islr	chr9 B	[illegible]	[illegible]	[illegible]
1432913_at	10.98	leucine rich repeat containing 52	Lrrc52	chr1 H2.3	[illegible]	[illegible]	[illegible]
1419409_at	10.83	late cornified envelope 1B	Lce1b	chr3 F1	[illegible]	[illegible]	[illegible]
1429334_at	10.79	RIKEN cDNA 2300002O18 gene	2300002O18Rik	chr1 B	[illegible]	[illegible]	[illegible]
1430466_at	10.78	RIKEN cDNA 2310005G13 gene	2310005G13Rik	chr16 C1.1	[illegible]	[illegible]	[illegible]
1453218_at	10.66	late cornified envelope 1C	Lce1c	chr3 F1	[illegible]	[illegible]	[illegible]
1455224_at	10.50	angiopoietin-like 1	Angptl1	chr1 H1	[illegible]	[illegible]	[illegible]
1453898_at	10.30	integrin beta 1 binding protein 3	Itgb1bp3	chr10 C1	[illegible]	[illegible]	[illegible]
1423010_at	10.27	sacsin	Sacs	chr14 D1|14 26.75 cM	[illegible]	[illegible]	[illegible]
1458455_at	9.88	actin-binding Rho activating protein	Abra	chr15 B3.1	[illegible]	[illegible]	[illegible]
1417543_at	9.75	ribosomal protein S6 kinase, polypeptide 2	Rps6ka2	chr17 F4|17 3.65 cM	[illegible]	[illegible]	[illegible]
1420350_at	9.61	late cornified envelope 1A2	Lce1a2	chr3 F1	[illegible]	[illegible]	[illegible]
1458368_at	9.58	myosin, heavy polypeptide 4, skeletal muscle	Myh4	chr11 B3|11 35.0 cM	[illegible]	[illegible]	[illegible]
1429598_at	9.56	RIKEN cDNA 2310042D19 gene	2310042D19Rik	chr4 E2	[illegible]	[illegible]	[illegible]
1420676_at	9.53	late cornified envelope 1A1	Lce1a1	chr3 F1	[illegible]	[illegible]	[illegible]
1451613_at	9.38	hornerin	Hrnr	chr3 F2	[illegible]	[illegible]	[illegible]
1420332_x_at	9.33	late cornified envelope 1D	Lce1d	chr3 F1	[illegible]	[illegible]	[illegible]
1416325_at	9.30	cysteine-rich secretory protein 1	Crisp1	chr17 B1|17 21.0 cM	[illegible]	[illegible]	[illegible]
1459003_at	9.22	four and a half LIM domains 1	Fhl1	chrX A6-A7.1	[illegible]	[illegible]	[illegible]
1420941_at	9.16	regulator of G-protein signaling 5	Rgs5	chr1 H2|1 86.5 cM	[illegible]	[illegible]	[illegible]
1419325_at	9.12	neuromedin U	Nmu	chr5 C3.3	[illegible]	[illegible]	[illegible]
1453623_a_at	8.82	RAD23a homolog (S. cerevisiae)	Rad23a	chr8 C3	[illegible]	[illegible]	[illegible]
1424362_at	8.79	phosphatidic acid phosphatase type 2 domain containing 3	Ppapdc3	chr2 B	[illegible]	[illegible]	[illegible]
1460281_at	8.77	ankyrin repeat and SOCS box-containing protein 15	Asb15	chr6 A3.1	[illegible]	[illegible]	[illegible]
1453224_at	8.70	zinc finger, AN1-type domain 5	Zfand5	chr19 B|19 15.0 cM	[illegible]	[illegible]	[illegible]
1420358_at	8.50	keratin associated protein 13	Krtap13	chr16 C3.3	[illegible]	[illegible]	[illegible]
1417576_a_at	8.36	OTU domain, ubiquitin aldehyde binding 2	Otub2	chr12 E	[illegible]	[illegible]	[illegible]
1420550_at	8.33	late cornified envelope 1F	Lce1f	chr3 F1	[illegible]	[illegible]	[illegible]
1422908_at	8.27	ATPase, (Na+)/K+ transporting, beta 4 polypeptide	Atp1b4	chrX A2	[illegible]	[illegible]	[illegible]
1422195_s_at	8.21	T-box 15	Tbx15	chr3 F2.2|3 49.0 cM	[illegible]	[illegible]	[illegible]
1433691_at	8.11	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	chr19 C3	[illegible]	[illegible]	[illegible]
1455090_at	7.98	angiopoietin-like 2	Angptl2	chr2 B	[illegible]	[illegible]	[illegible]
1427414_at	7.94	protein kinase, cAMP dependent regulatory, type II alpha	Prkar2a	chr9 F2	[illegible]	[illegible]	[illegible]
1416652_at	7.88	asporin	Aspn	chr13 B1	[illegible]	[illegible]	[illegible]
1456211_at	7.84	NLR family, pyrin domain containing 10	Nlrp10	chr7 E3	[illegible]	[illegible]	[illegible]
1450196_s_at	7.83	glycogen synthase 1, muscle	Gys1	chr7 B3|7 23.0 cM	[illegible]	[illegible]	[illegible]
1418592_at	7.83	DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	chr9 A5.3	[illegible]	[illegible]	[illegible]
1420940_x_at	7.80	regulator of G-protein signaling 5	Rgs5	chr1 H2|1 86.5 cM	[illegible]	[illegible]	[illegible]
1417033_at	7.73	ubiquitin-conjugating enzyme E2G 2	Ube2g2	chr10 C1|10 41.6 cM	[illegible]	[illegible]	[illegible]
1431233_at	7.67	cyclin M4	Cnnm4	chr1 B|1 20.2 cM	[illegible]	[illegible]	[illegible]
1428444_at	7.64	ankyrin repeat and SOCS box-containing protein 2	Asb2	chr12 E|12 50.0 cM	[illegible]	[illegible]	[illegible]
1426122_a_at	7.57	coronin, actin binding protein 6	Coro6	chr11 B5	[illegible]	[illegible]	[illegible]
1424178_at	7.57	transmembrane protein 38a	Tmem38a	chr8 B3.3	[illegible]	[illegible]	[illegible]
1419088_at	7.25	tissue inhibitor of metalloproteinase 3	Timp3	chr10 C1-D1|10 47.0 cM	[illegible]	[illegible]	[illegible]
1428980_at	7.23	keratinocyte expressed, proline-rich	Kprp	chr3 F1	[illegible]	[illegible]	[illegible]
1425439_a_at	7.17	solute carrier family 41, member 3	Slc41a3	chr6 D2	[illegible]	[illegible]	[illegible]
1417803_at	7.16	RIKEN cDNA 1110032A04 gene	1110032A04Rik	chr3 E3	[illegible]	[illegible]	[illegible]
1415988_at	7.13	high density lipoprotein (HDL) binding protein	Hdlbp	chr1 D|1 55.3 cM	[illegible]	[illegible]	[illegible]
1424518_at	7.13	RIKEN cDNA 2310016F22 gene /// cDNA sequence BC020489	2310016F22Rik /// BC020489	chr15 E1	[illegible]	[illegible]	[illegible]
1422967_a_at	7.11	transferrin receptor	Tfrc	chr16 B3|16 21.2 cM	[illegible]	[illegible]	[illegible]
1449986_at	7.09	RIKEN cDNA 2310034C09 gene	2310034C09Rik	chr16 C3.3	[illegible]	[illegible]	[illegible]
1420677_x_at	7.06	late cornified envelope 1A1	Lce1a1	chr3 F1	[illegible]	[illegible]	[illegible]
1422905_s_at	6.99	flavin containing monooxygenase 2	Fmo2	chr1 H1	[illegible]	[illegible]	[illegible]
1417645_at	6.97	sarcospan	Sspn	chr6 G3|6 71.55 cM	[illegible]	[illegible]	[illegible]
1418706_at	6.96	solute carrier family 38, member 3	Slc38a3	chr9 F1|9 63.0 cM	[illegible]	[illegible]	[illegible]
1434083_a_at	6.96	ELMO domain containing 1	Elmod1	chr9 A5.3	[illegible]	[illegible]	[illegible]
1421961_a_at	6.91	DnaJ (Hsp40) homolog, subfamily B, member 5	Dnajb5	chr4 B1	[illegible]	[illegible]	[illegible]
1417014_at	6.89	heat shock protein 8	Hspb8	chr5 F|5 59.0 cM	[illegible]	[illegible]	[illegible]
1451642_at	6.88	kinesin family member 1B	Kif1b	chr4 E|4 70.9 cM	[illegible]	[illegible]	[illegible]
1446771_at	6.86	Tubulin, alpha 8	Tuba8	chr6 F1	[illegible]	[illegible]	[illegible]
1451270_at	6.85	dual specificity phosphatase 18	Dusp18	chr11 A1	[illegible]	[illegible]	[illegible]
1431504_at	6.84	RIKEN cDNA 2310061N02 gene	2310061N02Rik	chr16 C3.3	[illegible]	[illegible]	[illegible]
1422230_s_at	6.80	cytochrome P450, family 2, subfamily a, polypeptide 4 /// cytochrome P450, famil	Cyp2a4 /// Cyp2a5	chr7 A3|7 6.5 cM	[illegible]	[illegible]	[illegible]
1454242_at	6.79	RIKEN cDNA 2310079G19 gene	2310079G19Rik	chr16 C3.3	[illegible]	[illegible]	[illegible]
1417229_at	6.78	calpain 1	Capn1	chr19 A|19 3.0 cM	[illegible]	[illegible]	[illegible]
1425911_a_at	6.78	fibroblast growth factor receptor 1	Fgfr1	chr8 A2|8 10.0 cM	[illegible]	[illegible]	[illegible]
1432173_at	6.73	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	Serpinb12	chr1 D	[illegible]	[illegible]	[illegible]
1436233_at	6.73	expressed sequence AI117581	AI117581	---	[illegible]	[illegible]	[illegible]
1454015_a_at	6.72	cadherin 13	Cdh13	chr8 E1|8 64.0 cM	[illegible]	[illegible]	[illegible]
1456255_at	6.70	expressed sequence AI314180	AI314180	chr4 B3	[illegible]	[illegible]	[illegible]
1458635_at	6.67	RIKEN cDNA 4832428D23 gene	4832428D23Rik	chr1 C1.1	[illegible]	[illegible]	[illegible]
1434449_at	6.66	aquaporin 4	Aqp4	chr18 A1|18 6.0 cM	[illegible]	[illegible]	[illegible]
1448541_at	6.62	kinesin light chain 1	Klc1	chr12 F1|12 57.0 cM	[illegible]	[illegible]	[illegible]
1449051_at	6.56	peroxisome proliferator activated receptor alpha	Ppara	chr15 E2|15 48.8 cM	[illegible]	[illegible]	[illegible]
1432004_a_at	6.48	dynamin 2	Dnm2	chr9 A3|9 7.0 cM	[illegible]	[illegible]	[illegible]
1419985_s_at	6.43	coiled-coil domain containing 69	Ccdc69	chr11 B1.3|11 28.5 cM	[illegible]	[illegible]	[illegible]
1439718_at	6.39	Adenosine deaminase	Ada	chr2 H3|2 94.0 cM	[illegible]	[illegible]	[illegible]
1425810_a_at	6.34	cysteine and glycine-rich protein 1	Csrp1	chr1 E4	[illegible]	[illegible]	[illegible]
1437751_at	6.29	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	chr5 C1	[illegible]	[illegible]	[illegible]
1418742_at	6.28	keratin 34	Krt34	chr11 D|11 58.3 cM	[illegible]	[illegible]	[illegible]
1425275_at	6.25	aspartate-beta-hydroxylase	Asph	chr4 A1	[illegible]	[illegible]	[illegible]
1427268_at	6.23	filaggrin /// similar to Filaggrin	Flg /// LOC620355 /// LOC675741	chr3 F2.1|3 42.6 cM	[illegible]	[illegible]	[illegible]
1443702_at	6.23	microtubule-associated protein 4	Mtap4	chr9 F2|9 58.0 cM	[illegible]	[illegible]	[illegible]
1420338_at	6.23	arachidonate 15-lipoxygenase	Alox15	chr11 B3|11 40.0 cM	[illegible]	[illegible]	[illegible]
1417673_at	6.21	growth factor receptor bound protein 14	Grb14	chr2 C1.3	[illegible]	[illegible]	[illegible]
1449615_s_at	6.20	high density lipoprotein (HDL) binding protein	Hdlbp	chr1 D|1 55.3 cM	[illegible]	[illegible]	[illegible]
1450828_at	6.18	synaptopodin 2	Synpo2	chr3 G3	[illegible]	[illegible]	[illegible]
1450747_at	6.17	kelch-like ECH-associated protein 1	Keap1	chr9 A3	[illegible]	[illegible]	[illegible]
1425270_at	6.14	kinesin family member 1B	Kif1b	chr4 E|4 70.9 cM	[illegible]	[illegible]	[illegible]
1428758_at	6.12	transmembrane protein 86A	Tmem86a	chr7 B3	[illegible]	[illegible]	[illegible]
1439151_at	6.08	methionine sulfoxide reductase B3	Msrb3	chr10 D2	[illegible]	[illegible]	[illegible]
1451751_at	6.06	DNA-damage-inducible transcript 4-like	Ddit4l	chr3 G3	[illegible]	[illegible]	[illegible]
1423476_at	6.06	solute carrier family 46, member 2	Slc46a2	chr4 B3|4 32.0 cM	[illegible]	[illegible]	[illegible]
1420534_at	5.98	guanylate cyclase 1, soluble, alpha 3	Gucy1a3	chr3 E3	[illegible]	[illegible]	[illegible]
1452957_at	5.96	keratin associated protein 3-3	Krtap3-3	chr11 D	[illegible]	[illegible]	[illegible]
1450974_at	5.93	tissue inhibitor of metalloproteinase 4	Timp4	chr6 E3|6 46.0 cM	[illegible]	[illegible]	[illegible]
1453657_at	5.92	RIKEN cDNA 2310065F04 gene	2310065F04Rik	chr11 B3	[illegible]	[illegible]	[illegible]
1449959_x_at	5.91	late cornified envelope 1H	Lce1h	chr3 F1	[illegible]	[illegible]	[illegible]
1452732_at	5.90	aspartic peptidase, retroviral-like 1	Asprv1	chr6 D1	[illegible]	[illegible]	[illegible]
1434958_at	5.89	sacsin	Sacs	chr14 D1|14 26.75 cM	[illegible]	[illegible]	[illegible]
1436713_s_at	5.88	GTL2, imprinted maternally expressed untranslated mRNA	Gtl2	chr12 F1|12 54.0 cM	[illegible]	[illegible]	[illegible]
1449872_at	5.87	heat shock protein 3	Hspb3	chr13 D2.2	[illegible]	[illegible]	[illegible]
1453724_a_at	5.87	serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpinf1	chr11 B5	[illegible]	[illegible]	[illegible]
1431382_a_at	5.81	CAP-GLY domain containing linker protein family, member 4	Clip4	chr17 E2	[illegible]	[illegible]	[illegible]
1434282_at	5.80	inhibitor of Bruton agammaglobulinemia tyrosine kinase	Ibtk	chr9 E3.1	[illegible]	[illegible]	[illegible]
1425274_at	5.77	aspartate-beta-hydroxylase	Asph	chr4 A1	[illegible]	[illegible]	[illegible]
1420954_a_at	5.76	adducin 1 (alpha)	Add1	chr5 B2|5 20.0 cM	[illegible]	[illegible]	[illegible]
1438849_at	5.75	keratin 78	Krt78	chr15 F3	[illegible]	[illegible]	[illegible]
1423281_at	5.70	stathmin-like 2	Stmn2	chr3 A1|3 6.6 cM	[illegible]	[illegible]	[illegible]
1429870_at	5.69	TRAF2 and NCK interacting kinase	Tnik	chr3 A3	[illegible]	[illegible]	[illegible]
1456968_at	5.67	Actinin alpha 2	Actn2	chr13 A1|13 7.0 cM	[illegible]	[illegible]	[illegible]
1418100_at	5.66	RIKEN cDNA A030009H04 gene	A030009H04Rik	chr11 B3	[illegible]	[illegible]	[illegible]
1425711_a_at	5.65	thymoma viral proto-oncogene 1	Akt1	chr12 F1-F2|12 57.0 cM	[illegible]	[illegible]	[illegible]
1421028_a_at	5.65	myocyte enhancer factor 2C	Mef2c	chr13 C3|13 45.0 cM	[illegible]	[illegible]	[illegible]
1425621_at	5.65	tripartite motif-containing 35	Trim35	chr14 D1	[illegible]	[illegible]	[illegible]
1460279_a_at	5.64	general transcription factor II I /// similar to General transcription factor II	Gtf2i /// LOC669007	chr5 G2|5 75.0 cM	[illegible]	[illegible]	[illegible]
1453973_s_at	5.61	RIKEN cDNA 2900057H02 gene	2900057H02Rik	---	[illegible]	[illegible]	[illegible]
1420537_at	5.61	potassium channel tetramerisation domain containing 4	Kctd4	chr14 D2	[illegible]	[illegible]	[illegible]
1428007_at	5.56	keratin associated protein 13-1	Krtap13-1	chr16 C3.3	[illegible]	[illegible]	[illegible]
1439658_at	5.55	leiomodin 3 (fetal)	Lmod3	chr6 D3	[illegible]	[illegible]	[illegible]
1456395_at	5.53	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	chr5 C1	[illegible]	[illegible]	[illegible]
1453435_a_at	5.52	flavin containing monooxygenase 2	Fmo2	chr1 H1	[illegible]	[illegible]	[illegible]
1432445_at	5.52	RIKEN cDNA 2310016G11 gene	2310016G11Rik	chr7 B3	[illegible]	[illegible]	[illegible]
1423405_at	5.52	tissue inhibitor of metalloproteinase 4	Timp4	chr6 E3|6 46.0 cM	[illegible]	[illegible]	[illegible]
1449902_at	5.51	late cornified envelope 1G	Lce1g	chr3 F1	[illegible]	[illegible]	[illegible]
1422904_at	5.51	flavin containing monooxygenase 2	Fmo2	chr1 H1	[illegible]	[illegible]	[illegible]
1434100_x_at	5.49	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	chr5 C1	[illegible]	[illegible]	[illegible]
1421290_at	5.48	heat shock protein family, member 7 (cardiovascular)	Hspb7	chr4 E1	[illegible]	[illegible]	[illegible]
1418855_at	5.48	late cornified envelope 1L	Lce1l	chr3 F1	[illegible]	[illegible]	[illegible]
AFFX-TransRecMur/X57349_5_at	5.47	transferrin receptor	Tfrc	chr16 B3|16 21.2 cM	[illegible]	[illegible]	[illegible]
1416188_at	5.45	GM2 ganglioside activator protein	Gm2a	chr11 B1.3|11 29.0 cM	[illegible]	[illegible]	[illegible]
1451441_at	5.43	RIKEN cDNA 2210415F13 gene	2210415F13Rik	chr11 B1.3	[illegible]	[illegible]	[illegible]
1449860_at	5.42	HIG1 domain family, member 1B	Higd1b	chr11 D	[illegible]	[illegible]	[illegible]
1425730_at	5.42	calcium channel, voltage-dependent, gamma subunit 6	Cacng6	chr7 A1|7 2.0 cM	[illegible]	[illegible]	[illegible]
1416204_at	5.37	glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	chr15 56.8 cM	[illegible]	[illegible]	[illegible]
1418652_at	5.37	chemokine (C-X-C motif) ligand 9	Cxcl9	chr5 E2|5 53.0 cM	[illegible]	[illegible]	[illegible]
1420741_x_at	5.36	late cornified envelope 1I	Lce1i	chr3 F1	[illegible]	[illegible]	[illegible]
1444139_at	5.35	DNA-damage-inducible transcript 4-like	Ddit4l	chr3 G3	[illegible]	[illegible]	[illegible]
1449082_at	5.32	microfibrillar associated protein 5	Mfap5	chr6 F1	[illegible]	[illegible]	[illegible]
1418632_at	5.30	ubiquitin-conjugating enzyme E2H	Ube2h	chr6 A3.3|6 6.5 cM	[illegible]	[illegible]	[illegible]
1425834_a_at	5.29	glycerol-3-phosphate acyltransferase, mitochondrial	Gpam	chr19 D2|19 52.0 cM	[illegible]	[illegible]	[illegible]
1448421_s_at	5.24	asporin	Aspn	chr13 B1	[illegible]	[illegible]	[illegible]
1452913_at	5.24	Purkinje cell protein 4-like 1	Pcp4l1	chr1 H3	[illegible]	[illegible]	[illegible]
1425273_s_at	5.23	epithelial membrane protein 2	Emp2	chr16 A1|16 2.4 cM	[illegible]	[illegible]	[illegible]
1418279_a_at	5.23	A kinase (PRKA) anchor protein 1	Akap1	chr11 C	[illegible]	[illegible]	[illegible]
1427168_a_at	5.21	procollagen, type XIV, alpha 1	Col14a1	chr15 D	[illegible]	[illegible]	[illegible]
1441897_at	5.20	RIKEN cDNA B230120H23 gene	B230120H23Rik	chr2 C3	[illegible]	[illegible]	[illegible]
1443832_s_at	5.19	serum deprivation response	Sdpr	chr1 C1.1	[illegible]	[illegible]	[illegible]
1440912_at	5.18	ring finger protein 39	Rnf39	chr17 B1	[illegible]	[illegible]	[illegible]
1450936_a_at	5.17	deoxyribonuclease 1-like 2	Dnase1l2	chr17 A3.3	[illegible]	[illegible]	[illegible]
1428595_at	5.15	solute carrier family 6 (neurotransmitter transporter), member 19	Slc6a19	chr13 C1	[illegible]	[illegible]	[illegible]
1425725_s_at	5.10	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	Ppp2r5c	chr12 F2|12 57.0 cM	[illegible]	[illegible]	[illegible]
1430579_at	5.08	TRAF2 and NCK interacting kinase /// region containing TRAF2 and NCK interacting	LOC674765 /// Tnik	chr3 A3	[illegible]	[illegible]	[illegible]
1428283_at	5.08	cytochrome P450, family 2, subfamily s, polypeptide 1	Cyp2s1	chr7 A3	[illegible]	[illegible]	[illegible]
1438651_a_at	5.07	angiotensin receptor-like 1	Agtrl1	chr2 E1	[illegible]	[illegible]	[illegible]
1438483_at	5.07	nitric oxide synthase 1, neuronal	Nos1	chr5 F|5 65.0 cM	[illegible]	[illegible]	[illegible]
1417649_at	5.06	cyclin-dependent kinase inhibitor 1C (P57)	Cdkn1c	chr7 F5|7 69.49 cM	[illegible]	[illegible]	[illegible]
1419518_at	5.04	tubulin, alpha 8	Tuba8	chr6 F1	[illegible]	[illegible]	[illegible]
1431554_a_at	5.04	annexin A9	Anxa9	chr3 F2	[illegible]	[illegible]	[illegible]
1425677_a_at	5.03	ankyrin 1, erythroid	Ank1	chr8 A2|8 9.5 cM	[illegible]	[illegible]	[illegible]
1423104_at	5.03	insulin receptor substrate 1	Irs1	chr1 C5|1 57.0 cM	[illegible]	[illegible]	[illegible]
1417358_s_at	5.02	sorbin and SH3 domain containing 1	Sorbs1	chr19 C3|19 36.5 cM	[illegible]	[illegible]	[illegible]
1455267_at	5.01	estrogen-related receptor gamma	Esrrg	chr1 H6	[illegible]	[illegible]	[illegible]
1425461_at	4.97	F-box and WD-40 domain protein 11	Fbxw11	chr11 A4	[illegible]	[illegible]	[illegible]
1423555_a_at	4.96	interferon-induced protein 44	Ifi44	chr3 H3	[illegible]	[illegible]	[illegible]
1439332_at	4.95	DNA-damage-inducible transcript 4-like	Ddit4l	chr3 G3	[illegible]	[illegible]	[illegible]
1425097_a_at	4.93	zinc finger protein 106	Zfp106	chr2 F1|2 67.2 cM	[illegible]	[illegible]	[illegible]
1443755_at	4.92	---	---	---	[illegible]	[illegible]	[illegible]
1455442_at	4.89	solute carrier family 6 (neurotransmitter transporter), member 19	Slc6a19	chr13 C1	[illegible]	[illegible]	[illegible]
1417802_at	4.89	RIKEN cDNA 1110032A04 gene	1110032A04Rik	chr3 E3	[illegible]	[illegible]	[illegible]
1429464_at	4.88	protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2	chr4 C6	[illegible]	[illegible]	[illegible]
1416779_at	4.85	serum deprivation response	Sdpr	chr1 C1.1	[illegible]	[illegible]	[illegible]
1435551_at	4.85	formin homology 2 domain containing 3	Fhod3	chr18 A2	[illegible]	[illegible]	[illegible]
1424737_at	4.84	thyroid hormone responsive SPOT14 homolog (Rattus)	Thrsp	chr7 E3	[illegible]	[illegible]	[illegible]
1449555_a_at	4.84	fetuin beta	Fetub	chr16 B|16 14.1 cM	[illegible]	[illegible]	[illegible]
1449334_at	4.84	tissue inhibitor of metalloproteinase 3	Timp3	chr10 C1-D1|10 47.0 cM	[illegible]	[illegible]	[illegible]
1432281_a_at	4.82	integrin beta 6	Itgb6	chr2 C3|2 34.0 cM	[illegible]	[illegible]	[illegible]
1420841_at	4.81	protein tyrosine phosphatase, receptor type, F	Ptprf	chr4 C6-D1	[illegible]	[illegible]	[illegible]
1432344_a_at	4.79	amyloid beta (A4) precursor-like protein 2	Aplp2	chr9 A2-B|9 13.0 cM	[illegible]	[illegible]	[illegible]
1440096_at	4.78	extracellular matrix protein 2, female organ and adipocyte specific	Ecm2	chr13 B1	[illegible]	[illegible]	[illegible]
1437774_at	4.78	RIKEN cDNA 1700020I14 gene	1700020I14Rik	chr2 E5	[illegible]	[illegible]	[illegible]
1460242_at	4.78	CD55 antigen	Cd55	chr1 E4|1 67.6 cM	[illegible]	[illegible]	[illegible]
1418536_at	4.76	similar to H-2 class I histocompatibility antigen, Q7 alpha chain precursor (QA-	LOC630509 /// LOC674192	---	[illegible]	[illegible]	[illegible]
1424010_at	4.76	microfibrillar-associated protein 4	Mfap4	chr11 B2|11 34.35 cM	[illegible]	[illegible]	[illegible]
1431030_a_at	4.75	ring finger protein 14	Rnf14	chr18 B3|18 17.0 cM	[illegible]	[illegible]	[illegible]
1428955_x_at	4.75	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	Slc9a3r2	chr17 A3.3	[illegible]	[illegible]	[illegible]
1422313_a_at	4.72	insulin-like growth factor binding protein 5	Igfbp5	chr1 C3|1 36.1 cM	[illegible]	[illegible]	[illegible]
1456180_at	4.71	similar to RNA binding motif protein 24 /// RNA binding motif protein 24	LOC380843 /// LOC638266 /// Rbm24	chr13 A5	[illegible]	[illegible]	[illegible]
1419748_at	4.71	ATP-binding cassette, sub-family D (ALD), member 2	Abcd2	chr15 E-F	[illegible]	[illegible]	[illegible]
1452670_at	4.71	myosin, light polypeptide 9, regulatory	Myl9	chr2 H1	[illegible]	[illegible]	[illegible]
1422919_at	4.70	HRAS-like suppressor	Hrasls	chr16 B2	[illegible]	[illegible]	[illegible]
1453152_at	4.67	MAM domain containing 2	Mamdc2	chr19 B	[illegible]	[illegible]	[illegible]
1451667_at	4.67	RIKEN cDNA C530043G21 gene	C530043G21Rik	chr1 H1	[illegible]	[illegible]	[illegible]
1422744_at	4.67	phosphorylase kinase alpha 1	Phka1	chrX D|X 39.0 cM	[illegible]	[illegible]	[illegible]
1431431_a_at	4.67	nitrogen fixation gene 1 (S. cerevisiae)	Nfs1	chr2 H1	[illegible]	[illegible]	[illegible]
1431422_a_at	4.66	dual specificity phosphatase 14	Dusp14	chr11 C|11 48.0 cM	[illegible]	[illegible]	[illegible]
1436736_x_at	4.66	DNA segment, human D4S114	D0H4S114	chr18 B1	[illegible]	[illegible]	[illegible]
1453552_at	4.65	RIKEN cDNA 2310014F07 gene	2310014F07Rik	---	[illegible]	[illegible]	[illegible]
1436484_at	4.65	RIKEN cDNA C030019I05 gene	C030019I05Rik	chr11 B1.1	[illegible]	[illegible]	[illegible]
1420816_at	4.65	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	chr5 G2	[illegible]	[illegible]	[illegible]
1453279_x_at	4.64	keratin 76	Krt76	chr15 F3	[illegible]	[illegible]	[illegible]
1448456_at	4.63	ceroid-lipofuscinosis, neuronal 8	Cln8	chr8 A1.1|8 6.0 cM	[illegible]	[illegible]	[illegible]
1421915_a_at	4.61	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	chr4 D1	[illegible]	[illegible]	[illegible]
1441801_at	4.61	potassium channel tetramerisation domain containing 4	Kctd4	chr14 D2	[illegible]	[illegible]	[illegible]
1445569_at	4.60	predicted gene, EG546611	EG546611	chr14 C1	[illegible]	[illegible]	[illegible]
1425102_a_at	4.60	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	Ace2	chrX F5|X 70.5 cM	[illegible]	[illegible]	[illegible]
1430514_a_at	4.58	CD99 antigen	Cd99	---	[illegible]	[illegible]	[illegible]
1425809_at	4.58	fatty acid binding protein 4, adipocyte	Fabp4	chr3 A1|3 13.9 cM	[illegible]	[illegible]	[illegible]
1417963_at	4.58	phospholipid transfer protein	Pltp	chr2 H3|2 93.0 cM	[illegible]	[illegible]	[illegible]
1415893_at	4.56	sphingosine phosphate lyase 1	Sgpl1	chr10 B4|10 32.0 cM	[illegible]	[illegible]	[illegible]
1418352_at	4.55	hydroxysteroid (17-beta) dehydrogenase 2	Hsd17b2	chr8 E1	[illegible]	[illegible]	[illegible]
1418979_at	4.54	aldo-keto reductase family 1, member C14	Akr1c14	chr13 A1	[illegible]	[illegible]	[illegible]
1425526_a_at	4.53	paired related homeobox 1	Prrx1	chr1 H2.1|1 85.4 cM	[illegible]	[illegible]	[illegible]
1431261_at	4.53	chloride intracellular channel 5	Clic5	chr17 C	[illegible]	[illegible]	[illegible]
1434917_at	4.51	cordon-bleu	Cobl	chr11 A1|11 6.5 cM	[illegible]	[illegible]	[illegible]
1460451_at	4.50	transmembrane protein 52	Tmem52	chr4 E2	[illegible]	[illegible]	[illegible]
1453988_a_at	4.50	insulin degrading enzyme	Ide	chr19 C2|19 25.0 cM	[illegible]	[illegible]	[illegible]
1453442_at	4.50	RIKEN cDNA 2310043M15 gene	2310043M15Rik	---	[illegible]	[illegible]	[illegible]
1434099_at	4.50	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	chr5 C1	[illegible]	[illegible]	[illegible]
1452138_a_at	4.50	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	Ace2	chrX F5|X 70.5 cM	[illegible]	[illegible]	[illegible]
1435635_at	4.49	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	Pcmtd1	chr1 A1	[illegible]	[illegible]	[illegible]
1444612_at	4.48	RIKEN cDNA 3222402P14 gene	3222402P14Rik	chr9 E4	[illegible]	[illegible]	[illegible]
1442368_at	4.47	potassium channel tetramerisation domain containing 12b	Kctd12b	chrX F3	[illegible]	[illegible]	[illegible]
1426051_a_at	4.46	centromere protein B	Cenpb	chr2 F1|2 73.9 cM	[illegible]	[illegible]	[illegible]
1421324_a_at	4.46	thymoma viral proto-oncogene 2	Akt2	chr7 B1|7 6.5 cM	[illegible]	[illegible]	[illegible]
1416805_at	4.45	RIKEN cDNA 1110032E23 gene	1110032E23Rik	chr3 E3	[illegible]	[illegible]	[illegible]
1422966_a_at	4.45	transferrin receptor	Tfrc	chr16 B3|16 21.2 cM	[illegible]	[illegible]	[illegible]
1441481_at	4.43	microfibrillar-associated protein 3-like	Mfap3l	chr8 B3.2	[illegible]	[illegible]	[illegible]
1420975_at	4.43	bromodomain adjacent to zinc finger domain, 1B	Baz1b	chr5 G2	[illegible]	[illegible]	[illegible]
1449009_at	4.42	T-cell specific GTPase	Tgtp	chr11 B1.2	[illegible]	[illegible]	[illegible]
1452742_at	4.42	trafficking protein, kinesin binding 1	Trak1	chr9 F4|9 71.0 cM	[illegible]	[illegible]	[illegible]
1452370_s_at	4.41	RIKEN cDNA B230208H17 gene	B230208H17Rik	chr2 A3	[illegible]	[illegible]	[illegible]
1429300_at	4.40	ankyrin repeat domain 9	Ankrd9	chr12 F1	[illegible]	[illegible]	[illegible]
1422949_at	4.40	nitric oxide synthase 1, neuronal	Nos1	chr5 F|5 65.0 cM	[illegible]	[illegible]	[illegible]
1459557_at	4.38	Zinc finger and BTB domain containing 16	Zbtb16	chr9 A5.3|9 23.0 cM	[illegible]	[illegible]	[illegible]
1429449_at	4.38	sterile alpha motif domain containing 4	Samd4	chr14 C1	[illegible]	[illegible]	[illegible]
1434621_at	4.38	cDNA sequence BC054438	BC054438	chr17 A3.3	[illegible]	[illegible]	[illegible]
1417634_at	4.37	superoxide dismutase 3, extracellular	Sod3	chr5 C1|5 31.0 cM	[illegible]	[illegible]	[illegible]
1431164_at	4.32	Ras-related GTP binding D	Rragd	chr4 A5|4 11.4 cM	[illegible]	[illegible]	[illegible]
1450839_at	4.31	DNA segment, human D4S114	D0H4S114	chr18 B1	[illegible]	[illegible]	[illegible]
1417932_at	4.30	interleukin 18	Il18	chr9 A5.3|9 29.0 cM	[illegible]	[illegible]	[illegible]
1419215_at	4.29	aldehyde oxidase 4	Aox4	chr1 23.2 cM	[illegible]	[illegible]	[illegible]
1436109_at	4.29	expressed sequence AI317395	AI317395	chr10 B1	[illegible]	[illegible]	[illegible]
1429679_at	4.29	leucine rich repeat containing 17	Lrrc17	chr5 A3	[illegible]	[illegible]	[illegible]
1431068_at	4.29	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	Rmnd5a	chr6 C1	[illegible]	[illegible]	[illegible]
1425272_at	4.28	epithelial membrane protein 2	Emp2	chr16 A1|16 2.4 cM	[illegible]	[illegible]	[illegible]
1459695_at	4.28	---	---	---	[illegible]	[illegible]	[illegible]
1450378_at	4.26	TAP binding protein	Tapbp	chr17 B1|17 18.41 cM	[illegible]	[illegible]	[illegible]
1443715_at	4.26	similar to RNA binding motif protein 24 /// RNA binding motif protein 24	LOC380843 /// LOC638266 /// Rbm24	chr13 A5	[illegible]	[illegible]	[illegible]
1418454_at	4.26	microfibrillar associated protein 5	Mfap5	chr6 F1	[illegible]	[illegible]	[illegible]
1456621_at	4.25	RIKEN cDNA D430015B01 gene	D430015B01Rik	chr6 B3	[illegible]	[illegible]	[illegible]
1432554_at	4.24	RIKEN cDNA 2310040G07 gene	2310040G07Rik	---	[illegible]	[illegible]	[illegible]
1457275_at	4.24	desmuslin	Dmn	chr7 C	[illegible]	[illegible]	[illegible]
1427490_at	4.24	ATP-binding cassette, sub-family B (MDR/TAP), member 7	Abcb7	chrX C-D|X 39.0 cM	[illegible]	[illegible]	[illegible]
1449029_at	4.23	MAP kinase-interacting serine/threonine kinase 2	Mknk2	chr10 C1	[illegible]	[illegible]	[illegible]
1421008_at	4.22	radical S-adenosyl methionine domain containing 2	Rsad2	chr12 A3	[illegible]	[illegible]	[illegible]
1453607_at	4.22	microfibrillar-associated protein 3-like	Mfap3l	chr8 B3.2	[illegible]	[illegible]	[illegible]
1424408_at	4.22	LIM and senescent cell antigen like domains 2	Lims2	chr18 B1	[illegible]	[illegible]	[illegible]
1421991_a_at	4.21	insulin-like growth factor binding protein 4	Igfbp4	chr11 D	[illegible]	[illegible]	[illegible]
1427652_x_at	4.20	synaptojanin 2	Synj2	chr17 A2-A3.1|17 3.3 cM	[illegible]	[illegible]	[illegible]
1447584_s_at	4.19	myc target 1	Myct1	chr10 A1	[illegible]	[illegible]	[illegible]
1427037_at	4.19	eukaryotic translation initiation factor 4, gamma 1	Eif4g1	chr16 B1	[illegible]	[illegible]	[illegible]
1456944_at	4.19	potassium voltage gated channel, Shaw-related subfamily, member 1	Kcnc1	chr7 B3|7 23.5 cM	[illegible]	[illegible]	[illegible]
1420892_at	4.19	wingless-related MMTV integration site 7B	Wnt7b	chr15 E2|15 46.9 cM	[illegible]	[illegible]	[illegible]
1444638_at	4.18	titin	Ttn	chr2 D|2 44.0 cM	[illegible]	[illegible]	[illegible]
AFFX-TransRecMur/X57349_3_at	4.17	transferrin receptor	Tfrc	chr16 B3|16 21.2 cM	[illegible]	[illegible]	[illegible]
1442325_at	4.17	TBC1 domain family, member 24	Tbc1d24	chr17 A3.3	[illegible]	[illegible]	[illegible]
1417502_at	4.17	tetraspanin 7	Tspan7	chrX A1.3-A2	[illegible]	[illegible]	[illegible]
1433493_at	4.16	RIKEN cDNA 5730472N09 gene	5730472N09Rik	chr2 B	[illegible]	[illegible]	[illegible]
1430715_at	4.15	RIKEN cDNA 2310014L17 gene	2310014L17Rik	chr7 A1	[illegible]	[illegible]	[illegible]
1449015_at	4.15	resistin like alpha	Retnla	chr16 B5|16 32.6 cM	[illegible]	[illegible]	[illegible]
1429342_s_at	4.13	RIKEN cDNA 2310021H06 gene	2310021H06Rik	chr2 H1	[illegible]	[illegible]	[illegible]
1429195_at	4.13	---	---	---	[illegible]	[illegible]	[illegible]
1425344_at	4.12	nuclear prelamin A recognition factor	Narf	chr11 E2	[illegible]	[illegible]	[illegible]
1441111_at	4.12	15 days embryo embryonic body below diaphragm cDNA, RIKEN full-length enriched l	---	---	[illegible]	[illegible]	[illegible]
1439127_at	4.12	expressed sequence AI314180	AI314180	chr4 B3	[illegible]	[illegible]	[illegible]
1421460_at	4.12	desmocollin 1	Dsc1	chr18 A2	[illegible]	[illegible]	[illegible]
1448538_a_at	4.11	DNA segment, Chr 4, Wayne State University 53, expressed	D4Wsu53e	chr4 D3|4 65.7 cM	[illegible]	[illegible]	[illegible]
1436644_x_at	4.10	transmembrane protein 25	Tmem25	chr9 A5.2	[illegible]	[illegible]	[illegible]
1425426_a_at	4.10	myocyte enhancer factor 2A	Mef2a	chr7 C|7 33.0 cM	[illegible]	[illegible]	[illegible]
1433499_at	4.09	RIKEN cDNA 2010005J08 gene	2010005J08Rik	chr11 A1	[illegible]	[illegible]	[illegible]
1444504_at	4.09	dehydrogenase/reductase (SDR family) member 7C	Dhrs7c	chr11 B3	[illegible]	[illegible]	[illegible]
1426139_a_at	4.08	chemokine (C-C motif) receptor-like 1	Ccrl1	chr9 F1	[illegible]	[illegible]	[illegible]
1422589_at	4.08	RAB3A, member RAS oncogene family	Rab3a	chr8 B3.3|8 32.6 cM	[illegible]	[illegible]	[illegible]
1427591_at	4.08	chloride channel 1	Clcn1	chr6 B2.1|6 22.5 cM	[illegible]	[illegible]	[illegible]
1434374_at	4.08	RIKEN cDNA B930006L02 gene	B930006L02Rik	chr7 E2	[illegible]	[illegible]	[illegible]
1432107_at	4.07	RIKEN cDNA 2310010M20 gene	2310010M20Rik	chr16 B2	[illegible]	[illegible]	[illegible]
1449461_at	4.06	retinol binding protein 7, cellular	Rbp7	chr4 E2	[illegible]	[illegible]	[illegible]
1460426_at	4.06	phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	chr3 F2.2|3 51.5 cM	[illegible]	[illegible]	[illegible]

KO Day 0 vs KO Day 1 (GCRMA > 2 Fold Changes 05-20-08 Both Experiments) Mouse 430_2 Arrays

Up Regulated Genes

p	Fold Change	Gene Title	Gene Symbol	Chromosomal Location	Gene Ontology Biological Process	Gene Ontology Cellular Component	Gene Ontology Molecular Function
1453511_at	16.64	RIKEN cDNA 2310007B03 gene	2310007B03Rik	chr1 D	[illegible]	[illegible]	[illegible]
1449902_at	12.13	late cornified envelope 1G	Lce1g	chr3 F1	[illegible]	[illegible]	[illegible]
1453898_at	12.03	integrin beta 1 binding protein 3	Itgb1bp3	chr10 C1	[illegible]	[illegible]	[illegible]
1451675_a_at	11.43	aminolevulinic acid synthase 2, erythroid	Alas2	chrX F3|X 63.0 cM	[illegible]	[illegible]	[illegible]
1434502_x_at	10.85	solute carrier family 4 (anion exchanger), member 1	Slc4a1	chr11 D|11 62.0 cM	[illegible]	[illegible]	[illegible]
1418493_a_at	10.62	synuclein, alpha	Snca	chr6 B3|6 29.0 cM	[illegible]	[illegible]	[illegible]
1430466_at	9.71	RIKEN cDNA 2310005G13 gene	2310005G13Rik	chr16 C1.1	[illegible]	[illegible]	[illegible]
1421421_at	9.68	angiopoietin-like 1	Angptl1	chr1 H1	[illegible]	[illegible]	[illegible]
1448021_at	9.46	RIKEN cDNA 4930431B09 gene	4930431B09Rik	chr3 F2.2	[illegible]	[illegible]	[illegible]
1451613_at	9.25	hornerin	Hrnr	chr3 F2	[illegible]	[illegible]	[illegible]
1419325_at	9.16	neuromedin U	Nmu	chr5 C3.3	[illegible]	[illegible]	[illegible]
1425631_at	8.39	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	chr19 C3	[illegible]	[illegible]	[illegible]
1422230_s_at	8.31	cytochrome P450, family 2, subfamily a, polypeptide 4 /// cytochrome P450, famil	Cyp2a4 /// Cyp2a5	chr7 A3|7 6.5 cM	[illegible]	[illegible]	[illegible]
1423016_a_at	8.27	glycophorin A	Gypa	chr8 C2|8 36.0 cM	[illegible]	[illegible]	[illegible]
1429334_at	8.11	RIKEN cDNA 2300002O18 gene	2300002O18Rik	chr1 B	[illegible]	[illegible]	[illegible]
1417808_at	8.04	RIKEN cDNA 2310050C09 gene	2310050C09Rik	chr3 F2.1	[illegible]	[illegible]	[illegible]
1455224_at	7.84	angiopoietin-like 1	Angptl1	chr1 H1	[illegible]	[illegible]	[illegible]
1449077_at	7.70	erythroid associated factor	Eraf	---	[illegible]	[illegible]	[illegible]
1417714_x_at	7.64	hemoglobin alpha, adult chain 1	Hba-a1	chr11 A4|11 16.0 cM	[illegible]	[illegible]	[illegible]
1425382_a_at	7.52	aquaporin 4	Aqp4	chr18 A1|18 6.0 cM	[illegible]	[illegible]	[illegible]
1419409_at	7.38	late cornified envelope 1B	Lce1b	chr3 F1	[illegible]	[illegible]	[illegible]
1420332_x_at	7.34	late cornified envelope 1D	Lce1d	chr3 F1	[illegible]	[illegible]	[illegible]
1423476_at	7.33	solute carrier family 46, member 2	Slc46a2	chr4 B3|4 32.0 cM	[illegible]	[illegible]	[illegible]
1451707_s_at	7.25	solute carrier family 41, member 3	Slc41a3	chr6 D2	[illegible]	[illegible]	[illegible]
1440435_at	7.24	kyphoscoliosis peptidase	Ky	chr9 F1|9 56.0 cM	[illegible]	[illegible]	[illegible]
1420550_at	6.98	late cornified envelope 1F	Lce1f	chr3 F1	[illegible]	[illegible]	[illegible]
1416652_at	6.96	asporin	Aspn	chr13 B1	[illegible]	[illegible]	[illegible]
1441801_at	6.89	potassium channel tetramerisation domain containing 4	Kctd4	chr14 D2	[illegible]	[illegible]	[illegible]
1418100_at	6.78	RIKEN cDNA A030009H04 gene	A030009H04Rik	chr11 B3	[illegible]	[illegible]	[illegible]
1453218_at	6.77	late cornified envelope 1C	Lce1c	chr3 F1	[illegible]	[illegible]	[illegible]
1434083_a_at	6.72	ELMO domain containing 1	Elmod1	chr9 A5.3	[illegible]	[illegible]	[illegible]
1420676_at	6.65	late cornified envelope 1A1	Lce1a1	chr3 F1	[illegible]	[illegible]	[illegible]

KO Day 0 vs WT Day 0 (GCRMA > 2 Fold Changes 05-20-08 Both Experiments) Mouse 430_2 Arrays

Up Regulated Genes

Probeset ID	Fold Change	Gene Title	Gene Symbol
1455869_at	5.71	Calcium/calmodulin-dependent protein kinase II, beta	Camk2b
1430703_at	5.59	---	---
1434502_x_at	5.45	solute carrier family 4 (anion exchanger), member 1	Slc4a1
1448021_at	4.34	RIKEN cDNA 4930431B09 gene	4930431B09Rik
1423016_a_at	4.22	glycophorin A	Gypa
1418493_a_at	4.13	synuclein, alpha	Snca
1425436_x_at	3.88	killer cell lectin-like receptor, subfamily A, member 3	Klra3
1451675_a_at	3.73	aminolevulinic acid synthase 2, erythroid	Alas2
1437358_at	3.69	WD repeat and FYVE domain containing 1	Wdfy1
1449077_at	3.48	erythroid associated factor	Eraf
1442089_at	3.36	---	---
1420599_at	3.27	RIKEN cDNA 2300006N05 gene /// hypothetical protein LOC670472 /// hypothetical p	2300006N05Rik /// LOC670472 /// LOC670482
1424749_at	3.22	WD repeat and FYVE domain containing 1	Wdfy1
1430509_at	3.21	---	---
1419394_s_at	3.03	S100 calcium binding protein A8 (calgranulin A)	S100a8
1436853_a_at	2.99	synuclein, alpha	Snca
1427179_at	2.99	keratin 33B	Krt33b
1435588_at	2.98	WD repeat and FYVE domain containing 1	Wdfy1
1449387_at	2.90	keratin 33A	Krt33a
1448752_at	2.89	carbonic anhydrase 2	Car2
1429993_s_at	2.84	spermatogenesis associated glutamate (E)-rich protein 4b	Speer4b
1448756_at	2.78	S100 calcium binding protein A9 (calgranulin B)	S100a9
1430669_at	2.74	keratin associated protein 4-7	Krtap4-7
1421494_at	2.66	RIKEN cDNA 1110033F04 gene	1110033F04Rik
1450723_at	2.65	ISL1 transcription factor, LIM/homeodomain	Isl1
1417714_x_at	2.64	hemoglobin alpha, adult chain 1	Hba-a1
1440852_at	2.60	isopentenyl-diphosphate delta isomerase 2	Idi2
1451774_at	2.58	predicted gene, OTTMUSG00000002196	OTTMUSG00000002196
1449902_at	2.57	late cornified envelope 1G	Lce1g
1440927_x_at	2.53	RIKEN cDNA A330102K04 gene	A330102K04Rik
1419311_at	2.53	tripartite motif protein 10	Trim10
1416464_at	2.47	solute carrier family 4 (anion exchanger), member 1	Slc4a1
1431650_at	2.47	RIKEN cDNA 1110054P19 gene	1110054P19Rik
1457307_at	2.46	RIKEN cDNA A330102K04 gene	A330102K04Rik
1429608_at	2.44	alcohol dehydrogenase 6A (class V)	Adh6a
1418480_at	2.35	pro-platelet basic protein	Ppbp
1449560_at	2.34	RIKEN cDNA 2310043L02 gene	2310043L02Rik
1417750_a_at	2.31	solute carrier family 25, member 37	Slc25a37
1429262_at	2.29	Ras association (RalGDS/AF-6) domain family 6	Rassf6
1421092_at	2.28	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antit	Serpina12
1452166_a_at	2.27	keratin 10	Krt10
1422720_at	2.23	ISL1 transcription factor, LIM/homeodomain	Isl1
1418304_at	2.21	protocadherin 21	Pcdh21
1451245_at	2.20	leucine rich repeat containing 3B	Lrrc3b
1441307_at	2.19	RIKEN cDNA A030010K20 gene	A030010K20Rik
1420904_at	2.14	interleukin 17 receptor A	Il17ra
1420905_at	2.14	interleukin 17 receptor A	Il17ra
1418100_at	2.10	RIKEN cDNA A030009H04 gene	A030009H04Rik
1428680_at	2.09	CDP-diacylglycerol synthase 1	Cds1
1435761_at	2.09	cDNA sequence BC100530	BC100530
1416105_at	2.07	nicotinamide nucleotide transhydrogenase	Nnt
1441629_at	2.07	Glutamate receptor interacting protein 1	Grip1
1421117_at	2.06	dystonin	Dst
1455889_at	2.06	male sterility domain containing 1	Mlstd1
1418496_at	2.05	forkhead box A1	Foxa1
1457140_s_at	2.05	RIKEN cDNA 4632411J06 gene	4632411J06Rik
1416076_at	2.04	cyclin B1, related sequence 1 /// cyclin B1 /// predicted gene, EG434175 /// sim	Ccnb1 /// Ccnb1-rs1 /// EG434175 /// LOC672788
1417808_at	2.04	RIKEN cDNA 2310050C09 gene	2310050C09Rik
1441801_at	2.04	potassium channel tetramerisation domain containing 4	Kctd4
1437842_at	2.03	phosphatidylinositol-specific phospholipase C, X domain containing 1	Plcxd1
1416309_at	2.03	nucleolar and spindle associated protein 1	Nusap1
1453145_at	2.02	RIKEN cDNA 4933439C20 gene	4933439C20Rik
1420562_at	2.02	secreted Ly6/Plaur domain containing 1	Slurp1

Down Regulated Genes

Probeset ID	Fold Change	Gene Title	Gene Symbol
1443100_at	-10.28	Thyroid hormone receptor beta	Thrb
1458368_at	-9.32	myosin, heavy polypeptide 4, skeletal muscle	Myh4
1421289_at	-8.85	heat shock protein family, member 7 (cardiovascular)	Hspb7
1450618_a_at	-8.23	small proline-rich protein 2A	Sprr2a
1425450_at	-6.73	chitinase 3-like 4	Chi3l4
1420338_at	-6.53	arachidonate 15-lipoxygenase	Alox15
1439016_x_at	-6.19	small proline-rich protein 2A	Sprr2a
1425451_s_at	-6.13	chitinase 3-like 3 /// chitinase 3-like 4	Chi3l3 /// Chi3l4
1420924_at	-6.01	tissue inhibitor of metalloproteinase 2	Timp2
1415959_at	-5.67	solute carrier family 2 (facilitated glucose transporter), member 4	Slc2a4
1453623_a_at	-5.66	RAD23a homolog (S. cerevisiae)	Rad23a
1417033_at	-5.52	ubiquitin-conjugating enzyme E2G 2	Ube2g2
1432646_a_at	-5.02	predicted gene, EG667653	EG667653
1441362_at	-4.86	Protein tyrosine phosphatase, receptor type, G	Ptprg
1426607_at	-4.84	predicted gene, EG633640	EG633640
1450196_s_at	-4.75	glycogen synthase 1, muscle	Gys1
1458659_at	-4.70	placenta specific 9	Plac9
1451961_a_at	-4.62	myelin basic protein	Mbp
1420841_at	-4.54	protein tyrosine phosphatase, receptor type, F	Ptprf
1425329_a_at	-4.49	cytochrome b5 reductase 3	Cyb5r3
1448541_at	-4.32	kinesin light chain 1	Klc1
1449551_at	-4.28	myosin IC	Myo1c
1453224_at	-4.26	zinc finger, AN1-type domain 5	Zfand5
1427414_at	-4.22	protein kinase, cAMP dependent regulatory, type II alpha	Prkar2a
1416601_a_at	-4.15	Down syndrome critical region homolog 1 (human)	Dscr1
1430514_a_at	-4.09	CD99 antigen	Cd99
AFFX-GapdhMur/M32599_5_at	-4.03	glyceraldehyde-3-phosphate dehydrogenase	Gapdh
1457324_at	-3.94	RIKEN cDNA 4933409K07 gene	4933409K07Rik
1425711_a_at	-3.92	thymoma viral proto-oncogene 1	Akt1
1422017_s_at	-3.90	RIKEN cDNA 4833439L19 gene	4833439L19Rik
1421991_a_at	-3.86	insulin-like growth factor binding protein 4	Igfbp4
1421290_at	-3.85	heat shock protein family, member 7 (cardiovascular)	Hspb7
1425810_a_at	-3.82	cysteine and glycine-rich protein 1	Csrp1
1425911_a_at	-3.77	fibroblast growth factor receptor 1	Fgfr1
1420954_a_at	-3.73	adducin 1 (alpha)	Add1
1420867_at	-3.72	transmembrane emp24 domain trafficking protein 2	Tmed2
1452590_a_at	-3.67	placenta specific 9	Plac9
1439127_at	-3.61	expressed sequence AI314180	AI314180
1417381_at	-3.58	complement component 1, q subcomponent, alpha polypeptide	C1qa
1450311_at	-3.49	solute carrier family 8 (sodium/calcium exchanger), member 3	Slc8a3
1417229_at	-3.47	calpain 1	Capn1
1417634_at	-3.46	superoxide dismutase 3, extracellular	Sod3
1426122_a_at	-3.44	coronin, actin binding protein 6	Coro6
1459003_at	-3.42	four and a half LIM domains 1	Fhl1
1449054_a_at	-3.42	poly(rC) binding protein 4	Pcbp4
1427610_at	-3.41	desmoplakin	Dsp
1416704_at	-3.33	mitogen activated protein kinase 14	Mapk14
1432436_a_at	-3.32	adenylate kinase 3	Ak3
1430980_a_at	-3.32	eukaryotic translation initiation factor 4A1	Eif4a1
1458624_at	-3.30	similar to RNA binding motif protein 24 /// RNA binding motif protein 24	LOC380843 /// Rbm24
1425834_a_at	-3.30	glycerol-3-phosphate acyltransferase, mitochondrial	Gpam
1443755_at	-3.28	---	---
1424518_at	-3.23	RIKEN cDNA 2310016F22 gene /// cDNA sequence BC020489	2310016F22Rik /// BC020489
1419088_at	-3.22	tissue inhibitor of metalloproteinase 3	Timp3
1445996_at	-3.22	---	---
1431292_a_at	-3.21	twinfilin, actin-binding protein, homolog 2 (Drosophila)	Twf2
1447937_a_at	-3.21	RIKEN cDNA 4933409K07 gene /// predicted gene, EG545605 /// similar to 4933409K0	4933409K07Rik /// EG545605 /// ENSMUSG00000073885 /// LOC545614 /// LOC622738 ///
1415997_at	-3.20	thioredoxin interacting protein	Txnip
1460279_a_at	-3.19	general transcription factor II I /// similar to General transcription factor II	Gtf2i /// LOC669007
1421324_a_at	-3.15	thymoma viral proto-oncogene 2	Akt2
1447939_a_at	-3.14	RIKEN cDNA 4933409K07 gene /// predicted gene, EG545605 /// hypothetical protein	4933409K07Rik /// EG545605 /// LOC665845
1449416_at	-3.09	frizzled homolog 4 (Drosophila)	Fzd4
1452429_s_at	-3.06	ATP-binding cassette, sub-family F (GCN20), member 1	Abcf1
1422959_s_at	-3.05	zinc finger protein 313	Zfp313
1428850_x_at	-3.03	CD99 antigen	Cd99
1431233_at	-3.03	cyclin M4	Cnnm4
1448605_at	-3.00	ras homolog gene family, member C	Rhoc
1431431_a_at	-2.98	nitrogen fixation gene 1 (S. cerevisiae)	Nfs1
1450379_at	-2.98	moesin	Msn
1424178_at	-2.97	transmembrane protein 38a	Tmem38a
1421002_at	-2.94	angiopoietin-like 2	Angptl2
1426051_a_at	-2.93	centromere protein B	Cenpb
1450114_at	-2.93	kinase suppressor of ras 1	Ksr1
1451441_at	-2.93	RIKEN cDNA 2210415F13 gene	2210415F13Rik
1425620_at	-2.93	transforming growth factor, beta receptor III	Tgfbr3
1427820_at	-2.92	---	---
1421239_at	-2.92	interleukin 6 signal transducer	Il6st
1425273_s_at	-2.92	epithelial membrane protein 2	Emp2
1417543_at	-2.89	ribosomal protein S6 kinase, polypeptide 2	Rps6ka2
1431274_a_at	-2.89	---	---
1450085_at	-2.88	angiopoietin-like 2	Angptl2
1456255_at	-2.88	expressed sequence AI314180	AI314180
1431382_a_at	-2.87	CAP-GLY domain containing linker protein family, member 4	Clip4
1419099_x_at	-2.87	stomatin	Stom
1416191_at	-2.86	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1
1449615_s_at	-2.86	high density lipoprotein (HDL) binding protein	Hdlbp
1425725_s_at	-2.86	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	Ppp2r5c
1448538_a_at	-2.86	DNA segment, Chr 4, Wayne State University 53, expressed	D4Wsu53e
1451841_a_at	-2.86	nuclear receptor co-repressor 2	Ncor2
1450747_at	-2.85	kelch-like ECH-associated protein 1	Keap1
1453307_a_at	-2.84	anaphase-promoting complex subunit 5	Anapc5
1417645_at	-2.84	sarcospan	Sspn
1451335_at	-2.83	placenta-specific 8	Plac8
1423446_at	-2.80	death-associated kinase 3	Dapk3
1427652_x_at	-2.79	synaptojanin 2	Synj2
1453556_x_at	-2.79	CD99 antigen	Cd99
1425394_at	-2.77	CDNA sequence BC023105	BC023105
1460281_at	-2.77	ankyrin repeat and SOCS box-containing protein 15	Asb15
1427844_a_at	-2.77	CCAAT/enhancer binding protein (C/EBP), beta	Cebpb
1454015_a_at	-2.76	cadherin 13	Cdh13
1420941_at	-2.74	regulator of G-protein signaling 5	Rgs5
1422853_at	-2.73	src homology 2 domain-containing transforming protein C1	Shc1
1437859_x_at	-2.71	eukaryotic translation initiation factor 5A	Eif5a
1435579_at	-2.70	RIKEN cDNA 4933409K07 gene	4933409K07Rik
1421895_at	-2.70	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x /// LOC673373
1431285_at	-2.70	mahogunin, ring finger 1	Mgrn1
1427102_at	-2.70	schlafen 4	Slfn4
1433804_at	-2.68	Janus kinase 1	Jak1
1422313_a_at	-2.68	insulin-like growth factor binding protein 5	Igfbp5
1417014_at	-2.67	heat shock protein 8	Hspb8
AFFX-TransRecMur/X57349_5_at	-2.67	transferrin receptor	Tfrc
1438683_at	-2.67	WAS protein family, member 2	Wasf2
1432419_a_at	-2.66	RIKEN cDNA 2700078K21 gene	2700078K21Rik
1434357_a_at	-2.65	karyopherin (importin) beta 1	Kpnb1
1416204_at	-2.64	glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1
1442019_at	-2.62	Recoverin	Rcvrn
1422007_at	-2.61	aquaporin 3	Aqp3
1451119_a_at	-2.61	fibulin 1	Fbln1
1451768_a_at	-2.60	solute carrier family 20, member 2	Slc20a2
1425444_a_at	-2.60	transforming growth factor, beta receptor II	Tgfbr2
1451743_at	-2.59	DNA segment, Chr 19, Wayne State University 162, expressed	D19Wsu162e
1418652_at	-2.59	chemokine (C-X-C motif) ligand 9	Cxcl9
1421915_a_at	-2.58	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3
1421961_a_at	-2.58	DnaJ (Hsp40) homolog, subfamily B, member 5	Dnajb5
1460460_a_at	-2.55	golgi reassembly stacking protein 2	Gorasp2
1449029_at	-2.55	MAP kinase-interacting serine/threonine kinase 2	Mknk2
1421378_s_at	-2.55	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1
1427457_a_at	-2.54	bone morphogenetic protein 1	Bmp1
1449888_at	-2.53	endothelial PAS domain protein 1	Epas1
1426004_a_at	-2.52	transglutaminase 2, C polypeptide	Tgm2
1450259_a_at	-2.52	signal transducer and activator of transcription 5A	Stat5a
1426179_a_at	-2.52	twisted gastrulation homolog 1 (Drosophila)	Twsg1
1417633_at	-2.51	superoxide dismutase 3, extracellular	Sod3
1424775_at	-2.51	2'-5' oligoadenylate synthetase 1A	Oas1a
1421313_s_at	-2.50	cortactin	Cttn
1431214_at	-2.50	hypothetical gene LOC433762	LOC433762
1422512_a_at	-2.50	opioid growth factor receptor	Ogfr
1426764_at	-2.50	ornithine decarboxylase antizyme 2	Oaz2
1417358_s_at	-2.48	sorbin and SH3 domain containing 1	Sorbs1
1423746_at	-2.47	thioredoxin domain containing 5	Txndc5
1415893_at	-2.47	sphingosine phosphate lyase 1	Sgpl1
1416691_at	-2.46	GTP binding protein 2	Gtpbp2
1416246_a_at	-2.46	coronin, actin binding protein 1A	Coro1a
AFFX-r2-Bs-dap-5_at	-2.45	---	---
1450472_s_at	-2.45	MAD homolog 3 (Drosophila)	Smad3
1434610_at	-2.45	plectin 1	Plec1
1449341_a_at	-2.45	stomatin	Stom
1420868_s_at	-2.45	transmembrane emp24 domain trafficking protein 2	Tmed2
1434374_at	-2.42	RIKEN cDNA B930006L02 gene	B930006L02Rik
1422522_at	-2.42	fragile X mental retardation, autosomal homolog 2	Fxr2
1452370_s_at	-2.42	RIKEN cDNA B230208H17 gene	B230208H17Rik
1448214_at	-2.41	pyruvate dehydrogenase (lipoamide) beta /// similar to pyruvate dehydrogenase (l	LOC620009 /// Pdhb
1418292_at	-2.41	arsA (bacterial) arsenite transporter, ATP-binding, homolog 1	Asna1
1451667_at	-2.41	RIKEN cDNA C530043G21 gene	C530043G21Rik
1424668_a_at	-2.40	cut-like 1 (Drosophila)	Cutl1
1427565_a_at	-2.40	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5
1426118_a_at	-2.40	translocase of outer mitochondrial membrane 40 homolog (yeast)	Tomm40
1434282_at	-2.40	inhibitor of Bruton agammaglobulinemia tyrosine kinase	Ibtk
1450462_at	-2.40	corticotropin releasing hormone receptor 2	Crhr2
1415819_a_at	-2.40	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	Ppp2r1a
1453839_a_at	-2.40	peptidase inhibitor 16	Pi16
1453740_a_at	-2.37	cyclin L2	Ccnl2
1420831_at	-2.37	quiescin Q6	Qscn6
1415798_at	-2.36	discoidin domain receptor family, member 1	Ddr1
1433493_at	-2.36	RIKEN cDNA 5730472N09 gene	5730472N09Rik
1425461_at	-2.36	F-box and WD-40 domain protein 11	Fbxw11
1431030_a_at	-2.36	ring finger protein 14	Rnf14
1416504_at	-2.36	Unc-51 like kinase 1 (C. elegans)	Ulk1
1439151_at	-2.35	methionine sulfoxide reductase B3	Msrb3
1441897_at	-2.34	RIKEN cDNA B230120H23 gene	B230120H23Rik
1427773_a_at	-2.34	Rab acceptor 1 (prenylated)	Rabac1
1415988_at	-2.34	high density lipoprotein (HDL) binding protein	Hdlbp
1418592_at	-2.34	DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4
1416157_at	-2.33	vinculin	Vcl
1420854_at	-2.33	elastin	Eln
1424808_at	-2.33	laminin, alpha 4	Lama4
1432349_a_at	-2.32	syncoilin	Sync
1456610_at	-2.32	jumonji domain containing 3	Jmjd3
1460635_at	-2.31	Fas-activated serine/threonine kinase	Fastk
1429449_at	-2.31	sterile alpha motif domain containing 4	Samd4
1416228_at	-2.31	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	Pin1
1452485_at	-2.31	phosphatase, orphan 1	Phospho1
1431828_a_at	-2.31	synaptojanin 2	Synj2
1415784_at	-2.30	vacuolar protein sorting 35	Vps35
1422967_a_at	-2.30	transferrin receptor	Tfrc
1429362_a_at	-2.30	splicing factor 3b, subunit 2	Sf3b2
1448320_at	-2.30	stromal interaction molecule 1	Stim1
1429148_at	-2.30	nuclear factor I/C	Nfic
1453973_s_at	-2.30	RIKEN cDNA 2900057H02 gene	2900057H02Rik
1449055_x_at	-2.29	poly(rC) binding protein 4	Pcbp4
1450977_s_at	-2.29	N-myc downstream regulated gene 1	Ndrg1
1421143_at	-2.29	diaphanous homolog 1 (Drosophila)	Diap1
1452742_at	-2.29	trafficking protein, kinesin binding 1	Trak1
1425730_at	-2.29	calcium channel, voltage-dependent, gamma subunit 6	Cacng6
1427408_a_at	-2.29	thyroid hormone receptor associated protein 3	Thrap3
1455548_at	-2.28	discs, large homolog-associated protein 4 (Drosophila)	Dlgap4
1422526_at	-2.28	acyl-CoA synthetase long-chain family member 1	Acsl1
1424791_a_at	-2.28	basal cell adhesion molecule	Bcam
1436665_a_at	-2.28	latent transforming growth factor beta binding protein 4	Ltbp4
1460717_at	-2.27	testis-specific protein, Y-encoded-like 1	Tspyl1
1450089_a_at	-2.26	signal recognition particle receptor, B subunit	Srprb
1429464_at	-2.26	protein kinase, AMP-activated, alpha 2 catalytic subunit	Prkaa2
1432004_a_at	-2.26	dynamin 2	Dnm2
1418393_a_at	-2.26	integrin alpha 7	Itga7
1440342_at	-2.25	RIKEN cDNA G530011O06 gene	G530011O06Rik
1421721_a_at	-2.25	aryl hydrocarbon receptor nuclear translocator	Arnt
1445569_at	-2.25	predicted gene, EG546611	EG546611
1451721_a_at	-2.25	histocompatibility 2, class II antigen A, beta 1	H2-Ab1
1452024_a_at	-2.25	LIM domain binding 1	Ldb1
1424907_a_at	-2.24	phenylalanyl-tRNA synthetase, alpha subunit	Farsa
1449002_at	-2.24	pleckstrin homology-like domain, family A, member 3	Phlda3
1450676_at	-2.24	transcription elongation factor B (SIII), polypeptide 3	Tceb3
1432913_at	-2.23	leucine rich repeat containing 52	Lrrc52
1429859_a_at	-2.23	ADP-ribosylation factor-like 2 binding protein	Arl2bp
1421187_at	-2.22	chemokine (C-C motif) receptor 2	Ccr2
1417752_at	-2.22	coronin, actin binding protein 1C	Coro1c
1420975_at	-2.22	bromodomain adjacent to zinc finger domain, 1B	Baz1b
1435134_at	-2.22	arylacetamide deacetylase-like 1	Aadacl1
1447938_at	-2.22	similar to 4933409K07Rik protein	LOC545614
1456080_a_at	-2.21	serine incorporator 3	Serinc3
1425576_at	-2.21	S-adenosylhomocysteine hydrolase-like 1	Ahcyl1
1427533_at	-2.21	ALS2 C-terminal like	Als2cl
1438639_x_at	-2.21	RIKEN cDNA 4933417E01 gene	4933417E01Rik
1424484_at	-2.20	MOB1, Mps One Binder kinase activator-like 1B (yeast)	Mobk1b
1425726_x_at	-2.20	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	Ppp2r5c
1425621_at	-2.20	tripartite motif-containing 35	Trim35
1421848_at	-2.20	solute carrier family 22 (organic cation transporter), member 5	Slc22a5
1451290_at	-2.20	microtubule-associated protein 1 light chain 3 alpha	Map1lc3a
1418632_at	-2.19	ubiquitin-conjugating enzyme E2H	Ube2h
1417350_at	-2.19	pallidin	Pldn
1452097_a_at	-2.19	dual specificity phosphatase 7 /// similar to dual specificity phosphatase 7	Dusp7 /// LOC674944
1453724_a_at	-2.19	serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpinf1
1428664_at	-2.19	vasoactive intestinal polypeptide	Vip
1416188_at	-2.19	GM2 ganglioside activator protein	Gm2a
1419098_at	-2.18	stomatin	Stom
AFFX-GapdhMur/M32599_M_at	-2.18	glyceraldehyde-3-phosphate dehydrogenase	Gapdh
1418188_a_at	-2.18	Metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	Malat1
1425610_s_at	-2.17	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	Galnt2
1443866_at	-2.17	leucine-rich repeats and transmembrane domains 1	Lrtm1
1424115_at	-2.17	protein phosphatase 5, catalytic subunit	Ppp5c
1442675_at	-2.17	---	---
1443715_at	-2.16	similar to RNA binding motif protein 24 /// RNA binding motif protein 24	LOC380843 /// LOC638266 /// Rbm24
1425474_a_at	-2.16	vacuolar protein sorting 39 (yeast)	Vps39
1449073_at	-2.16	filamin C, gamma (actin binding protein 280)	Flnc
1420652_at	-2.16	arginine-tRNA-protein transferase 1	Ate1

KO Day 1 vs WT Day 1 (GCRMA > 2 Fold Changes 05-20-08 Both Experiments) Mouse 430_2 Arrays

Up Regulated Genes

Probeset ID	Fold Change	Gene Title	Gene Symbol	Chromosomal Location	Gene Ontology Biological Process	Gene Ontology Cellular Component	Gene Ontology Molecular Function
1427451_a_at	9.21	cDNA sequence BC018473	BC018473	chr11 E2	---	---	---
1425450_at	8.93	chitinase 3-like 4	Chi3l4	chr3 F2.3	0005975 // carbohydrate metabolic process // inferred from electronic annotation	---	0003824 // catalytic activity // inferred from electronic annotation /// 0004553
1420338_at	8.25	arachidonate 15-lipoxygenase	Alox15	chr11 B3|11 40.0 cM	0005975 // carbohydrate metabolic process // --- /// 0006118 // electron transpo	---	0004052 // arachidonate 12-lipoxygenase activity // inferred from electronic ann
1425451_s_at	5.90	chitinase 3-like 3 /// chitinase 3-like 4	Chi3l3 /// Chi3l4	chr3 F2.3 /// chr3 F2.3|3 50.5 cM	0005975 // carbohydrate metabolic process // inferred from electronic annotation	0016023 // cytoplasmic membrane-bound vesicle // inferred from direct assay	0003824 // catalytic activity // inferred from electronic annotation /// 0004553
1424749_at	3.69	WD repeat and FYVE domain containing 1	Wdfy1	chr1 C4	---	---	0008270 // zinc ion binding // inferred from electronic annotation
1426039_a_at	3.61	arachidonate lipoxygenase, epidermal	Alox12e	chr11 B3|11 40.0 cM	0006118 // electron transport // inferred from electronic annotation /// 0006691	---	0004052 // arachidonate 12-lipoxygenase activity // inferred from electronic ann
1437358_at	3.52	WD repeat and FYVE domain containing 1	Wdfy1	chr1 C4	---	---	0008270 // zinc ion binding // inferred from electronic annotation
1418742_at	3.38	keratin 34	Krt34	chr11 D|11 58.3 cM	0007010 // cytoskeleton organization and biogenesis // inferred from electronic	0005882 // intermediate filament // inferred from electronic annotation	0005198 // structural molecule activity // inferred from electronic annotation /
1442089_at	3.37	---	---	---	---	---	---
1417808_at	3.25	RIKEN cDNA 2310050C09 gene	2310050C09Rik	chr3 F2.1	0006118 // electron transport // inferred from electronic annotation	---	0009055 // electron carrier activity // inferred from electronic annotation
1420409_at	3.21	keratin 35	Krt35	chr11 D	---	0005882 // intermediate filament // inferred from electronic annotation	0005198 // structural molecule activity // inferred from electronic annotation
1421672_at	3.16	interleukin 17A	Il17a	chr1 A	0006954 // inflammatory response // inferred from electronic annotation	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from electronic annotation
1441307_at	3.12	RIKEN cDNA A030010K20 gene	A030010K20Rik	chr11 D	---	0005882 // intermediate filament // inferred from electronic annotation /// 0045	0005515 // protein binding // inferred from physical interaction
1418652_at	3.04	chemokine (C-X-C motif) ligand 9	Cxcl9	chr5 E2|5 53.0 cM	0006954 // inflammatory response // inferred from electronic annotation /// 0006	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from electronic annotation /// 0008009
1418930_at	2.95	chemokine (C-X-C motif) ligand 10	Cxcl10	chr5 E2|5 53.0 cM	0006118 // electron transport // --- /// 0006935 // chemotaxis // inferred from	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from electronic annotation /// 0008009
1435588_at	2.94	WD repeat and FYVE domain containing 1	Wdfy1	chr1 C4	---	---	0008270 // zinc ion binding // inferred from electronic annotation
1430703_at	2.86	---	---	---	---	---	---
1455869_at	2.73	Calcium/calmodulin-dependent protein kinase II, beta	Camk2b	chr11 A1|11 0.5 cM	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenoty	0005954 // calcium- and calmodulin-dependent protein kinase complex // traceable	0000166 // nucleotide binding // inferred from electronic annotation /// 0004672
1417164_at	2.71	dual specificity phosphatase 10	Dusp10	chr1 H5	0006470 // protein amino acid dephosphorylation // --- /// 0006470 // protein am	0005634 // nucleus // --- /// 0005634 // nucleus // inferred from electronic ann	0000158 // protein phosphatase type 2A activity // --- /// 0000163 // protein ph
1418536_at	2.70	similar to H-2 class I histocompatibility antigen, Q7 alpha chain precursor (QA-	LOC630509 /// LOC674192	---	0002474 // antigen processing and presentation of peptide antigen via MHC class	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1419413_at	2.70	chemokine (C-C motif) ligand 17	Ccl17	chr8 D1|8 45.0 cM	0006935 // chemotaxis // traceable author statement /// 0006955 // immune respon	0005576 // extracellular region // --- /// 0005576 // extracellular region // in	0005125 // cytokine activity // traceable author statement /// 0008009 // chemok
1432173_at	2.65	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	Serpinb12	chr1 D	0042177 // negative regulation of protein catabolic process // inferred from seq	0005737 // cytoplasm // inferred from sequence or structural similarity	0004866 // endopeptidase inhibitor activity // inferred from electronic annotati
1451774_at	2.63	predicted gene, OTTMUSG00000002196	OTTMUSG00000002196	chr11 D|11	---	0005882 // intermediate filament // inferred from electronic annotation /// 0045	---
1416105_at	2.62	nicotinamide nucleotide transhydrogenase	Nnt	chr13 D2|13 64.0 cM	0006118 // electron transport // inferred from electronic annotation /// 0015992	0005739 // mitochondrion // inferred from direct assay /// 0005739 // mitochondr	0008746 // NAD(P) transhydrogenase activity // inferred from electronic annotati
1419409_at	2.62	late cornified envelope 1B	Lce1b	chr3 F1	---	---	---
1426181_a_at	2.61	interleukin 24	Il24	chr1 E4	0006955 // immune response // --- /// 0006955 // immune response // inferred fro	0005576 // extracellular region // inferred from direct assay /// 0005576 // ext	0005125 // cytokine activity // inferred from sequence or structural similarity
1439718_at	2.57	Adenosine deaminase	Ada	chr2 H3|2 94.0 cM	0006163 // purine nucleotide metabolic process // inferred from mutant phenotype	0005737 // cytoplasm // inferred from direct assay	0004000 // adenosine deaminase activity // inferred from direct assay /// 000400
1454883_at	2.53	expressed sequence AI987692	AI987692	chr15 D1	---	---	---
1418174_at	2.51	D site albumin promoter binding protein	Dbp	chr7 B3|7 23.0 cM	0006350 // transcription // inferred from electronic annotation /// 0006355 // r	0005634 // nucleus // inferred from electronic annotation	0003677 // DNA binding // inferred from electronic annotation /// 0003700 // tra
1453145_at	2.49	RIKEN cDNA 4933439C20 gene	4933439C20Rik	---	0008654 // phospholipid biosynthetic process // inferred from electronic annotat	---	0004609 // phosphatidylserine decarboxylase activity // inferred from electronic
1427268_at	2.48	filaggrin /// similar to Filaggrin	Flg /// LOC620355 /// LOC675741	chr3 F2.1|3 42.6 cM	0007010 // cytoskeleton organization and biogenesis // traceable author statemen	0001533 // cornified envelope // inferred from direct assay	0005509 // calcium ion binding // inferred from electronic annotation
1453218_at	2.43	late cornified envelope 1C	Lce1c	chr3 F1	---	---	---
1452957_at	2.43	keratin associated protein 3-3	Krtap3-3	chr11 D	---	0005882 // intermediate filament // inferred from electronic annotation /// 0045	0005198 // structural molecule activity // inferred from electronic annotation
1429334_at	2.41	RIKEN cDNA 2300002O18 gene	2300002O18Rik	chr1 B	0008152 // metabolic process // inferred from electronic annotation /// 0009253	0005615 // extracellular space // ---	0003796 // lysozyme activity // inferred from electronic annotation /// 0016787
1443702_at	2.41	microtubule-associated protein 4	Mtap4	chr9 F2|9 58.0 cM	0007017 // microtubule-based process // inferred from electronic annotation ///	0005874 // microtubule // inferred from electronic annotation /// 0005875 // mic	0005519 // cytoskeletal regulatory protein binding // inferred from electronic a
1420350_at	2.40	late cornified envelope 1A2	Lce1a2	chr3 F1	---	---	0005515 // protein binding // inferred from physical interaction /// 0042802 //
1415837_at	2.38	kallikrein 1	Klk1	chr7 B3|7 23.0 cM	0006508 // proteolysis // inferred from electronic annotation /// 0006508 // pro	0005615 // extracellular space // ---	0004252 // serine-type endopeptidase activity // inferred from electronic annota
1457867_at	2.37	sphingosine-1-phosphate phosphotase 2	Sgpp2	chr1 C4	---	0005783 // endoplasmic reticulum // inferred from electronic annotation /// 0016	0016787 // hydrolase activity // inferred from electronic annotation
1420358_at	2.36	keratin associated protein 13	Krtap13	chr16 C3.3	---	0005882 // intermediate filament // inferred from electronic annotation	---
1460336_at	2.35	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Ppargc1a	chr5 C1	0001659 // thermoregulation // inferred from sequence or structural similarity /	0005634 // nucleus // --- /// 0005634 // nucleus // inferred from sequence or st	0000166 // nucleotide binding // inferred from electronic annotation /// 0003676
1440435_at	2.31	kyphoscoliosis peptidase	Ky	chr9 F1|9 56.0 cM	0007517 // muscle development // inferred from mutant phenotype /// 0007528 // n	---	---
1429342_s_at	2.31	RIKEN cDNA 2310021H06 gene	2310021H06Rik	chr2 H1	---	---	0008289 // lipid binding // inferred from electronic annotation
1420599_at	2.30	RIKEN cDNA 2300006N05 gene /// hypothetical protein LOC670472 /// hypothetical p	2300006N05Rik /// LOC670472 /// LOC670482	chr11 D	---	0005882 // intermediate filament // inferred from electronic annotation /// 0045	---
1453279_x_at	2.30	keratin 76	Krt76	chr15 F3	---	0005882 // intermediate filament // inferred from electronic annotation	0005198 // structural molecule activity // inferred from electronic annotation
1419215_at	2.30	aldehyde oxidase 4	Aox4	chr1 23.2 cM	0006118 // electron transport // --- /// 0006118 // electron transport // inferr	---	0004031 // aldehyde oxidase activity // inferred from sequence or structural sim
1429496_x_at	2.30	RIKEN cDNA 2300002M23 gene	2300002M23Rik	chr17 B1	---	0005615 // extracellular space // ---	---
1458624_at	2.29	similar to RNA binding motif protein 24 /// RNA binding motif protein 24	LOC380843 /// Rbm24	chr13 A5	0016068 // type I hypersensitivity // inferred from electronic annotation	---	0000166 // nucleotide binding // inferred from electronic annotation /// 0003676
1444139_at	2.28	DNA-damage-inducible transcript 4-like	Ddit4l	chr3 G3	---	---	---
1416033_at	2.27	transmembrane protein 109	Tmem109	chr19 A	---	0005615 // extracellular space // --- /// 0016020 // membrane // inferred from e	---
1427365_at	2.25	RIKEN cDNA 5430421N21 gene	5430421N21Rik	chr15 F2|15 58.71 cM	---	0005882 // intermediate filament // inferred from electronic annotation	0005198 // structural molecule activity // inferred from electronic annotation
1430731_at	2.25	keratin associated protein 2-4	Krtap2-4	chr11 D	---	0005882 // intermediate filament // inferred from electronic annotation /// 0045	---
1422667_at	2.25	keratin 15	Krt15	chr11 D|11 58.5 cM	0007010 // cytoskeleton organization and biogenesis // inferred from electronic	0005882 // intermediate filament // inferred from electronic annotation	0005198 // structural molecule activity // inferred from electronic annotation /
1424761_at	2.25	cDNA sequence BC011487	BC011487	chr6 B2.1	---	---	---
1427797_s_at	2.24	cathepsin E /// predicted gene, EG622147 /// predicted gene, EG665955 /// predic	Ctse /// EG622147 /// EG665955 /// EG666402 /// EG667328 /// EG667538 /// EG6682	chr1 F|1 69.1 cM /// chr10 A1 /// chr10 A3 /// chr10 B3 /// chr11 B5 /// chr11 C	0006278 // RNA-dependent DNA replication // inferred from electronic annotation	0005615 // extracellular space // --- /// 0005768 // endosome // inferred from d	0003676 // nucleic acid binding // inferred from electronic annotation /// 00036
1456573_x_at	2.24	nicotinamide nucleotide transhydrogenase	Nnt	chr13 D2|13 64.0 cM	0006118 // electron transport // inferred from electronic annotation /// 0015992	0005739 // mitochondrion // inferred from direct assay /// 0005739 // mitochondr	0008746 // NAD(P) transhydrogenase activity // inferred from electronic annotati
1449986_at	2.22	RIKEN cDNA 2310034C09 gene	2310034C09Rik	chr16 C3.3	---	---	---
1425102_a_at	2.22	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	Ace2	chrX F5|X 70.5 cM	0006508 // proteolysis // --- /// 0006508 // proteolysis // inferred from electr	0005576 // extracellular region // inferred from electronic annotation /// 00160	0004180 // carboxypeptidase activity // traceable author statement /// 0004180 /
1450618_a_at	2.20	small proline-rich protein 2A	Sprr2a	chr3 F1|3 45.2 cM	0006412 // translation // inferred from electronic annotation /// 0007566 // emb	0001533 // cornified envelope // non-traceable author statement /// 0005622 // i	0003735 // structural constituent of ribosome // inferred from electronic annota
1431650_at	2.20	RIKEN cDNA 1110054P19 gene	1110054P19Rik	chr11 D	---	0005882 // intermediate filament // inferred from electronic annotation /// 0045	0005515 // protein binding // inferred from physical interaction
1422179_at	2.18	gap junction membrane channel protein beta 4	Gjb4	chr4 D1-D3|4 57.5 cM	0007154 // cell communication // inferred from electronic annotation /// 0007267	0005615 // extracellular space // --- /// 0005921 // gap junction // inferred fr	0005243 // gap-junction forming channel activity // inferred from electronic ann
1458455_at	2.17	actin-binding Rho activating protein	Abra	chr15 B3.1	0000060 // protein import into nucleus, translocation // inferred from direct as	0005856 // cytoskeleton // inferred from electronic annotation /// 0005886 // pl	0003713 // transcription coactivator activity // inferred from direct assay ///
1445420_at	2.16	Myocyte enhancer factor 2C	Mef2c	chr13 C3|13 45.0 cM	0001974 // blood vessel remodeling // inferred from mutant phenotype /// 0006350	0005634 // nucleus // --- /// 0005634 // nucleus // inferred from electronic ann	0003677 // DNA binding // inferred from direct assay /// 0003677 // DNA binding
1419684_at	2.15	chemokine (C-C motif) ligand 8	Ccl8	chr11 C|11 47.0 cM	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // infl	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from electronic annotation /// 0008009
1448107_x_at	2.15	kallikrein 1	Klk1	chr7 B3|7 23.0 cM	0006508 // proteolysis // inferred from electronic annotation /// 0006508 // pro	0005615 // extracellular space // ---	0004252 // serine-type endopeptidase activity // inferred from electronic annota
1418283_at	2.15	claudin 4	Cldn4	chr5 G2|5 75.0 cM	0016338 // calcium-independent cell-cell adhesion // inferred from sequence or s	0005615 // extracellular space // --- /// 0005923 // tight junction // inferred	0005198 // structural molecule activity // inferred from electronic annotation /
1419591_at	2.14	melanoma-derived leucine zipper, extra-nuclear factor	Mlze	chr15 D1	---	0005737 // cytoplasm // inferred from sequence or structural similarity	---
1420677_x_at	2.14	late cornified envelope 1A1	Lce1a1	chr3 F1	---	---	---
1451961_a_at	2.13	myelin basic protein	Mbp	chr18 E2-E4|18 55.0 cM	0042552 // myelination // inferred from direct assay	0043209 // myelin sheath // inferred from direct assay	0005198 // structural molecule activity // inferred from electronic annotation /
1443361_at	2.13	Tetraspanin 9	Tspan9	chr6 F3	---	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1431213_a_at	2.13	hypothetical gene LOC433762 /// predicted gene, EG668462 /// predicted gene, EG6	EG668462 /// EG668581 /// LOC433762 /// LOC670993 /// LOC673100	chr12 A1.2 /// chr4 D2.3	0015074 // DNA integration // inferred from electronic annotation	0019028 // viral capsid // inferred from electronic annotation	0003676 // nucleic acid binding // inferred from electronic annotation /// 00036
1416325_at	2.12	cysteine-rich secretory protein 1	Crisp1	chr17 B1|17 21.0 cM	---	0005576 // extracellular region // inferred from electronic annotation /// 00055	---
1446484_at	2.12	Myocyte enhancer factor 2C	Mef2c	chr13 C3|13 45.0 cM	0001974 // blood vessel remodeling // inferred from mutant phenotype /// 0006350	0005634 // nucleus // --- /// 0005634 // nucleus // inferred from electronic ann	0003677 // DNA binding // inferred from direct assay /// 0003677 // DNA binding
1456211_at	2.12	NLR family, pyrin domain containing 10	Nlrp10	chr7 E3	0006952 // defense response // ---	---	0000166 // nucleotide binding // inferred from electronic annotation /// 0005524
1422565_s_at	2.12	nuclear factor I/C	Nfic	chr10 C1|10 43.0 cM	0006260 // DNA replication // inferred from electronic annotation /// 0006350 //	0005622 // intracellular // inferred from electronic annotation /// 0005634 // n	0003677 // DNA binding // inferred from electronic annotation /// 0003700 // tra
1450488_at	2.11	chemokine (C-C motif) ligand 24	Ccl24	chr5 G1	0006935 // chemotaxis // inferred from direct assay /// 0006935 // chemotaxis //	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from direct assay /// 0005125 // cytoki
1420550_at	2.11	late cornified envelope 1F	Lce1f	chr3 F1	---	---	0005515 // protein binding // inferred from physical interaction
1420676_at	2.10	late cornified envelope 1A1	Lce1a1	chr3 F1	---	---	---
1439332_at	2.10	DNA-damage-inducible transcript 4-like	Ddit4l	chr3 G3	---	---	---
1417803_at	2.10	RIKEN cDNA 1110032A04 gene	1110032A04Rik	chr3 E3	---	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1449555_a_at	2.09	fetuin beta	Fetub	chr16 B|16 14.1 cM	---	0005615 // extracellular space // ---	0004869 // cysteine protease inhibitor activity // inferred from electronic anno
1420332_x_at	2.09	late cornified envelope 1D	Lce1d	chr3 F1	---	---	---
1431504_at	2.08	RIKEN cDNA 2310061N02 gene	2310061N02Rik	chr16 C3.3	---	---	0005515 // protein binding // inferred from physical interaction
1421494_at	2.07	RIKEN cDNA 1110033F04 gene	1110033F04Rik	chr11 D	---	0005882 // intermediate filament // inferred from electronic annotation /// 0045	0005515 // protein binding // inferred from physical interaction
1456968_at	2.06	Actinin alpha 2	Actn2	chr13 A1|13 7.0 cM	0006936 // muscle contraction // inferred from physical interaction /// 0030035	0005865 // striated muscle thin filament // traceable author statement /// 00059	0003779 // actin binding // inferred from electronic annotation /// 0005509 // c
1451755_a_at	2.06	apolipoprotein B editing complex 1	Apobec1	chr6 F1|6 54.5 cM	0006381 // mRNA editing // inferred from mutant phenotype /// 0006397 // mRNA pr	---	0004126 // cytidine deaminase activity // inferred from sequence or structural s
1419043_a_at	2.05	interferon inducible GTPase 1	Iigp1	chr18 D3	0019221 // cytokine and chemokine mediated signaling pathway // traceable author	0005783 // endoplasmic reticulum // inferred from electronic annotation /// 0016	0000166 // nucleotide binding // inferred from electronic annotation /// 0003924
1454242_at	2.05	RIKEN cDNA 2310079G19 gene	2310079G19Rik	chr16 C3.3	---	---	---
1417802_at	2.04	RIKEN cDNA 1110032A04 gene	1110032A04Rik	chr3 E3	---	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1452138_a_at	2.03	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	Ace2	chrX F5|X 70.5 cM	0006508 // proteolysis // --- /// 0006508 // proteolysis // inferred from electr	0005576 // extracellular region // inferred from electronic annotation /// 00160	0004180 // carboxypeptidase activity // traceable author statement /// 0004180 /
1438467_at	2.02	macrophage galactose N-acetyl-galactosamine specific lectin 2	Mgl2	chr11 B3	---	0016020 // membrane // inferred from electronic annotation	0005529 // sugar binding // inferred from electronic annotation /// 0030246 // c
1450606_at	2.02	phenylethanolamine-N-methyltransferase	Pnmt	chr11 D	0042423 // catecholamine biosynthetic process // inferred from electronic annota	---	0004603 // phenylethanolamine N-methyltransferase activity // inferred from elec
1428980_at	2.00	keratinocyte expressed, proline-rich	Kprp	chr3 F1	---	---	---
1427751_a_at	2.00	keratin 36	Krt36	chr11 D	0007010 // cytoskeleton organization and biogenesis // inferred from electronic	0005882 // intermediate filament // inferred from electronic annotation	0005198 // structural molecule activity // inferred from electronic annotation /

Down Regulated Genes

Probeset ID	Fold Change	Gene Title	Gene Symbol	Chromosomal Location	Gene Ontology Biological Process	Gene Ontology Cellular Component	Gene Ontology Molecular Function
1421806_at	-6.07	defensin beta 3	Defb3	chr8 A4	0006952 // defense response // inferred from electronic annotation /// 0042742 /	0005576 // extracellular region // inferred from electronic annotation /// 00056	---
1443100_at	-5.97	Thyroid hormone receptor beta	Thrb	chr14 A3	0006350 // transcription // inferred from electronic annotation /// 0006355 // r	0005634 // nucleus // traceable author statement /// 0005634 // nucleus // infer	0003677 // DNA binding // inferred from electronic annotation /// 0003700 // tra
1418666_at	-5.85	pentraxin related gene	Ptx3	chr3 E1|3 33.8 cM	0001878 // response to yeast // inferred from mutant phenotype /// 0008228 // op	0005615 // extracellular space // ---	0001872 // zymosan binding // inferred from mutant phenotype
1422604_at	-5.28	urate oxidase	Uox	chr3 H2|3 75.0 cM	0006144 // purine base metabolic process // traceable author statement /// 00061	0005739 // mitochondrion // inferred from direct assay /// 0005777 // peroxisome	0004846 // urate oxidase activity // traceable author statement /// 0004846 // u
1452590_a_at	-5.22	placenta specific 9	Plac9	chr14 B	---	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1449366_at	-4.89	matrix metallopeptidase 8	Mmp8	chr9 A1	0000270 // peptidoglycan metabolic process // inferred from electronic annotatio	0005578 // proteinaceous extracellular matrix // inferred from electronic annota	0004222 // metalloendopeptidase activity // inferred from electronic annotation
1450297_at	-4.42	interleukin 6	Il6	chr5 B1|5 17.0 cM	0001781 // neutrophil apoptosis // inferred from direct assay /// 0001781 // neu	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from direct assay /// 0005125 // cytoki
1455241_at	-4.19	cDNA sequence BC037703	BC037703	chr3 F2.2	---	---	---
1458659_at	-3.87	placenta specific 9	Plac9	chr14 B	---	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1417160_s_at	-3.68	extracellular proteinase inhibitor	Expi	chr11 C	---	---	0004866 // endopeptidase inhibitor activity // --- /// 0004866 // endopeptidase
1418722_at	-3.34	neutrophilic granule protein	Ngp	chr9 F2	0006952 // defense response // --- /// 0006952 // defense response // inferred f	0005576 // extracellular region // --- /// 0005576 // extracellular region // in	0004869 // cysteine protease inhibitor activity // --- /// 0004869 // cysteine p
1419427_at	-3.32	colony stimulating factor 3 (granulocyte)	Csf3	chr11 D|11 57.0 cM	0006955 // immune response // inferred from electronic annotation /// 0030851 //	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // non-traceable author statement /// 0005125 // cy
1447939_a_at	-3.31	RIKEN cDNA 4933409K07 gene /// predicted gene, EG545605 /// hypothetical protein	4933409K07Rik /// EG545605 /// LOC665845	chr4 A5 /// chr4 A5|4	---	---	---
1450616_at	-3.30	eosinophil-associated, ribonuclease A family, member 5	Ear5	chr14 C1	---	0005615 // extracellular space // ---	0003676 // nucleic acid binding // inferred from electronic annotation /// 00045
1419209_at	-3.17	chemokine (C-X-C motif) ligand 1	Cxcl1	chr5 E-F|5 51.0 cM	0000074 // regulation of progression through cell cycle // inferred from electro	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from electronic annotation /// 0008009
1419728_at	-3.10	chemokine (C-X-C motif) ligand 5	Cxcl5	chr5 E2|5 53.0 cM	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // infl	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from electronic annotation /// 0008009
1424832_at	-3.06	RIKEN cDNA 4732429D16 gene	4732429D16Rik	chr11 E2	---	---	---
1447937_a_at	-3.02	RIKEN cDNA 4933409K07 gene /// predicted gene, EG545605 /// similar to 4933409K0	4933409K07Rik /// EG545605 /// ENSMUSG00000073885 /// LOC545614 /// LOC622738 //	chr4 A5 /// chr4 A5|4	---	---	---
1445996_at	-3.02	---	---	---	---	---	---
1441362_at	-2.97	Protein tyrosine phosphatase, receptor type, G	Ptprg	chr14 A2|14 2.0 cM	0006470 // protein amino acid dephosphorylation // inferred from electronic anno	0005615 // extracellular space // --- /// 0005886 // plasma membrane // inferred	0004089 // carbonate dehydratase activity // inferred from electronic annotation
1442074_at	-2.92	C-type lectin domain family 2, member g	Clec2g	chr6 F3	0045671 // negative regulation of osteoclast differentiation // inferred from di	0005615 // extracellular space // --- /// 0016021 // integral to membrane // ---	0005529 // sugar binding // --- /// 0005529 // sugar binding // inferred from el
1429960_at	-2.89	RIKEN cDNA 4930438A08 gene	4930438A08Rik	chr11 B1.3	0006118 // electron transport // inferred from electronic annotation	---	0016491 // oxidoreductase activity // inferred from electronic annotation /// 00
1419725_at	-2.83	solute carrier family 26, member 4	Slc26a4	chr12 B1	0006810 // transport // inferred from electronic annotation /// 0007605 // senso	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	0005215 // transporter activity // inferred from electronic annotation /// 00082
1422562_at	-2.80	Ras-related associated with diabetes	Rrad	chr8 D3	0007264 // small GTPase mediated signal transduction // inferred from electronic	0016020 // membrane // inferred from electronic annotation	0000166 // nucleotide binding // inferred from electronic annotation /// 0005516
1420310_at	-2.78	---	---	---	---	---	---
1448214_at	-2.78	pyruvate dehydrogenase (lipoamide) beta /// similar to pyruvate dehydrogenase (l	LOC620009 /// Pdhb	chr1 A1 /// chr14 A1	0006096 // glycolysis // --- /// 0006096 // glycolysis // inferred from electron	0005739 // mitochondrion // inferred from direct assay /// 0005739 // mitochondr	0004739 // pyruvate dehydrogenase (acetyl-transferring) activity // --- /// 0004
1425606_at	-2.69	solute carrier family 5 (iodide transporter), member 8	Slc5a8	chr10 C1	0006810 // transport // inferred from electronic annotation /// 0006811 // ion t	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	0005215 // transporter activity // inferred from electronic annotation
1457644_s_at	-2.69	chemokine (C-X-C motif) ligand 1	Cxcl1	chr5 E-F|5 51.0 cM	0000074 // regulation of progression through cell cycle // inferred from electro	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from electronic annotation /// 0008009
1458382_a_at	-2.68	zinc fingers and homeoboxes protein 1	Zhx1	---	0006350 // transcription // inferred from electronic annotation /// 0006355 // r	0005622 // intracellular // inferred from electronic annotation /// 0005634 // n	0003676 // nucleic acid binding // inferred from electronic annotation /// 00036
1430612_at	-2.65	RIKEN cDNA 1810033B17 gene	1810033B17Rik	chr8 A1|8 0.38 cM	---	---	---
1441493_at	-2.64	ELKS/RAB6-interacting/CAST family member 1	Erc1	chr6 F1	0006810 // transport // inferred from electronic annotation /// 0015031 // prote	0005737 // cytoplasm // inferred from direct assay	0005515 // protein binding // inferred from physical interaction /// 0017137 //
1427348_at	-2.59	zinc finger CCCH type containing 12A	Zc3h12a	chr4 D2.2	---	---	---
1435579_at	-2.57	RIKEN cDNA 4933409K07 gene	4933409K07Rik	chr4 A5	---	---	---
1450322_s_at	-2.54	schlafen 3 /// schlafen 4	Slfn3 /// Slfn4	chr11 C	0008285 // negative regulation of cell proliferation // inferred from direct ass	---	---
1428738_a_at	-2.54	DNA segment, Chr 14, ERATO Doi 449, expressed	D14Ertd449e	chr14 B	---	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1427820_at	-2.54	---	---	---	---	---	---
1457324_at	-2.53	RIKEN cDNA 4933409K07 gene	4933409K07Rik	chr4 A5	---	---	---
1447284_at	-2.50	triggering receptor expressed on myeloid cells 1	Trem1	chr17 C	---	0005615 // extracellular space // --- /// 0016020 // membrane // inferred from e	0004872 // receptor activity // inferred from electronic annotation
1421921_at	-2.48	serine (or cysteine) peptidase inhibitor, clade A, member 3M	Serpina3m	chr12 E	---	---	0004866 // endopeptidase inhibitor activity // inferred from electronic annotati
1452406_x_at	-2.45	erythroid differentiation regulator 1	Erdr1	---	---	---	---
1421811_at	-2.45	thrombospondin 1 /// similar to thrombospondin 1	LOC640441 /// Thbs1	chr2 F1-F3|2 65.0 cM	0006954 // inflammatory response // inferred from mutant phenotype /// 0007155 /	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005198 // structural molecule activity // inferred from electronic annotation /
1417130_s_at	-2.44	angiopoietin-like 4	Angptl4	chr17 B1	0001666 // response to hypoxia // inferred from sequence or structural similarit	0005576 // extracellular region // inferred from expression pattern /// 0005576	0004857 // enzyme inhibitor activity // inferred from direct assay /// 0004857 /
1448728_a_at	-2.44	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, ze	Nfkbiz	chr16 C1.2-C1.3	0006355 // regulation of transcription, DNA-dependent // --- /// 0006954 // infl	0005634 // nucleus // inferred from direct assay	0003677 // DNA binding // --- /// 0003700 // transcription factor activity // --
1422029_at	-2.43	chemokine (C-C motif) ligand 20	Ccl20	chr1 C5|1 52.0 cM	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // infl	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from direct assay /// 0005125 // cytoki
1427747_a_at	-2.42	lipocalin 2	Lcn2	chr2 A3|2 27.0 cM	0006810 // transport // inferred from electronic annotation	---	0005215 // transporter activity // inferred from electronic annotation /// 00054
1424938_at	-2.42	six transmembrane epithelial antigen of the prostate 1	Steap1	chr5 A1|5 3.0 cM	0006118 // electron transport // inferred from electronic annotation /// 0006810	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	0005506 // iron ion binding // inferred from electronic annotation /// 0005507 /
1424509_at	-2.41	CD177 antigen	Cd177	chr7 A3	---	---	---
1434484_at	-2.40	RIKEN cDNA 1100001G20 gene	1100001G20Rik	chr11 C	---	---	---
1457108_at	-2.37	Interleukin 1 receptor, type II	Il1r2	chr1 B|1 19.5 cM	0007166 // cell surface receptor linked signal transduction // inferred from ele	0005887 // integral to plasma membrane // inferred from electronic annotation //	0004872 // receptor activity // inferred from electronic annotation /// 0004907
1420657_at	-2.37	uncoupling protein 3 (mitochondrial, proton carrier)	Ucp3	chr7 E2|7 50.0 cM	0000303 // response to superoxide // inferred from mutant phenotype /// 0006631	0005739 // mitochondrion // inferred from mutant phenotype /// 0005739 // mitoch	0005215 // transporter activity // inferred from electronic annotation /// 00054
1460302_at	-2.31	thrombospondin 1 /// similar to thrombospondin 1	LOC640441 /// Thbs1	chr2 F1-F3|2 65.0 cM	0006954 // inflammatory response // inferred from mutant phenotype /// 0007155 /	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005198 // structural molecule activity // inferred from electronic annotation /
1437060_at	-2.30	olfactomedin 4	Olfm4	chr14 D3	---	0005615 // extracellular space // inferred from direct assay	---
1447891_at	-2.30	Transforming, acidic coiled-coil containing protein 2	Tacc2	chr7 F4	---	0005634 // nucleus // inferred from electronic annotation	0005515 // protein binding // inferred from sequence or structural similarity
1451054_at	-2.28	orosomucoid 1	Orm1	chr4 C1|4 31.4 cM	0006810 // transport // inferred from electronic annotation /// 0006953 // acute	0005615 // extracellular space // ---	0005215 // transporter activity // inferred from electronic annotation /// 00054
1431705_a_at	-2.25	mucolipin 2	Mcoln2	chr3 H2	0006810 // transport // inferred from electronic annotation /// 0006811 // ion t	0016020 // membrane // --- /// 0016020 // membrane // inferred from electronic a	0005216 // ion channel activity // --- /// 0005216 // ion channel activity // in
1427102_at	-2.23	schlafen 4	Slfn4	chr11 C	---	---	---
1444232_at	-2.22	protein kinase, cGMP-dependent, type I	Prkg1	chr19 C2	0001764 // neuron migration // inferred from mutant phenotype /// 0006468 // pro	0005794 // Golgi apparatus // inferred from direct assay /// 0005952 // cAMP-dep	0000166 // nucleotide binding // inferred from electronic annotation /// 0004672
1417851_at	-2.19	chemokine (C-X-C motif) ligand 13	Cxcl13	chr5 E3	0006935 // chemotaxis // inferred from electronic annotation /// 0006954 // infl	0005576 // extracellular region // inferred from electronic annotation /// 00056	0005125 // cytokine activity // inferred from electronic annotation /// 0008009
1450808_at	-2.19	formyl peptide receptor 1	Fpr1	chr17 A3.2|17 10.2 cM	0006935 // chemotaxis // traceable author statement /// 0007165 // signal transd	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	0001584 // rhodopsin-like receptor activity // inferred from electronic annotati
1420992_at	-2.19	ankyrin repeat domain 1 (cardiac muscle)	Ankrd1	chr19 C3	0006357 // regulation of transcription from RNA polymerase II promoter // inferr	0005634 // nucleus // inferred from direct assay /// 0005634 // nucleus // infer	0003714 // transcription corepressor activity // inferred from direct assay ///
1420804_s_at	-2.18	C-type lectin domain family 4, member d	Clec4d	chr6 F3|6 56.5 cM	0006955 // immune response // inferred from electronic annotation	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	0004872 // receptor activity // inferred from electronic annotation /// 0005529
1438050_x_at	-2.17	predicted gene, EG668383	EG668383	chr12 A1.2	---	---	---
1429029_at	-2.16	sphingomyelin synthase 2	Sgms2	chr3 G3	0006629 // lipid metabolic process // inferred from electronic annotation /// 00	0005794 // Golgi apparatus // inferred from electronic annotation /// 0005794 //	0016301 // kinase activity // inferred from electronic annotation /// 0016740 //
1440865_at	-2.15	interferon induced transmembrane protein 6	Ifitm6	chr7 F5	0009607 // response to biotic stimulus // inferred from electronic annotation	0016021 // integral to membrane // inferred from electronic annotation	---
1439200_x_at	-2.14	---	---	---	---	---	---
1417741_at	-2.14	liver glycogen phosphorylase	Pygl	chr12 C2|12 30.0 cM	0005975 // carbohydrate metabolic process // inferred from electronic annotation	---	0000166 // nucleotide binding // inferred from electronic annotation /// 0003824
1455271_at	-2.14	hypothetical protein LOC620695	LOC620695	chr2 E1	---	---	---
1454713_s_at	-2.14	histidine decarboxylase	Hdc	chr2 E5-G	0006519 // amino acid and derivative metabolic process // inferred from electron	---	0003824 // catalytic activity // inferred from electronic annotation /// 0004398
1420991_at	-2.13	ankyrin repeat domain 1 (cardiac muscle)	Ankrd1	chr19 C3	0006357 // regulation of transcription from RNA polymerase II promoter // inferr	0005634 // nucleus // inferred from direct assay /// 0005634 // nucleus // infer	0003714 // transcription corepressor activity // inferred from direct assay ///
1452117_a_at	-2.13	FYN binding protein	Fyb	chr15 A1	0045576 // mast cell activation // inferred from mutant phenotype	0005634 // nucleus // inferred from electronic annotation	---
1425663_at	-2.13	interleukin 1 receptor antagonist	Il1rn	chr2 A3|2 10.0 cM	0006629 // lipid metabolic process // inferred from mutant phenotype /// 0006954	0005576 // extracellular region // inferred from electronic annotation /// 00058	0004872 // receptor activity // inferred from electronic annotation /// 0005149
1440815_x_at	-2.12	hypothetical protein LOC624112	LOC624112	chr14 B	---	---	---
1453181_x_at	-2.11	phospholipid scramblase 1	Plscr1	chr9 E3.3	0009615 // response to virus // inferred from electronic annotation /// 0030099	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	0005509 // calcium ion binding // inferred from electronic annotation /// 000551
1426607_at	-2.09	predicted gene, EG633640	EG633640	chr13 D2.3	---	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1419219_at	-2.09	cytochrome P450, family 4, subfamily f, polypeptide 18	Cyp4f18	chr8 C1	0006118 // electron transport // inferred from electronic annotation /// 0006118	0005615 // extracellular space // --- /// 0005783 // endoplasmic reticulum // in	0003676 // nucleic acid binding // --- /// 0004497 // monooxygenase activity //
1449533_at	-2.08	transmembrane protein 100	Tmem100	chr11 C	---	0016020 // membrane // inferred from electronic annotation /// 0016021 // integr	---
1449876_at	-2.07	protein kinase, cGMP-dependent, type I	Prkg1	chr19 C2	0001764 // neuron migration // inferred from mutant phenotype /// 0006464 // pro	0005794 // Golgi apparatus // inferred from direct assay /// 0005952 // cAMP-dep	0000166 // nucleotide binding // inferred from electronic annotation /// 0004672
1417483_at	-2.07	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, ze	Nfkbiz	chr16 C1.2-C1.3	0006355 // regulation of transcription, DNA-dependent // --- /// 0006954 // infl	0005634 // nucleus // inferred from direct assay	0003677 // DNA binding // --- /// 0003700 // transcription factor activity // --
1416600_a_at	-2.06	Down syndrome critical region homolog 1 (human)	Dscr1	chr16 C4|16 62.0 cM	0019722 // calcium-mediated signaling // inferred from electronic annotation ///	0005634 // nucleus // inferred from direct assay /// 0005737 // cytoplasm // inf	---
1449254_at	-2.06	secreted phosphoprotein 1	Spp1	chr5 E5|5 56.0 cM	0001503 // ossification // inferred from electronic annotation /// 0006916 // an	0005576 // extracellular region // non-traceable author statement /// 0005578 //	0005125 // cytokine activity // non-traceable author statement /// 0005125 // cy
1438148_at	-2.06	gene model 1960, (NCBI)	Gm1960	chr5 E2	0006955 // immune response // inferred from electronic annotation	0005576 // extracellular region // inferred from electronic annotation	0005125 // cytokine activity // inferred from electronic annotation /// 0008009
1444487_at	-2.06	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)	Lrat	chr3 E3	0006653 // lecithin metabolic process // traceable author statement /// 0006776	0005783 // endoplasmic reticulum // inferred from electronic annotation /// 0016	0008374 // O-acyltransferase activity // inferred from direct assay /// 0008415
1439764_s_at	-2.05	insulin-like growth factor 2 mRNA binding protein 2	Igf2bp2	chr16 B1	0006417 // regulation of translation // inferred from electronic annotation	---	0000166 // nucleotide binding // inferred from electronic annotation /// 0003676
1428663_at	-2.03	RIKEN cDNA 5133401H06 gene	5133401H06Rik	---	---	---	---
1448561_at	-2.02	neutrophil cytosolic factor 2	Ncf2	chr1 G3|1 76.1 cM	0006742 // NADP catabolic process // inferred from sequence or structural simila	0001669 // acrosome // inferred from direct assay /// 0005737 // cytoplasm // in	0005488 // binding // inferred from electronic annotation /// 0016175 // superox
1425829_a_at	-2.01	STEAP family member 4	Steap4	chr5 A1	0006118 // electron transport // inferred from electronic annotation /// 0006810	0005886 // plasma membrane // inferred from sequence or structural similarity //	0005506 // iron ion binding // inferred from electronic annotation /// 0005507 /
1425415_a_at	-2.01	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter	Slc1a1	chr19 C1	0006810 // transport // inferred from electronic annotation /// 0006835 // dicar	0005887 // integral to plasma membrane // inferred from electronic annotation //	0005386 // carrier activity // inferred from electronic annotation /// 0015293 /
1460555_at	-2.00	RIKEN cDNA 6330500D04 gene	6330500D04Rik	chr13 A3.2	---	---	---