Supplementary Table 1. The genes regulated by dexamethasone treatment in the rat liver

Gene Name*	Gene Symbol	Mean	Median	p-Value
RT1 class Ib, locus Aw2	RT1-Aw2	-5.593229642	-5.593229642	5.11E-05
ribonucleotide reductase M2 (mapped)	Rrm2	-5.148483224	-5.148483224	7.84E-06
serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antipeptidase, antitrypsin), member 7	Serpina7	-4.338990085	-4.338990085	5.80E-05
similar to indolethylamine N-methyltransferase	LOC368066	-3.975678082	-3.975678082	4.10E-05
cyclin-dependent kinase inhibitor 3 (predicted)	Cdkn3_predicted	-3.808443113	-3.808443113	1.37E-05
RT1 class Ib gene, H2-TL-like, grc region (N1)	RT1-N1	-3.373370936	-3.373370936	7.27E-05
ect2 oncogene (predicted)	Ect2_predicted	-3.350168588	-3.350168588	0.00020606
unknown gene	NA	-3.284346975	-3.284346975	8.56E-05
ribonucleotide reductase M2 (mapped)	Rrm2	-3.224176104	-3.224176104	0.000451123
cell division cycle 2 homolog A (S. pombe)	Cdc2a	-3.196434398	-3.196434398	1.04E-05
cyclin A2	Ccna2	-3.193890649	-3.193890649	1.64E-05
integral membrane transport protein UST4r	UST4r	-3.075352788	-3.075352788	1.91E-05
unknown gene	NA	-3.001627445	-3.001627445	1.98E-05
NS5A (hepatitis C virus) transactivated protein 9	Ns5atp9	-2.979374866	-2.979374866	1.08E-05
RT1 class Ib, locus Aw2	RT1-Aw2	-2.899160528	-2.899160528	0.000928447
hydroxysteroid (17-beta) dehydrogenase 2	Hsd17b2	-2.753479131	-2.753479131	0.000104517
aldehyde dehydrogenase family 1, member A1	Aldh1a1	-2.7351609	-2.7351609	2.09E-06
antigen identified by monoclonal antibody Ki-67 (predicted)	Mki67_predicted	-2.674465871	-2.674465871	0.000406635
ATP-binding cassette, sub-family G (WHITE), member 5	Abcg5	-2.588780399	-2.588780399	2.29E-05
cyclin B2	Ccnb2	-2.578176951	-2.578176951	0.00020413
solute carrier organic anion transporter family, member 1a4	Slco1a4	-2.489216481	-2.489216481	8.28E-06
cyclin D1	Ccnd1	-2.434073538	-2.434073538	4.31E-05
similar to hypothetical protein MGC37914 (predicted)	RGD1307603_predicted	-2.407491926	-2.407491926	3.40E-06
solute carrier family 17 (sodium phosphate), member 3	Slc17a3	-2.376576508	-2.376576508	2.61E-06
cyclin B1	Ccnb1	-2.373163953	-2.373163953	6.56E-05
cyclin B1	Ccnb1	-2.357115822	-2.357115822	2.80E-05
RT1 class I, CE12	RT1-CE12	-2.280854876	-2.280854876	0.000269075
sulfotransferase family, cytosolic, 1C, member 2	Sult1c2	-2.263329132	-2.263329132	7.65E-05
cytoskeleton associated protein 2 (predicted)	Ckap2_predicted	-2.214273723	-2.214273723	1.62E-05
solute carrier organic anion transporter family, member 1a4	Slco1a4	-2.213473927	-2.213473927	1.45E-06
pregnancy-induced growth inhibitor	Okl38	-2.196523519	-2.196523519	1.16E-07
solute carrier family 34 (sodium phosphate), member 2	Slc34a2	-2.173449825	-2.173449825	5.96E-05
budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) (predicted)	Bub1_predicted	-2.157882186	-2.157882186	3.19E-05
cell division cycle associated 3	Cdca3	-2.153217937	-2.153217937	0.003219246
spindle pole body component 25 homolog (S. cerevisiae)	Spbc25	-2.145772796	-2.145772796	4.97E-05
kinesin family member 20A (predicted)	Kif20a_predicted	-2.133266185	-2.133266185	0.000115375
enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Ehhadh	-2.121013069	-2.121013069	1.37E-05
TRAF4 associated factor 1	Traf4af1	-2.099597485	-2.099597485	0.000148375
sulfotransferase family, cytosolic, 1C, member 1	Sult1c1	-2.056321635	-2.056321635	5.77E-06
cell division cycle 20 homolog (S. cerevisiae)	Cdc20	-2.051310421	-2.051310421	2.92E-05
RT1 class II, locus Bb	RT1-Bb	-2.039373956	-2.039373956	3.18E-05
neuronal regeneration related protein	Nrep	-2.03322068	-2.03322068	1.15E-05
epoxide hydrolase 1, microsomal	Ephx1	-2.032016875	-2.032016875	9.69E-07
lysyl oxidase	Lox	-2.023827009	-2.023827009	9.63E-06
dedicator of cytokinesis 11	Dock11	-1.99058609	-1.99058609	0.000107171
ubiquitin-conjugating enzyme E2C (predicted)	Ube2c_predicted	-1.988089155	-1.988089155	2.23E-05
similar to paired immunoglobin-like type 2 receptor alpha	LOC685020	-1.980933207	-1.980933207	2.07E-05
SH3 and cysteine rich domain 3 (predicted)	Stac3_predicted	-1.97840037	-1.97840037	8.49E-07
lysyl oxidase	Lox	-1.966225917	-1.966225917	8.77E-07
unknown gene	NA	-1.929131819	-1.929131819	7.99E-05

protein regulator of cytokinesis 1 (predicted)	Prc1_predicted	-1.918259773	-1.918259773	0.001580351
DEP domain containing 1a (predicted)	Depdc1a_predicted	-1.884487225	-1.884487225	0.000874673
CD5 antigen-like	Cd5l	-1.867246622	-1.867246622	9.46E-06
similar to Ig kappa chain (predicted)	RGD1562855_predicted	-1.865135404	-1.865135404	1.01E-07
similar to RIKEN cDNA 6530401L14 gene	RGD1309107	-1.851058012	-1.851058012	8.65E-06
carbonic anhydrase 3	Ca3	-1.838987935	-1.838987935	3.10E-05
steroid 5 alpha-reductase 1	Srd5a1	-1.834833522	-1.834833522	4.49E-05
cyclin D1	Ccnd1	-1.832285934	-1.832285934	7.73E-06
chemokine (C-X-C motif) ligand 1	Cxcl1	-1.828157044	-1.828157044	0.000227294
hyaluronan mediated motility receptor (RHAMM)	Hmmr	-1.826975814	-1.826975814	0.000385885
similar to RIKEN cDNA 9230117N10	RGD1311155	-1.81172709	-1.81172709	3.87E-06
fatty acid desaturase 1	Fads1	-1.81077951	-1.81077951	2.06E-07
sialophorin	Spn	-1.806046611	-1.806046611	0.000482706
DDHD domain containing 1	Ddhd1	-1.804609368	-1.804609368	0.00010371
claudin 10 (predicted)	Cldn10_predicted	-1.798465998	-1.798465998	6.85E-05
topoisomerase (DNA) 2 alpha	Top2a	-1.798139413	-1.798139413	0.00048669
Rac GTPase-activating protein 1 (predicted)	Racgap1_predicted	-1.795893236	-1.795893236	0.000249684
cyclin D1	Ccnd1	-1.793195151	-1.793195151	1.59E-05
similar to Shc SH2-domain binding protein 1	LOC687121	-1.780426552	-1.780426552	1.55E-05
unknown gene	NA	-1.771887093	-1.771887093	0.000268855
similar to Ab2-095	RGD1309079	-1.740296116	-1.740296116	0.000981129
cell division cycle 20 homolog (S. cerevisiae)	Cdc20	-1.736716293	-1.736716293	0.000280682
sulfotransferase family, cytosolic, 1C, member 2	Sult1c2	-1.730058634	-1.730058634	9.94E-05
RT1 class Ib, locus Aw2	RT1-Aw2	-1.725870934	-1.725870934	6.64E-05
cytochrome P450, family 26, subfamily b, polypeptide 1	Cyp26b1	-1.723356802	-1.723356802	0.001822548
cell division cycle associated 1	Cdca1	-1.717973671	-1.717973671	0.003518529
syncollin	Sycn	-1.715862633	-1.715862633	2.85E-05
allograft inflammatory factor 1	Aif1	-1.699716696	-1.699716696	3.87E-05
SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	Smc4l1	-1.699704572	-1.699704572	4.85E-05
PDZ binding kinase (predicted)	Pbk_predicted	-1.695377625	-1.695377625	1.02E-05
immunoglobulin heavy chain (alpha polypeptide) (mapped)	Igha_mapped	-1.689540162	-1.689540162	0.000110832
asp (abnormal spindle)-like, microcephaly associated (Drosophila) (predicted)	Aspm_predicted	-1.688778319	-1.688778319	3.15E-06
nucleolar and spindle associated protein 1 (predicted)	Nusap1_predicted	-1.683672858	-1.683672858	4.99E-05
Iroquois related homeobox 1 (Drosophila) (predicted)	Irx1_predicted	-1.660336565	-1.660336565	0.000287434
candidate mediator of the p53-dependent G2 arrest	Rprm	-1.644918928	-1.644918928	2.27E-05
similar to RIKEN cDNA 9230117N10	RGD1311155	-1.63269329	-1.63269329	2.73E-05
coronin, actin binding protein 1A	Coro1a	-1.60318117	-1.60318117	0.00372972
lymphocyte antigen 86 (predicted)	Ly86_predicted	-1.602801397	-1.602801397	1.94E-05
similar to C-C chemokine receptor type 11 (C-C CKR-11) (CCR-11) (Chemokine receptor-like 1)	LOC685243	-1.601863727	-1.601863727	6.28E-05
CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	-1.601796118	-1.601796118	3.17E-07
RT1 class II, locus Da	RT1-Da	-1.593065	-1.593065	0.000222195
chemokine (C-C motif) ligand 6	Ccl6	-1.588666962	-1.588666962	5.27E-05
cytochrome P450, family 4, subfamily a, polypeptide 14	Cyp4a14	-1.586532967	-1.586532967	0.001016108
retinol binding protein 1, cellular	Rbp1	-1.575928543	-1.575928543	9.45E-05
EGF-like module containing, mucin-like, hormone receptor-like sequence 1	Emr1	-1.564315529	-1.564315529	0.000949409
SRY-box containing gene 4 (predicted)	Sox4_predicted	-1.55520287	-1.55520287	0.00047255
kallikrein B, plasma 1	Klkb1	-1.55431913	-1.55431913	4.43E-05
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6 (mapped)	Serpina6	-1.55291586	-1.55291586	3.05E-05
CD38 antigen	Cd38	-1.552274735	-1.552274735	0.000127895
stearoyl-Coenzyme A desaturase 2	Scd2	-1.547126586	-1.547126586	1.33E-05
carbonic anhydrase 1 (predicted)	Car1_predicted	-1.53903187	-1.53903187	1.60E-06
chemokine (C-X-C motif) ligand 12	Cxcl12	-1.536265161	-1.536265161	4.51E-05
annexin A3	Anxa3	-1.535584724	-1.535584724	0.001069394
steroid sensitive gene 1	Ssg1	-1.534213679	-1.534213679	1.62E-05
unknown gene	NA	-1.529833756	-1.529833756	0.000726184

spindle pole body component 24 homolog (S. cerevisiae) (predicted)	Spbc24_predicted	-1.524056671	-1.524056671	0.001503708
similar to immunoglobulin heavy chain 6 (Igh-6)	RGD1359202	-1.52307536	-1.52307536	1.56E-05
cytochrome P450, family 4, subfamily a, polypeptide 14	Cyp4a14	-1.522559192	-1.522559192	4.22E-05
M-phase phosphoprotein 1 (predicted)	Mphosph1_predicted	-1.505619542	-1.505619542	0.000632374
aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	Akr7a3	-1.503402746	-1.503402746	0.000158906
cytochrome P450, subfamily 51	Cyp51	-1.489379492	-1.489379492	1.24E-05
serum/glucocorticoid regulated kinase	Sgk	-1.488980786	-1.488980786	1.98E-05
sulfotransferase, estrogen preferring	Ste	-1.47985711	-1.47985711	3.73E-06
Cytochrome P450, family 2, subfamily b, polypeptide 2	Cyp2b2	-1.478414759	-1.478414759	6.13E-06
unknown gene	NA	-1.468891594	-1.468891594	3.66E-07
fatty acid desaturase 2	Fads2	-1.466830361	-1.466830361	0.00011421
similar to kIAA0367	RGD1311350	-1.466158793	-1.466158793	0.000694222
similar to aldo-keto reductase family 1, member C12 (predicted)	RGD1562954_predicted	-1.46467477	-1.46467477	0.000107416
chemokine (C-C motif) ligand 5	Ccl5	-1.460353301	-1.460353301	2.62E-05
ephrin A1	Efna1	-1.458083931	-1.458083931	4.67E-05
N-acetyltransferase 8 (camello like)	Nat8	-1.453863727	-1.453863727	0.000259134
a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (predicted)	Adamts9_predicted	-1.431296094	-1.431296094	0.001162062
similar to ENSANGP00000020885 (predicted)	RGD1563825_predicted	-1.428603031	-1.428603031	5.90E-05
similar to DNA repair protein RAD51 homolog 1 (predicted)	RGD1563603_predicted	-1.427956099	-1.427956099	0.000135696
similar to RIKEN cDNA 2810433K01 (predicted)	RGD1310784_predicted	-1.422748555	-1.422748555	0.000662239
unknown gene	NA	-1.414980241	-1.414980241	5.79E-06
ficolin A	Fcna	-1.413877121	-1.413877121	0.001014316
interleukin 1 beta	Il1b	-1.412584123	-1.412584123	0.001209983
unknown gene	NA	-1.407681191	-1.407681191	0.003488597
insulin-like growth factor binding protein, acid labile subunit	Igfals	-1.404224425	-1.404224425	0.000346177
tubulin, beta 5	Tubb5	-1.399302582	-1.399302582	6.53E-07
alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	Adh7	-1.398800012	-1.398800012	0.000159645
ephrin A1	Efna1	-1.398695197	-1.398695197	0.00123929
annexin A3	Anxa3	-1.395785344	-1.395785344	3.10E-06
unknown gene	NA	-1.393249978	-1.393249978	0.000121068
v-raf murine sarcoma 3611 viral oncogene homolog	Araf	-1.39321066	-1.39321066	7.73E-05
RT1 class Ib, locus Aw2	RT1-Aw2	-1.386409008	-1.386409008	6.05E-05
gamma-aminobutyric acid (GABA) B receptor 1	Gabbr1	-1.386158698	-1.386158698	6.30E-05
adenosine A3 receptor	Adora3	-1.386004782	-1.386004782	0.000670013
NADPH oxidase 4	Nox4	-1.384521914	-1.384521914	5.68E-05
unknown gene	NA	-1.377699795	-1.377699795	0.00014694
arginine vasopressin receptor 1A	Avpr1a	-1.373094733	-1.373094733	0.000108185
glutathione S-transferase Yc2 subunit	Yc2	-1.367620336	-1.367620336	0.000220581
RT1 class II, locus Ba	RT1-Ba	-1.36580726	-1.36580726	4.89E-05
HRAS like suppressor 3	Hrasls3	-1.360279301	-1.360279301	0.001020377
similar to netrin G1 (predicted)	RGD1563465_predicted	-1.360079824	-1.360079824	0.001484761
cytochrome P450, subfamily 51	Cyp51	-1.359174355	-1.359174355	2.66E-06
lamin B1	Lmnb1	-1.356301489	-1.356301489	0.000217945
similar to Glutathione S-transferase, theta 3 (predicted)	RGD1562732_predicted	-1.355844277	-1.355844277	7.44E-05
TRAF2 binding protein	LOC310877	-1.354929335	-1.354929335	4.51E-05
unknown gene	NA	-1.352040415	-1.352040415	0.005110375
transcription elongation factor A (SII)-like 1	Tceal1	-1.351461442	-1.351461442	0.000191239
kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	Kmo	-1.34872645	-1.34872645	6.85E-05
carbonic anhydrase 8	Car8	-1.347037975	-1.347037975	3.31E-07
kinesin family member C1	Kifc1	-1.334966481	-1.334966481	0.000223777
guanylate nucleotide binding protein 2	Gbp2	-1.334157569	-1.334157569	0.000690411
solute carrier family 17 (sodium phosphate), member 2 (predicted)	Slc17a2_predicted	-1.33234599	-1.33234599	5.41E-06
prostaglandin E receptor 3 (subtype EP3)	Ptger3	-1.327891241	-1.327891241	0.000202752
unknown gene	NA	-1.325431296	-1.325431296	0.001943858
proteosome (prosome, macropain) subunit, beta type 9	Psmb9	-1.322026628	-1.322026628	0.000360454

stathmin 1	Stmn1	-1.321882102	-1.321882102	0.000114424
ubiquitin D	Ubd	-1.31976269	-1.31976269	0.001054299
protein kinase C, delta binding protein	Prkcdbp	-1.316220984	-1.316220984	1.10E-05
integrin alpha L	Itgal	-1.309312779	-1.309312779	0.000181657
unknown gene	NA	-1.308416793	-1.308416793	3.19E-05
caveolin 2	Cav2	-1.306940133	-1.306940133	0.000734299
protein kinase C, beta 1	Prkcb1	-1.304218531	-1.304218531	2.34E-06
pituitary tumor-transforming 1	Pttg1	-1.302152149	-1.302152149	8.86E-06
neurofibromatosis 1	Nf1	-1.29799792	-1.29799792	7.01E-05
unknown gene	NA	-1.297577442	-1.297577442	0.000210881
poliovirus receptor-related 2 (herpesvirus entry mediator B)	Pvrl2	-1.297250851	-1.297250851	0.000537347
cytochrome P450, subfamily 2A, polypeptide 1	Cyp2a2	-1.290575725	-1.290575725	1.46E-09
carnitine O-octanoyltransferase	Crot	-1.281809225	-1.281809225	0.000353638
PYD and CARD domain containing	Pycard	-1.278199743	-1.278199743	0.004657237
CD8 antigen, alpha chain	Cd8a	-1.271651805	-1.271651805	0.010194527
regulator of G-protein signaling 18	Rgs18	-1.269862067	-1.269862067	7.35E-06
interleukin 13 receptor, alpha 1	Il13ra1	-1.268598922	-1.268598922	9.77E-05
adaptor-related protein complex 1, sigma 2 subunit (predicted)	Ap1s2_predicted	-1.26542726	-1.26542726	0.003893065
carboxylesterase 3	Ces3	-1.25829127	-1.25829127	0.000120007
sterol-C4-methyl oxidase-like	Sc4mol	-1.257344338	-1.257344338	4.80E-06
unknown gene	NA	-1.257342554	-1.257342554	0.000443724
carnitine O-octanoyltransferase	Crot	-1.256613819	-1.256613819	0.000102642
ATP-binding cassette, sub-family G (WHITE), member 8	Abcg8	-1.253683006	-1.253683006	0.00366781
kinesin family member 22	Kif22	-1.251415605	-1.251415605	0.000308709
CD14 antigen	Cd14	-1.251116133	-1.251116133	9.17E-06
chemokine (C-X-C motif) ligand 12	Cxcl12	-1.242825326	-1.242825326	0.00034001
TAR DNA binding protein	Tardbp	-1.242759876	-1.242759876	3.35E-05
CD53 antigen	Cd53	-1.24045523	-1.24045523	8.99E-05
myosin VC (predicted)	Myo5c_predicted	-1.239359061	-1.239359061	0.002675205
claudin 3	Cldn3	-1.239009243	-1.239009243	0.000133482
cytochrome b-245, alpha polypeptide	Cyba	-1.233911826	-1.233911826	0.000565129
membrane-spanning 4-domains, subfamily A, member 1 (predicted)	Ms4a1_predicted	-1.231384981	-1.231384981	7.11E-05
similar to ctla-2-beta protein (141 AA) (predicted)	RGD1565540_predicted	-1.230527815	-1.230527815	0.000215147
granzyme A	Gzma	-1.226240445	-1.226240445	0.002191236
similar to hypothetical protein MGC5528 (predicted)	RGD1561749_predicted	-1.222382797	-1.222382797	0.007868108
serine/threonine kinase 6	Stk6	-1.221008022	-1.221008022	1.04E-05
kinesin family member 11	Kif11	-1.220888759	-1.220888759	0.00112485
caveolin 2	Cav2	-1.220640918	-1.220640918	0.000708814
chemokine (C-X-C motif) ligand 12	Cxcl12	-1.220518678	-1.220518678	5.90E-05
phospholipase A2, group IVA (cytosolic, calcium-dependent)	Pla2g4a	-1.219674624	-1.219674624	0.000421394
transcription factor 19	Tcf19	-1.217660539	-1.217660539	0.00041913
unknown gene	NA	-1.217550143	-1.217550143	2.30E-05
caveolin 2	Cav2	-1.216933405	-1.216933405	0.000181098
ring finger and KH domain containing 3 (predicted)	Rkhd3_predicted	-1.214862137	-1.214862137	0.000235293
Fc fragment of IgG, low affinity IIIa, receptor	Fcgr3a	-1.214528783	-1.214528783	5.52E-05
acid phosphatase-like 2	Acpl2	-1.211781271	-1.211781271	1.44E-05
fibrinogen-like 2	Fgl2	-1.208609818	-1.208609818	0.000100039
aldehyde dehydrogenase 1 family, member B1	Aldh1b1	-1.205606913	-1.205606913	0.000199224
interferon induced transmembrane protein 1 (predicted)	Ifitm1_predicted	-1.204490216	-1.204490216	5.45E-07
SRY-box containing gene 4 (predicted)	Sox4_predicted	-1.201857374	-1.201857374	0.001295563
interleukin 13 receptor, alpha 1	Il13ra1	-1.190146401	-1.190146401	0.000682508
membrane interacting protein of RGS16	Mir16	-1.185342011	-1.185342011	0.000164494
acyl-CoA synthetase long-chain family member 5	Acsl5	-1.179941441	-1.179941441	0.000426269
unknown gene	NA	-1.178807995	-1.178807995	0.000862553
immunoglobulin joining chain	Igj	-1.178448235	-1.178448235	0.000199741

chemokine (C-C motif) ligand 6	Ccl6	-1.174393213	-1.174393213	1.05E-06
aurora kinase B	Aurkb	-1.172759853	-1.172759853	0.000973905
similar to MGC68837 protein (predicted)	RGD1565710_predicted	-1.164608214	-1.164608214	0.003244479
3-hydroxybutyrate dehydrogenase, type 1	Bdh1	-1.162272558	-1.162272558	0.000375058
annexin A3	Anxa3	-1.160231354	-1.160231354	0.000114851
cytochrome P450, family 2, subfamily c, polypeptide 7	Cyp2c7	-1.15568524	-1.15568524	3.87E-05
similar to SPI6	MGC94010	-1.154491703	-1.154491703	1.07E-08
unknown gene	NA	-1.154393943	-1.154393943	3.50E-05
carbonic anhydrase 3	Ca3	-1.15368062	-1.15368062	6.78E-07
integrin beta 2	Itgb2	-1.151880353	-1.151880353	0.002212021
complement component 1, q subcomponent, alpha polypeptide	C1qa	-1.151171766	-1.151171766	0.000180048
kinesin family member 23 (predicted)	Kif23_predicted	-1.149134206	-1.149134206	0.000108864
3'-phosphoadenosine 5'-phosphosulfate synthase 2 (predicted)	Papss2_predicted	-1.148064235	-1.148064235	1.16E-06
caveolin 2	Cav2	-1.146239419	-1.146239419	0.012967368
unknown gene	NA	-1.144170799	-1.144170799	0.000831818
growth arrest specific 6	Gas6	-1.139137991	-1.139137991	5.35E-05
similar to small nuclear RNA activating complex, polypeptide 5	LOC691501	-1.137338811	-1.137338811	0.000558459
S100 calcium binding protein A9 (calgranulin B)	S100a9	-1.135726914	-1.135726914	5.74E-05
folate receptor 2 (fetal) (predicted)	Folr2_predicted	-1.13409833	-1.13409833	0.001628358
prostaglandin D2 synthase 2	Ptgds2	-1.131244127	-1.131244127	0.000176105
chondrolectin (predicted)	Chodl_predicted	-1.130854469	-1.130854469	0.011991145
unknown gene	NA	-1.130491722	-1.130491722	0.00288942
guanylate cyclase 1, soluble, beta 2	Gucy1b2	-1.130205112	-1.130205112	0.000495986
high mobility group box 2	Hmgb2	-1.129570281	-1.129570281	0.000757492
napsin A aspartic peptidase	Napsa	-1.12917338	-1.12917338	0.001702312
hypothetical LOC310540	MGC72614	-1.125514808	-1.125514808	0.00111578
similar to solute carrier family 17 (sodium phosphate), member 4	LOC679784	-1.125362614	-1.125362614	6.92E-06
copine VIII (predicted)	Cpne8_predicted	-1.123674453	-1.123674453	0.00014891
CD68 antigen	Cd68	-1.12104455	-1.12104455	0.000188624
potassium channel tetramerisation domain containing 12 (predicted)	Kctd12_predicted	-1.114846988	-1.114846988	1.00E-05
minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	Mcm6	-1.113081884	-1.113081884	0.000324329
unknown gene	NA	-1.109137026	-1.109137026	0.001259762
unknown gene	NA	-1.108433353	-1.108433353	1.22E-05
similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2	LOC498279	-1.104268199	-1.104268199	7.51E-05
hematopoietically expressed homeobox	Hhex	-1.10235898	-1.10235898	2.28E-05
unknown gene	NA	-1.102028519	-1.102028519	1.70E-06
aldehyde oxidase 1	Aox1	-1.09916877	-1.09916877	5.57E-06
thyroid hormone receptor interactor 13	Trip13	-1.097251174	-1.097251174	0.00049312
unknown gene	NA	-1.093037179	-1.093037179	9.38E-06
leukotriene C4 synthase	Ltc4s	-1.092214481	-1.092214481	1.99E-05
S100 calcium binding protein A8 (calgranulin A)	S100a8	-1.091015343	-1.091015343	0.009879121
similar to killer activatory receptor-like protein p91D (predicted)	RGD1562625_predicted	-1.088368913	-1.088368913	0.000191916
unknown gene	NA	-1.085277892	-1.085277892	0.000417971
transforming growth factor beta 1 induced transcript 4	Tgfb1i4	-1.083731915	-1.083731915	4.98E-05
bone morphogenetic protein 2	Bmp2	-1.082905267	-1.082905267	3.94E-07
transforming, acidic coiled-coil containing protein 3	Tacc3	-1.082108177	-1.082108177	0.000306107
cathepsin E	Ctse	-1.081676459	-1.081676459	0.001513917
isopentenyl-diphosphate delta isomerase	Idi1	-1.081363043	-1.081363043	0.000120184
glutathione S-transferase, theta 2	Gstt2	-1.080522293	-1.080522293	6.07E-05
dual specificity phosphatase 6	Dusp6	-1.079707105	-1.079707105	2.04E-05
hemogen	Hemgn	-1.078642536	-1.078642536	0.000249108
retinol dehydrogenase 11	Rdh11	-1.074046347	-1.074046347	1.80E-05
Tyro protein tyrosine kinase binding protein	Tyrobp	-1.073818448	-1.073818448	2.24E-06
unknown gene	NA	-1.072234737	-1.072234737	0.000166937
RT1 class II, locus Bb	RT1-Bb	-1.069815775	-1.069815775	0.000291396

unknown gene	NA	-1.068318543	-1.068318543	0.002236394
similar to Diphosphoinositol polyphosphate phosphohydrolase 3 alpha (DIPP-3 alpha)	LOC680248	-1.064110856	-1.064110856	4.85E-05
superoxide dismutase 3, extracellular	Sod3	-1.060617644	-1.060617644	5.78E-05
alpha-2u globulin PGCL1	LOC259246	-1.060488985	-1.060488985	0.000638299
Tumor necrosis factor receptor superfamily, member 6	Tnfrsf6	-1.059483916	-1.059483916	0.004499446
nuclear factor, erythroid derived 2	Nfe2	-1.059363175	-1.059363175	0.006772332
Ttk protein kinase (predicted)	Ttk_predicted	-1.058041962	-1.058041962	0.000283778
carboxylesterase 1	Ces1	-1.05740739	-1.05740739	3.00E-05
receptor (calcitonin) activity modifying protein 2	Ramp2	-1.057026562	-1.057026562	1.02E-07
unknown gene	NA	-1.054804495	-1.054804495	1.23E-05
unknown gene	NA	-1.054105736	-1.054105736	0.000474483
RT1 class II, locus Ba	RT1-Ba	-1.053780908	-1.053780908	0.000374848
SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (predicted)	Smc2l1_predicted	-1.052126291	-1.052126291	0.01129515
J domain protein 1	LOC619393	-1.051478016	-1.051478016	3.03E-05
dickkopf homolog 4 (Xenopus laevis) (predicted)	Dkk4_predicted	-1.051310142	-1.051310142	0.000496865
secretory leukocyte peptidase inhibitor	Slpi	-1.050890626	-1.050890626	0.000168164
unknown gene	NA	-1.050887117	-1.050887117	0.003979265
nuclear factor, erythroid derived 2, like 2	Nfe2l2	-1.049812474	-1.049812474	4.34E-05
phospholipid transfer protein (predicted)	Pltp_predicted	-1.049358525	-1.049358525	0.000574965
malic enzyme 1	Me1	-1.0491146	-1.0491146	3.85E-05
erythroid associated factor (predicted)	Eraf_predicted	-1.049006846	-1.049006846	0.000167788
similar to Stabilin-2 precursor (Hyaluronan receptor for endocytosis)	LOC691926	-1.043766741	-1.043766741	0.0004291
unknown gene	NA	-1.038855442	-1.038855442	0.000160244
CD8 antigen, alpha chain	Cd8a	-1.03747774	-1.03747774	5.24E-06
aldo-keto reductase family 1, member D1	Akr1d1	-1.032879395	-1.032879395	0.000157685
prostaglandin E receptor 3 (subtype EP3)	Ptger3	-1.030693014	-1.030693014	3.21E-07
complement factor D (adipsin)	Cfd	-1.028031401	-1.028031401	0.000701318
RT1 class Ib, locus Aw2	RT1-Aw2	-1.02795016	-1.02795016	0.001236599
serine (or cysteine) proteinase inhibitor, clade E, member 2	Serpine2	-1.02587391	-1.02587391	4.30E-07
dual specificity phosphatase 6	Dusp6	-1.025631815	-1.025631815	1.77E-05
Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene	Cyp2a1	-1.023962025	-1.023962025	0.000103465
hydroxysteroid 11-beta dehydrogenase 2	Hsd11b2	-1.023463177	-1.023463177	1.06E-05
similar to shippo 1 (predicted)	RGD1564322_predicted	-1.022717038	-1.022717038	0.001390907
choline/ethanolamine phosphotransferase 1	Cept1	-1.020812467	-1.020812467	7.96E-07
RAS-related C3 botulinum substrate 2	Rac2	-1.019934253	-1.019934253	1.95E-05
SH3 domain binding glutamic acid-rich protein-like 3 (predicted)	Sh3bgrl3_predicted	-1.017192925	-1.017192925	0.000161372
similar to Expressed sequence AW146242 (predicted)	RGD1306494_predicted	-1.011723899	-1.011723899	0.002089612
gamma-2a immunoglobulin heavy chain	IgG-2a	-1.010052988	-1.010052988	0.000313588
one cut domain, family member 1	Onecut1	0.987728293	0.987728293	0.000764765
unknown gene	NA	0.98955641	0.98955641	0.000285417
unknown gene	NA	0.993867129	0.993867129	0.003628715
myxovirus (influenza virus) resistance 1	Mx1	0.994159658	0.994159658	9.73E-05
branched chain ketoacid dehydrogenase E1, alpha polypeptide	Bckdha	0.995005613	0.995005613	0.015254297
similar to RIKEN cDNA 5730557B15 (predicted)	RGD1564227_predicted	0.999752938	0.999752937	0.000604758
similar to T-cell activation protein phosphatase 2C (predicted)	RGD1310383_predicted	1.000792461	1.000792461	0.003443779
interferon-related developmental regulator 1	Ifrd1	1.001656593	1.001656593	0.000174303
unknown gene	NA	1.002052938	1.002052938	0.004988888
myosin Ib	Myo1b	1.003455156	1.003455156	0.00035124
similar to myocardial ischemic preconditioning upregulated protein 2 (predicted)	RGD1565589_predicted	1.004522936	1.004522936	0.00342525
similar to diacylglycerol kinase, delta 130kDa isoform 1 (predicted)	RGD1563309_predicted	1.004732317	1.004732317	8.85E-05
dehydrodolichyl diphosphate synthase	Dhdds	1.006418048	1.006418048	0.000246452
metallothionein 1a	Mt1a	1.006420337	1.006420337	0.008516356
dolichol-phosphate (beta-D) mannosyltransferase 1 (predicted)	Dpm1_predicted	1.0066162	1.0066162	0.001385114
solute carrier family 30 (zinc transporter), member 2	Slc30a2	1.007427026	1.007427026	0.001171315
unknown gene	NA	1.007529749	1.007529749	5.32E-05

unknown gene	NA	1.008257408	1.008257408	0.000435923
unknown gene	NA	1.008665025	1.008665025	0.000189675
plasticity-related protein 3	LOC298062	1.008685177	1.008685177	0.004726201
unknown gene	NA	1.010577229	1.010577229	0.000299438
RAB30, member RAS oncogene family	Rab30	1.017529369	1.017529369	1.09E-05
DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Ddx27	1.017729516	1.017729516	1.61E-05
protease, serine, 32 (predicted)	Prss32_predicted	1.01809829	1.01809829	0.014562285
protocadherin alpha 4	Pcdha4	1.02027235	1.02027235	0.000531865
unknown gene	NA	1.020315118	1.020315118	0.000417625
pantothenate kinase 2 (Hallervorden-Spatz syndrome) (predicted)	Pank2_predicted	1.023846022	1.023846022	0.002280356
unknown gene	NA	1.025174887	1.025174887	0.000137051
ectodermal-neural cortex 1	Enc1	1.025420396	1.025420396	9.24E-05
fatty acid synthase	Fasn	1.028414036	1.028414036	1.53E-05
chloride intracellular channel 2	Clic2	1.029612499	1.029612499	0.000252497
unknown gene	NA	1.030748433	1.030748433	0.000771519
RGD1564391 (predicted)	RGD1564391_predicted	1.030883557	1.030883557	0.001429997
unknown gene	NA	1.031543989	1.031543989	0.00010138
unknown gene	NA	1.03247871	1.03247871	0.000230345
nuclear receptor subfamily 1, group I, member 2	Nr1i2	1.032724668	1.032724668	5.64E-05
alcohol dehydrogenase 6 (class V)	Adh6	1.036337245	1.036337245	0.002217778
FCH and double SH3 domains 2 (predicted)	Fchsd2_predicted	1.037006066	1.037006066	0.001246558
unknown gene	NA	1.037883326	1.037883326	1.42E-05
sulfotransferase family 1A, phenol-preferring, member 1	Sult1a1	1.039516665	1.039516665	1.46E-07
peroxisomal membrane protein 4	Pxmp4	1.043430126	1.043430126	0.000619405
unknown gene	NA	1.045087034	1.045087034	0.000900661
interferon-induced protein with tetratricopeptide repeats 2	Ifit2	1.04533073	1.04533073	5.15E-06
nuclear factor I/B	Nfib	1.049224585	1.049224585	0.000184722
unknown gene	NA	1.049676636	1.049676636	9.48E-05
S-adenosylhomocysteine hydrolase	Ahcy	1.052989735	1.052989735	4.24E-06
syntaxin 5a	Stx5a	1.053254505	1.053254505	0.003882607
unknown gene	NA	1.054727078	1.054727078	0.000430739
similar to mKIAA0613 protein (predicted)	RGD1564875_predicted	1.05551086	1.05551086	4.35E-05
interferon-induced protein with tetratricopeptide repeats 2	Ifit2	1.057142727	1.057142727	1.22E-06
thymidylate kinase family LPS-inducible member (predicted)	Tyki_predicted	1.057875901	1.057875901	8.25E-05
unknown gene	NA	1.058481515	1.058481515	0.009975546
unknown gene	NA	1.058758964	1.058758964	0.000224944
unknown gene	NA	1.059411558	1.059411558	1.83E-05
unknown gene	NA	1.061436434	1.061436434	0.008279793
interleukin 6 receptor, alpha	Il6ra	1.062859245	1.062859245	0.000174276
abhydrolase domain containing 6	Abhd6	1.065789757	1.065789757	0.001255857
basic helix-loop-helix domain containing, class B2	Bhlhb2	1.066667865	1.066667865	0.000251251
unknown gene	NA	1.067239116	1.067239116	0.009690042
inositol 1,4,5-triphosphate receptor 1	Itpr1	1.069525957	1.069525957	3.17E-05
interferon regulatory factor 7	Irf7	1.070195555	1.070195555	0.000130065
branched chain keto acid dehydrogenase E1, beta polypeptide	Bckdhb	1.07828558	1.07828558	2.82E-05
microtubule-associated protein 7 (predicted)	Mtap7_predicted	1.07987826	1.07987826	0.000204104
similar to homolog of Human holocarboxylase synthetase gene HLCS (predicted)	RGD1565360_predicted	1.080460351	1.080460351	0.001591323
histone cluster 2, H2aa (predicted)	Hist2h2aa_predicted	1.083078553	1.083078553	0.000438934
DnaJ (Hsp40) homolog, subfamily B, member 6	Dnajb6	1.084664931	1.084664931	0.000982196
aspartoacylase	Aspa	1.08560529	1.08560529	0.001067319
unknwon gene	NA	1.088383428	1.088383428	0.000155931
unknwon gene	NA	1.089494832	1.089494832	1.47E-05
thioesterase superfamily member 2 (predicted)	Them2_predicted	1.09465055	1.09465055	5.66E-05
similar to Ext1	LOC299907	1.094798941	1.094798941	0.000353179
similar to Proline oxidase, mitochondrial precursor (Proline dehydrogenase)	LOC680409	1.095406356	1.095406356	4.51E-05

transmembrane protein 86A (predicted)	Tmem86a_predicted	1.096770355	1.096770355	0.004594484
unknwon gene	NA	1.102804325	1.102804325	0.000195572
24-dehydrocholesterol reductase	Dhcr24	1.1067042	1.1067042	2.35E-05
similar to RIKEN cDNA 1810014F10 gene (predicted)	RGD1311186_predicted	1.110156143	1.110156143	3.62E-05
butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase)	Bbox1	1.110448345	1.110448345	4.05E-05
unknwon gene	NA	1.113608076	1.113608076	7.94E-05
aconitase 2, mitochondrial	Aco2	1.114206109	1.114206109	0.001810377
glucose-6-phosphatase, catalytic	G6pc	1.12222331	1.12222331	2.24E-05
hypoxanthine guanine phosphoribosyl transferase	Hprt	1.125438097	1.125438097	9.49E-05
similar to hypothetical protein D4Ertd89e	RGD1305703	1.126359265	1.126359265	2.38E-05
unknwon gene	NA	1.130267945	1.130267945	2.64E-06
Protein kinase, interferon-inducible double stranded RNA dependent	Prkr	1.13232141	1.13232141	0.002990459
proprotein convertase subtilisin/kexin type 5	Pcsk5	1.134426189	1.134426189	2.48E-05
unknwon gene	NA	1.134488194	1.134488194	0.025856692
signal transducer and activator of transcription 1	Stat1	1.137156136	1.137156136	2.64E-06
RNA (guanine-7-) methyltransferase	Rnmt	1.141972618	1.141972618	0.003340707
arachidonate 5-lipoxygenase	Alox5	1.144029969	1.144029969	0.001719428
regulator of G-protein signaling 16	Rgs16	1.144442332	1.144442332	0.001598821
unknwon gene	NA	1.145153487	1.145153487	0.005213872
similar to RIKEN cDNA B630019K06 (predicted)	RGD1560784_predicted	1.149009034	1.149009034	0.000401945
Kruppel-like factor 9	Klf9	1.151269918	1.151269918	8.51E-06
unknwon gene	NA	1.151478539	1.151478539	0.000743893
hypothetical protein LOC619561	LOC619561	1.152462202	1.152462202	7.70E-05
similar to T-cell activation protein phosphatase 2C (predicted)	RGD1310383_predicted	1.153744226	1.153744226	0.000240988
forkhead box O1A	Foxo1a	1.164995441	1.164995441	0.000644795
DnaJ (Hsp40) homolog, subfamily B, member 9	Dnajb9	1.165197972	1.165197972	0.000447428
sulfotransferase family, cytosolic, 2B, member 1 (predicted)	Sult2b1_predicted	1.165979312	1.165979312	0.000509994
anterior pharynx defective 1b homolog (C. elegans)	Aph1b	1.166419586	1.166419586	0.000477187
unknwon gene	NA	1.166464544	1.166464544	0.001664881
unknwon gene	NA	1.166546844	1.166546844	0.00048996
RNA binding motif protein 5	Rbm5	1.170279445	1.170279445	0.000168586
ubiquitin-conjugating enzyme E2B, RAD6 homolog (S. cerevisiae)	Ube2b	1.173086509	1.173086509	2.15E-05
Nucleoside 2-deoxyribosyltransferase domain containing protein RGD620382	RGD620382	1.173579756	1.173579756	0.000180511
fatty acid synthase	Fasn	1.175254733	1.175254733	4.42E-05
unknwon gene	NA	1.176738039	1.176738039	2.29E-05
unknwon gene	NA	1.184760372	1.184760372	0.000101222
betaine-homocysteine methyltransferase	Bhmt	1.194092145	1.194092145	3.71E-06
tribbles homolog 3 (Drosophila)	Trib3	1.199381791	1.199381791	0.001212442
myosin Ib	Myo1b	1.199440588	1.199440588	1.79E-05
nuclear receptor binding factor 2	Nrbf2	1.201542004	1.201542004	0.000716488
chemokine (C-X-C motif) ligand 10	Cxcl10	1.20175307	1.20175307	0.003768636
S100 calcium binding protein G	S100g	1.20304723	1.20304723	0.002600502
alpha-2,6-sialyltransferase ST6GalNAc IV	siat7D	1.20926761	1.20926761	0.000159934
similar to Beta-sarcoglycan (Beta-SG) (43 kDa dystrophin-associated glycoprotein) (43DAG)	LOC680229	1.213349638	1.213349638	0.003638768
similar to low density lipoprotein receptor-related protein binding protein (predicted)	RGD1565715_predicted	1.217003927	1.217003927	0.002415851
glycine N-methyltransferase	Gnmt	1.22200569	1.22200569	4.35E-05
unknwon gene	NA	1.223709229	1.223709229	9.32E-05
similar to hypothetical protein FLJ13448	RGD1359509	1.230366319	1.230366319	0.000561556
unknwon gene	NA	1.233744835	1.233744835	0.000216887
FBJ murine osteosarcoma viral oncogene homolog	Fos	1.238460864	1.238460864	0.000823299
orosomucoid 1	Orm1	1.24098738	1.24098738	1.05E-05
malate dehydrogenase 1, NAD (soluble)	Mdh1	1.241092459	1.241092459	5.44E-05
inositol hexaphosphate kinase 2	Ihpk2	1.247735109	1.247735109	0.00047355
myotubularin related protein 7 (predicted)	Mtmr7_predicted	1.249041573	1.249041573	0.000424142
solute carrier family 37 (glycerol-6-phosphate transporter), member 4	Slc37a4	1.250274328	1.250274328	3.63E-05

protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	1.251896438	1.251896438	0.000299838
proprotein convertase subtilisin/kexin type 5	Pcsk5	1.262540696	1.262540696	0.000159444
zeta-chain (TCR) associated protein kinase 70 (mapped)	Zap70	1.273112083	1.273112083	1.98E-07
dolichol-phosphate (beta-D) mannosyltransferase 1 (predicted)	Dpm1_predicted	1.285165015	1.285165015	1.03E-05
similar to mesenchymal stem cell protein DSC54 (predicted)	RGD1564528_predicted	1.285567871	1.285567871	0.00173755
protein tyrosine phosphatase, receptor type, G	Ptprg	1.289427808	1.289427808	3.83E-05
sterol carrier protein 2	Scp2	1.295958916	1.295958916	7.20E-05
phytanoyl-CoA 2-hydroxylase 2	Phyh2	1.302058275	1.302058275	4.18E-06
serine protease inhibitor, Kazal type 1	Spink1	1.303207722	1.303207722	0.000871408
ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	1.304621292	1.304621292	1.62E-05
signal transducer and activator of transcription 1	Stat1	1.306913706	1.306913706	0.000334026
solute carrier family 3, member 1	Slc3a1	1.307106893	1.307106893	6.38E-05
hepatic protein EIIH	Eiih	1.30910529	1.30910529	0.000122879
phosphoenol carboxykinase	Pepck	1.309609424	1.309609424	0.006321522
hydroxysteroid (17-beta) dehydrogenase 9	Hsd17b9	1.310561495	1.310561495	4.97E-05
ubiquitin-conjugating enzyme E2B, RAD6 homolog (S. cerevisiae)	Ube2b	1.314165967	1.314165967	6.43E-05
transient receptor potential cation channel, subfamily M, member 2	Trpm2	1.318248182	1.318248182	5.67E-05
glutamate oxaloacetate transaminase 1	Got1	1.319117268	1.319117268	4.39E-05
cyclin-dependent kinase inhibitor 1A	Cdkn1a	1.324280421	1.324280421	7.56E-05
fibroblast growth factor 21	Fgf21	1.328152734	1.328152734	0.000237391
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Herpud1	1.340381543	1.340381543	0.000139153
protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	1.344806151	1.344806151	0.000104517
similar to histocompatibility 28	LOC310968	1.349206531	1.349206531	1.93E-05
proline rich 2	Pnrc1	1.351841327	1.351841327	0.000126403
basic helix-loop-helix domain containing, class B2	Bhlhb2	1.353505184	1.353505184	0.000152851
potential ubiquitin ligase	Herc6	1.356266474	1.356266474	0.018607026
calcium-sensing receptor like 1	Casrl1	1.356870312	1.356870312	2.98E-05
lectin, galactose binding, soluble 5	Lgals5	1.359291663	1.359291663	2.75E-05
unknwon gene	NA	1.364152265	1.364152265	0.001278811
unknwon gene	NA	1.364552108	1.364552108	6.49E-05
protocadherin alpha 4	Pcdha4	1.377988458	1.377988458	0.001382188
glyceronephosphate O-acyltransferase	Gnpat	1.384434028	1.384434028	0.000259765
carnitine palmitoyltransferase 1a, liver	Cpt1a	1.387686918	1.387686918	7.70E-07
unknwon gene	NA	1.395359705	1.395359705	6.95E-05
microtubule-associated protein 1b	Map1b	1.395774689	1.395774689	7.80E-05
thyroid hormone responsive protein	Thrsp	1.397995348	1.397995348	3.89E-05
angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	Agt	1.40259302	1.40259302	1.97E-05
FK506 binding protein 5	Fkbp5	1.404077798	1.404077798	0.000400178
unknwon gene	NA	1.404738446	1.404738446	8.18E-06
endothelin receptor type A	Ednra	1.408370365	1.408370365	0.00056749
cyclin-dependent kinase inhibitor 1A	Cdkn1a	1.408578239	1.408578239	0.000211744
carnitine palmitoyltransferase 1a, liver	Cpt1a	1.414872264	1.414872264	6.56E-05
similar to hypothetical protein BC011981 (predicted)	RGD1310609_predicted	1.422134034	1.422134034	0.001890032
unknwon gene	NA	1.432172221	1.432172221	0.000232817
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	Mafb	1.433080366	1.433080366	1.86E-06
unknwon gene	NA	1.434260739	1.434260739	0.000658203
solute carrier family 2, member 5	Slc2a5	1.440390107	1.440390107	0.000736607
forkhead box O1A	Foxo1a	1.450937143	1.450937143	0.000587058
insulin-like growth factor binding protein 1	Igfbp1	1.45187632	1.45187632	1.92E-05
rhomboid, veinlet-like 7 (Drosophila) (predicted)	Rhbdl7_predicted	1.458824452	1.458824452	4.62E-05
hypothetical protein LOC619558	LOC619558	1.460112194	1.460112194	1.48E-05
2',5'-oligoadenylate synthetase 1, 40/46kDa	Oas1	1.462798748	1.462798748	3.50E-06
unknwon gene	NA	1.463386572	1.463386572	1.43E-06
splicing factor 3b, subunit 1	Sf3b1	1.465161441	1.465161441	8.69E-05
guanylate cyclase 2C	Gucy2c	1.466970384	1.466970384	0.001203956

2'-5' oligoadenylate synthetase-like 1	Oasl1	1.471302813	1.471302813	0.000294296
solute carrier family 38, member 2	Slc38a2	1.490463238	1.490463238	1.21E-05
basic helix-loop-helix domain containing, class B, 8	Bhlhb8	1.49460773	1.49460773	0.000300185
acetyl-coenzyme A carboxylase alpha	Acaca	1.500771601	1.500771601	2.91E-06
amine oxidase, copper containing 3	Aoc3	1.50128825	1.50128825	2.60E-05
signal transducer and activator of transcription 1	Stat1	1.503881453	1.503881453	1.34E-05
nuclear protein 1	Nupr1	1.507918878	1.507918878	2.64E-05
dual specificity phosphatase 1	Dusp1	1.512003391	1.512003391	1.02E-05
thyroid hormone responsive protein	Thrsp	1.51754742	1.51754742	6.80E-05
solute carrier family 41, member 3	Slc41a3	1.517602899	1.517602899	7.50E-05
unknwon gene	NA	1.520456489	1.520456489	1.67E-06
megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human) (predicted)	Mlc1_predicted	1.543213696	1.543213696	0.000154635
WDNM1 homolog	LOC360228	1.543887475	1.543887475	6.85E-05
hypothetical protein LOC685448	LOC685448	1.548647058	1.548647058	0.000818367
similar to CG1998-PA	LOC691221	1.552042413	1.552042413	0.000387713
dual specificity phosphatase 1	Dusp1	1.570849015	1.570849015	0.000229571
protein tyrosine phosphatase, receptor type, G	Ptprg	1.580955898	1.580955898	6.36E-05
unknwon gene	NA	1.587129106	1.587129106	7.77E-06
thyroid hormone responsive protein	Thrsp	1.605204213	1.605204213	9.76E-06
protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	1.61428765	1.61428765	0.000520637
similar to hypothetical protein D4Ertd89e	RGD1305703	1.618482589	1.618482589	0.00644234
unknwon gene	NA	1.622590668	1.622590668	0.000612255
endothelin receptor type A	Ednra	1.630456903	1.630456903	0.000569308
unknwon gene	NA	1.633764686	1.633764686	0.000623873
hypothetical protein LOC685448	LOC685448	1.641710587	1.641710587	6.69E-07
lipoprotein lipase	Lpl	1.651260134	1.651260134	2.21E-05
similar to ankyrin repeat and SOCs box-containing protein 5	LOC361187	1.652101428	1.652101428	0.002341155
unknwon gene	NA	1.652621478	1.652621478	9.58E-07
microtubule-associated protein 1 light chain 3 beta	Map1lc3b	1.657481173	1.657481173	7.37E-07
sperm specific antigen 2 (predicted)	Ssfa2_predicted	1.658539815	1.658539815	0.005857011
unknwon gene	NA	1.675525685	1.675525685	3.78E-05
retinol dehydrogenase 2	Rdh2	1.67553581	1.67553581	4.75E-06
zinc finger protein 655	Zfp655	1.681612195	1.681612195	0.000969995
benzodiazepine receptor, peripheral	Bzrp	1.690123105	1.690123105	2.75E-05
P450 (cytochrome) oxidoreductase	Por	1.696944119	1.696944119	1.90E-05
acetyl-coenzyme A carboxylase alpha	Acaca	1.700603066	1.700603066	0.000832624
unknwon gene	NA	1.711129847	1.711129847	0.000621269
AA926063gene	AA926063	1.712293647	1.712293647	0.000105231
FK506 binding protein 5	Fkbp5	1.72503502	1.72503502	0.000146219
lectin, galactose binding, soluble 9	Lgals9	1.729298527	1.729298527	2.99E-05
similar to mKIAA0613 protein (predicted)	RGD1564875_predicted	1.736268048	1.736268048	0.000955114
unknwon gene	NA	1.740289043	1.740289043	0.000546046
decorin	Dcn	1.745423557	1.745423557	2.08E-05
similar to BTEB3 protein (predicted)	RGD1565099_predicted	1.751757858	1.751757858	0.000304907
unknwon gene	NA	1.759118624	1.759118624	0.000370174
plasticity-related protein 3	LOC298062	1.771018526	1.771018526	2.80E-06
phospholipase A2, group XIIA (predicted)	Pla2g12a_predicted	1.782487572	1.782487572	0.000401055
similar to mKIAA0212 protein (predicted)	RGD1563633_predicted	1.783833367	1.783833367	5.65E-06
similar to leiomodin 2 (cardiac)	LOC296935	1.784942648	1.784942648	0.000552054
arylsulfatase B	Arsb	1.788632096	1.788632096	5.23E-05
unknwon gene	NA	1.820772383	1.820772383	5.18E-05
P450 (cytochrome) oxidoreductase	Por	1.853237221	1.853237221	0.000208161
camello-like 1	Cml1	1.853557535	1.853557535	1.54E-05
interferon-induced protein with tetratricopeptide repeats 3	Ifit3	1.8590584	1.8590584	9.01E-05
similar to Beta-sarcoglycan (Beta-SG) (43 kDa dystrophin-associated glycoprotein) (43DAG)	LOC680229	1.871302452	1.871302452	6.80E-06

nicotinamide N-methyltransferase (predicted)	Nnmt_predicted	1.884454456	1.884454456	1.51E-06
similar to hypothetical protein FLJ10154	RGD1310061	1.892774715	1.892774715	8.21E-05
metallothionein 1a	Mt1a	1.898499595	1.898499595	4.10E-07
solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	Slc25a25	1.89979856	1.89979856	4.15E-06
potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	Kcnn2	1.90014453	1.90014453	0.000195314
transformation related protein 53 inducible nuclear protein 1	Trp53inp1	1.916572365	1.916572365	0.000532333
solute carrier family 13 (sodium-dependent citrate transporter), member 5	Slc13a5	1.930393911	1.930393911	4.45E-05
similar to mKIAA0212 protein (predicted)	RGD1563633_predicted	1.943182955	1.943182955	6.02E-05
glutamic pyruvic transaminase 1, soluble	Gpt1	1.968022721	1.968022721	1.20E-05
ubiquitin specific peptidase 18	Usp18	1.983659525	1.983659525	6.68E-08
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	Pfkfb1	1.98856786	1.98856786	8.06E-05
unknwon gene	NA	2.011213835	2.011213835	0.000273751
unknwon gene	NA	2.013876153	2.013876153	0.001129352
myxovirus (influenza virus) resistance 2	Mx2	2.031112452	2.031112452	0.000222142
interferon-induced protein 44	Ifi44	2.04205433	2.04205433	6.78E-05
TSC22 domain family 3	Tsc22d3	2.046871264	2.046871264	0.000142741
unknwon gene	NA	2.061026033	2.061026033	0.000457885
unknwon gene	NA	2.061593849	2.061593849	5.83E-06
unknwon gene	NA	2.097513001	2.097513001	1.56E-05
odorant binding protein I f	Obp1f	2.101993824	2.101993824	3.68E-06
similar to mKIAA0613 protein (predicted)	RGD1564875_predicted	2.116359334	2.116359334	4.02E-05
TSC22 domain family 3	Tsc22d3	2.142806678	2.142806678	0.000136727
cytochrome P450, 4a12	Cyp4a12	2.15073155	2.15073155	0.000218916
serine dehydratase	Sds	2.158189247	2.158189247	2.39E-06
major histocompatibility complex, class II, DM alpha	Hla-dma	2.172076089	2.172076089	4.27E-06
similar to mKIAA0212 protein (predicted)	RGD1563633_predicted	2.177260979	2.177260979	0.000240758
connective tissue growth factor	Ctgf	2.190620819	2.190620819	6.00E-05
osteomodulin	Omd	2.206579623	2.206579623	4.97E-07
minichromosome maintenance deficient 10 (S. cerevisiae) (predicted)	Mcm10_predicted	2.263963989	2.263963989	0.000708609
2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	Acmsd	2.313012997	2.313012997	2.18E-07
unknwon gene	NA	2.416445811	2.416445811	0.000105611
zinc finger and BTB domain containing 16	Zbtb16	2.425056235	2.425056235	7.19E-08
lipin 1	Lpin1	2.43126298	2.43126298	4.10E-06
minichromosome maintenance deficient 10 (S. cerevisiae) (predicted)	Mcm10_predicted	2.478222013	2.478222013	2.14E-05
cytochrome P450, 4a12	Cyp4a12	2.486084107	2.486084107	2.38E-06
endothelin receptor type A	Ednra	2.606051431	2.606051431	5.99E-05
cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (predicted)	Cidea_predicted	2.609818002	2.609818002	5.66E-05
cytochrome P450, family 1, subfamily a, polypeptide 1	Cyp1a1	2.614499069	2.614499069	3.42E-05
unknwon gene	NA	2.637634674	2.637634674	2.58E-07
2-5 oligoadenylate synthetase 1B	Oas1b	2.650854969	2.650854969	8.34E-06
unknwon gene	NA	2.682847195	2.682847195	1.43E-05
major urinary protein 5	Mup5	2.781589674	2.781589674	0.000201177
similar to RIKEN cDNA 5730410E15 gene (predicted)	RGD1564335_predicted	2.782926495	2.782926495	4.61E-07
hypothetical LOC300207 (predicted)	RGD1305928_predicted	2.967308924	2.967308924	7.16E-05
unknwon gene	NA	2.979808223	2.979808223	0.000175758
unknwon gene	NA	3.052019392	3.052019392	1.72E-05
ubiquitin specific peptidase 2	Usp2	3.134782256	3.134782256	6.87E-06
major urinary protein 5	Mup5	3.176082924	3.176082924	2.19E-05
myxovirus (influenza virus) resistance 2	Mx2	3.226306387	3.226306387	1.82E-05
similar to Metallothionein-2 (MT-2) (Metallothionein-II) (MT-II)	LOC689415	3.268792679	3.268792679	4.49E-07
unknwon gene	NA	3.269240392	3.269240392	7.45E-07
similar to myoferlin isoform b	LOC679806	3.343665326	3.343665326	6.13E-07
CCR4 carbon catabolite repression 4-like (S. cerevisiae)	Ccrn4l	3.38858723	3.38858723	7.73E-06
hypothetical LOC298504 (predicted)	RGD1310174_predicted	3.402352599	3.402352599	1.14E-06
similar to MASK-4E-BP3 protein	LOC679725	3.458587815	3.458587815	4.03E-07

interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted	3.50350591	3.50350591	1.31E-05
unknwon gene	NA	3.739352236	3.739352236	1.55E-05
similar to retinoid binding protein 7 (predicted)	RGD1562168_predicted	4.103689998	4.103689998	2.44E-06
alpha-2-macroglobulin	A2m	4.21849825	4.21849825	1.63E-06
zinc finger protein 354A	Zfp354a	4.288363943	4.288363943	4.20E-07
solute carrier family 5 (sodium/glucose cotransporter), member 11	Slc5a11	4.505495582	4.505495582	5.84E-07
carboxylesterase 2 (intestine, liver)	Ces2	6.099239765	6.099239765	2.51E-05

* Genes up- or down-regulated by over 2-fold are shown.