Supplementary Table 3. The genes regulated by dexamethasone and AICAR treatment in the rat liver

Gene Name*	Gene Symbol	Mean	Median	p-Value
CD5 antigen-like	Cd5l	-6.963810854	-6.963810854	3.49E-08
chemokine (C-C motif) ligand 6	Ccl6	-5.769641193	-5.769641193	2.35E-07
complement component 1, q subcomponent, beta polypeptide	C1qb	-5.423493864	-5.423493864	0.00015815
complement component 1, q subcomponent, alpha polypeptide	C1qa	-5.16580036	-5.16580036	1.12E-06
RT1 class II, locus Bb	RT1-Bb	-4.816885841	-4.816885841	3.78E-05
RT1 class Ib, locus Aw2	RT1-Aw2	-4.6803517	-4.6803517	1.22E-07
C-type lectin domain family 4, member f	Clec4f	-4.64300143	-4.64300143	5.27E-07
SH3 and cysteine rich domain 3 (predicted)	Stac3_predicted	-4.541304296	-4.541304296	9.15E-07
ribonucleotide reductase M2 (mapped)	Rrm2	-4.493093171	-4.493093171	1.89E-06
allograft inflammatory factor 1	Aif1	-4.430588687	-4.430588687	1.56E-05
ficolin A	Fcna	-4.370945722	-4.370945722	3.16E-05
complement component 1, q subcomponent, gamma polypeptide	C1qg	-4.357618774	-4.357618774	0.00046502
similar to paired immunoglobin-like type 2 receptor alpha	LOC685020	-4.273456637	-4.273456637	8.69E-06
EGF-like module containing, mucin-like, hormone receptor-like sequence 1	Emr1	-3.967634048	-3.967634048	1.47E-05
cytochrome b-245, beta polypeptide	Cybb	-3.86839397	-3.86839397	3.67E-05
nuclear receptor subfamily 0, group B, member 2	Nr0b2	-3.857620768	-3.857620768	5.90E-06
unknown gene	NA	-3.782569916	-3.782569916	0.00030753
CD163 antigen (predicted)	Cd163_predicted	-3.759257772	-3.759257772	5.87E-06
annexin A3	Anxa3	-3.669128045	-3.669128045	6.26E-07
CD163 antigen (predicted)	Cd163_predicted	-3.573066952	-3.573066952	2.47E-05
RT1 class II, locus Da	RT1-Da	-3.478259816	-3.478259816	3.87E-07
colony stimulating factor 1 receptor	Csf1r	-3.426246626	-3.426246626	8.75E-06
retinoic acid receptor responder (tazarotene induced) 1	Rarres1	-3.362981653	-3.362981653	1.30E-06
arginine vasopressin receptor 1A	Avpr1a	-3.362449046	-3.362449046	3.87E-06
guanylate nucleotide binding protein 2	Gbp2	-3.327561328	-3.327561328	8.04E-05
phospholipase A2, group IIA (platelets, synovial fluid)	Pla2g2a	-3.319858189	-3.319858189	1.07E-05
membrane-spanning 4-domains, subfamily A, member 11 (predicted)	Ms4a11_predicted	-3.318918143	-3.318918143	0.00021547
prostaglandin-endoperoxide synthase 1	Ptgs1	-3.305097829	-3.305097829	3.23E-05
cathepsin S	Ctss	-3.256600301	-3.256600301	1.96E-05
similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2	LOC498279	-3.228727244	-3.228727244	3.92E-05
CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	Cd74	-3.228197784	-3.228197784	3.17E-06
unknown gene	NA	-3.156217553	-3.156217553	3.09E-05
Fc receptor, IgG, low affinity III	Fcgr3	-3.065090703	-3.065090703	2.75E-07
RT1 class II, locus Bb	RT1-Bb	-3.018494314	-3.018494314	1.49E-07
cyclin A2	Ccna2	-3.001280243	-3.001280243	0.00019902
v-raf murine sarcoma 3611 viral oncogene homolog	Araf	-2.987797854	-2.987797854	0.00111294
CD68 antigen	Cd68	-2.952267751	-2.952267751	4.18E-05
RT1 class II, locus Ba	RT1-Ba	-2.925178437	-2.925178437	6.35E-06
cyclin-dependent kinase inhibitor 3 (predicted)	Cdkn3_predicted	-2.890028372	-2.890028372	0.00032085
membrane-spanning 4-domains, subfamily A, member 6B	Ms4a6b	-2.880606912	-2.880606912	2.28E-06
neuronal regeneration related protein	Nrep	-2.857860701	-2.857860701	1.36E-07
lipopolysaccharide binding protein	Lbp	-2.84882248	-2.84882248	1.44E-06
complement factor D (adipsin)	Cfd	-2.837870541	-2.837870541	0.00225577
Fc fragment of IgG, low affinity IIIa, receptor	Fcgr3a	-2.832606426	-2.832606426	8.25E-06
protein kinase C, beta 1	Prkcb1	-2.829742259	-2.829742259	4.40E-07
nuclear receptor subfamily 1, group D, member 2	Nr1d2	-2.820340024	-2.820340024	2.57E-06
RT1 class II, locus Ba	RT1-Ba	-2.804996032	-2.804996032	4.34E-05
unknown gene	NA	-2.802116337	-2.802116337	6.19E-07
RGD1566254 (predicted)	RGD1566254_predicted	-2.77146063	-2.77146063	3.56E-05
chemokine (C-X-C motif) ligand 12	Cxcl12	-2.747624214	-2.747624214	8.21E-06

sulfotransferase family, cytosolic, 1C, member 1	Sult1c1	-2.73128432	-2.73128432	2.89E-07
nuclear receptor subfamily 1, group D, member 2	Nr1d2	-2.706685195	-2.706685195	6.53E-05
ect2 oncogene (predicted)	Ect2_predicted	-2.701953251	-2.701953251	2.38E-05
regulator of G-protein signaling 18	Rgs18	-2.694809053	-2.694809053	1.11E-05
RT1 class Ib, locus Aw2	RT1-Aw2	-2.688413162	-2.688413162	6.32E-07
lymphocyte antigen 86 (predicted)	Ly86_predicted	-2.649619624	-2.649619624	0.00025301
NS5A (hepatitis C virus) transactivated protein 9	Ns5atp9	-2.635594675	-2.635594675	3.76E-07
ubiquitin D	Ubd	-2.635470982	-2.635470982	3.51E-06
dendritic cell inhibitory receptor 3	Dcir3	-2.622839239	-2.622839239	0.00041405
annexin A3	Anxa3	-2.615571702	-2.615571702	0.00017547
cyclin B1	Ccnb1	-2.607439618	-2.607439618	2.13E-05
NADPH oxidase 4	Nox4	-2.605872342	-2.605872342	1.51E-05
fibrinogen-like 2	Fgl2	-2.603806132	-2.603806132	6.97E-06
serine protease inhibitor, Kazal type 1	Spink1	-2.578804273	-2.578804273	3.25E-07
Fc receptor, IgG, low affinity III	Fcgr3	-2.576968545	-2.576968545	5.12E-05
integrin alpha L	Itgal	-2.568222889	-2.568222889	0.00012711
CD53 antigen	Cd53	-2.558039665	-2.558039665	2.96E-06
cell division cycle 2 homolog A (S. pombe)	Cdc2a	-2.51630032	-2.51630032	0.00065824
similar to aldo-keto reductase family 1, member C12 (predicted)	RGD1562954_predicted	-2.504476298	-2.504476298	8.69E-07
glucose-6-phosphatase, catalytic	G6pc	-2.500830551	-2.500830551	1.58E-06
protein tyrosine phosphatase, receptor type, C	Ptprc	-2.486252329	-2.486252329	3.56E-05
chemokine (C-X-C motif) ligand 12	Cxcl12	-2.470173268	-2.470173268	4.11E-05
RT1 class Ib, locus Aw2	RT1-Aw2	-2.451188482	-2.451188482	3.96E-05
hydroxysteroid (17-beta) dehydrogenase 2	Hsd17b2	-2.428304709	-2.428304709	2.09E-07
pleckstrin homology domain containing, family B (evectins) member 1	Plekhb1	-2.424417955	-2.424417955	2.62E-06
steroid 5 alpha-reductase 1	Srd5a1	-2.422837623	-2.422837623	2.35E-06
CD38 antigen	Cd38	-2.396376764	-2.396376764	4.40E-05
similar to Ab2-095	RGD1309079	-2.374305146	-2.374305146	6.32E-06
growth arrest specific 6	Gas6	-2.363516325	-2.363516325	2.35E-05
serine protease inhibitor, Kazal type 1	Spink1	-2.334803576	-2.334803576	8.68E-07
unknown gene	NA	-2.331736138	-2.331736138	8.04E-06
ATP-binding cassette, sub-family G (WHITE), member 5	Abcg5	-2.327419512	-2.327419512	0.00035248
unknown gene	NA	-2.310652557	-2.310652557	0.0004505
fatty acid desaturase 1	Fads1	-2.302906154	-2.302906154	1.33E-06
integrin beta 2	Itgb2	-2.296235685	-2.296235685	6.16E-05
cyclin B1	Ccnb1	-2.287295752	-2.287295752	0.00021606
unknown gene	NA	-2.271663164	-2.271663164	1.17E-05
similar to killer activatory receptor-like protein p91D (predicted)	RGD1562625_predicted	-2.249738936	-2.249738936	5.34E-05
ribonuclease, RNase A family 4	Rnase4	-2.24800642	-2.24800642	9.72E-07
unknown gene	NA	-2.239132555	-2.239132555	4.04E-06
aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	Akr7a3	-2.232451301	-2.232451301	8.50E-07
Axl receptor tyrosine kinase	Axl	-2.230030373	-2.230030373	0.00045407
secretory leukocyte peptidase inhibitor	Slpi	-2.227808162	-2.227808162	9.03E-08
pregnancy-induced growth inhibitor	Okl38	-2.211140372	-2.211140372	2.77E-07
hypothetical protein LOC690768	LOC690768	-2.210738714	-2.210738714	1.67E-05
stearoyl-Coenzyme A desaturase 1	Scd1	-2.209501566	-2.209501566	1.58E-06
serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antipeptidase, antitrypsin), member 7	Serpina7	-2.209351849	-2.209351849	1.53E-05
solute carrier family 1 (glial high affinity glutamate transporter), member 3	Slc1a3	-2.198604194	-2.198604194	3.80E-05
cyclin B2	Ccnb2	-2.196100653	-2.196100653	6.06E-05
ADP-ribosyltransferase 2b	Art2b	-2.170972181	-2.170972181	0.00031448
protocadherin alpha 4	Pcdha4	-2.155072864	-2.155072864	6.43E-07
immunoglobulin superfamily, member 6	Igsf6	-2.150944817	-2.150944817	0.00028991
C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 6	Clecsf6	-2.148764428	-2.148764428	0.00078719
nuclear receptor subfamily 1, group D, member 1	Nr1d1	-2.142884374	-2.142884374	0.00045199
interleukin 1 beta	Il1b	-2.124248262	-2.124248262	0.00383957

phospholipase A2, group IVA (cytosolic, calcium-dependent)	Pla2g4a	-2.119699687	-2.119699687	0.000448
unknown gene	NA	-2.112698384	-2.112698384	0.00020568
chemokine (C-X-C motif) ligand 12	Cxcl12	-2.108649662	-2.108649662	1.02E-05
PYD and CARD domain containing	Pycard	-2.095323189	-2.095323189	0.00019376
ribonucleotide reductase M2 (mapped)	Rrm2	-2.078859741	-2.078859741	0.00010911
cytochrome b-245, alpha polypeptide	Cyba	-2.075195543	-2.075195543	6.55E-07
steroid sensitive gene 1	Ssg1	-2.065868023	-2.065868023	7.41E-07
unknown gene	NA	-2.065665614	-2.065665614	0.0011035
similar to indolethylamine N-methyltransferase	LOC368066	-2.055669825	-2.055669825	0.00014717
unknown gene	NA	-2.051808214	-2.051808214	3.58E-06
B-cell leukemia/lymphoma 2 related protein A1	Bcl2a1	-2.050077313	-2.050077313	1.61E-06
annexin A3	Anxa3	-2.023692137	-2.023692137	0.00025629
glucose-6-phosphatase, catalytic	G6pc	-2.009146725	-2.009146725	2.31E-07
antigen identified by monoclonal antibody Ki-67 (predicted)	Mki67_predicted	-2.004172307	-2.004172307	0.00101446
Fc receptor, IgG, high affinity I	Fcgr1	-2.003954464	-2.003954464	0.00037591
TRAF2 binding protein	LOC310877	-2.003837892	-2.003837892	0.00043168
malic enzyme 1	Me1	-1.990049052	-1.990049052	3.68E-07
unknown gene	NA	-1.989211295	-1.989211295	2.36E-06
RT1 class Ib, locus Aw2	RT1-Aw2	-1.967836754	-1.967836754	0.00130138
unknown gene	NA	-1.957953219	-1.957953219	0.00449035
unknown gene	NA	-1.946347299	-1.946347299	1.12E-05
unknown gene	NA	-1.944411016	-1.944411016	3.73E-06
similar to Reticulocalbin-1 precursor	LOC502737	-1.921256335	-1.921256335	6.70E-06
similar to kIAA0367	RGD1311350	-1.903749676	-1.903749676	0.0001406
lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)	Lrat	-1.896734253	-1.896734253	2.89E-05
Cytochrome P450, family 2, subfamily b, polypeptide 2	Cyp2b2	-1.895885737	-1.895885737	1.55E-06
thyroid hormone responsive protein	Thrsp	-1.8897756	-1.8897756	3.72E-08
solute carrier organic anion transporter family, member 1a4	Slco1a4	-1.871893625	-1.871893625	6.39E-07
kelch-like 24 (Drosophila)	Klhl24	-1.871464606	-1.871464606	8.02E-05
unknown gene	NA	-1.865760594	-1.865760594	0.00166066
TRAF4 associated factor 1	Traf4af1	-1.860450126	-1.860450126	0.0001947
similar to RIKEN cDNA 6530401L14 gene	RGD1309107	-1.856963841	-1.856963841	0.00036296
ornithine aminotransferase	Oat	-1.856250305	-1.856250305	2.39E-06
kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	Kmo	-1.855745004	-1.855745004	1.30E-06
phospholipid transfer protein (predicted)	Pltp_predicted	-1.852304848	-1.852304848	0.00021077
similar to Diphosphoinositol polyphosphate phosphohydrolase 3 alpha (DIPP-3 alpha) (DIPP3 alpha)	LOC680248	-1.850211008	-1.850211008	6.53E-07
fibrinogen-like 2	Fgl2	-1.846423014	-1.846423014	6.42E-06
lymphocyte antigen 6 complex, locus B	Ly6b	-1.845847036	-1.845847036	0.00063574
ATP-binding cassette, sub-family G (WHITE), member 8	Abcg8	-1.844051662	-1.844051662	0.00064713
immunoglobulin heavy chain (alpha polypeptide) (mapped)	Igha_mapped	-1.825167553	-1.825167553	1.42E-05
lysosomal-associated protein transmembrane 5	Laptm5	-1.819907588	-1.819907588	5.20E-05
prostaglandin D2 synthase 2	Ptgds2	-1.819636842	-1.819636842	0.0001695
purinergic receptor P2Y, G-protein coupled, 13	P2ry13	-1.814963983	-1.814963983	0.00945179
thyroid hormone responsive protein	Thrsp	-1.812541071	-1.812541071	2.48E-06
lymphocyte cytosolic protein 1	Lcp1	-1.810177845	-1.810177845	1.87E-05
thyroid hormone responsive protein	Thrsp	-1.808928133	-1.808928133	4.59E-07
ribonuclease, RNase A family 4	Rnase4	-1.80722447	-1.80722447	1.15E-06
unknown gene	NA	-1.795279494	-1.795279494	4.74E-08
kallikrein B, plasma 1	Klkb1	-1.791327825	-1.791327825	1.32E-08
adenosine A3 receptor	Adora3	-1.775153303	-1.775153303	0.00308773
unknown gene	NA	-1.76608819	-1.76608819	2.47E-07
fibrinogen-like 2	Fgl2	-1.764736849	-1.764736849	0.00092434
cytochrome P450, subfamily 2A, polypeptide 1	Cyp2a2	-1.75932215	-1.75932215	2.81E-06
cysteine-rich protein 2	Crip2	-1.748655938	-1.748655938	6.58E-06
budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) (predicted)	Bub1_predicted	-1.742505471	-1.742505471	0.00014017

Bcl2 modifying factor	Bmf	-1.74088613	-1.74088613	3.66E-05
chemokine (C-C motif) ligand 6	Ccl6	-1.737653942	-1.737653942	4.89E-05
solute carrier family 17 (sodium phosphate), member 2 (predicted)	Slc17a2_predicted	-1.73341429	-1.73341429	1.44E-05
similar to myo-inositol 1-phosphate synthase A1	LOC290651	-1.724491957	-1.724491957	0.00012483
unknown gene	NA	-1.721190699	-1.721190699	1.56E-05
unknown gene	NA	-1.714651133	-1.714651133	2.15E-06
3-hydroxybutyrate dehydrogenase, type 1	Bdh1	-1.708269991	-1.708269991	1.36E-08
cell division cycle associated 3	Cdca3	-1.707420406	-1.707420406	0.0009046
coactosin-like 1 (Dictyostelium) (predicted)	Cotl1_predicted	-1.69964866	-1.69964866	0.0007805
similar to ctla-2-beta protein (141 AA) (predicted)	RGD1565540_predicted	-1.697404162	-1.697404162	1.77E-05
major histocompatibility complex, class II, DM beta	Hla-dmb	-1.695434151	-1.695434151	9.11E-06
unknown gene	NA	-1.69182317	-1.69182317	0.00028229
unknown gene	NA	-1.691140946	-1.691140946	0.00024945
solute carrier organic anion transporter family, member 1a4	Slco1a4	-1.684838079	-1.684838079	8.68E-06
unknown gene	NA	-1.684272074	-1.684272074	0.00057128
unknown gene	NA	-1.681990839	-1.681990839	0.00014292
similar to epithelial stromal interaction 1 isoform a (predicted)	RGD1563207_predicted	-1.67805076	-1.67805076	0.00123743
Rho, GDP dissociation inhibitor (GDI) beta	Arhgdib	-1.67788286	-1.67788286	6.15E-05
unknown gene	NA	-1.676943116	-1.676943116	0.00019074
osteoglycin (predicted)	Ogn_predicted	-1.673210389	-1.673210389	1.14E-05
Rac GTPase-activating protein 1 (predicted)	Racgap1_predicted	-1.671391591	-1.671391591	0.00035275
ring finger protein 125 (predicted)	Rnf125_predicted	-1.667939683	-1.667939683	2.51E-06
cyclin G2 (predicted)	Ccng2_predicted	-1.661123813	-1.661123813	0.00014989
guanylate nucleotide binding protein 4 (predicted)	Gbp4_predicted	-1.658430694	-1.658430694	0.00028995
hyaluronan mediated motility receptor (RHAMM)	Hmmr	-1.658388758	-1.658388758	1.32E-05
granzyme A	Gzma	-1.653958603	-1.653958603	0.00088589
unknown gene	NA	-1.650549309	-1.650549309	8.80E-05
unknown gene	NA	-1.644946887	-1.644946887	3.66E-05
chemokine (C-X-C motif) ligand 9	Cxcl9	-1.639230014	-1.639230014	2.57E-05
unknown gene	NA	-1.635857745	-1.635857745	1.61E-05
protocadherin alpha 4	Pcdha4	-1.632876823	-1.632876823	0.00015195
kinesin family member 20A (predicted)	Kif20a_predicted	-1.626504203	-1.626504203	2.60E-06
kelch-like 24 (Drosophila)	Klhl24	-1.625302014	-1.625302014	0.00036449
similar to scavenger receptor type A SR-A (predicted)	RGD1564316_predicted	-1.615075197	-1.615075197	8.77E-05
pyruvate kinase, liver and red blood cell	Pklr	-1.61425115	-1.61425115	3.68E-06
similar to phospholipase D family, member 4	LOC362792	-1.614034975	-1.614034975	0.00204089
similar to RIKEN cDNA D130038B21	RGD1305890	-1.61378298	-1.61378298	4.61E-08
osteoglycin (predicted)	Ogn_predicted	-1.613353578	-1.613353578	0.00039852
coronin, actin binding protein 1A	Coro1a	-1.61204536	-1.61204536	4.20E-05
solute carrier family 17 (sodium phosphate), member 3	Slc17a3	-1.608057831	-1.608057831	1.19E-05
sialic acid binding Ig-like lectin 5 (predicted)	Siglec5_predicted	-1.607092477	-1.607092477	0.00073899
epidermal growth factor receptor	Egfr	-1.605275073	-1.605275073	2.19E-07
cytoskeleton associated protein 2 (predicted)	Ckap2_predicted	-1.605026232	-1.605026232	0.0005001
similar to solute carrier family 17 (sodium phosphate), member 4	LOC679784	-1.601477244	-1.601477244	4.56E-06
solute carrier family 22 (organic anion transporter), member 8	Slc22a8	-1.600696543	-1.600696543	9.51E-06
unknown gene	NA	-1.599609572	-1.599609572	0.00039209
protein regulator of cytokinesis 1 (predicted)	Prc1_predicted	-1.596668718	-1.596668718	0.00041528
chemokine (C-C motif) ligand 5	Ccl5	-1.593502894	-1.593502894	0.0001642
chaperone, ABC1 activity of bc1 complex like (S. pombe)	Cabc1	-1.593062572	-1.593062572	7.03E-06
cytochrome P450, family 26, subfamily b, polypeptide 1	Cyp26b1	-1.588788616	-1.588788616	2.23E-06
unknown gene	NA	-1.588461365	-1.588461365	0.00082949
capping protein (actin filament), gelsolin-like	Capg	-1.588040332	-1.588040332	0.00098919
unknown gene	NA	-1.58702288	-1.58702288	1.51E-05
similar to ecotropic viral integration site 2A	LOC685433	-1.584622274	-1.584622274	0.00051258
lysophospholipase	LOC246266	-1.579572022	-1.579572022	6.54E-05

heme oxygenase (decycling) 1	Hmox1	-1.576386514	-1.576386514	2.28E-05
alcohol dehydrogenase 4 (class II), pi polypeptide	Adh4	-1.572130593	-1.572130593	0.00017892
minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	Mcm6	-1.572010337	-1.572010337	0.00025824
neurofibromatosis 1	Nf1	-1.570821095	-1.570821095	0.00115488
kelch-like 24 (Drosophila)	Klhl24	-1.570472158	-1.570472158	4.34E-06
crystallin, mu	Crym	-1.569810051	-1.569810051	1.16E-05
similar to TPR repeat-containing protein KIAA1043	LOC304558	-1.567918359	-1.567918359	0.00198069
unknown gene	NA	-1.564927112	-1.564927112	0.0004536
purinergic receptor P2Y, G-protein coupled, 13	P2ry13	-1.563268856	-1.563268856	0.00017578
chemokine (C-X-C motif) ligand 9	Cxcl9	-1.561190143	-1.561190143	1.56E-05
leukocyte immunoglobulin-like receptor	Lilrc1	-1.554965552	-1.554965552	0.00052082
microtubule-associated protein 7 (predicted)	Mtap7_predicted	-1.553770948	-1.553770948	0.00101808
malic enzyme 1	Me1	-1.542569467	-1.542569467	1.29E-05
unknown gene	NA	-1.528945141	-1.528945141	0.00135042
membrane-spanning 4-domains, subfamily A, member 11 (predicted)	Ms4a11_predicted	-1.527309314	-1.527309314	0.00148327
lysosomal-associated protein transmembrane 5	Laptm5	-1.520070204	-1.520070204	3.48E-06
leukotriene C4 synthase	Ltc4s	-1.517939641	-1.517939641	0.00102684
similar to Expressed sequence AW146242 (predicted)	RGD1306494_predicted	-1.517759946	-1.517759946	0.00013225
nuclear factor, erythroid derived 2	Nfe2	-1.517349696	-1.517349696	0.0031632
serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6 (mapped)	Serpina6	-1.506775225	-1.506775225	7.68E-08
cysteine and glycine-rich protein 1	Csrp1	-1.505431461	-1.505431461	3.46E-05
similar to Ras-related protein Rap-1b precursor (GTP-binding protein smg p21B)	LOC363897	-1.50402813	-1.50402813	0.0001853
aldehyde oxidase 1	Aox1	-1.50044917	-1.50044917	1.84E-05
sulfotransferase family, cytosolic, 1C, member 2	Sult1c2	-1.49869779	-1.49869779	1.47E-06
Tyro protein tyrosine kinase binding protein	Tyrobp	-1.49837435	-1.49837435	7.40E-05
secreted acidic cysteine rich glycoprotein	Sparc	-1.498017371	-1.498017371	0.00019687
unknown gene	NA	-1.495757361	-1.495757361	0.00052795
uroplakin 1B	Upk1b	-1.493723989	-1.493723989	0.00411615
CD83 antigen (predicted)	Cd83_predicted	-1.489501999	-1.489501999	2.14E-06
cell division cycle 20 homolog (S. cerevisiae)	Cdc20	-1.489048111	-1.489048111	0.00379146
insulin-like growth factor binding protein, acid labile subunit	Igfals	-1.484201637	-1.484201637	5.22E-05
unknown gene	NA	-1.483999698	-1.483999698	0.00117895
actinin, alpha 1	Actn1	-1.483595109	-1.483595109	0.00022467
fatty acid desaturase 2	Fads2	-1.479937866	-1.479937866	4.13E-07
protein kinase C, delta binding protein	Prkcdbp	-1.478745697	-1.478745697	1.61E-05
plasminogen activator, urokinase	Plau	-1.476830921	-1.476830921	0.00150286
similar to N-acetylneuraminate pyruvate lyase	LOC304860	-1.476280155	-1.476280155	0.00061225
cytochrome P450, family 1, subfamily a, polypeptide 2	Cyp1a2	-1.475689905	-1.475689905	7.13E-06
unknown gene	NA	-1.47265043	-1.47265043	0.00047591
hairy and enhancer of split 6 (Drosophila)	Hes6	-1.465479478	-1.465479478	5.11E-05
ubiquitin-conjugating enzyme E2C (predicted)	Ube2c_predicted	-1.464537643	-1.464537643	0.00013189
similar to interferon-inducible GTPase	RGD1309362	-1.464269458	-1.464269458	2.01E-06
unknown gene	NA	-1.462461385	-1.462461385	0.00368713
unknown gene	NA	-1.462272339	-1.462272339	0.00032552
unknown gene	NA	-1.449735832	-1.449735832	8.86E-05
RT1 class Ib, locus Aw2	RT1-Aw2	-1.446302586	-1.446302586	2.40E-05
cytochrome b-245, beta polypeptide	Cybb	-1.44542433	-1.44542433	0.00055956
PDZ and LIM domain 1 (elfin)	Pdlim1	-1.44280955	-1.44280955	3.41E-08
similar to immunoglobulin superfamily containing leucine-rich repeat	LOC686539	-1.442664039	-1.442664039	0.00026813
cd36 antigen	Cd36	-1.442512439	-1.442512439	3.52E-06
interferon regulatory factor 8	Irf8	-1.441990671	-1.441990671	1.69E-05
transmembrane 4 superfamily member 13	Tm4sf13	-1.441634621	-1.441634621	0.00039136
AA926063gene	AA926063	-1.438326923	-1.438326923	0.00379127
claudin 10 (predicted)	Cldn10_predicted	-1.435062227	-1.435062227	0.0010791
src-like adaptor	Sla	-1.432378762	-1.432378762	0.00274691

lectin, galactose binding, soluble 3	Lgals3	-1.432075699	-1.432075699	4.97E-07
unknown gene	NA	-1.423700669	-1.423700669	8.54E-05
napsin A aspartic peptidase	Napsa	-1.422609667	-1.422609667	0.00127185
glycoprotein, synaptic 2	Gpsn2	-1.421980806	-1.421980806	4.40E-06
stathmin 1	Stmn1	-1.417752448	-1.417752448	1.84E-06
CD38 antigen	Cd38	-1.413226058	-1.413226058	0.00132212
phosphoenolpyruvate carboxykinase	Pepck	-1.410387708	-1.410387708	0.00034999
carboxylesterase 1	Ces1	-1.40821785	-1.40821785	7.91E-05
similar to solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	LOC301113	-1.405607185	-1.405607185	0.00013514
adaptor-related protein complex 1, sigma 2 subunit (predicted)	Ap1s2_predicted	-1.40210209	-1.40210209	1.27E-05
cd36 antigen	Cd36	-1.400083192	-1.400083192	0.00066939
MARVEL (membrane-associating) domain containing 1	Mrvldc1	-1.399420549	-1.399420549	6.48E-05
folate receptor 2 (fetal) (predicted)	Folr2_predicted	-1.399386308	-1.399386308	5.59E-05
interleukin 18 binding protein	Il18bp	-1.398555639	-1.398555639	5.22E-05
potassium channel tetramerisation domain containing 12 (predicted)	Kctd12_predicted	-1.397816915	-1.397816915	5.71E-06
fatty acid synthase	Fasn	-1.392417111	-1.392417111	4.25E-05
lipocalin 2	Lcn2	-1.390129382	-1.390129382	4.68E-05
similar to Shc SH2-domain binding protein 1	LOC687121	-1.388756278	-1.388756278	0.00020429
mesoderm specific transcript	Mest	-1.383276097	-1.383276097	0.00064875
RT1 class II, locus Bb	RT1-Bb	-1.379413204	-1.379413204	9.33E-05
cystathionase (cystathionine gamma-lyase)	Cth	-1.37927116	-1.37927116	1.46E-07
unc-93 homolog B1 (C. elegans)	Unc93b1	-1.374159805	-1.374159805	0.00010156
carbonic anhydrase 3	Ca3	-1.37031102	-1.37031102	5.39E-06
sequestosome 1	Sqstm1	-1.367208865	-1.367208865	1.41E-05
sequestosome 1	Sqstm1	-1.366595169	-1.366595169	2.16E-06
ephrin A1	Efna1	-1.363543982	-1.363543982	2.02E-06
solute carrier family 6 (neurotransmitter transporter, glycine), member 9	Slc6a9	-1.362835092	-1.362835092	7.23E-06
Ena-vasodilator stimulated phosphoprotein	Evl	-1.362812762	-1.362812762	7.68E-05
acid phosphatase 5, tartrate resistant	Acp5	-1.361915561	-1.361915561	0.00027455
hydroxyacid oxidase 2 (long chain)	Hao2	-1.35994066	-1.35994066	1.06E-07
syncollin	Sycn	-1.357373545	-1.357373545	0.00089369
solute carrier family 15, member 3	Slc15a3	-1.356916399	-1.356916399	0.00052136
procollagen, type XIV, alpha 1 (predicted)	Col14a1_predicted	-1.354658351	-1.354658351	9.15E-06
hypothetical LOC310540	MGC72614	-1.350495011	-1.350495011	0.00013091
unknown gene	NA	-1.350221476	-1.350221476	0.00403881
cd86 antigen	Cd86	-1.348393783	-1.348393783	1.04E-05
hemopoietic cell kinase	Hck	-1.348393058	-1.348393058	4.38E-05
unknown gene	NA	-1.346856171	-1.346856171	0.00464169
arrestin, beta 2	Arrb2	-1.344840083	-1.344840083	9.21E-06
similar to DNA segment, Chr 11, ERATO Doi 18, expressed	RGD1309472	-1.340529165	-1.340529165	0.00015965
similar to Dedicator of cytokinesis protein 10 (Protein zizimin 3) (predicted)	RGD1561963_predicted	-1.340396115	-1.340396115	0.00414325
interferon regulatory factor 1	Irf1	-1.339938774	-1.339938774	4.53E-05
mesenchyme homeobox 2	Meox2	-1.339820893	-1.339820893	0.0001202
calcium/calmodulin-dependent protein kinase II, delta	Camk2d	-1.3381198	-1.3381198	0.00072698
calcium binding and coiled coil domain 1	Calcoco1	-1.336923576	-1.336923576	0.00060339
acyl-Coenzyme A oxidase 3, pristanoyl	Acox3	-1.33386777	-1.33386777	1.60E-05
pleckstrin	Plek	-1.328324281	-1.328324281	0.00082805
plasmalemma vesicle associated protein	Plvap	-1.326616368	-1.326616368	3.57E-05
protein kinase C, beta 1	Prkcb1	-1.320850188	-1.320850188	1.30E-05
enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Ehhadh	-1.320492884	-1.320492884	0.00033751
unknown gene	NA	-1.319407451	-1.319407451	1.08E-05
nucleolar and spindle associated protein 1 (predicted)	Nusap1_predicted	-1.316657462	-1.316657462	0.00016535
solute carrier family 35, member D2 (predicted)	Slc35d2_predicted	-1.315560317	-1.315560317	0.0001287
SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1` (predicted)	Smarcad1_predicted	-1.314333148	-1.314333148	0.00015819
solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	-1.313830039	-1.313830039	0.00080181

growth hormone receptor	Ghr	-1.312981229	-1.312981229	0.00035501
acyl-CoA synthetase short-chain family member 2 (predicted)	Acss2_predicted	-1.3094304	-1.3094304	6.52E-06
EH-domain containing 3	Ehd3	-1.305946929	-1.305946929	0.00021282
similar to AVIEF	LOC365948	-1.305698905	-1.305698905	0.00154161
ephrin A1	Efna1	-1.305265109	-1.305265109	0.000155
procollagen, type 1, alpha 1	Col1a1	-1.305156986	-1.305156986	8.94E-05
solute carrier family 19 (thiamine transporter), member 2	Slc19a2	-1.305118445	-1.305118445	1.09E-06
antigen identified by monoclonal antibody MRC OX-2 receptor	Mox2r	-1.301382839	-1.301382839	0.0004592
similar to RIKEN cDNA 5830404H04	RGD735112	-1.2986855	-1.2986855	0.00010154
mannan-binding lectin serine peptidase 1	Masp1	-1.298538113	-1.298538113	3.85E-07
unknown gene	NA	-1.297425629	-1.297425629	6.37E-05
flavin containing monooxygenase 5	Fmo5	-1.292677943	-1.292677943	4.19E-06
unknown gene	NA	-1.291025044	-1.291025044	8.58E-06
leucine rich repeat containing 33	Lrrc33	-1.289486616	-1.289486616	2.75E-05
protein tyrosine phosphatase, non-receptor type 18	Ptpn18	-1.287465801	-1.287465801	1.83E-06
interferon induced transmembrane protein 1 (predicted)	Ifitm1_predicted	-1.279018988	-1.279018988	1.63E-06
lanC (bacterial lantibiotic synthetase component C)-like 1	Lancl1	-1.277981364	-1.277981364	0.00015789
amyloid beta (A4) precursor protein	App	-1.274823101	-1.274823101	0.00018788
stearoyl-Coenzyme A desaturase 2	Scd2	-1.268800574	-1.268800574	0.00017384
unknown gene	NA	-1.268111199	-1.268111199	2.58E-05
kininogen 1	Kng1	-1.267794089	-1.267794089	0.00021409
similar to Glutathione S-transferase, theta 3 (predicted)	RGD1562732_predicted	-1.266902051	-1.266902051	7.21E-06
unknown gene	Bckdhb	-1.266859835	-1.266859835	2.72E-05
NA	NA	-1.264065863	-1.264065863	6.98E-07
zinc finger protein 367	Zfp367	-1.259957798	-1.259957798	0.00261545
tRNA phosphotransferase 1 (predicted)	Trpt1_predicted	-1.256147149	-1.256147149	0.00019255
unknown gene	NA	-1.255064156	-1.255064156	0.00076864
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	-1.254493967	-1.254493967	5.47E-05
similar to Aa2-174	RGD1309578	-1.251137109	-1.251137109	5.14E-05
unknown gene	NA	-1.245442819	-1.245442819	1.06E-05
ankyrin repeat and BTB (POZ) domain containing 1	Abtb1	-1.245076039	-1.245076039	1.38E-05
aldo-keto reductase family 1, member B4 (aldose reductase)	Akr1b4	-1.241639354	-1.241639354	0.00010882
tweety homolog 3 (Drosophila) (predicted)	Ttyh3_predicted	-1.239996495	-1.239996495	0.00015795
immunoglobulin superfamily, member 10	Igsf10	-1.238578251	-1.238578251	5.31E-06
unknown gene	NA	-1.238036938	-1.238036938	0.00023571
embigin	Emb	-1.236901328	-1.236901328	0.0001001
CD5 antigen-like	Cd5l	-1.236603003	-1.236603003	0.00270603
similar to antigen identified by monoclonal antibody MRC OX-2 receptor (predicted)	RGD1563387_predicted	-1.236369714	-1.236369714	7.85E-06
unknown gene	NA	-1.236150462	-1.236150462	0.00024072
cell division cycle 20 homolog (S. cerevisiae)	Cdc20	-1.235946107	-1.235946107	0.0005458
SH3 domain binding glutamic acid-rich protein-like 3 (predicted)	Sh3bgrl3_predicted	-1.235518739	-1.235518739	4.99E-06
RAB11B, member RAS oncogene family	Rab11b	-1.235195804	-1.235195804	0.00012546
transmembrane 6 superfamily member 1 (predicted)	Tm6sf1_predicted	-1.23516664	-1.23516664	0.00040827
Iroquois related homeobox 1 (Drosophila) (predicted)	Irx1_predicted	-1.233888517	-1.233888517	0.00074212
aminolevulinic acid synthase 2	Alas2	-1.230766587	-1.230766587	0.00013057
pyruvate kinase, liver and red blood cell	Pklr	-1.227463717	-1.227463717	0.00067008
unknown gene	NA	-1.226542795	-1.226542795	0.00562609
superoxide dismutase 3, extracellular	Sod3	-1.224143433	-1.224143433	1.56E-05
lymphocyte cytosolic protein 2	Lcp2	-1.223739602	-1.223739602	0.00233935
osteoglycin (predicted)	Ogn_predicted	-1.222462404	-1.222462404	4.00E-05
unknown gene	NA	-1.218940967	-1.218940967	6.53E-05
IQ motif containing GTPase activating protein 1 (predicted)	Iqgap1_predicted	-1.218136971	-1.218136971	2.74E-06
RAS-related C3 botulinum substrate 2	Rac2	-1.217401473	-1.217401473	0.00026909
caspase 1	Casp1	-1.217236176	-1.217236176	0.00018047
osteoglycin (predicted)	Ogn_predicted	-1.214605193	-1.214605193	0.00405444

carbonic anhydrase 8	Car8	-1.214291258	-1.214291258	9.52E-07
SH3-domain GRB2-like 3	Sh3gl3	-1.2122152	-1.2122152	2.35E-05
unknown gene	NA	-1.210705791	-1.210705791	6.63E-05
deoxyribonuclease I-like 3	Dnase1l3	-1.207445226	-1.207445226	1.14E-05
metallothionein 1a	Mt1a	-1.20650915	-1.20650915	3.44E-05
similar to N-acetylglucosaminyltrasnferase IVb (predicted)	RGD1562836_predicted	-1.205922517	-1.205922517	1.47E-05
Cytochrome P450 IIA1 (hepatic steroid hydroxylase IIA1) gene	Cyp2a1	-1.20358641	-1.20358641	2.57E-05
similar to hypothetical protein FLJ11127	LOC310190	-1.202542139	-1.202542139	0.0006516
unknown gene	NA	-1.199324606	-1.199324606	2.54E-07
unknown gene	NA	-1.19751573	-1.19751573	0.00507635
amyloid beta (A4) precursor-like protein 2	Aplp2	-1.197187458	-1.197187458	4.08E-05
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	Galnt1	-1.196754808	-1.196754808	0.00124715
interleukin 13 receptor, alpha 1	Il13ra1	-1.192543056	-1.192543056	0.00051685
zinc finger, FYVE domain containing 1 (predicted)	Zfyve1_predicted	-1.192358446	-1.192358446	0.00112499
hematopoietic cell signal transducer	Hcst	-1.189146704	-1.189146704	0.00316447
unknown gene	NA	-1.187807643	-1.187807643	0.00172071
similar to gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	MGC125167	-1.185962595	-1.185962595	0.00015143
cadherin 11	Cdh11	-1.181868467	-1.181868467	0.00261088
proteosome (prosome, macropain) subunit, beta type 8	Psmb8	-1.181577077	-1.181577077	1.81E-05
epoxide hydrolase 1, microsomal	Ephx1	-1.181522905	-1.181522905	2.02E-06
Bruton agammaglobulinemia tyrosine kinase	Btk	-1.181104153	-1.181104153	0.00011
parathymosin	Ptms	-1.179739573	-1.179739573	0.00035011
solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	Slc13a3	-1.178702496	-1.178702496	4.98E-05
cytochrome P450, family 2, subfamily c, polypeptide 23	Cyp2c23	-1.17600381	-1.17600381	3.33E-06
unknown gene	NA	-1.173287326	-1.173287326	0.00079541
unknown gene	NA	-1.169354357	-1.169354357	0.00019474
transcription factor 19	Tcf19	-1.168108991	-1.168108991	0.00069505
similar to CG4025-PA	LOC679937	-1.16784417	-1.16784417	0.00244631
GLI pathogenesis-related 1 (glioma)	Glipr1	-1.16761223	-1.16761223	0.00026805
calcitonin receptor-like	Calcrl	-1.167049944	-1.167049944	0.00350928
cytochrome b5 reductase 3	Cyb5r3	-1.164259397	-1.164259397	1.37E-05
unknown gene	NA	-1.163405414	-1.163405414	0.0005242
similar to solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	LOC301113	-1.162569042	-1.162569042	0.00012892
N-myc downstream regulated gene 2	Ndrg2	-1.1608748	-1.1608748	9.52E-07
glucan (1,4-alpha-), branching enzyme 1	Gbe1	-1.160617925	-1.160617925	8.20E-08
similar to Ig kappa chain (predicted)	RGD1562855_predicted	-1.159911105	-1.159911105	8.99E-05
unknown gene	NA	-1.159596331	-1.159596331	0.00065866
disabled homolog 2 (Drosophila)	Dab2	-1.159390187	-1.159390187	0.00011175
complement component 9	C9	-1.158276505	-1.158276505	5.22E-07
DDHD domain containing 1	Ddhd1	-1.157719393	-1.157719393	0.00023882
t-complex 11 (mouse) like 2	Tcp11l2	-1.156039743	-1.156039743	3.94E-06
complement component 6	C6	-1.155371625	-1.155371625	2.06E-05
mitogen-activated protein kinase 9	Mapk9	-1.152631996	-1.152631996	6.45E-05
unknown gene	NA	-1.152392747	-1.152392747	6.99E-05
similar to chromosome 6 open reading frame 80; chemokine C-C motif receptor-like 1 adjacent	RGD1310326	-1.151843693	-1.151843693	7.15E-05
Cd200 antigen	Cd200	-1.151532979	-1.151532979	0.00195408
unknown gene	NA	-1.150469902	-1.150469902	6.21E-05
procollagen, type XIV, alpha 1 (predicted)	Col14a1_predicted	-1.149983587	-1.149983587	0.0001544
guanine nucleotide binding protein, gamma 2	Gng2	-1.149912375	-1.149912375	0.00012929
EH-domain containing 3	Ehd3	-1.149302369	-1.149302369	6.58E-05
similar to MGC47262 protein	RGD1561028	-1.148388739	-1.148388739	0.00016748
unknown gene	NA	-1.147579108	-1.147579108	1.16E-05
epidermal growth factor	Egf	-1.147360305	-1.147360305	0.0001627
Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	Fgr	-1.146362716	-1.146362716	1.02E-05
unknown gene	NA	-1.146263926	-1.146263926	0.0004311

motile sperm domain containing 3	Mospd3	-1.143510982	-1.143510982	0.00011684
formyltetrahydrofolate dehydrogenase	Fthfd	-1.143445005	-1.143445005	2.98E-07
fractured callus expressed transcript 1	Fxc1	1.126108782	1.126108782	0.00047332
unknown gene	NA	1.126122173	1.126122173	2.40E-05
myosin Ib	Myo1b	1.126608604	1.126608604	2.19E-06
DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	Ddx39	1.13039178	1.13039178	8.23E-06
choline phosphotransferase 1	Chpt1	1.131011443	1.131011443	5.13E-06
nucleosome assembly protein 1-like 1	Nap1l1	1.132197995	1.132197995	0.00018986
unknown gene	NA	1.132200623	1.132200623	0.00012986
similar to RIKEN cDNA 0610008C08 (predicted)	RGD1565289_predicted	1.134637781	1.134637781	3.23E-05
mitochondrial acyl-CoA thioesterase 1	Mte1	1.136834341	1.136834341	1.36E-06
matrix Gla protein	Mgp	1.137485981	1.137485981	3.38E-07
unknown gene	NA	1.138007646	1.138007646	0.01127426
arachidonate 5-lipoxygenase	Alox5	1.138212594	1.138212594	1.33E-05
transmembrane protein 33	Tmem33	1.138482096	1.138482096	2.22E-06
similar to outer dense fiber of sperm tails 2-like	LOC685425	1.138526995	1.138526995	0.00093276
similar to hypothetical protein D4Ertd89e	RGD1305703	1.148188312	1.148188312	1.55E-05
kelch-like 2, Mayven (Drosophila) (predicted)	Klhl2_predicted	1.148197944	1.148197944	3.34E-05
unknown gene	NA	1.152971519	1.152971519	0.00042544
recombination activating gene 1 activating protein 1 (predicted)	Rag1ap1_predicted	1.154613971	1.154613971	0.00035366
SEC23B (S. cerevisiae) (predicted)	Sec23b_predicted	1.155722364	1.155722364	2.56E-05
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a) (predicted)	Ndufa7_predicted	1.156944163	1.156944163	0.00057261
sperm associated antigen 9 (predicted)	Spag9_predicted	1.157573349	1.157573349	9.53E-05
similar to mitochondrial carrier family protein	RGD1308774	1.15766719	1.15766719	0.01838514
MTERF domain containing 1	Mterfd1	1.159389355	1.159389355	4.19E-05
similar to RIKEN cDNA G430041M01 (predicted)	RGD1562563_predicted	1.161521822	1.161521822	0.00084615
zinc finger protein 386 (Kruppel-like)	Znf386	1.162070568	1.162070568	0.00015728
similar to NOGO-interacting mitochondrial protein (predicted)	RGD1563384_predicted	1.163542407	1.163542407	2.26E-05
mitochondrial ribosomal protein L49	Mrpl49	1.165587877	1.165587877	2.09E-05
similar to BolA domain-containing protein like (11.4 kD) (1P25) (predicted)	RGD1305975_predicted	1.166229616	1.166229616	0.00019114
similar to Neural Wiskott-Aldrich syndrome protein (N-WASP)	LOC682507	1.166917824	1.166917824	1.60E-06
translocase of inner mitochondrial membrane 8 homolog b (yeast)	Timm8b	1.167048585	1.167048585	5.51E-06
protein tyrosine phosphatase, receptor type, R	Ptprr	1.167447958	1.167447958	0.00096045
protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	1.168768015	1.168768015	4.78E-05
similar to WD repeat domain 36	LOC688637	1.169384619	1.169384619	0.0002161
sterol carrier protein 2	Scp2	1.171339709	1.171339709	0.00200128
unknown gene	NA	1.172836166	1.172836166	4.12E-05
Jun oncogene	Jun	1.17332214	1.17332214	7.92E-05
cytosolic acyl-CoA thioesterase 1	Cte1	1.17351306	1.17351306	4.00E-05
phytanoyl-CoA hydroxylase	Phyh	1.17395867	1.17395867	1.70E-09
similar to AMME syndrome candidate gene 1 protein homolog (predicted)	RGD1561004_predicted	1.175192956	1.175192956	0.00102779
MHC class II region expressed gene KE2	Ke2	1.176202824	1.176202824	5.42E-05
glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	1.177251027	1.177251027	0.00047967
TSC22 domain family 3	Tsc22d3	1.178529255	1.178529255	1.35E-05
interferon-induced protein 44	Ifi44	1.181085071	1.181085071	2.30E-05
dolichol-phosphate (beta-D) mannosyltransferase 1 (predicted)	Dpm1_predicted	1.182579497	1.182579497	0.00350833
unknown gene	NA	1.18484943	1.18484943	1.85E-05
potential ubiquitin ligase	Herc6	1.191172866	1.191172866	0.00305227
unknown gene	NA	1.192441317	1.192441317	7.64E-05
elastin microfibril interfacer 2 (predicted)	Emilin2_predicted	1.192728786	1.192728786	0.00012676
NudC domain containing 1 (predicted)	Nudcd1_predicted	1.196280872	1.196280872	0.0006771
basic helix-loop-helix domain containing, class B, 8	Bhlhb8	1.196589894	1.196589894	0.00018672
unknown gene	NA	1.198379011	1.198379011	0.00037608
similar to MAPK-interacting and spindle-stabilizing protein (predicted)	RGD1311455_predicted	1.200874257	1.200874257	1.72E-05
zinc finger and BTB domain containing 16	Zbtb16	1.202180731	1.202180731	0.00339535

mitochondrial ribosomal protein L47	Mrpl47	1.204936698	1.204936698	9.75E-06
cerebellar degeneration-related 2	Cdr2	1.207086252	1.207086252	0.00022152
hypothetical protein LOC680080	LOC680080	1.207473241	1.207473241	4.85E-06
RGD1566320 (predicted)	RGD1566320_predicted	1.208620194	1.208620194	9.47E-06
cytochrome b5 type B	Cyb5b	1.209695641	1.209695641	7.14E-07
dead end homolog 1 (zebrafish)	Dnd1	1.21083416	1.21083416	0.00089494
similar to RIKEN cDNA 1110067D22 (predicted)	RGD1307414_predicted	1.211036022	1.211036022	5.59E-06
S100 calcium binding protein A10 (calpactin)	S100a10	1.211738972	1.211738972	4.98E-07
hypothetical LOC305552 (predicted)	RGD1309501_predicted	1.212133268	1.212133268	0.00230732
similar to neuregulin 4	LOC686216	1.212515419	1.212515419	0.00088516
unknown gene	NA	1.214770826	1.214770826	8.08E-06
solute carrier family 25 (mitochondrial carrier, glutamate), member 22	Slc25a22	1.215256931	1.215256931	1.18E-05
translocase of inner mitochondrial membrane 8 homolog a (yeast)	Timm8a	1.215347872	1.215347872	4.04E-05
unknown gene	NA	1.216256949	1.216256949	0.00351572
unknown gene	NA	1.217348118	1.217348118	0.00067132
lipoprotein lipase	Lpl	1.221827369	1.221827369	7.06E-05
cytochrome P450, 4a12	Cyp4a12	1.221837414	1.221837414	2.47E-05
heat shock 70kD protein 1A	Hspa1a	1.222281785	1.222281785	8.38E-07
sal-like 1 (Drosophila) (predicted)	Sall1_predicted	1.222558209	1.222558209	4.66E-05
putatative 28 kDa protein	LOC289809	1.222928699	1.222928699	0.00011581
similar to PAK/PLC-interacting protein 1	MGC125015	1.225380645	1.225380645	0.00018718
glutamic pyruvate transaminase (alanine aminotransferase) 2 (predicted)	Gpt2_predicted	1.22713669	1.22713669	7.60E-06
nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	Nucks	1.228109578	1.228109578	0.00013804
similar to low density lipoprotein receptor-related protein binding protein (predicted)	RGD1565715_predicted	1.229611327	1.229611327	2.71E-05
ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	1.230333838	1.230333838	2.08E-05
ornithine decarboxylase 1	Odc1	1.230453994	1.230453994	8.00E-06
cysteine rich protein 61	Cyr61	1.230575443	1.230575443	0.00133165
unknown gene	NA	1.230946482	1.230946482	1.96E-05
unknown gene	NA	1.233121226	1.233121226	8.24E-07
chaperonin subunit 8 (theta) (predicted)	Cct8_predicted	1.233648902	1.233648902	0.0001823
unknown gene	NA	1.234149491	1.234149491	0.00245826
similar to RIKEN cDNA 2610002M06 (predicted)	RGD1566265_predicted	1.235589128	1.235589128	0.00011039
unknown gene	NA	1.236160992	1.236160992	8.91E-06
protein kinase, cAMP-dependent, regulatory, type 2, alpha	Prkar2a	1.236839325	1.236839325	0.00017855
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hmgcr	1.239526277	1.239526277	1.62E-05
similar to Eph receptor A4 (predicted)	RGD1560587_predicted	1.239897533	1.239897533	0.0002644
kinesin family member 21A (predicted)	Kif21a_predicted	1.240836042	1.240836042	8.37E-07
unknown gene	NA	1.242752754	1.242752754	1.15E-05
glyceronephosphate O-acyltransferase	Gnpat	1.242856443	1.242856443	7.85E-05
similar to WAP four-disulfide core 6-like 1	LOC685153	1.245176295	1.245176295	6.47E-06
glutamic pyruvate transaminase (alanine aminotransferase) 2 (predicted)	Gpt2_predicted	1.24972126	1.24972126	0.00083915
nucleophosmin 1	Npm1	1.250989073	1.250989073	2.37E-05
similar to histone H2b-616 (predicted)	RGD1561543_predicted	1.253795363	1.253795363	4.38E-05
tripartite motif protein 36 (predicted)	Trim36_predicted	1.254242587	1.254242587	0.00028693
urinary protein 2	Rup2	1.255033915	1.255033915	0.0001692
epoxide hydrolase 2, cytoplasmic	Ephx2	1.261161644	1.261161644	1.42E-06
phosphatidylserine-specific phospholipase A1	Pspla1	1.261326543	1.261326543	4.16E-05
homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	Herpud1	1.26489078	1.26489078	0.0002444
eukaryotic translation initiation factor 1A	Eif1a	1.265117001	1.265117001	6.98E-05
fibulin 2	Fbln2	1.26516699	1.26516699	0.00014931
unknown gene	NA	1.266104345	1.266104345	0.0014135
similar to ovary-specific acidic protein	LOC689931	1.266839916	1.266839916	0.00124188
unknown gene	NA	1.27051151	1.27051151	6.58E-05
biogenesis of lysosome-related organelles complex-1, subunit 2	Bloc1s2	1.271433588	1.271433588	0.00070669
unknown gene	NA	1.272733624	1.272733624	1.51E-05

WAP four-disulfide core domain 3 (predicted)	Wfdc3_predicted	1.275287802	1.275287802	4.29E-05
calcyclin binding protein	Cacybp	1.278795837	1.278795837	2.03E-05
cyclin G1	Ccng1	1.284210999	1.284210999	3.76E-06
minichromosome maintenance deficient 10 (S. cerevisiae) (predicted)	Mcm10_predicted	1.284311804	1.284311804	1.57E-06
crystallin, alpha B	Cryab	1.285668277	1.285668277	0.00043989
similar to Neural Wiskott-Aldrich syndrome protein (N-WASP)	LOC682507	1.296514423	1.296514423	4.67E-05
nardilysin, N-arginine dibasic convertase 1	Nrd1	1.297729513	1.297729513	5.55E-05
unknown gene	NA	1.29788691	1.29788691	6.51E-06
RNA binding motif protein 3	Rbm3	1.29816696	1.29816696	2.18E-05
RAB30, member RAS oncogene family	Rab30	1.299642259	1.299642259	2.26E-06
unknown gene	NA	1.300333491	1.300333491	0.00043382
similar to erythroid differentiation-related factor 1 (predicted)	RGD1306820_predicted	1.306016147	1.306016147	2.14E-05
similar to RIKEN cDNA 2700002I20	RGD1307279	1.308567783	1.308567783	2.10E-06
similar to Serine/threonine protein kinase 24 (predicted)	RGD1561742_predicted	1.310255261	1.310255261	5.95E-06
unknown gene	NA	1.311692771	1.311692771	1.43E-05
ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	1.312187361	1.312187361	1.55E-05
unknown gene	NA	1.312748819	1.312748819	0.00021461
amphoterin induced gene and ORF 3	Amigo3	1.316425311	1.316425311	0.00011691
unknown gene	NA	1.31672522	1.31672522	0.00011136
casein kinase II, alpha 1 polypeptide	Csnk2a1	1.320953127	1.320953127	1.85E-05
acyl-Coenzyme A oxidase 2, branched chain	Acox2	1.323138179	1.323138179	3.00E-06
acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	1.323446194	1.323446194	5.73E-05
similar to Beta-sarcoglycan (Beta-SG) (43 kDa dystrophin-associated glycoprotein) (43DAG)	LOC680229	1.323981272	1.323981272	0.01411096
interleukin 1 receptor antagonist	Il1rn	1.325440642	1.325440642	3.19E-06
similar to Aig1 protein (predicted)	RGD1562920_predicted	1.32884464	1.32884464	2.95E-05
synaptic vesicle glycoprotein 2b	Sv2b	1.330377921	1.330377921	9.72E-06
unknown gene	NA	1.33535085	1.33535085	1.91E-05
similar to Protein C8orf4 (Thyroid cancer protein 1) (TC-1)	LOC684871	1.338086632	1.338086632	3.83E-05
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	Pfkfb1	1.35083145	1.35083145	3.30E-05
unknown gene	NA	1.356670001	1.356670001	0.00024968
unknown gene	NA	1.359456869	1.359456869	0.00024078
hydroxysteroid (17-beta) dehydrogenase 7	Hsd17b7	1.362274742	1.362274742	0.00013877
gamma-glutamyl hydrolase	Ggh	1.365741486	1.365741486	4.83E-06
peroxiredoxin 6	Prdx6	1.36921022	1.36921022	0.0012333
similar to Protein C6orf115	LOC685045	1.370037252	1.370037252	0.0002381
unknown gene	NA	1.372147198	1.372147198	7.25E-06
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hmgcr	1.373227719	1.373227719	3.86E-06
peptidylprolyl isomerase (cyclophilin)-like 3	Ppil3	1.374797474	1.374797474	0.00014469
unknown gene	NA	1.375217461	1.375217461	0.00140317
leukocyte cell-derived chemotaxin 2 (predicted)	Lect2_predicted	1.37922144	1.37922144	9.51E-06
unknown gene	NA	1.382758156	1.382758156	0.00014114
growth arrest specific 5	Gas5	1.384010224	1.384010224	3.94E-05
protein tyrosine phosphatase, receptor type, G	Ptprg	1.384312637	1.384312637	5.28E-05
unknown gene	NA	1.386869036	1.386869036	2.29E-05
similar to Acylphosphatase, muscle type isozyme (Acylphosphate phosphohydrolase)	LOC682245	1.386930759	1.386930759	0.00092587
alpha-fetoprotein	Afp	1.390933752	1.390933752	7.39E-05
unknown gene	NA	1.395737728	1.395737728	0.00317308
betaine-homocysteine methyltransferase	Bhmt	1.402478325	1.402478325	2.18E-06
SRY-box containing gene 17 (predicted)	Sox17_predicted	1.404969444	1.404969444	1.20E-05
transferrin	Tf	1.410464257	1.410464257	0.00015474
endothelial cell-specific molecule 1	Esm1	1.413624422	1.413624422	2.77E-05
cryptochrome 1 (photolyase-like)	Cry1	1.414151925	1.414151925	1.48E-05
unknown gene	NA	1.418031087	1.418031087	0.0028715
similar to Eph receptor A4 (predicted)	RGD1560587_predicted	1.422248504	1.422248504	0.00094969
zinc finger protein 189 (predicted)	Zfp189_predicted	1.427737747	1.427737747	8.71E-06

nicotinamide N-methyltransferase (predicted)	Nnmt_predicted	1.431167962	1.431167962	4.39E-07
unknown gene	NA	1.43780869	1.43780869	1.11E-06
citrate lyase beta like	Clybl	1.442871504	1.442871504	0.00017167
unknown gene	NA	1.450626966	1.450626966	4.58E-05
DNA-damage inducible transcript 3	Ddit3	1.453632495	1.453632495	0.00044353
RGD1565641 (predicted)	RGD1565641_predicted	1.458584741	1.458584741	2.64E-05
unknown gene	NA	1.461717988	1.461717988	4.92E-07
similar to ankyrin repeat and SOCs box-containing protein 5	LOC361187	1.464193794	1.464193794	0.00027564
similar to Pinin	LOC368070	1.464841348	1.464841348	2.09E-06
unknown gene	NA	1.466596245	1.466596245	0.0010171
abhydrolase domain containing 6	Abhd6	1.468792638	1.468792638	0.00032723
signal-induced proliferation-associated 1 like 1	Sipa1l1	1.46988464	1.46988464	0.00038402
leucine rich repeat (in FLII) interacting protein 1	Lrrfip1	1.471696547	1.471696547	0.00011498
unknown gene	NA	1.473084787	1.473084787	6.99E-05
translocase of inner mitochondrial membrane 8 homolog a (yeast)	Timm8a	1.474703136	1.474703136	3.13E-06
unknown gene	NA	1.476394481	1.476394481	0.00074648
eukaryotic translation initiation factor 1A	Eif1a	1.479048793	1.479048793	0.00014451
unknown gene	NA	1.479716033	1.479716033	0.00167822
regulator of G-protein signaling 5	Rgs5	1.487937321	1.487937321	0.00017314
unknown gene	NA	1.491104958	1.491104958	1.50E-05
transformation related protein 53 inducible nuclear protein 1	Trp53inp1	1.492753585	1.492753585	4.50E-05
hypothetical protein LOC685545	LOC685545	1.492996254	1.492996254	0.00011459
similar to RIKEN cDNA 2810055F11 (predicted)	RGD1305721_predicted	1.506778262	1.506778262	3.29E-06
unknown gene	NA	1.512892374	1.512892374	0.00091641
heat shock protein 1, alpha	Hspca	1.514701928	1.514701928	3.21E-06
G0/G1 switch gene 2	G0s2	1.52725748	1.52725748	6.09E-06
prominin 1	Prom1	1.534840912	1.534840912	3.16E-05
unknown gene	NA	1.536127042	1.536127042	0.00332201
unknown gene	NA	1.5405141	1.5405141	1.97E-05
hypothetical protein LOC685888	LOC685888	1.54527686	1.54527686	2.51E-05
unknown gene	NA	1.546274471	1.546274471	9.99E-05
unknown gene	NA	1.549847101	1.549847101	0.00019722
unknown gene	NA	1.550203284	1.550203284	9.86E-06
protein C receptor, endothelial	Procr	1.551327557	1.551327557	3.43E-05
TSC22 domain family 3	Tsc22d3	1.552693128	1.552693128	9.36E-07
heat shock 105kDa/110kDa protein 1	Hsph1	1.553150402	1.553150402	2.47E-06
unknown gene	NA	1.554043768	1.554043768	4.62E-05
decorin	Dcn	1.559298048	1.559298048	7.43E-05
heterogeneous nuclear ribonucleoprotein A1	Hnrpa1	1.563940158	1.563940158	4.73E-05
unknown gene	NA	1.567997264	1.567997264	0.00057655
mitochondrial acyl-CoA thioesterase 1	Mte1	1.571402665	1.571402665	9.22E-05
unknown gene	NA	1.575146561	1.575146561	1.12E-07
aconitase 2, mitochondrial	Aco2	1.575802698	1.575802698	0.0008149
zinc finger protein 354A	Zfp354a	1.577204117	1.577204117	9.65E-06
transmembrane protein 33	Tmem33	1.586324475	1.586324475	6.23E-05
nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (predicted)	Nfkbiz_predicted	1.591639137	1.591639137	4.25E-06
unknown gene	NA	1.593776996	1.593776996	2.91E-05
dehydrodolichyl diphosphate synthase	Dhdds	1.597165723	1.597165723	7.07E-07
similar to RIKEN cDNA 2410005O16	LOC500419	1.597258633	1.597258633	0.0004094
unknown gene	NA	1.604598235	1.604598235	8.51E-06
periplakin (predicted)	Ppl_predicted	1.605080382	1.605080382	0.00178737
fatty acid binding protein 2, intestinal	Fabp2	1.61039051	1.61039051	0.00025119
ladinin (predicted)	Lad1_predicted	1.61090444	1.61090444	4.51E-05
nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate	Nucks	1.614455371	1.614455371	3.75E-06
unknown gene	NA	1.615869641	1.615869641	0.00079996

claudin 1	Cldn1	1.630574366	1.630574366	6.16E-05
similar to RIKEN cDNA A030007L17; EST AA673177 (predicted)	RGD1304876_predicted	1.630634685	1.630634685	0.00036676
methylthioadenosine phosphorylase (predicted)	Mtap_predicted	1.632184182	1.632184182	0.00070725
hypothetical protein LOC619558	LOC619558	1.634955465	1.634955465	3.59E-07
similar to Sulfide:quinone oxidoreductase, mitochondrial precursor	LOC691966	1.636781253	1.636781253	2.32E-05
similar to RIKEN cDNA 1700023M03	RGD1305457	1.637290214	1.637290214	0.00023494
transmembrane protein 2 (predicted)	Tmem2_predicted	1.637691528	1.637691528	0.00061115
glutamic pyruvic transaminase 1, soluble	Gpt1	1.643504375	1.643504375	1.04E-06
ubiquitin specific peptidase 18	Usp18	1.645804146	1.645804146	2.36E-05
chemokine (C-C motif) ligand 2	Ccl2	1.648038909	1.648038909	4.39E-07
unknown gene	NA	1.655357908	1.655357908	6.83E-05
hypoxanthine guanine phosphoribosyl transferase	Hprt	1.66062988	1.66062988	0.0002004
dynamin 1-like	Dnm1l	1.664549844	1.664549844	0.00037899
similar to Beta-sarcoglycan (Beta-SG) (43 kDa dystrophin-associated glycoprotein) (43DAG)	LOC680229	1.667101012	1.667101012	0.00211447
aldo-keto reductase family 1, member B7	Akr1b7	1.681685796	1.681685796	2.00E-06
electron-transfer-flavoprotein, beta polypeptide	Etfb	1.698290226	1.698290226	0.00037419
dodecenoyl-coenzyme A delta isomerase	Dci	1.705401022	1.705401022	2.16E-06
similar to mKIAA0212 protein (predicted)	RGD1563633_predicted	1.707636061	1.707636061	1.73E-05
myo-inositol oxygenase	Miox	1.710988048	1.710988048	9.26E-05
NudC domain containing 1 (predicted)	Nudcd1_predicted	1.71444008	1.71444008	9.11E-05
ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	1.715660953	1.715660953	3.89E-05
unknown gene	NA	1.731220099	1.731220099	6.24E-06
cysteine-rich with EGF-like domains 2	Creld2	1.740860288	1.740860288	6.41E-07
unknown gene	NA	1.758754145	1.758754145	3.07E-05
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	B3galt3	1.759100384	1.759100384	4.58E-07
ubiquitin specific peptidase 33	Usp33	1.76953683	1.76953683	3.48E-05
cell growth regulator with EF hand domain 1	Cgref1	1.771025339	1.771025339	0.00044924
zinc finger protein 655	Zfp655	1.776171026	1.776171026	1.16E-06
glutamate oxaloacetate transaminase 1	Got1	1.779272474	1.779272474	6.86E-07
rat senescence marker protein 2A gene, exons 1 and 2	Smp2a	1.788123894	1.788123894	3.02E-06
similar to TSC22 domain family protein 2 (TSC22-related-inducible leucine zipper protein 4)	LOC499624	1.78858305	1.78858305	0.00075344
osteomodulin	Omd	1.802602079	1.802602079	2.78E-06
unknown gene	NA	1.814129766	1.814129766	0.0002064
similar to mKIAA0212 protein (predicted)	RGD1563633_predicted	1.83654004	1.83654004	4.08E-08
unknown gene	NA	1.837351575	1.837351575	1.97E-05
unknown gene	NA	1.846754167	1.846754167	3.58E-06
far upstream element (FUSE) binding protein 1	Fubp1	1.852315648	1.852315648	2.75E-05
protein disulfide isomerase associated 3	Pdia3	1.882655826	1.882655826	5.63E-05
interferon-related developmental regulator 1	Ifrd1	1.904888896	1.904888896	3.61E-05
myxovirus (influenza virus) resistance 2	Mx2	1.932624983	1.932624983	6.15E-05
microtubule-associated protein 1 light chain 3 beta	Map1lc3b	1.941365012	1.941365012	5.84E-07
connective tissue growth factor	Ctgf	1.944440011	1.944440011	0.00050316
transferrin receptor	Tfrc	1.94931939	1.94931939	8.01E-08
development and differentiation enhancing (predicted)	Ddef1_predicted	1.965627031	1.965627031	1.40E-06
hepcidin antimicrobial peptide	Hamp	1.989567055	1.989567055	3.63E-07
regulator of G-protein signaling 4	Rgs4	2.00125496	2.00125496	0.0001261
unknown gene	NA	2.01368737	2.01368737	0.00064572
heat shock 105kDa/110kDa protein 1	Hsph1	2.026892311	2.026892311	5.55E-05
unknown gene	NA	2.03244598	2.03244598	6.98E-05
cytochrome P450, family 17, subfamily a, polypeptide 1	Cyp17a1	2.036698286	2.036698286	8.83E-06
similar to myoferlin isoform b	LOC679806	2.054601651	2.054601651	0.00014703
deoxyribonuclease II beta	Dnase2b	2.083545102	2.083545102	0.00074556
rhomboid, veinlet-like 7 (Drosophila) (predicted)	Rhbdl7_predicted	2.101102481	2.101102481	2.98E-05
similar to mKIAA0212 protein (predicted)	RGD1563633_predicted	2.109889005	2.109889005	4.43E-05
transmembrane protein 55A	Tmem55a	2.110685812	2.110685812	1.47E-05

similar to hypothetical protein D4Ertd89e	RGD1305703	2.11792085	2.11792085	1.57E-05
similar to hypothetical protein MGC52110 (predicted)	RGD1565095_predicted	2.127176075	2.127176075	3.63E-05
unknown gene	NA	2.149567461	2.149567461	1.85E-05
aspartyl aminopeptidase	Dnpep	2.152869924	2.152869924	6.06E-05
hypothetical LOC300207 (predicted)	RGD1305928_predicted	2.167194402	2.167194402	2.80E-05
transmembrane protein 55A	Tmem55a	2.168095172	2.168095172	1.47E-06
thrombospondin 1	Thbs1	2.197295176	2.197295176	0.00311051
FK506 binding protein 5	Fkbp5	2.206630299	2.206630299	0.00010203
neuropeptide Y	Npy	2.223461673	2.223461673	3.62E-06
similar to expressed sequence AW413625 (predicted)	RGD1560913_predicted	2.239714185	2.239714185	4.96E-09
acetyl-Coenzyme A acetyltransferase 2	Acat2	2.242655328	2.242655328	5.21E-05
thrombospondin 1	Thbs1	2.287819048	2.287819048	1.82E-05
unknown gene	NA	2.32118446	2.32118446	2.40E-07
RT1 class I, CE12	RT1-CE12	2.346089474	2.346089474	2.74E-06
odorant binding protein I f	Obp1f	2.359137951	2.359137951	1.22E-05
transferrin receptor	Tfrc	2.395368817	2.395368817	1.27E-05
regulator of G-protein signaling 4	Rgs4	2.418139144	2.418139144	0.00036244
FK506 binding protein 5	Fkbp5	2.479391841	2.479391841	5.86E-07
unknown gene	NA	2.55266562	2.55266562	0.00014176
bromodomain adjacent to zinc finger domain protein 1B	Baz1b	2.565138961	2.565138961	6.52E-07
hypothetical LOC298504 (predicted)	RGD1310174_predicted	2.567244108	2.567244108	1.15E-06
cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (predicted)	Cidea_predicted	2.610136176	2.610136176	1.53E-06
similar to Protein diaphanous homolog 3 (Diaphanous-related formin-3) (DRF3) (mDIA2) (p134mDIA2)	LOC290396	2.74700457	2.74700457	4.11E-05
period homolog 2 (Drosophila)	Per2	2.752665021	2.752665021	2.74E-06
solute carrier family 5 (sodium/glucose cotransporter), member 11	Slc5a11	2.828754605	2.828754605	0.00042452
ubiquitin specific peptidase 2	Usp2	2.844572356	2.844572356	2.26E-07
interferon, alpha-inducible protein (clone IFI-15K) (predicted)	G1p2_predicted	2.94206362	2.94206362	3.17E-07
major urinary protein 5	Mup5	2.946149683	2.946149683	6.10E-05
guanylate cyclase 2C	Gucy2c	2.982155248	2.982155248	5.01E-06
similar to MASK-4E-BP3 protein	LOC679725	3.074508418	3.074508418	1.20E-06
phospholipase A2, group XIIA (predicted)	Pla2g12a_predicted	3.095135913	3.095135913	1.28E-06
unknown gene	NA	3.159748469	3.159748469	1.17E-07
fatty acid binding protein 4, adipocyte	Fabp4	3.330785557	3.330785557	1.05E-06
unknown gene	NA	3.337559077	3.337559077	4.35E-06
major urinary protein 5	Mup5	3.505184594	3.505184594	6.15E-06
similar to retinoid binding protein 7 (predicted)	RGD1562168_predicted	3.582798178	3.582798178	0.00052251
hypothetical protein LOC680687	LOC680687	3.91474711	3.91474711	9.85E-05
calcium-sensing receptor like 1	Casrl1	4.073699664	4.073699664	2.26E-06
RT1 class Ib gene, H2-TL-like, grc region (N1)	RT1-N1	4.31118505	4.31118505	1.11E-06
unknown gene	NA	4.587307215	4.587307215	8.53E-08
carboxylesterase 2 (intestine, liver)	Ces2	5.096243081	5.096243081	1.31E-06
aldehyde dehydrogenase family 1, subfamily A4	Aldh1a4	5.177644748	5.177644748	1.96E-08
alpha-2-macroglobulin	A2m	6.153903954	6.153903954	2.81E-06

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