

Table S3. Lung genes (n=318) significantly different between wild-type (Gsr-WT) and glutathione reductase-deficient (Gsr-KO) mice at PND56 (moderated t-test, p < 0.01).

Blue(-): fold lower in Gsr-KO. Red : fold higher in Gsr-KO.

p [Corr]	[C3H/HeN, P56][raw]	[Gsr-KO, P56][raw]	RefSeq Transcript ID	FD @PND56	Gene Symbol	Gene Title	Gene Ontology Biological Process
1.61E-04	1048.2871	101.53538	NM_010344	-10.32	<i>Gsr</i>	glutathione reductase	0006749 // glutathione metabolic process // inferred by curator//0006749 // glutathione metabolic process // not recorded//0007283 // spermatogenesis // not r
0.04568	1695.0776	668.1192	NM_172399//XM_006508	-2.54	<i>Ndnf</i>	neuron-derived neurotrophic factor	0001525 // angiogenesis // not recorded//0001764 // neuron migration // not recorded//0002931 // response to ischemia // inferred from direct assay//0007263 // nec
0.040763	1907.629	848.30896	NM_054077//XM_006525	-2.25	<i>Prepl</i>	proline arginine-rich end leucine-rich repeat	0007409 // axonogenesis // ---//0007569 // cell aging // inferred from direct assay//0018146 // keratan sulfate biosynthetic process // not recorded//0042340 // kera
0.041704	434.2309	221.01195	NM_001081161//NM_00_	-1.95	<i>Fam117a1</i>	family with sequence similarity 171, member A1	
0.026022	593.0906	305.6782	NM_009252//XM_011244	-1.94	<i>Serpina3n</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3N	0006953 // acute-phase response // inferred from electronic annotation//0010466 // negative regulation of peptidase activity // inferred from electronic annotation//
0.034382	111.22671	57.724236	NM_021332	-1.93	<i>Glyr</i>	glycylglycine-like peptide 1 receptor	0006190 // response to stress // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface rece
0.038405	338.4938	177.95528	NM_145434	-1.90	<i>Nr1d1</i>	nuclear receptor subfamily 1, group D, member 1	000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0005978 // glycogen biosynthetic process // inferred from mutant p
0.043007	1053.2932	563.1152	NM_007734	-1.87	<i>Col4a3</i>	collagen, type IV, alpha 3	0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic process // not recorded//0007155 // cell adhesion // inferred from electronic annot.
0.04941	2822.9595	1516.9738	NM_009371//NM_02957	-1.86	<i>Tajfb2</i>	transforming growth factor, beta receptor II	0001569 // patterning of blood vessels // inferred from mutant phenotype//0001570 // vasculogenesis // inferred from mutant phenotype//0001701 // in utero embri
0.038405	1639.2592	889.60785	NM_009538	-1.84	<i>Plagl1</i>	pleiomorphic adenoma gene-like 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006357 // regulation of transcription from RNA polymerase II promoter // inferred fr
0.024562	513.21954	279.34222	NM_027289//XM_006518	-1.84	<i>Ntsdc2</i>	5'-nucleotidase domain containing 2	0006470 // protein dephosphorylation // ---//0016311 // dephosphorylation // ---
0.038405	2763.3057	1514.9174	NM_009502//XM_006518	-1.82	<i>Vcl</i>	vinculin	0002009 // morphogenesis of an epithelium // not recorded//0007155 // cell adhesion // inferred from direct assay//0007160 // cell-matrix adhesion // inferred from
0.038405	2526.5679	1398.8287	NM_010740	-1.81	<i>Cd93</i>	CD93 antigen	0002230 // positive regulation of defense response to virus by host // not recorded//0007155 // cell adhesion // inferred from electronic annotation//0016337 // singl
0.0401	4443.3164	269.60785	NM_011595	-1.79	<i>Timpp3</i>	tissue inhibitor of metalloproteinase 3	0007417 // central nervous system development // inferred from electronic annotation//0007568 // aging // inferred from electronic annotation//0009612 // respons
0.04941	480.23367	269.20834	NM_027946	-1.78	<i>Dcaf7</i>	DDI1 and CUL4 associated factor 7	0007275 // multicellular organismal development // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from electronic annotati
0.038405	1142.0466	645.12634	NM_033565//XM_006498	-1.77	<i>Klf7</i>	Kruppel-like factor 7 (ubiquitous)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.041949	1290.8439	733.1305	NM_007590	-1.76	<i>Calm3</i>	calmodulin 3	0000086 // G2/M transition of mitotic cell cycle // inferred from direct assay//0001975 // response to amphetamine // inferred from electronic annotation//0002027 //
0.038405	3275.4446	1875.4241	NM_008306//XM_006525	-1.75	<i>Nds1</i>	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	0000165 // MAPK cascade // inferred from mutant phenotype//0000271 // polysaccharide biosynthetic process // inferred from mutant phenotype//0003279 // cardi
0.038405	1098.0709	630.346	NM_019472//XM_006525	-1.74	<i>Myo10</i>	myosin X	0006810 // transport // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0008152 // metabolic process // i
0.040179	483.47977	277.98203	NM_001199113//NM_00_	-1.74	<i>Slc29a1</i>	solute carrier family 29 (nucleoside transporters), member 1	0006810 // transport // inferred from electronic annotation//0007595 // lactation // inferred from electronic annotation//0015858 // nucleoside transport // inferred f
0.04232	2567.0747	1476.0676	NM_001159941//NM_02_	-1.74	<i>Kctd10</i>	potassium channel tetramerisation domain containing 10	0016567 // protein ubiquitination // inferred from sequence or structural similarity//0016567 // protein ubiquitination // inferred from electronic annotation//004316:
0.022647	1067.3907	614.3084	NM_025446//XM_006518	-1.74	<i>Aig1</i>	androgen-induced 1	
0.024493	157.4052	90.6929	NM_007619//XM_006508	-1.74	<i>Cbl</i>	Casitas B-lineage lymphoma	0006468 // protein phosphorylation // inferred from sequence or structural similarity//0007166 // cell surface receptor signaling pathway // inferred from electronic an
0.028133	2361.1665	1361.4855	NM_153423//XM_006538	-1.73	<i>Waf2f2</i>	WAS protein family, member 2	0001525 // angiogenesis // inferred from mutant phenotype//0001667 // ameoboid-type cell migration // inferred from mutant phenotype//0006897 // endocytosis /
0.037886	259.154	149.68216	NM_001201470//NM_01_	-1.73	<i>Paps2</i>	3'-phosphoadenosine 5'-phosphosulfate synthase 2	0001003 // sulfate assimilation // inferred from direct assay//0007596 // blood coagulation // inferred from mutant phenotype//0008152 // metabolic process // infer
0.038405	500.5909	289.55228	NM_023755//XM_006525	-1.73	<i>Tjfc2l1</i>	transcription factor CP2-like 1	000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0009092 // cell morphogenesis // inferred from mutant
0.038405	1474.4878	854.76874	NM_001277928//NM_00_	-1.73	<i>Lamb3</i>	laminin, beta 3	0007155 // cell adhesion // inferred from electronic annotation//0035987 // endodermal cell differentiation // inferred from electronic annotation//0050873 // brow
0.046012	123.13911	71.58008	NM_025310	-1.72	<i>Ftsj3</i>	FtsJ homolog 3 (E. coli)	0000453 // enzyme-directed rRNA 2'-O-methylation // inferred from electronic annotation//0000463 // maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-r
0.0486	4349.991	2534.636	NM_080555	-1.72	<i>Ptp3</i>	phosphophilip phosphatase 3	0001568 // blood vessel development // inferred from mutant phenotype//0001702 // gastrulation with mouth forming second // inferred from mutant phenotype//0
0.024493	1178.2483	687.4245	NM_001166584//NM_00_	-1.71	<i>Tea1</i>	TEA domain family member 1	0003143 // embryonic heart tube morphogenesis // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred from electronic annotation,
0.038405	8260.866	4822.33	NM_007929	-1.71	<i>Emp2</i>	epithelial membrane protein 2	0001765 // membrane raft assembly // inferred from direct assay//0001913 // T cell mediated cytotoxicity // inferred from direct assay//0001952 // regulation of cell-l
0.038405	972.1052	571.09314	NM_001024955//NM_00_	-1.70	<i>Plk3r1</i>	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p	0001678 // cellular glucose homeostasis // inferred from direct assay//0001934 // positive regulation of protein phosphorylation // not recorded//0001953 // negative
0.038405	2010.098	1185.7617	NM_019760	-1.70	<i>Serinc1</i>	serine incorporator 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006658 // phosphatidylserine metabolic process // not recorded//0000665 // sphingolipid
0.032292	5139.1206	3044.7122	NM_009931//XR_378656	-1.69	<i>Col1a1</i>	collagen, type I, alpha 1	0001525 // angiogenesis // inferred from electronic annotation//0001569 // patterning of blood vessels // not recorded//0007420 // brain development // not recorde
0.04034	3779.0332	2240.2678	NM_001164036//NM_00_	-1.69	<i>Ly6e</i>	lymphocyte antigen 6 complex, locus E	0001701 // in utero embryonic development // inferred from mutant phenotype//0003025 // adrenal gland development // inferred from mutant phenotype//0003526
0.047911	231.7017	137.50171	NM_021506//NM_19867	-1.69	<i>Sh3f1</i>	SH3 domain containing ring finger 1	0006915 // apoptotic process // inferred from electronic annotation//0016567 // protein ubiquitination // inferred from electronic annotation//0043066 // negative re
0.038405	957.0747	568.5649	NM_172530	-1.68	<i>She</i>	src homology 2 domain-containing transforming protein E	
0.038405	390.36908	232.65388	NM_013813//XM_006525	-1.68	<i>Epb41b3</i>	erythrocyte membrane protein band 4.1 like 3	0001558 // regulation of cell growth // inferred from electronic annotation//0002175 // protein localization to paranode region of axon // inferred from mutant phenot
0.045263	1538.4482	917.0651	NM_001163354//NM_01_	-1.68	<i>Cytk3</i>	cytohesin 3	0001692 // vesicle-mediated transport // ---//0032012 // regulation of ARF protein signal transduction // inferred from electronic annotation//0043547 // positive reg,
0.038405	2406.5662	1434.6732	NM_001081146//NM_00_	-1.68	<i>Prickle2</i>	prickle homolog 2 (Drosophila)	0031175 // neuron-projection development // inferred from mutant phenotype//0045197 // establishment or maintenance of epithelial cell apical/basal polarity // infe
0.038405	74.02675	44.182262	NM_053147	-1.68	<i>Pcdhb22</i>	protocadherin beta 22	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from elect
0.042664	919.9881	552.4643	NM_144552//XM_006518	-1.67	<i>Sinx6p6</i>	syntaxin binding protein 6 (amisyn)	0006887 // exocytosis // not recorded//0006893 // Golgi to plasma membrane transport // not recorded//0016192 // vesicle-mediated transport // inferred from elect
0.038405	5288.5454	3176.2969	NM_009932	-1.67	<i>Col2a2</i>	collagen, type IV, alpha 2	0001525 // angiogenesis // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from direct assay//00016525 // negative regula
0.04034	94.17975	56.642086	NM_001113246//NM_00_	-1.66	<i>Chimerin1</i>	chimerin 1	0007165 // signal transduction // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//0008045 // m
0.038405	1183.4149	714.85333	NM_007901	-1.66	<i>S1pr1</i>	sphingosine-1-phosphate receptor 1	0001525 // angiogenesis // inferred from direct assay//0001955 // blood vessel maturation // inferred from mutant phenotype//0003245 // cardiac muscle tissue gro
0.026847	731.1027	441.8175	NM_153393//XM_011244	-1.65	<i>Col23a1</i>	collagen, type XXIII, alpha 1	0072027 // protein homotrimerization // not recorded
0.03755	440.11227	267.1456	NM_001195031//NM_05_	-1.65	<i>Pag1</i>	phosphoprotein associated with glycosphingolipid microdomains 1	0002250 // adaptive immune response // inferred from electronic annotation//0002376 // immune system process // inferred from electronic annotation//0035556 //
0.038405	191.66026	117.12714	NM_001286468//NM_02_	-1.64	<i>RhoGAP24</i>	Rho GTPase activating protein 24	0001525 // angiogenesis // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007275 // multicellular organ
0.048819	831.3	510.80463	NM_001085492//XM_00_	-1.63	<i>Rere</i>	arginine glutamic acid dipeptide (RE) repeats	000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006338 // chromatin remodeling // inferred fr
0.024562	1328.2279	820.05664	NM_178357	-1.62	<i>Klf11</i>	Kruppel-like factor 11	0000083 // regulation of transcription involved in G1/S transition of mitotic cell cycle // not recorded//0000122 // negative regulation of transcription from RNA polyme
0.048611	1729.504	1073.1603	NM_009320//XM_006505	-1.61	<i>Slc6a6</i>	solute carrier family 6 (neurotransmitter transporter, tauroine), member 6	0001762 // beta-alanine transport // inferred from direct assay//0006810 // transport // inferred from electronic annotation//0006836 // neurotransmitter transport //
0.041117	574.2601	363.6274	NM_010332	-1.61	<i>Ednra</i>	endothelin receptor type A	0001569 // patterning of blood vessels // inferred from genetic interaction//0001666 // response to hypoxia // inferred from mutant phenotype//0001701 // in utero e
0.04568	1159.851	724.24347	NM_001136065//NM_00_	-1.60	<i>Hpk2</i>	homeodomain interacting protein kinase 2	000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001934 // positive regulation of protein phosphorylat
0.038405	123.47199	77.43215	NM_030556//XM_006498	-1.59	<i>Slc19a3</i>	solute carrier family 19, member 3	0006810 // transport // inferred from electronic annotation//0015884 // folic acid transport // not recorded//0015888 // thiamine transport // not recorded//004272
0.0401	2224.1606	1395.728	NM_033314//XM_006518	-1.59	<i>Slc20a1</i>	solute carrier organic anion transporter family, member 2a1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015732 // prostaglandin transport // in
0.024562	208.39694	131.20868	NM_178395//XM_006508	-1.59	<i>Zdhc2</i>	zinc finger, DHHC domain containing 2	0006612 // protein targeting to membrane // ---//0018230 // peptidyl-L-cysteine S-palmitoylation // ---//0018345 // protein palmitoylation // inferred from direct assa
0.048728	443.21927	280.0098	NM_020510	-1.58	<i>Frd2</i>	frizzled homolog 2 (Drosophila)	0003149 // membranous septum morphogenesis // inferred from genetic interaction//0003150 // muscular septum morphogenesis // inferred from genetic interaction
0.038405	294.4626	186.95341	NM_008005//NR_102395	-1.58	<i>Fgf18</i>	fibroblast growth factor 18	0001503 // ossification // inferred from mutant phenotype//0001525 // angiogenesis // inferred from mutant phenotype//0001957 // intramembranous ossification //
0.038405	221.46472	140.78758	NM_001190448//NM_01_	-1.57	<i>Ddc</i>	dopa decarboxylase	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0007623 // circadian rhythm // inferred from electronic annotation//0009636
0.04789	30.130987	19.231869		-1.57	<i>Igkv15-103</i>	immunoglobulin kappa chain variable 15-103	0006898 // receptor-mediated endocytosis // ---//0006910 // phagocytosis, recognition // ---//0006911 // phagocytosis, engulfment // ---//0006958 // complement ac
0.038405	136.74263	87.35392	NM_001081349//NM_00_	-1.57	<i>Slc43a1</i>	solute carrier family 43, member 1	0006810 // transport // inferred from electronic annotation//0006865 // amino acid transport // inferred from electronic annotation//0015804 // neutral amino acid tr
0.048728	1049.4797	674.76886	NM_001098799//XM_00_	-1.56	<i>Tox2</i>	TOX high mobility group box family member 2	0006338 // chromatin remodeling // not recorded//0006355 // regulation of transcription, DNA-templated // not recorded//0045944 // positive regulation of transcrip
0.038405	678.3445	436.1575	NM_198023//XM_006518	-1.56	<i>Rcor1</i>	REST corepressor 1	000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic
0.038405	329.11517	213.00853	NM_015755//XM_011244	-1.55	<i>Hunk</i>	horizontally upregulated Neu-associated kinase	0006468 // protein phosphorylation // inferred from direct assay//00016310 // phosphorylation // inferred from electronic annotation//0035556 // intracellular signal t
0.040179	799.8799	521.3591	NM_183186//XM_006518	-1.53	<i>Foxn3</i>	forkhead box protein 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.041134	2590.2878	1688.9473	NM_001080774//NM_00_	-1.53	<i>Myo1c</i>	myosin IC	0006605 // protein targeting // not recorded//0006612 // protein targeting to membrane // not recorded//0006810 // transport // inferred from direct assay//00081:
0.038405	2260.475	1475.6559	NM_001170341//NM_14_	-1.53	<i>Mjfl2</i>	myeloid leukemia factor 2	0006952 // defense response // not recorded
0.041209	148.01059	96.73844	NM_020505//NM_14613	-1.53	<i>Vav3</i>	vav 3 oncogene	0001525 // angiogenesis // inferred from electronic annotation//0006906 // vesicle fusion // inferred from genetic interaction//0006974 // cellular response to DNA d
0.042664	3332.377	2182.652	NM_139149//XM_006507	-1.53	<i>Fuz1</i>	fused in sarcoma	0007127 // cellular response to calcium ion // not recorded//1903506 // regulation of nucleic acid-templated transcription // inferred from electronic annotation
0.04941	314.04416	205.67297	NM_027265//NM_13443	-1.53	<i>Il17rd</i>	interleukin 17 receptor D	0019221 // cytokine-mediated signaling pathway // not recorded
0.038405	1085.1791	712.9826	NM_001304757//NM_00_	-1.52	<i>Col13a1</i>	collagen, type XIII, alpha 1	0001503 // ossification // inferred from electronic annotation//0001763 // morphogenesis of a branching structure // inferred from expression pattern//0001958 // en
0.038405	716.9844	471.4302	NM_001271584//NM_00_	-1.52	<i>Dnaic5</i>	Dnal (Hsp40) homolog, subfamily C, member 5	0043524 // negative regulation of neuron apoptotic process // inferred from genetic interaction
0.048728	461.2156	304.12143	NM_177839//XM_006498	-1.52	<i>Tnn</i>	tenascin N	0007160 // cell-matrix adhesion // inferred from direct assay//0007409 // axonogenesis // inferred from direct assay//0016049 // cell growth // inferred from direct as
0.038405	522.45447	344.89117	NM_008029	-1.51	<i>Fit4</i>	FMS-like tyrosine kinase 4	0001525 // angiogenesis // inferred from electronic annotation//0001934 // positive regulation of protein phosphorylation // not recorded//0001938 // positive regula
0.038405	366.60474	242.18045	NM_001042779//NM_00_	-1.51	<i>Sema3b</i>	sema domain, immunoglobulin domain (Ig), short basic domain, semaphorin 3B	0001755 // neural crest cell migration // not recorded//0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous s
0.041704	192.55879	127.45899	NM_001081420//XM_01_	-1.51	<i>Fam206a</i>	family with sequence similarity 206, member A	
0.024562	32.793064	21.708841	NM_001301370//NM_18_	-1.51	<i>Syt14</i>	synaptotagmin XIV	0006906 // vesicle fusion // ---//0016079 // synaptic vesicle exocytosis // not recorded//0017158 // regulation of calcium ion-dependent exocytosis // ---//0048791 //

p [Corr]	[C3H/HeN, P56][raw]	[Gsr-KO, P56][raw]	RefSeq Transcript ID	FD @PND56	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.032292	165.37949	109.610146	NM_001163154//NM_00_1-51		<b>Etv1</b>	ets variant 1	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
0.038405	877.2441	582.276	NM_001081098//NM_011-151		<b>Zfp362</b>	zinc finger protein 362	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation // 0015031 // protein transport // inferred from electronic annotation // 001000
0.04941	1159.0638	769.6117	NM_001040459//NM_00_1-51		<b>Shroom4</b>	shroom family member 4	0000902 // cell morphogenesis // inferred from sequence or structural similarity // 0007015 // actin filament organization // inferred from direct assay // 0007275 // mu
0.038405	855.61957	568.6709	NM_1133685	-1.50	<b>Rab31</b>	RAB31, member RAS oncogene family	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation // 0015031 // protein transport // inferred from electronic annotation // 001000
0.043007	3468.1067	2307.2063	NM_001276481//NM_00_1-50		<b>Dag1</b>	dyagroglycan 1	0002011 // morphogenesis of an epithelial sheet // inferred from mutant phenotype // 0006509 // membrane protein ectodomain proteolysis // not recorded // 000660
0.04941	1402.9282	935.90622	NM_0052994//NM_006514-150		<b>Spack2</b>	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	0007165 // signal transduction // inferred from electronic annotation // 0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay // 0001980C
0.040434	562.2537	375.09845	NM_023785	-1.50	<b>Pppb</b>	pro-platelet basic protein	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant phenotype // 0002690 // positive regulation of leukocyte chemotaxis // not r
0.049711	1739.3824	1163.3354	NM_0111239	-1.50	<b>Ranbp1</b>	RAN binding protein 1	0007051 // spindle organization // inferred from direct assay // 0010976 // positive regulation of neuron projection development // not recorded // 00035690 // cellular n
0.040698	178.26881	119.235756	NM_001135657//NM_00_1-50		<b>Ptpri1//Gm38718/</b>	protein tyrosine phosphatase, receptor type, 1 // predicted gene, 3	0001570 // vasculogenesis // inferred from mutant phenotype // 0001954 // positive regulation of cell-matrix adhesion // inferred from direct assay // 0006470 // protei
0.041949	432.15854	289.1162	NM_199299//NM_006534-149		<b>Jade2</b>	jade family PHD finger 2	0043966 // histone H3 acetylation // not recorded // 0043981 // histone H4-K4 acetylation // not recorded // 0043982 // histone H4-K8 acetylation // not recorded // 004
0.028116	276.0881	184.87575	NM_001080813//NM_02_1-49		<b>Rab11fp1</b>	RAB11 family interacting protein 1 (class I)	0006810 // transport // inferred from electronic annotation // 0015031 // protein transport // inferred from electronic annotation // 0045055 // regulated secretory pat
0.046461	272.19382	182.57698	NM_139294//NM_006505-149		<b>Braf</b>	Braf transforming gene	0000165 // MAPK cascade // not recorded // 0000186 // activation of MAPKK activity // not recorded // 00002318 // myeloid progenitor cell differentiation // inferred fr
0.047179	892.29755	599.9184	NM_010415	-1.49	<b>Hbecf</b>	heparin-binding EGF-like growth factor	0001525 // angiogenesis // non-traceable author statement // 0001832 // blastocyst growth // traceable author statement // 0007173 // epidermal growth factor recept
0.038405	1397.2965	939.61255	NM_001024624	-1.49	<b>Cdk15</b>	cyclin-dependent kinase-like 5	0001764 // neuron migration // not recorded // 0006468 // protein phosphorylation // inferred from electronic annotation // 0016310 // phosphorylation // inferred fr
0.038405	340.83203	229.91806	NM_001003671//NM_00_1-48		<b>Pcdha11//Pcdha10</b>	protocadherin alpha 11 // protocadherin alpha 10 // protocadherin	0007155 // cell adhesion // inferred from electronic annotation // 0007155 // cell adhesion // traceable author statement // 0007156 // homophilic cell adhesion via plas
0.04941	3203.1	2173.2795	NM_001029836//NM_00_1-47		<b>Npnt</b>	nephronectin	0001657 // ureteric bud development // inferred from mutant phenotype // 0001658 // branching involved in ureteric bud morphogenesis // inferred from mutant phen
0.04941	3227.47	2193.964	NM_001025600//NM_00_1-47		<b>Cadm1</b>	cell adhesion molecule 1	0001889 // liver development // not recorded // 0002376 // immune system process // inferred from electronic annotation // 0006915 // apoptotic process // inferred fr
0.038405	261.20563	177.58998	NM_001003671//NM_00_1-47		<b>Pcdha11//Pcdha10</b>	protocadherin alpha 11 // protocadherin alpha 10 // protocadherin	0007155 // cell adhesion // inferred from electronic annotation // 0007155 // cell adhesion // traceable author statement // 0007156 // homophilic cell adhesion via plas
0.048728	2347.2542	1598.9901	NM_172145//NM_006505-147		<b>Evai1b</b>	eva-1 homolog B (C. elegans)	0098779 // mitophagy in response to mitochondrial depolarization // not recorded
0.043007	1352.7505	922.9179	NM_007478//NM_011242-147		<b>Arf3</b>	ADP-ribosylation factor 3	0006810 // transport // inferred from electronic annotation // 0007264 // small GTPase mediated signal transduction // inferred from electronic annotation // 0015031 /
0.041704	83.124756	56.806545	NM_013475//NM_006534-146		<b>Apj</b>	apolipoprotein H	0001937 // negative regulation of endothelial cell proliferation // not recorded // 0006641 // triglyceride metabolic process // not recorded // 0007596 // blood coagulat
0.043007	75.47448	51.586594	NM_013848//NM_006505-146		<b>Ermapp</b>	erythroblast membrane-associated protein	
0.041117	497.23718	339.93472	NM_001005740//NM_00_1-46		<b>Phactr1//Chst11</b>	phosphatase and actin regulator 1 // carboxypeptidase sulfotransferase	0031032 // actomyosin structure organization // inferred from mutant phenotype // 0031032 // actomyosin structure organization // not recorded // 0031532 // actin cy
0.04941	1123.7413	768.2795	NM_001038625//NM_02_1-46		<b>Srtad2</b>	SERTA domain containing 2	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.04941	936.5158	604.2987	NM_001313977//NM_00_1-46		<b>Pekc</b>	protein kinase C, eta	0006468 // protein phosphorylation // not recorded // 0010744 // positive regulation of macrophage derived foam cell differentiation // inferred from mutant phenotyp
0.04356	447.06488	305.67294	NM_178608	-1.46	<b>Reep1</b>	receptor accessory protein 1	0032386 // regulation of intracellular transport // inferred from direct assay // 0051205 // protein insertion into membrane // not recorded // 0071786 // endoplasmic re
0.038405	3695.5808	2528.6582	NM_001001183//NM_00_1-46		<b>Tram204</b>	transmembrane protein 204	0001945 // lymph vessel development // inferred from genetic interaction // 0001945 // lymph vessel development // inferred from mutant phenotype // 00030947 // req
0.04232	7164.845	4905.9795	NM_032398//NM_011242-146		<b>Plvap</b>	plasmaless vesicle associated protein 2	0000165 // MAPK cascade // not recorded // 0002693 // positive regulation of cellular extravasation // inferred from mutant phenotype // 0002693 // positive regulati
0.04232	476.4661	326.4861	NM_025729//NM_006521-146		<b>Tab3</b>	TGF-beta activated kinase 1/MAP3K7 binding protein 3	0016310 // phosphorylation // inferred from electronic annotation
0.049219	209.23053	143.5325	NM_001290489//NM_02_1-46		<b>Med27</b>	mediator complex subunit 27	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.049219	1171.1486	804.0398	NM_010228//NM_006504-146		<b>Fit1</b>	FMS-like tyrosine kinase 1	0001525 // angiogenesis // inferred from mutant phenotype // 0001525 // angiogenesis // traceable author statement // 0001569 // patterning of blood vessels // infern
0.038405	257.90628	177.10294	NM_033622//NM_006504-146		<b>Tnfr1f3b</b>	tumor necrosis factor (ligand) superfamily, member 13b	0001782 // B cell homeostasis // inferred from mutant phenotype // 0002636 // positive regulation of germinal center formation // inferred from mutant phenotype // 0
0.04941	2174.0627	1493.8977	NM_011202//NM_20124-146		<b>Mrip1</b>	myosin phosphatase Rho interacting protein	0001934 // positive regulation of protein phosphorylation // not recorded // 0032507 // maintenance of protein location in cell // not recorded // 0035509 // negative re
0.049545	2060.2314	1416.2219	NM_175341//NM_20751-145		<b>Mbnl2</b>	muscleblind-like 2	000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from mutant phenotype // 0000381 // regulation of alternative mRNA splicing, via splicee
0.038405	949.74506	654.44745	NM_018884//NM_006504-145		<b>Pdm3</b>	PDZ domain containing RING finger 3	0007528 // neuromuscular junction development // inferred from mutant phenotype // 0016567 // protein ubiquitination // inferred from direct assay
0.043007	301.5806	208.10634	NM_001163505//NM_14_1-45		<b>Ait3</b>	atastin GTPase 3	0007029 // endoplasmic reticulum organization // not recorded // 0007030 // Golgi organization // not recorded // 0008152 // metabolic process // inferred from electr
0.04201	452.33777	312.7535	NM_024286//NM_006514-145		<b>Popdc3</b>	popye domain containing 3	0042391 // regulation of membrane potential // inferred from genetic interaction
0.041117	4692.4355	3246.059	NM_001289895//NM_02_1-45		<b>Tns1</b>	tensin 1	0007044 // cell-substrate junction assembly // inferred from mutant phenotype // 0010761 // fibroblast migration // inferred from mutant phenotype // 0035556 // intra
0.038405	219.95209	152.24667	NM_022980	-1.44	<b>Rcan3</b>	regulator of calcineurin 3	0019722 // calcium-mediated signaling // inferred from electronic annotation // 0050790 // regulation of catalytic activity // -- // 0070884 // regulation of calcineurin-NF
0.04232	344.3199	238.81123	NM_183106//NM_006504-144		<b>Tct17</b>	retrotransposon repeat domain 17	0030030 // cell projection organization // inferred from electronic annotation // 0030041 // actin filament polymerization // not recorded // 0044782 // cilium organizati
0.044532	344.19833	239.34137	NM_010731//NM_006514-144		<b>Zbtb7a</b>	zinc finger and BTB domain containing 7a	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0006351 // transcription, DNA-templated // inferred fr
0.04789	535.3437	372.38577	NM_0010037136//NM_17_1-44		<b>Argap1</b>	ARF-GAP with GTPase domain, ankyrin repeat and PH domain 1	0006810 // transport // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0007264 // small GTPase mediat
0.049568	421.48666	293.28323	NM_001145830//NM_01_1-44		<b>Pfcb1</b>	phospholipase C, beta 1	0000086 // G2/M transition of mitotic cell cycle // inferred from direct assay // 0000086 // G2/M transition of mitotic cell cycle // non-traceable author statement // 000
0.038405	243.71495	169.61202	NM_001043355//NM_00_1-44		<b>Map6</b>	microtubule-associated protein 6	0000226 // microtubule cytoskeleton organization // inferred from electronic annotation // 0006810 // transport // inferred from electronic annotation // 00032418 // lysi
0.048728	1404.8986	977.93884	NM_145130//NM_006505-144		<b>Lncp3</b>	lysophosphatidylcholine acyltransferase 3	0006629 // lipid metabolic process // inferred from electronic annotation // 0006644 // phospholipid metabolic process // inferred from electronic annotation // 000865-
0.047646	571.37335	444.2544	NM_025664	-1.44	<b>Sxpr1</b>	sorting nexin 9	000281 // mitotic cytokinesis // not recorded // 0006810 // transport // inferred from electronic annotation // 0006886 // intracellular protein transport // inferred fr
0.038405	1207.6235	841.2943	NM_001285805//NM_01_1-44		<b>Zbtb20</b>	zinc finger and BTB domain containing 20	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype // 0006351 // transcription, DNA-templated // infe
0.04941	3716.0823	2591.874	NM_009128	-1.43	<b>Sdc2</b>	stearyl-Coenzyme A desaturase 2	0006629 // lipid metabolic process // inferred from electronic annotation // 0006631 // fatty acid metabolic process // inferred from electronic annotation // 00006633 //
0.038405	927.2107	646.7869	NM_147219//NM_006534-143		<b>Abc5a</b>	ATP-binding cassette, sub-family A (ABC1), member 5	0006810 // transport // inferred from electronic annotation // 0008152 // metabolic process // inferred from electronic annotation // 0010745 // negative regulation of r
0.048611	348.89117	243.37679	NM_021439//NM_006514-143		<b>Phactr1//Phactr1</b>	carbohydrate sulfotransferase 11 // phosphatase and actin regulat	0002063 // chondrocyte development // inferred from mutant phenotype // 0005975 // carbohydrate metabolic process // inferred from electronic annotation // 00075
0.04232	659.69305	461.06625	NM_198631//NM_006544-143		<b>Zc3h4</b>	zinc finger CCHC-type containing 4	
0.042435	1120.1317	783.55286	NM_001204915//NM_17_1-43		<b>Reep3</b>	receptor accessory protein 3	0006998 // nuclear envelope organization // not recorded // 0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // inferred
0.040179	701.4039	490.79355	NM_001081016//NM_01_1-43		<b>Zc3h7b</b>	zinc finger CCHC type containing 7b	
0.038405	525.3361	368.1724	NM_001081750	-1.43	<b>Zfp664</b>	zinc finger protein 664	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // not recorded
0.04941	1364.7068	957.38416	NM_010590	-1.43	<b>Ajuab</b>	ajuba LIM protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype // 0001666 // response to hypoxia // not recorded,
0.048728	344.255	242.27428	NM_001276461//NM_00_1-42		<b>Asp1</b>	ARF-GAP with SH3 domain, ankyrin repeat and PH domain1	0030030 // cell projection organization // inferred from electronic annotation // 0043547 // positive regulation of GTPase activity // inferred from electronic annotation/
0.049864	189.51044	133.46808	NM_026186	-1.42	<b>Cwc25</b>	CWC25 spliceosome-associated protein homolog (S. cerevisiae)	
0.047853	1317.6952	928.29004	NM_028763	-1.42	<b>Cbx6</b>	chromobox 6	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic
0.044232	473.55157	333.81567	NM_001311112//NM_17_1-42		<b>Ccd126</b>	coiled-coil domain containing 126	0006487 // protein N-linked glycosylation // inferred from electronic annotation
0.04789	2008.2811	1417.9764	NM_175414//NM_006505-142		<b>Tspan9</b>	tetraspanin 9	0007166 // cell surface receptor signaling pathway // not recorded
0.048728	304.9978	215.579	NM_009199	-1.41	<b>Sic1a</b>	solute carrier family 1 (neuronal/epithelial high affinity glutamate t	0006810 // transport // inferred from electronic annotation // 0006835 // dicarboxylic acid transport // inferred from electronic annotation // 0010460 // positive regulat
0.048728	292.65384	207.17819	NM_176958	-1.41	<b>Hif1a</b>	hypoxia-inducible factor 1, alpha subunit inhibitor	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.04941	192.37997	136.22414	NM_029037	-1.41	<b>Ponk</b>	protein-O-mannose kinase	0001764 // neuron migration // inferred from mutant phenotype // 0006468 // protein phosphorylation // inferred from electronic annotation // 0006493 // protein O-li
0.041117	331.8189	235.22113	NM_021528//NM_006504-141		<b>Chst12</b>	carbohydrate sulfotransferase 12	0005975 // carbohydrate metabolic process // inferred from electronic annotation // 0016051 // carbohydrate biosynthesis process // inferred from electronic annotatio
0.049864	254.88866	180.70114	NM_201519//NM_006514-141		<b>Map4k5</b>	mitogen-activated protein kinase kinase kinase 5	0000165 // MAPK cascade // not recorded // 0000185 // activation of MAPKK activity // -- // 0000185 // activation of MAPKK activity // inferred from electronic annota
0.04941	213.7468	151.6481	NM_013818//NM_006524-141		<b>Gtpbp1</b>	GTP binding protein 1	0006413 // translational initiation // -- // 0008152 // metabolic process // inferred from electronic annotation // 0006104 // positive regulation of mRNA catabolic proce
0.044232	519.01294	368.33963	NM_008881	-1.41	<b>Plexn1</b>	plexin A1	0007165 // signal transduction // inferred from electronic annotation // 0014910 // regulation of smooth muscle cell migration // inferred from mutant phenotype // 000
0.04941	4282.401	3046.8162	NM_172621//NM_006524-141		<b>Clic5</b>	chloride intracellular channel 5	0002021 // response to dietary excess // inferred from mutant phenotype // 0002024 // diet induced thermogenesis // inferred from mutant phenotype // 0006749 // gl
0.04232	505.34937	360.12274	NM_001003955//NM_17_1-40		<b>Rab11fp5</b>	RAB11 family interacting protein 5 (class I)	0006810 // transport // inferred from electronic annotation // 0015031 // protein transport // inferred from electronic annotation // 0035773 // insulin secretion involv
0.0401	513.92395	366.2639	NM_001003529//NM_00_1-40		<b>Tulp4</b>	tubby like protein 4	0016567 // protein ubiquitination // inferred from electronic annotation // 0035556 // intracellular signal transduction // inferred from electronic annotation // 0061512
0.038405	384.71835	275.97717	NM_001001883//NM_17_1-39		<b>Hecw2</b>	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	0016567 // protein ubiquitination // not recorded // 0042787 // protein ubiquitination involved in ubiquitin-dependent protein catabolic process // --
0.048728	879.9232	632.8017	NM_183016//NM_006514-139		<b>Cdc42bbp</b>	CDC42 binding protein kinase beta	0006468 // protein phosphorylation // not recorded // 0016310 // phosphorylation // inferred from electronic annotation // 0016477 // cell migration // not recorded //
0.04941	1067.7323	769.5822	NM_181415//NM_006524-139		<b>Attractin1</b>	attractin like 1	0007186 // G-protein coupled receptor signaling pathway // inferred from physical interaction
0.044568	254.41515	183.1787	NM_177409	-1.38	<b>Tram2</b>	translocating chain-associated membrane protein 2	0006810 // transport // inferred from electronic annotation // 0015031 // protein transport // inferred from electronic annotation // 0032964 // collagen biosynthetic pri
0.041117	238.1474	172.13155	NM_030256//NM_006514-138		<b>C9orf2</b>	B cell CLL/lymphoma 9-like	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.04941	83.60875	60.45419	NM_019732//NM_006534-138		<b>Rum3</b>	runf related transcription factor 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay // 0001503 // ossification // not recorded // 0002062 // ct
0.0486	919.9784	665.8952	NM_026301//NM_006524-138		<b>Rif125</b>	runt finger protein 125	0002250 // adaptive immune response // inferred from electronic annotation // 0002376 // immune system process // inferred from electronic annotation // 0016567 //
0.041704	266.5603	193.26584	NM_029397//NM_170594-138		<b>Rbm12</b>	RNA binding motif protein 12	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.049711							

p [Corr]	[C3H/HeN, P56][raw]	[Gsr-KO, P56][raw]	RefSeq Transcript ID	FD @PND56	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.04941	506.8478	368.49817	NM_001253890//NM_001-1.38		<b>Prkar1b</b>	protein kinase, cAMP dependent regulatory, type I beta	0001932 // regulation of protein phosphorylation // inferred from electronic annotation//0006468 // protein phosphorylation // traceable author statement//0007611
0.048728	309.95627	226.64578	NM_001039079//NM_001-1.37		<b>Prkcz</b>	protein kinase C, zeta	0000226 // microtubule cytoskeleton organization // inferred from genetic interaction//0000226 // microtubule cytoskeleton organization // inferred from mutant ph
0.045259	318.1437	233.03137	NM_001146687//NM_001-1.37		<b>Pip5k1c</b>	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma	0006887 // exocytosis // inferred from electronic annotation//0006897 // endocytosis // inferred from electronic annotation//0006909 // phagocytosis // inferred from
0.04941	147.24838	100.05353	NM_001040026//XM_000-1.36		<b>Sco1</b>	SCO cytochrome oxidase deficient homologue 1 (yeast)	0006825 // copper ion transport // inferred from electronic annotation//0006878 // cellular copper ion homeostasis // inferred from electronic annotation//0008535 /
0.04941	259.1912	190.93745	NM_053273	-1.36	<b>Ttyh2</b>	twenty homolog 2 (Drosophila)	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821 // chloride transport // inferre
0.04941	391.65328	289.13334	NM_029770//XM_006511-1.35		<b>Unc5b</b>	unc-5 homolog B (C. elegans)	0001525 // angiogenesis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0007165 // signal transduction /
0.04232	249.01794	184.08096	NM_001114361//NM_001-1.35		<b>Emil4</b>	echinoderm microtubule associated protein like 4	0007026 // negative regulation of microtubule depolymerization // inferred from mutant phenotype
0.044264	200.35493	148.59875	NM_033509//XM_006491-1.35		<b>Vangl2</b>	vang-like 2 (van gogh, Drosophila)	0001569 // patterning of blood vessels // traceable author statement//0001736 // establishment of planar polarity // inferred from genetic interaction//0001736 // est
0.038405	97.365265	72.2618	NM_025519	-1.35	<b>Chmp4c</b>	charged multivesicular body protein 4C	0000920 // cell separation after cytokinesis // not recorded//0006810 // transport // inferred from electronic annotation//0006997 // nucleus organization // not reco
0.038405	128.85724	95.66023	NM_145700//XM_006511-1.35		<b>Ackr4</b>	atypical chemokine receptor 4	0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0006935 // chemotaxis // inferred from electronic annotation//0007165 // signal tr
0.049303	134.66531	100.621735	NM_178793//XM_006524-1.34		<b>Ccbe1</b>	collagen and calcium binding EGF domains 1	0001525 // angiogenesis // inferred from electronic annotation//0001946 // lymphangiogenesis // inferred from mutant phenotype//0001946 // lymphangiogenesis //
0.04941	353.18076	264.94797	NM_001042623//NM_001-1.33		<b>Phc1</b>	polyhomeotic-like 1 (Drosophila)	0007275 // multicellular organismal development // inferred from electronic annotation//0016574 // histone ubiquitination // not recorded//0071300 // cellular respo
0.045259	36.328278	27.450245	NM_013596//XR_385979-1.32		<b>Mcsr</b>	melanocortin 5 receptor	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation,
0.04941	57.860466	44.106277	NM_008730	-1.31	<b>Nptx1</b>	neuronal pentraxin 1	0006839 // mitochondrial transport // not recorded//0035865 // cellular response to potassium ion // not recorded//0043653 // mitochondrial fragmentation involv
0.041949	163.54807	124.994736	NM_175022	-1.31	<b>Prr12</b>	proline rich 12	
0.04941	324.36267	248.02576	NM_001081149//XM_000-1.31		<b>Kat6a</b>	K[lysine] acetyltransferase 6A	0003007 // heart morphogenesis // inferred from genetic interaction//0003007 // heart morphogenesis // inferred from mutant phenotype//0006334 // nucleosome
0.049864	367.79852	281.6287	NM_001256104//NM_14-1.31		<b>Slc10a3</b>	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	0006810 // transport // inferred from electronic annotation//0010033 // response to organic substance // inferred from direct assay//0015721 // bile acid and bile salt
0.04941	161.53345	127.06176	NM_001038607//NM_001-1.27		<b>Kcnh1</b>	potassium voltage-gated channel, subfamily H (eag-related), member 1	0000160 // phosphorelay signal transduction system // inferred from electronic annotation//0001964 // startle response // not recorded//0006810 // transport // infe
0.049219	562.8476	735.7147	NM_182805	1.31	<b>Gp95t</b>	glutamic pyruvic transaminase, soluble	0009058 // biosynthetic process // inferred from electronic annotation//0042853 // L-alanine catabolic process // inferred from electronic annotation
0.049864	691.3509	924.1627	NM_0011155//XM_006538-1.34		<b>Ppp5c</b>	protein phosphatase 5, catalytic subunit	0001933 // negative regulation of protein phosphorylation // not recorded//0006470 // protein dephosphorylation // not recorded//0007165 // signal transduction //
0.048728	1232.7087	1668.4021	NM_028281//XM_006511-1.35		<b>Pcb2d</b>	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of	0006729 // tetrahydrobiopterin biosynthetic process // inferred from electronic annotation//0045893 // positive regulation of transcription, DNA-templated // not reco
0.042825	860.3127	1167.1267	NM_009676//XM_006491-1.36		<b>Aox1</b>	aldehyde oxidase 1	0005514 // oxidation-reduction process // inferred from electronic annotation
0.038405	3502.844	4765.1333	NM_025650	1.36	<b>Uqc11</b>	ubiquinol-cytochrome c reductase, complex III subunit XI	0006810 // transport // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic annotation//1902600 // hydrogen ion
0.04941	1140.442	1560.2775	NM_001114970//NM_001-1.37		<b>Slc16a11</b>	solute carrier family 16 (monocarboxylic acid transporters), member 11	0006629 // lipid metabolic process // not recorded//0006810 // transport // inferred from electronic annotation//0015718 // monocarboxylic acid transport // ---//00
0.0489	872.35706	1197.4795	NM_001302138//NM_001-1.37		<b>Vamp17</b>	vesicle-associated membrane protein 17	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // not recorded//0006888 // ER to Golgi vesicle-mediated transport // not record
0.038713	540.09784	741.47784	NM_144844//XM_006511-1.37		<b>Pcca</b>	propionyl-Coenzyme A carboxylase, alpha polypeptide	0008152 // metabolic process // inferred from electronic annotation
0.049864	621.2741	415.4482	NM_007713//XM_006511-1.38		<b>Clk3</b>	CDK-like kinase 3	0006468 // protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not recorded//0016310 // phosphorylation // inferred from e
0.049219	1558.7548	2147.0571	NM_001010930//NM_001-1.38		<b>Gml12540//Mrps3</b>	predicted gene 12540//mitochondrial ribosomal protein 533	
0.0486	3012.044	4194.0224	NR_003513//NR_131212-1.38		<b>Neat1</b>	nuclear paraspeckle assembly transcript 1 (non-protein coding)	0030575 // nuclear body organization // inferred from mutant phenotype//0043954 // cellular component maintenance // inferred from direct assay//0043954 // cellu
0.041197	236.48164	326.7122	XM_977361	1.38	<b>Tcrb-1//LOC6550</b>	T cell receptor beta, joining region//T cell receptor beta-2 chain C	region-like//T cell receptor beta, constant region 1//T cell receptor beta, constant 2
0.045259	485.95206	675.1463	NM_026765//XM_006500-1.39		<b>Uck1</b>	uridine-cytidine kinase 1-like 1	0006206 // pyrimidine nucleobase metabolic process // not recorded//0006222 // UMP biosynthetic process // ---//0006222 // UMP biosynthetic process // inferred fr
0.048728	296.35696	412.21576	NM_138951	1.39	<b>Ttc36</b>	tetratricopeptide repeat domain 36	
0.038405	843.4365	1173.7635	NM_016665//XM_006531-1.39		<b>Str13</b>	stimulated by retinoic acid 13	0000712 // resolution of meiotic recombination intermediates // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular resp
0.044264	1082.6326	1507.5061	NM_007620	1.39	<b>Cbr1</b>	carboxyl reductase 1	0008152 // metabolic process // inferred from electronic annotation//0017144 // drug metabolic process // not recorded//0030855 // epithelial cell differentiation // i
0.048728	616.8076	870.6265	NM_026686	1.41	<b>Tefm</b>	transcription elongation factor, mitochondrial	0006119 // oxidative phosphorylation // not recorded//0006259 // DNA metabolic process // not recorded//0006351 // transcription, DNA-templated // inferred from
0.038405	1103.6636	1574.5457	NM_025353//XM_006531-1.43		<b>Uqcq</b>	ubiquinol-cytochrome c reductase, complex III subunit VII	0006810 // transport // inferred from electronic annotation//0021539 // subthalamus development // inferred from expression pattern//0021548 // pons developer
0.041134	498.89755	711.9223	NM_001286217//NM_001-1.43		<b>Fuocm</b>	fucoase mutarotase	0005996 // monosaccharide metabolic process // inferred from electronic annotation//0006004 // fucoase metabolic process // inferred from direct assay//0036065 //
0.044232	19.238907	27.458847		1.43	<b>C76798</b>	expressed sequence C76798	
0.041197	1766.3695	2552.7488	NM_025559	1.45	<b>Mien1</b>	migration and invasion enhancer 1	0006915 // apoptotic process // inferred from electronic annotation//0030335 // positive regulation of cell migration // not recorded//0043066 // negative regulation
0.046012	1141.71	1650.7617	NM_027204	1.45	<b>Mrp12</b>	mitochondrial ribosomal protein L12	0006390 // transcription from mitochondrial promoter // not recorded//0006412 // translation // inferred from sequence or structural similarity//0045893 // positive
0.047179	292.8371	424.46414	NM_027460//XM_011251-1.45		<b>Slc25a33</b>	solute carrier family 25, member 33	0000002 // mitochondrial genome maintenance // not recorded//0002082 // regulation of oxidative phosphorylation // not recorded//0006264 // mitochondrial DNA
0.049711	439.25894	637.5859	NM_011220	1.45	<b>Pts</b>	6-pyruvyl-tetrahydropterin synthase	0006729 // tetrahydrobiopterin biosynthetic process // inferred from direct assay
0.04941	4502.7183	6539.9336	NM_025641	1.45	<b>Ahr</b>	ubiquinol-cytochrome c reductase hinge protein	0006122 // mitochondrial electron transport, ubiquinol to cytochrome c // inferred from electronic annotation//0006810 // transport // inferred from electronic annota
0.046012	37.01822	53.875175	NM_001081070//XM_000-1.46		<b>Pdia2</b>	protein disulfide isomerase associated 2	0006457 // protein folding // traceable author statement//0006457 // protein folding // inferred from electronic annotation//0008152 // metabolic process // inferred
0.038405	349.09006	485.4858	XM_977361	1.46	<b>LOC65506//Tcrb</b>	T cell receptor beta-2 chain C region-like//T cell receptor beta, constant 2//T cell receptor beta, joining region//T cell receptor beta, variable 26	0018023 // peptidyl-lysine trimethylation // inferred from mutant phenotype//0032259 // methylation // inferred from electronic annotation//1904733 // negative reg
0.0486	318.0146	464.25732	NM_001252094//NM_001-1.46		<b>Mettl20</b>	methyltransferase like 20	0008283 // cell proliferation // not recorded//0042127 // regulation of cell proliferation // not recorded//0042254 // ribosome biogenesis // not recorded//1902895 /
0.045259	661.1228	970.5638	NM_153547//NM_17884-1.47		<b>Zbtb11</b>	zinc finger and BTB domain containing 11	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.039357	235.25885	346.95377	NM_001040686//NM_001-1.47		<b>Zfp692</b>	zinc finger protein 692	
0.037386	721.05054	1069.5739	NM_173026//XM_011242-1.48		<b>Zbtb11</b>	zinc finger and BTB domain containing 11	
0.038405	951.30585	1425.4102	NM_025349//XM_006511-1.50		<b>Lsm7</b>	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0000398 // mRNA splicing, via spliceosome // inferred from electronic annotation//0006396 // RNA processing // not recorded//0006397 // mRNA processing // infer
0.04941	310.8811	466.65048	NM_001145948//NM_001-1.50		<b>Ttc39a</b>	tetratricopeptide repeat domain 39A	
0.04723	457.8883	692.8698	NM_001160378//NM_001-1.51		<b>Fam46a</b>	family with sequence similarity 46, member A	0010468 // regulation of gene expression // not recorded//0030193 // regulation of blood coagulation // not recorded
0.044568	40.306248	61.026524		1.51	<b>A930007D18rik</b>	RIKEN cDNA A930007D18 gene	
0.038405	61.677505	63.433083	NM_009162	1.52	<b>Srg5</b>	secretogranin V	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from direct assay//0007218 // neuropeptide signalr
0.038405	260.5462	397.86157	XM_977361	1.53	<b>LOC65506//Tcrb</b>	T cell receptor beta-2 chain C region-like//T cell receptor beta, constant 2//T cell receptor beta, joining region//T cell receptor beta, variable 26	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.040334	428.5794	657.0457	NM_001114879//NM_001-1.53		<b>Fam208a</b>	family with sequence similarity 208, member A	0006779 // porphyrin-containing compound biosynthetic process // not recorded//0006810 // transport // not recorded//0007420 // brain development // not record
0.038405	306.48367	469.9942	NM_023732//XM_006491-1.53		<b>Acb6b</b>	ATP-binding cassette, sub-family B (MDR/TAP), member 6	0002082 // regulation of oxidative phosphorylation // inferred from mutant phenotype//0002082 // regulation of oxidative phosphorylation // not recorded//0034551
0.041949	1135.9435	1747.348	NM_028063//XM_006524-1.54		<b>Uqc2c</b>	ubiquinol-cytochrome c reductase complex assembly factor 2	0007368 // determination of left/right symmetry // inferred from mutant phenotype//0007507 // heart development // inferred from mutant phenotype
0.041949	53.28974	82.348274	NM_027725//XM_027636-1.55		<b>Daw1</b>	dynein assembly factor with WDR repeat domains 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic ann
0.049336	2274.0522	3525.3977	NM_170777	1.55	<b>Elof1</b>	elongation factor 1 homolog (ELF1, S. cerevisiae)	
0.049864	836.24603	1297.9843	NM_001037913//XM_000-1.55		<b>Ccdc107</b>	coiled-coil domain containing 107	
0.04941	711.8731	1107.1307	NM_021788	1.56	<b>Sap30</b>	sin3 associated polypeptide	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000183 // chromatin silencing at rDNA // traceable au
0.038405	170.08076	265.13123	NM_027829//XM_006514-1.56		<b>Izumo4</b>	IZUMO family member 4	
0.049864	103.268234	161.00058	NM_029801//XM_006500-1.56		<b>Tsac</b>	TSK6 activating co-chaperone	0045860 // positive regulation of protein kinase activity // not recorded//1904030 // negative regulation of cyclin-dependent protein kinase activity // ---
0.038405	267.83148	419.3986	NM_026633//XM_006524-1.57		<b>Fam195a</b>	family with sequence similarity 195, member A	
0.04941	272.86652	428.1105	NM_001164190//NM_001-1.57		<b>Mtm1</b>	X-linked myotubular myopathy gene 1	0006470 // protein dephosphorylation // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006810 // transport // inferred fr
0.038405	666.018	1062.4897	NM_009402	1.60	<b>Pglyrp1</b>	peptidoglycan recognition protein 1	0002221 // pattern recognition receptor signaling pathway // not recorded//0002376 // immune system process // inferred from electronic annotation//0006915 // a
0.038405	26.72522	42.908756		1.61	<b>C77805</b>	expressed sequence C77805	
0.038405	904.64264	1464.0131	NM_030677	1.62	<b>Gpx2</b>	glutathione peroxidase 2	0001659 // temperature homeostasis // inferred from genetic interaction//0002862 // negative regulation of inflammatory response to antigenic stimulus // inferred fr
0.04941	529.1728	873.3403	NM_001033261//XM_000-1.65		<b>Zfc3h1</b>	zinc finger, C3H1-type containing chemokine (C-X-C motif) ligand 2	0006396 // RNA processing // inferred from electronic annotation
0.038405	30.241604	50.01674	NM_009140	1.65	<b>Cxcl2</b>	chemokine (C-X-C motif) ligand 2	0001975 // response to amphetamine // inferred from electronic annotation//0002237 // response to molecule of bacterial origin // inferred from direct assay//00026
0.043007	228.67743	378.75113	NM_030075//XM_006511-1.66		<b>Klhdcb8</b>	kelch domain containing 8B	
0.04941	416.41345	697.16455	NM_001254761//NM_001-1.67		<b>Rnf128</b>	ring finger protein 128	0016567 // protein ubiquitination // inferred from direct assay//0016567 // protein ubiquitination // inferred from electronic annotation//0016567 // protein ubiquitin
0.038405	45.30973	75.9462	NM_001110506//NM_001-1.68		<b>Efcab12</b>	EF-hand calcium binding domain 12	
0.038405	19.481081	33.880554		1.74	<b>AU021001</b>	expressed sequence AU021001	
0.038405	311.3006	545.1864	NM_007931//XR_374059-1.75		<b>Endog</b>	endonuclease G	0001701 // in utero embryonic development // inferred from mutant phenotype//0006308 // DNA catabolic process // traceable author statement//0006309 // apopt
0.046461	47.03804	83.95114	NM_001164785//NM_001-1.78		<b>Adams20</b>	a disintegrin-like and metallopeptidase (repolyrin type) with thrombospondin type 1 motifs	0006508 // proteolysis // inferred from direct assay//0007229 // integrin-mediated signaling pathway // inferred from electronic annotation//0009967 // positive regu
0.038405	259.65488	464.33987	NM_133660//XM_006531-1.79		<b>Ces1e</b>	carboxylesterase 1E	0008152 // metabolic process // inferred from electronic annotation//0016042 // lipid catabolic process // ---

p [Corr]	[C3H/HeN, P56][raw]	[Gsr-KO, P56][raw]	RefSeq Transcript ID	FD @PND56	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.038405	108.183136	193.67982	XR_870188//XR_870189	1.79	<b>Gm29782</b>	predicted gene, 29782	
0.033755	807.6589	1450.5835	NR_045471//NR_130109	1.80	<b>Fendrr</b>	Foxf1 adjacent non-coding developmental regulatory RNA	0009791 // post-embryonic development // inferred from mutant phenotype//0031061 // negative regulation of histone methylation // inferred from mutant phenotyp
0.035203	152.70503	275.17526	NM_001081069	1.80	<b>Rgs11</b>	regulator of G-protein signaling 11	0007186 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal transduction // inferred from electri
0.026847	269.7194	510.2515	NM_013487//XM_006505	1.89	<b>Cd3d</b>	CD3 antigen, delta polypeptide	0006461 // protein complex assembly // non-traceable author statement//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//C
0.038405	151.41887	293.8693	NM_177290//XM_006516	1.94	<b>Irgb8</b>	integrin beta 8	0001573 // ganglioside metabolic process // inferred from mutant phenotype//0007155 // cell adhesion // inferred from electronic annotation//0007160 // cell-matrix
0.049711	1115.6477	2169.2866	NM_001290740//NM_01	1.94	<b>Cwc22//Xdh</b>	CWC22 spliceosome-associated protein homolog (S. cerevisiae)//>	0000398 // mRNA splicing, via spliceosome // not recorded//0001933 // negative regulation of protein phosphorylation // not recorded//0001937 // negative regulatic
0.04941	422.68167	846.8321	NM_001302559//NM_01	2.00	<b>Sjfn4//Sjfn3</b>	schlafen 4//schlafen 3	0008285 // negative regulation of cell proliferation // inferred from direct assay
0.022647	82.04181	172.38866	NM_001254953//XM_006	2.10	<b>Ankrd66</b>	ankyrin repeat domain 66	
0.038405	2049.9666	4665.2554	NM_001281830//NM_02	2.28	<b>Ijz712a</b>	interferon, alpha-inducible protein 27 like 2A	0007568 // aging // inferred from direct assay//0009615 // response to virus // inferred from direct assay
0.033755	455.56992	1119.032	NM_011315	2.46	<b>Saa3</b>	serum amyloid A 3	0006953 // acute-phase response // inferred from electronic annotation//0007252 // i-kappaB phosphorylation // inferred from direct assay//0035634 // response to s
0.023287	111.20848	277.16113	NM_001291131//NM_00	2.49	<b>Asgr1</b>	asialoglycoprotein receptor 1	0006897 // endocytosis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // not recorded//0031668 // cellular response to extracellu
0.030801	241.65337	618.6185	NM_144930//XR_387740	2.56	<b>Ces1f</b>	carboxylesterase 1F	0019626 // short-chain fatty acid catabolic process // inferred from direct assay