

Table S1. Lung genes (n=908) significantly different between wild-type (Gsr-WT) and glutathione reductase-deficient (Gsr-KO) mouse embryos at E19 (moderated t-test, p < 0.01).

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

[C3H/HeN][raw]	[Gsr-KO][raw]	p [Corr]	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
905.6041	27.324053	0.0090494	NM_029562//NM_006521	-32.87	Cyp2d26	cytochrome P450, family 2, subfamily d, polypeptide 26	0006805 // xenobiotic metabolic process // not recorded//0007565 // female pregnancy // inferred from electronic annotation//0019369 // arachidonic acid metabolic pr
1424.7395	53.878025	0.0089693	NM_001039555//NM_0061	-35.90	Cyp2c68	cytochrome P450, family 2, subfamily c, polypeptide 68	0006805 // xenobiotic metabolic process // not recorded//0019373 // epoxigenase P450 pathway // not recorded//0042738 // exogenous drug catabolic process // not re
2265.2947	103.28793	0.0020859	NM_175628//NM_011241	-21.63	A2m	alpha-2-macroglobulin	0001869 // negative regulation of complement activation, lectin pathway // not recorded//0007565 // female pregnancy // inferred from electronic annotation//0010466
556.89984	28.522108	0.0097449	NM_019775	-19.54	Cpb2	carboxypeptidase B2 (plasma)	0003311 // positive regulation of extracellular matrix constituent secretion // not recorded//0006508 // proteolysis // inferred from electronic annotation//0007596 // acute-phase respons
247.28	13.300347	0.0098942	NM_022884	-18.58	Bhmt2	betaine-homocysteine methyltransferase 2	0009086 // methionine biosynthetic process // not recorded//0003259 // methylation // inferred from electronic annotation//0055114 // 5-methylmethionine metabolic p
467.52148	25.764864	0.0089772	NM_001304800//NM_008	-18.34	Hsd3b1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	0006694 // steroid biosynthetic process // not recorded//0008152 // metabolic process // inferred from electronic annotation//0003477 // oxidation-reduction process //
445.74228	28.955765	0.0097449	NM_001277944//NM_001	-15.45	Apoc2//Apoc4-apoc2	apolipoprotein C-II//Apoc4-Apoc2 readthrough	0006629 // lipid metabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // infer
2766.6523	174.52327	0.0098942	NM_010168//NM_011239	-15.31	F2	coagulation factor II	0001934 // positive regulation of protein phosphorylation // not recorded//0006508 // proteolysis // inferred from electronic annotation//0006953 // acute-phase respons
218.12827	17.254292	0.0089693	NM_009244//NM_009247	-12.92	Serpina1b//Serpina1e	SERP (or cysteine) peptidase inhibitor, clade A, member 1B//serine (or cysteine) pe	0001701 // in utero embryonic development // inferred from mutant phenotype//0006487 // protein N-linked glycosylation // inferred from direct assay//0006953 // ac
167.1455	13.147254	0.0099958	NM_009467	-12.76	Ugt2b5	UDP glucuronosyltransferase 2 family, polypeptide B5	0008152 // metabolic process // inferred from electronic annotation//0009813 // flavonoid biosynthetic process // not recorded//0032870 // cellular response to hormone
140.85959	13.687359	0.0096679		-10.27	A195470	expressed sequence A195470	
515.03235	54.43274	0.008943	NM_133653//NM_006518	-9.57	Mst1a	methionine adenosyltransferase I, alpha	0006556 // s-adenosylmethionine biosynthetic process // not recorded//0006730 // one-carbon metabolic process // inferred from electronic annotation//0051260 // pro
203.04868	22.982317	0.009631	NM_007618	-8.96	Serpine6	serine (or cysteine) peptidase inhibitor, clade A, member 6	0006810 // transport // inferred from electronic annotation//0008211 // glucocorticoid metabolic process // inferred from mutant phenotype//0010951 // negative regula
399.35556	45.383698	0.0089693	NM_001109045//NM_007	-8.94	Ang8	angiotensinogen	0006810 // regulation of blood vessel size by renin-angiotensin // inferred from mutant phenotype//0006833 // water transport // inferred from mutant phenotype // not recorded
911.0561	105.31718	0.0096878	NM_008878	-8.59	Serpinf2	serine (or cysteine) peptidase inhibitor, clade F, member 2	0002034 // regulation of blood vessel size by renin-angiotensin // inferred from mutant phenotype//0006953 // acute-phase response // inferred from electronic annotation
654.0267	76.74889	0.0090057	NM_0118816	-8.42	Apom	apolipoprotein M	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation//0009749 // response to glucose // inferred
176.56389	21.89735	0.0085929	NM_001291131//NM_001	-8.14	Asgr1	asialoglycoprotein receptor 1	0006897 // endocytosis // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // not recorded//0031668 // cellular response to extracellular s
238.05107	30.172365	0.0067139	NM_008290//NM_006530	-7.98	Hsd17b2	hydroxy-steroid (17-beta) dehydrogenase 2	0001701 // in utero embryonic development // inferred from mutant phenotype//0001890 // placenta development // inferred from mutant phenotype//0006623 // lipid i
167.2239	21.232779	0.0017344	NM_205769	-7.76	Crh	corticotropin releasing hormone	0001934 // positive regulation of protein phosphorylation // not recorded//0001963 // synaptic transmission, dopaminergic // not recorded//0006704 // glucocorticoid bic
296.46375	39.088787	7.20E-05	NM_001111143	-7.60	Cym	chymosin	0006508 // proteolysis // not recorded//0030163 // protein catabolic process // not recorded
797.0761	116.83812	1.35E-05	NM_010344	-6.80	Gsr	glutathione reductase	0006749 // glutathione metabolic process // inferred by curator//0006749 // glutathione metabolic process // not recorded//0007283 // spermatogenesis // not recorded//
115.41196	18.958382	0.0095588	NM_010001	-6.08	Cyp2c37	cytochrome P450, family 2, subfamily c, polypeptide 37	0006805 // xenobiotic metabolic process // not recorded//0019373 // epoxigenase P450 pathway // not recorded//0042738 // exogenous drug catabolic process // not re
382.43787	65.28365	0.0089693	NM_032540//NM_006506	-5.93	Kel	cell blood group	0006508 // proteolysis // inferred from electronic annotation//0006874 // cellular calcium ion homeostasis // inferred from genetic interaction//0008361 // regulation of IC
278.97556	51.960957	0.0099126	NM_145146	-5.43	Afm	afamin	0006810 // transport // inferred from electronic annotation//0051180 // vitamin transport // not recorded
119.14806	41.986256	0.008832	NM_001012306//NM_001	-5.28	Hsd3b2//Hsd3b3//Hsd3b6	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2//hyd	0006694 // steroid biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0055114 // oxidatio
1808.1936	388.49655	0.0063393	NM_008469	-4.72	Krt15	keratin 15	0008779 // mitophagy in response to mitochondrial depolarization // not recorded
238.20706	51.728527	0.0094153	NM_008243//NM_006511	-4.64	Mst1	macrose stimulating 1 (hepatocyte growth factor-like)	0006508 // proteolysis // inferred from electronic annotation//0007283 // spermatogenesis // inferred from electronic annotation//0007566 // embryo implantation // inf
414.3533	102.813614	0.0075335	NM_001122683//NM_175	-4.40	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	0008152 // metabolic process // inferred from electronic annotation//0055114 // oxidation-reduction process // not recorded
540.4503	128.9482	0.008644	NM_008156//NM_011244	-4.22	Gpld1	glycosylphosphatidylinositol specific phospholipase D1	0001503 // ossification // inferred from expression pattern//0002042 // cell migration involved in sprouting angiogenesis // not recorded//0002062 // chondrocyte differer
14453.229	3323.1257	0.0081374	NM_001177544//NM_178	-4.20	Hist1h2aa//Hist1h2ap	histone cluster 1, H2a//histone cluster 1, H2ap	0006629 // chromatin organization // not recorded//0006342 // chromatin silencing // not recorded//0008285 // negative regulation of cell proliferation // not record
292.10898	70.59229	0.0085929	NM_001290011//NM_001	-4.15	Pemt	phosphatidylethanolamine N-methyltransferase	0006625 // lipid metabolic process // inferred from electronic annotation//0006644 // phospholipid metabolic process // inferred from electronic annotation//0006650 // i
309.9616	75.63072	0.009037	NM_133686	-4.13	Qprt	quinolate phosphoribosyltransferase	0009435 // NAD biosynthetic process // not recorded//0019363 // pyridine nucleotide biosynthetic process // inferred from electronic annotation//0034213 // quinolinate
127.1686	13.112123	0.0096679	NM_153193//NM_006501	-4.12	Hsd3b2//Hsd3b3//Hsd3b6	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2//hyd	0006694 // steroid biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0055114 // oxidatio
106.652466	27.08468	0.0068697	NM_008260	-4.00	Foxa3	forkhead box A3	0001678 // cellular glucose homeostasis // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
293.85028	74.839554	0.0090012	NM_030703//NM_011247	-3.98	Cpn1	carboxypeptidase N, polypeptide 1	0006508 // proteolysis // not recorded//0006518 // peptide metabolic process // --//0010815 // bradykinin-catabolic process // not recorded//0016485 // protein process
269.92487	75.49332	0.0089066	NM_009034	-3.59	Rbp2	retinol binding protein 2, cellular	0001523 // retinoid metabolic process // traceable author statement//0006776 // vitamin A metabolic process // inferred from electronic annotation//0006810 // transport
952.7804	282.42905	0.0017344	NM_001291128//NM_001	-3.44	Nnat	neuronal	0007275 // retinoid organismal development // inferred from electronic annotation//0007420 // brain development // inferred from electronic annotation//0009749 //
96.26743	28.237905	0.0090404	NM_138595	-3.44	Glic	glycine decarboxylase	0006520 // cellular amino acid metabolic process // inferred from electronic annotation//0006544 // glycine metabolic process // inferred from electronic annotation//000
188.70776	55.884327	0.0029632	NM_001480210//NM_0065	-3.43	BC005512//Gm29673//Gm	RIKEN cDNA BC005512//predicted gene, 29673//predicted gene 6958	
103.52489	21.22533	0.0099254	NM_001161355//NM_001	-3.35	Tmd2	T cell immunoglobulin and mucin domain containing 2	
113.84464	55.278667	0.0087842	NM_001305992//NM_008	-3.25	Ggt1	gamma-glutamyltransferase 1	0002682 // regulation of immune system process // inferred from mutant phenotype//0006508 // proteolysis // inferred from electronic annotation//0006536 // glutamat
558.37537	179.16898	0.0086932	NM_001217129//NM_009	-3.20	Tk1	thymidine kinase 1	0001889 // liver development // inferred from electronic annotation//0009157 // deoxyribonucleoside monophosphate biosynthetic process // inferred from direct assay//
1139.0332	361.4583	0.002626	NM_026515//NR_379450	-3.18	2810417H13R1K	RIKEN cDNA 2810417H13R1K gene	0006260 // DNA replication // not recorded//0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // not r
1181.2656	375.74295	0.0012309	NM_001252627//NM_001	-3.17	Cdh16	cadherin 16	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // DNA inferred from electronic
380.86133	119.52265	0.0080529	NM_019538//NM_006541	-3.16	Plac1	placental specific protein 1	0001890 // placenta development // inferred from expression pattern//0001890 // placenta development // inferred from electronic annotation//0007275 // multicelluar
1602.6293	508.9842	0.0086932	NM_001110251//NM_013	-3.15	Hmbs	hydroxymethylbilane synthase	0001666 // response to hypoxia // inferred from electronic annotation//0006779 // porphyrin-containing compound biosynthetic process // inferred from electronic annota
281.24805	88.69928	0.0058237	NM_001025779//NM_011	-3.14	Cdc6	cell division cycle 6	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from electronic annotation//0007049 // cell cycle // in
508.85938	176.28032	0.0080529	NM_0013548//NM_013550	-2.97	Hist1h3a//Hist1h3b//Hist1	histone cluster 1, H3a//histone cluster 1, H3b//histone cluster 1, H3c//histone cluster 1, H3d//histone cluster 1, H3e//histone cluster 1, H3f//histone cluster 1, H3g//histone cluster 1, H3i//histone cluster 1, H3j//histone cluster 1, H3k//histone cluster 1, H3l//histone cluster 1, H3m//histone cluster 1, H3n//histone cluster 1, H3o//histone cluster 1, H3p//histone cluster 1, H3q//histone cluster 1, H3r//histone cluster 1, H3s//histone cluster 1, H3t//histone cluster 1, H3u//histone cluster 1, H3v//histone cluster 1, H3w//histone cluster 1, H3x//histone cluster 1, H3y//histone cluster 1, H3z//histone cluster 1	
2075.968	715.2055	0.0051715	NM_008185//NM_006513	-2.88	Gstt1	glutathione S-transferase, theta 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000183 // chromatin silencing at rDNA // traceable author
141.70409	57.50415	0.0063203	NM_0082039	-2.81	Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	0006304 // DNA modification // not recorded//0006749 // glutathione metabolic process // inferred from direct assay//0006749 // glutathione metabolic process // infer
321.0904	116.72456	0.0076866	NM_011976//NR_386476	-2.76	Sema04g	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short	0001755 // neural crest cell migration // not recorded//0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous syst
1009.33734	378.059	0.0046248	NM_001012272//NM_001	-2.69	Birc5	baculoviral IAP repeat-containing 5	0000086 // G2/M transition of mitotic cell cycle // not recorded//0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype//0000910 // cytoki
485.58954	180.9112	0.0087842	NM_008698//NM_006514	-2.68	Nipsnap1	4-nitrophenylphosphate domain and non-neuronal SNAP25-like protein homolog 1	0019233 // sensory perception of pain // inferred from mutant phenotype
747.8198	282.82642	0.003657	NM_001302540//NM_008	-2.66	Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation//0006270 // DNA replication initiation // inferred from electronic annotation//0007049 // cell cycle // in
546.5247	216.97443	0.0065464	NM_009903	-2.61	Cldn4	claudin 4	0007565 // female pregnancy // inferred from electronic annotation//0007623 // circadian rhythm // inferred from electronic annotation//0016338 // calcium-indepen
104.69458	40.579697	0.0089567	NM_001033264//NM_001	-2.61	Gls2	glutaminase 2 (liver, mitochondrial)	0006537 // L-serine biosynthetic process // not recorded//0006541 // glutamine metabolic process // inferred from electronic annotation//0006543 // glutamine catabo
3438.888	1293.1224	0.0075737	NM_001081117//NM_006	-2.59	Mki67	antigen identified by monoclonal antibody Ki 67	0006259 // DNA metabolic process // inferred from electronic annotation//0007126 // meiotic nuclear division // inferred from direct assay//0000283 // cell proliferation /
617.7388	238.86847	0.0089693	NM_016966//NR_076393	-2.58	Gm6756//Phgdh	3-phosphoglycerate dehydrogenase pseudogene //3-phosphoglycerate dehydrogena	0006541 // glutamine metabolic process // inferred from mutant phenotype//0006544 // glycine metabolic process // inferred from mutant phenotype//0006563 // L-seri
314.12036	125.28604	0.0063393	NM_172505//NM_198652	-2.56	6430706D22R1K//A730008H	RIKEN cDNA 6430706D22 gene//RIKEN cDNA A730008H23 gene//Holliday junction	0007049 // cell cycle // inferred from electronic annotation//0007059 // chromosome segregation // not recorded//0034080 // CENP-A containing nucleosome assembly //
154.00896	60.946278	0.0084703	NM_133995	-2.55	Ubp1	ureidopropionase, beta	0001889 // liver development // not recorded//0006807 // nitrogen compound metabolic process // inferred from mutant phenotype//0008152 // metabolic process //
65.52462	25.925991	0.0048754	NM_021886//NM_006517	-2.55	Cenph	centromere protein H	0007059 // chromosome segregation // not recorded//0007067 // mitotic nuclear division // not recorded//0051382 // kinetochore assembly // inferred from electronic a
508.1461	201.18913	0.0040953	NM_00111078//NM_001	-2.52	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA p
371.50165	148.30985	0.002626	NM_011496//NM_006532	-2.52	Aurkb	aurora kinase B	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0002903 // negative regulation of B cell apoptotic process // not record
1818.8318	277.27985	0.0076944	NM_009104	-2.50	Rrm2	ribonucleotide reductase 2	0006260 // DNA replication // inferred from electronic annotation//0009186 // deoxyribonucleoside diphosphate metabolic process // inferred from electronic annotation//
392.26077	159.18124	0.0035996	NM_178683//NM_006517	-2.50	Depdc1b	DEP domain containing 1B	0007165 // signal transduction // inferred from electronic annotation//0016477 // cell migration // not recorded//0030177 // positive regulation of Wnt signaling pathway
279.2767	113.36384	0.008644	NM_013548//NM_145073	-2.49	Hist1h3a//Hist1h3f//Hist1h	histone cluster 1, H3a//histone cluster 1, H3f//histone cluster 1, H3g//histone cluster 1, H3h//histone cluster 1, H3i//histone cluster 1, H3j//histone cluster 1, H3k//histone cluster 1, H3l//histone cluster 1, H3m//histone cluster 1, H3n//histone cluster 1, H3o//histone cluster 1, H3p//histone cluster 1, H3q//histone cluster 1, H3r//histone cluster 1, H3s//histone cluster 1, H3t//histone cluster 1, H3u//histone cluster 1, H3v//histone cluster 1, H3w//histone cluster 1, H3x//histone cluster 1, H3y//histone cluster 1, H3z//histone cluster 1	
179.56654	71.97339	0.0017344	NM_007634//NM_006523	-2.49	Cnrf	cyclin F	0000183 // chromatin silencing at rDNA // traceable author statement//0002230 // positive regulation of defense response to virus by host // not recorded//0006334 // nu
2582.6367	1037.7747	0.0057447	NM_0118187	-2.49	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	0000320 // re-entry into mitotic cell cycle // inferred from mutant phenotype//0001890 // placenta development // inferred from mutant phenotype//0007049 // cell cycle
1772.6205	714.39276	0.004449	NM_001205339//NM_177	-2.47	Psat1	phosphoserine aminotransferase 1	0000185 // activation of MAPKKK activity // not recorded//0000186 // activation of MAPKK activity // inferred from direct assay//0006465 // negative regulation of protein
607.43964	254.67839	0.0098942	NM_001302139//NM_001	-2.44	Cenpa	centromere protein A	0006564 // L-serine biosynthetic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0008652 // cellular
1361.0616	560.9477	0.0046722	NM_009828	-2.44	Cnna2	cyclin A2	0000132 // establishment of mitotic spindle orientation // not recorded//0051382 // kinetochore assembly // not recorded//0071459 // protein localization to chromosom
288.41794	120.441124	0.0083164	NM_178203//NM_178206	-2.42	Hist1h3b//Hist1h3h//Hist1h	histone cluster 1, H3b//histone cluster 1, H3h//histone cluster	

[C3H/HeN][raw]	[Gsr-KO][raw]	p [Corr]	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
1079.798	600.12305	0.0071653	NM_010721	-1.82	Lmnb1	lamin B1	0031662 // positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle // non-traceable author statement
244.46936	132.68498	0.0097449	NM_011234	-1.82	Rad51	RAD51 homolog	0000724 // double-strand break repair via homologous recombination // inferred from direct assay // 0000724 // double-strand break repair via homologous recombination, 0000728 // mitotic cell cycle // not recorded // 0007018 // microtubule-based movement // not recorded // 0007049 // cell cycle // inferred from electronic annotation // 0007015 // actin filament organization // not recorded // 0007264 // microtubule signal transduction // inferred from electronic annotation
325.85416	177.58089	0.0083164	NM_173762	-1.82	Cenpe	centromere protein E	
280.84192	156.38338	0.0030958	NM_175092	-1.81	Rhof	ras homolog gene family, member f	
141.25345	77.62626	0.0056196	NM_001310502 // NM_172	-1.81	Ankle1	ankyrin repeat and LEM domain containing 1	
266.02588	144.89935	0.008644	NM_008644 // NM_0112466	-1.81	Sgol1	shogunin-like 1 (S. pombe)	0007049 // cell cycle // inferred from electronic annotation // 0007059 // chromosome segregation // not recorded // 0007067 // mitotic nuclear division // inferred from electronic annotation // 0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0006821 // chloride transport // inferred from electronic annotation // 0003070 // heart morphogenesis // traceable author statement // 0007165 // signal transduction // inferred from direct assay // 0007204 // positive regulation of cytosolic c // 0006470 // protein dephosphorylation // not recorded // 0007049 // cell cycle // inferred from electronic annotation // 00016311 // dephosphorylation // -- // 00023052 // sig // 0030041 // actin filament polymerization // inferred from mutant phenotype // 0030041 // actin filament polymerization // not recorded // 0031175 // neuron projection development // 0007018 // microtubule-based movement // not recorded // 0007019 // cell cycle // inferred from electronic annotation // 0000700 // mitotic sister chromatid segregation // not recorded // 0007013 // microtubule depolymerization // not recorded // 0007049 // cell cycle // inferred from electronic annotation // 0000700 // mitotic sister chromatid segregation // not recorded // 0001032 // establishment of mitotic spindle orientation // not recorded // 0007049 // cell cycle // inferred from electronic annotation // 0042168 // heme metabolic process // inferred by curator
2471.4858	1356.2666	0.0093457	NM_0135446 // NM_0112411	-1.79	Hebp1	heme binding protein 1	0042552 // myelination // not recorded // 15902043 // positive regulation of extrinsic apoptotic signaling pathway via death domain receptors // inferred from direct assay
2314.4055	1279.117	0.0042446	NM_001171187 // NM_010	-1.78	Mpl	myelin and lymphocyte protein, T cell differentiation protein	0006915 // apoptotic process // inferred from electronic annotation // 0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // in
238.49878	133.22519	0.0065811	NM_001141975 // NM_001	-1.78	Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // inferred from direct assay // 0001836 // release of cytochrome c from mitochondria // r
110.138535	61.08116	0.0090044	NM_018754	-1.78	Sfn	stratfin	0000070 // mitotic sister chromatid segregation // inferred from mutant phenotype // 0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear
663.7102	382.0576	0.0087756	NM_019499 // NM_006506	-1.76	Msd21l	MAD2 mitotic arrest deficient-like 1	0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // inferred from electronic annotation // 00051301 // cell division // inferred
75.18874	42.93687	0.0084703	NM_001042653 // NM_011	-1.76	LOC100862416 // LOC100862	protein Mts18-beta-like // Opa interacting protein 5	0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // inferred from electronic annotation // 0007088 // regulation of mitotic n
214.85017	122.0136	0.002626	NM_175265 // NM_006519	-1.76	Bora	bora, aurora kinase A activator	0000070 // mitotic sister chromatid segregation // not recorded // 0000278 // mitotic cell cycle // not recorded // 0007018 // microtubule-based movement // not recorded //
289.10873	162.40288	0.0063393	NM_197959 // NM_011249	-1.75	Kif18b	kinessin family member 18B	0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
89.550385	15.170246	0.0093601	NM_008652 // NM_006498	-1.75	Mybl2	myeloblastosis oncogene-like 2	0000380 // alternative mRNA splicing, via spliceosome // inferred from direct assay // 0006397 // mRNA processing // inferred from electronic annotation // 0006810 // trans
3723.599	2118.052	0.0085929	NM_001039129 // NM_001	-1.75	Gm10052 // Gm5803 // Hnmrg	heterogeneous nuclear ribonucleoprotein A1 pseudogene // predicted gene 5803 // h	
189.54427	108.06164	0.0085929	NM_001162998	-1.74	Smm16	small integral membrane protein 6	
1744.2056	1007.732	0.0066692	NM_008969 // NM_006497	-1.74	Ptgs1	prostaglandin-endoperoxide synthase 1	0001516 // prostaglandin biosynthetic process // inferred from mutant phenotype // 0001516 // prostaglandin biosynthetic process // not recorded // 0006629 // lipid metabol
321.54047	185.32677	0.0068697	NM_001163763 // NM_001	-1.72	Tcf19	transcription factor 19	
373.47095	219.88608	0.0085912	NM_001081062	-1.72	Ccno	cyclin O	
1369.9546	801.1917	0.0068707	NM_0023223	-1.72	Cdc20	cell division cycle 20	0006284 // base-excision repair // not recorded // 0007049 // cell cycle // not recorded // 0030030 // cell projection organization // inferred from electronic annotation // 000
405.17148	241.57718	0.0068697	NM_0097238 // NM_138	-1.71	Aldh7a1	aldehyde dehydrogenase family 7, member A1	0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division // inferred from electronic annotation // 0007399 // nervous system develop
121.321014	100.065291	0.0056291	NM_0009764 // NM_006532	-1.71	Brcs1	breast cancer 1, early onset	0008152 // metabolic process // inferred from electronic annotation // 0019285 // glycine betaine biosynthetic process from choline // inferred from electronic annotation // 000
198.91296	114.78199	0.0084641	NM_001110265 // NM_001	-1.71	Ttk	Ttk protein kinase	0000724 // double-strand break repair via homologous recombination // not recorded // 0006260 // DNA replication // inferred from mutant phenotype // 0006281 // DNA r
197.26901	114.24718	0.0063393	NM_001081407 // NM_030	-1.71	Plb1	phospholipase B1	0006468 // protein phosphorylation // inferred from electronic annotation // 0007093 // mitotic cell cycle checkpoint // inferred from electronic annotation // 00016310 // ph
1097.7009	649.7863	0.0063393	NM_0027324 // NM_006516	-1.71	Sfkn1	sideroflexin 1	0006629 // lipid metabolic process // inferred from electronic annotation // 0006644 // phospholipid metabolic process // not recorded // 0016042 // lipid catabolic process, s
3455.324	1978.3197	0.0065291	NM_016904	-1.71	Cks1b	CDC28 protein kinase 1b	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0006826 // iron ion transport // inferred fro
1097.9629	652.45746	0.0089693	NM_009103	-1.70	Rrm1	ribonucleotide reductase M1	0007049 // cell cycle // inferred from electronic annotation // 00045859 // regulation of protein kinase activity // inferred from electronic annotation // 00051301 // cell division
154.63812	91.652245	0.0087842	NM_0197777 // NM_006529	-1.70	Ikbe	inhibitor of kappaB kinase epsilon1	000278 // mitotic cell cycle // inferred from electronic annotation // 0006206 // pyrimidine nucleobase metabolic process // inferred from electronic annotation // 0000260
126.2824	74.05487	0.0085929	NM_009434 // NM_006508	-1.69	Phlda2	pleckstrin homology-like domain, family A, member 2	0006468 // protein phosphorylation // not recorded // 0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation // 0007252 // h-kappa p1
897.0389	538.2648	0.004422	NM_134022	-1.69	633040307Rik	RIKEN cDNA 633040307 gene	0001890 // placenta development // inferred from direct assay // 0009887 // organ morphogenesis // inferred from mutant phenotype // 0010468 // regulation of gene expr
599.1347	326.11835	0.0075984	NM_001310659 // NM_008	-1.68	Igfbp2	insulin-like growth factor binding protein 2	0001558 // regulation of cell growth // inferred from electronic annotation // 0007165 // signal transduction // inferred from electronic annotation // 0007565 // female preg
91.67897	54.652256	0.0080529	NM_012012 // NM_006496	-1.67	Exo1	exonuclease 1	0002376 // immune system process // inferred from electronic annotation // 0002455 // humoral immune response mediated by circulating immunoglobulin // inferred from
347.5209	209.89442	0.0066381	NM_008446 // NM_006527	-1.67	Kif4	kinessin family member 4	0000281 // mitotic cytokinesis // not recorded // 0007018 // microtubule-based movement // not recorded // 0008152 // metabolic process // inferred from electronic anno
1016.0242	618.9151	0.0097017	NM_025912 // NM_006500	-1.67	Fam210b	family with sequence similarity 210, member B	
200.88041	145.02652	0.0071653	NM_011132	-1.66	Pole	polymerase (DNA directed), epsilon	0000082 // G1/S transition of mitotic cell cycle // not recorded // 0000731 // DNA synthesis involved in DNA repair // not recorded // 0001701 // in utero embryonic develop
163.5017	97.06772	0.0063393	NM_013542	-1.66	Gzmb	granzyme B	0001913 // T cell mediated cytotoxicity // inferred from mutant phenotype // 0006508 // proteolysis // inferred from electronic annotation // 0006915 // apoptotic process, DN
934.4133	574.4162	0.006796	NM_176838 // NM_006531	-1.65	Esrp2	epithelial splicing regulated protein 2	0006397 // mRNA processing // inferred from electronic annotation // 0008380 // RNA splicing // inferred from electronic annotation // 00043484 // regulation of RNA splicing
399.2814	247.41849	0.0069718	NM_138653 // NM_006537	-1.65	Bspry	B-box and SPRY domain containing	0006810 // transport // inferred from electronic annotation // 0006811 // ion transport // inferred from electronic annotation // 0006816 // calcium ion transport // inferre
626.9157	389.03702	0.0090404	NM_001159646 // NM_023	-1.64	Dut	deoxyuridine triphosphatase	0006226 // dUMP biosynthetic process // not recorded // 0043497 // regulation of protein heterodimerization activity // not recorded // 0046080 // dUTP metabolic process
272.6889	166.64886	0.0065754	NM_007633	-1.63	Ccne1	cyclin E1	0000082 // G1/S transition of mitotic cell cycle // inferred from electronic annotation // 0001547 // antral ovarian follicle growth // inferred from electronic annotation // 000
1442.2517	886.77435	0.004326	NM_001289724 // NM_001	-1.63	Silp	stem-loop binding protein	0006397 // mRNA processing // inferred from electronic annotation // 0006398 // mRNA 3'-end processing by stem-loop binding and cleavage // inferred from direct assay //,
681.90967	423.89102	0.0055381	NM_198937	-1.63	Hn1l	hematological and neurological expressed 1-like	
81.28702	49.95855	0.0068697	NM_029249 // NM_006514	-1.63	Parpbbp	PARP1 binding protein	0006281 // DNA repair // inferred from electronic annotation // 0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation // 2000042 // m
158.24734	96.889694	0.0046248	NM_001110162 // NM_175	-1.62	Cdca2	cell division cycle associated 2	0007049 // cell cycle // inferred from electronic annotation // 0007059 // chromosome segregation // inferred from direct assay // 0007067 // mitotic nuclear division // infc
121.6674	75.24433	0.0068697	NM_183064 // NM_006527	-1.61	Kif20b	kinessin family member 20B	0001843 // neural tube closure // inferred from mutant phenotype // 0007018 // microtubule-based movement // inferred from electronic annotation // 0007049 // cell cycl
75.92991	47.093437	0.0066692	NM_001122958 // NM_001	-1.61	Rad54l	RAD54 like (S. cerevisiae)	0000724 // double-strand break repair via homologous recombination // inferred from genetic interaction // 0000724 // double-strand break repair via homologous recomb
344.59515	216.81549	0.0065754	NM_024257	-1.61	Hdh3	haloacid dehalogenase-like hydrolase domain containing 3	0008152 // metabolic process // inferred from electronic annotation
100.83858	62.93387	0.0063393	NM_201364 // NM_006496	-1.60	BC055324	cDNA sequence BC055324	
317.17	199.7879	0.0084354	NM_181589 // NM_006500	-1.59	Kcap2l	cytoskeleton associated protein 2-like	
203.13467	126.308655	0.0080529	NM_001163495 // NM_027	-1.59	Arhgap19	Rho GTPase activating protein 19	0007165 // signal transduction // inferred from electronic annotation // 0043547 // positive regulation of GTPase activity // inferred from electronic annotation
1103.5352	702.88635	0.0086932	NM_134081	-1.59	Dnajc9	Dnaj (Hsp40) homolog, subfamily C, member 9	0032781 // positive regulation of ATPase activity // not recorded // 0035176 // social behavior // inferred from electronic annotation
63.379673	203.8792	0.0046248	NM_001163766 // NM_134	-1.59	Wdr90	WD repeat domain 90	
63.379288	39.879528	0.0096878	NM_01311124 // NM_001	-1.59	Celf5	CUGBP, Elav-like family member 5	
671.19885	429.11035	0.0079038	NM_024184	-1.59	Asf1b	anti-silencing function 1B histone chaperone	0006333 // chromatin assembly or disassembly // inferred from electronic annotation // 0006334 // nucleosome assembly // inferred from direct assay // 0006335 // DNA re
645.78125	413.081	0.0089693	NM_011950	-1.59	Mapk13	mitogen-activated protein kinase 13	0000165 // MAPK cascade // not recorded // 0006351 // transcription, DNA-templated // inferred from electronic annotation // 0006355 // regulation of transcription, DNA-1
759.81165	487.55862	0.0085589	NM_026384	-1.59	Dgat2	diacylglycerol O-acyltransferase 2	0006071 // glycerol metabolic process // inferred from electronic annotation // 0006629 // lipid metabolic process // inferred from electronic annotation // 0010867 // positi
2548.035	1558.9877	0.0087791	NM_172543 // NM_006532	-1.57	Fam117a	family with sequence similarity 117, member A	
1813.1226	1152.7639	0.0098452	NM_011358 // NM_006532	-1.57	Srsf2	serine/arginine-rich splicing factor 2	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from direct assay // 0006397 // mRNA processing // inferred from electronic annotation // 000
892.33356	575.13965	0.0090944	NM_026598	-1.57	Ebp1	emopamil binding protein-like	0016125 // steroid metabolic process // inferred from electronic annotation
256.2794	163.40034	0.0065464	NM_019487	-1.57	Hebp2	heme binding protein 2	0010917 // negative regulation of mitochondrial membrane potential // not recorded // 0010940 // positive regulation of necrotic cell death // not recorded // 0025794 // pc
222.41306	141.4752	0.0068697	NM_026412 // NM_006499	-1.56	Knstrn	kinetochore-localized astrin/SPAG5 binding	0000070 // mitotic sister chromatid segregation // not recorded // 0007049 // cell cycle // inferred from electronic annotation // 0007051 // spindle organization // not rec
61.122593	39.136593	0.0075124	NM_183287 // NM_006522	-1.56	2610318N02Rik	RIKEN cDNA 2610318N02 gene	
23.524618	14.733796	0.0084703	NM_001162954 // NM_011	-1.56	Gm8267	predicted gene 8267	
25.98156	16.873371	0.0096878	NM_01034882	-1.55	Kbtbd6	kelch repeat and BTB (POZ) domain containing 6	0016567 // protein ubiquitination // not recorded
70.1359	50.64932	0.003657	NM_146218 // NM_006530	-1.55	Rfwd3	ring finger and WD repeat domain 3	0002230 // positive regulation of defense response to virus by host // not recorded // 0006281 // DNA repair // inferred from electronic annotation // 0006974 // cellular res
262.974	168.92628	0.0097449	NM_009773 // NM_006498	-1.55	Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	0006468 // protein phosphorylation // inferred from electronic annotation // 0006915 // apoptotic process // inferred from electronic annotation // 0007049 // cell cycle // h
195.14597	123.61147	0.0071653	NM_001190161 // NM_019	-1.55	Psrc1	perlecan/serine-rich collod-coll 1	0001578 // microtubule bundle formation // inferred from direct assay // 0007049 // cell cycle // inferred from electronic annotation // 0007067 // mitotic nuclear division //
1528.5718	997.962	0.0051715	NM_001035226 // NM_134	-1.54	Xpo1	exportin 1, CRM1 homolog (yeast)	0000055 // ribosomal large subunit export from nucleus // not recorded // 0000056 // ribosomal small subunit export from nucleus // not recorded // 0000122 // negative re
2498.0105	1610.6658	0.0075048	NM_001039129 // NM_001	-1.54	Gm10052 // Gm5803 // Hnmrg	heterogeneous nuclear ribonucleoprotein A1 pseudogene // predicted gene 5803 // h	
113.88868	73.41951	0.0085208	NM_007263	-1.54	Apd1t	apoptosis-inducing, TAF9-like domain 1	0000712 // resolution of meiotic recombination intermediates // inferred from sequence or structural similarity // 0000712 // resolution of meiotic recombination intermed
260.19714	171.23952	0.0059002	NM_009951	-1.54	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	0006403 // RNA localization // not recorded // 0006417 // regulation of translation // inferred from electronic annotation // 0006810 // transport // inferred from electronic
487.11728	320.79062	0.0085929	NM_153783 // NM_006536	-1.54	Paox	polyamine oxidase (exo-N4-amino)	0006598 // polyamine catabolic process // inferred from direct assay // 0006598 // polyamine catabolic process // not recorded // 0008215 // spermine metabolic process //
85.46114	55.791164	0.0051039	NM_175563	-1.52	Prr11	proline rich 11	0051726 // regulation of cell cycle // not recorded
762.26917	509.4285	0.0084641	NM_025649	-1.52	Mad211bp	MAD2L1 binding protein	0007093 // mitotic cell cycle checkpoint // not recorded // 0007094 // mitotic spindle assembly checkpoint // not recorded // 0007096 // regulation of exit from mitosis // no
34.702877	22.945415	0.0071292	NM_024720	-1.52	2700099C18Rik	NDC80 homolog, kinetochore complex component pseudogene	
2016.1809	1315.6638	0.0070902	NM_025968 // NM_011250	-1.51	Ptgr1	prostaglandin reductase 1	0006693 // prostaglandin metabolic process // inferred from electronic annotation // 0009636 // response to toxic substance // inferred from electronic annotation // 000551
117.59393	77.464584	0.0087842	NM_019670 // NM_006519	-1.51	Diaph3	diaphanous-related formin 3	0007283 // spermatogenesis // inferred from electronic annotation // 0016043 // cellular component organization //

[C3H/HeN][raw]	[Gsr-KO][raw]	p [Corr]	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
841.2377	568.9676	0.008466	NM_010516	-1.50	Cyr61	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation//0001649 // osteoblast differentiation // inferred from genetic interaction//0001934 // positive
39.233936	26.668457	0.008644	NM_001039154//NM_001-1.50		Cdh8	cadherin 8	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from electronic
242.73042	162.77852	0.0080529	NM_010892//NM_006497:-1.49		Nek2	NIMA (Never in mitosis gene a)-related expressed kinase 2	0000070 // mitotic sister chromatid segregation // inferred from mutant phenotype//0001824 // blastocyst development // inferred from mutant phenotype//0006468 //
382.83978	261.87766	0.0089693	NM_0028354//NM_006515:-1.49		Tdp1	tyrosyl-DNA phosphodiesterase 1	0000012 // single strand break repair // inferred from mutant phenotype//0000012 // single strand break repair // not recorded//0006281 // DNA repair // inferred from r
118.30512	79.17589	0.0097449	NM_172520//NM_006538:-1.48		Arhgef19	Rho guanine nucleotide exchange factor (GEF) 19	0032956 // regulation of actin cytoskeleton organization // not recorded//0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation//
329.81055	227.59697	0.0094249	NM_001163633//NM_001-1.48		Wnt7b	wingless-type NMMTV integration site family, member 7B	0001525 // angiogenesis // inferred from genetic interaction//0001525 // inferred from mutant phenotype//0001701 // in utero embryonic development //
726.72424	499.79703	0.0084423	NM_001289524//NM_001-1.48		Lrrcd4	leucine rich repeat containing 4	
2794.6465	1870.1539	0.0070902	NM_009698	-1.47	Aprt	adenine phosphoribosyl transferase	0006166 // purine ribonucleoside salvage // inferred from genetic interaction//0006166 // purine ribonucleoside salvage // inferred from mutant phenotype//0006168 // a
567.54504	390.1537	0.0051094	NM_0026908//NM_006519:-1.47		Cab39l	calcium binding protein 39-like	
365.44797	250.73454	0.0084055	NM_0263003//NM_006509:-1.47		Alkbh8	alkB, alkylation repair homolog 8 (E. coli)	
818.74744	567.2709	0.0079038	NM_001190711//NM_013-1.47		Dbp4	DBF4 homolog (S. cerevisiae)	0002098 // tRNA wobble uridine modification // inferred from direct assay//0002098 // tRNA wobble uridine modification // not recorded//0006974 // cellular response to
45.819626	31.684292	0.0099354	NM_0273663//NM_0112411:-1.46		Chp2	calcineurin-like EF hand protein 2	0006260 // DNA replication // inferred from electronic annotation//0006468 // protein phosphorylation // --//0007049 // cell cycle // inferred from electronic annotation//
200.00963	136.01129	0.0064729	NM_016662//XR_873434-1.46		Mxd3	MAX dimerization protein 3	0006810 // transport // inferred from electronic annotation//0006814 // sodium ion transport // not recorded//0006885 // regulation of pH // not recorded//0008284 //
461.896	322.12955	0.0066908	NM_146013//NM_006514:-1.46		Sec14a	SEC14-like lipid binding 4	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
65.65217	45.232828	0.0065276	NM_033603	-1.46	Ann	anninoseless	0006810 // transport // inferred from electronic annotation
4909.1685	3253.606	0.0083164	NM_001161624//NM_009-1.46		Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0001501 // skeletal system development // inferred d
1072.6212	747.982	0.0066692	NM_025433	-1.45	Rpl71	ribosomal protein L71-like 1	0000463 // maturation of LSU-rRNA from tritricotronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) // --//0001825 // blastocyst formation // inferred from mutant phen
184.24342	126.50013	0.0085533	NM_001168356//NM_134-1.45		Bnip1	BCL2/adenovirus E1B 19kD interacting protein like N-methylpurine-DNA glycosylase	0006915 // apoptotic process // not recorded//0008285 // negative regulation of cell proliferation // not recorded//0004009 // regulation of growth rate // not rec
198.97799	138.8105	0.0088935	NM_0108821//NM_006514:-1.44		Mpg	N-methylpurine-DNA glycosylase	0003281 // ventricular septum development // inferred from mutant phenotype//0006281 // DNA repair // inferred from electronic annotation//0006284 // base-excision
3658.6804	2501.2078	0.0096782	NM_001164609//NM_001-1.44		Gm15453//Rbm3	predicted gene 15453//RNA binding motif protein 3	0006412 // translation // inferred from direct assay//0006417 // regulation of translation // inferred from direct assay//0009409 // response to cold // inferred from direct
39.6612	279.79776	0.007891	NM_001114045//NM_001-1.44		Nde1	nuclear distribution gene E homolog 1 (A nidulans)	0000132 // establishment of mitotic spindle orientation // not recorded//0001764 // neuron migration // inferred from mutant phenotype//0007020 // microtubule nuclea
65.56716	45.494156	0.0084073	NM_058214//NM_006521:-1.44		Recq4	RecQ protein-like 4	0000733 // DNA strand renaturation // not recorded//0001501 // skeletal system development // inferred from mutant phenotype//0006260 // DNA replication // not rec
63.784115	44.54083	0.0098942	NM_0027664//NM_0112411:-1.44		Rimkb	RECQ modification protein rimk-like family member B	0006464 // cellular protein modification process // inferred from electronic annotation
2562.9326	1751.9767	0.0066754	NM_001078167//NM_173-1.43		Srsf1	serine/arginine-rich splicing factor 1	0000380 // alternative mRNA splicing, via spliceosome // not recorded//0000395 // mRNA 5'-splice site recognition // not recorded//0001701 // in utero embryonic develo
131.15442	225.59178	0.0090494	NM_007658//NM_006511:-1.43		Cdc25a	cell division cycle 25A	0000082 // G1/S transition of mitotic cell cycle // not recorded//0000087 // mitotic M phase // inferred from electronic annotation//0006470 // protein dephosphorylation
3946.533	2687.9207	0.0082244	NM_0106655	-1.43	Kpna2	karyopherin (importin) alpha 2	0006606 // protein import into nucleus // inferred from direct assay//0006607 // NLS-bearing protein import into nucleus // not recorded//0006810 // transport // inferre
1170.7817	828.69446	0.0095304	NM_0011570//NM_207176-1.43		Tes	testis derived transcript	0008285 // negative regulation of cell proliferation // not recorded//0042127 // regulation of cell proliferation // inferred from electronic annotation
103.7571	71.90184	0.0076866	NM_001039556//NM_001-1.43		Rad54b//Fsbp	RAD54 homolog B (S. cerevisiae)//fibrinogen silencer binding protein	0000724 // double-strand break repair via homologous recombination // inferred from genetic interaction//0000724 // double-strand break repair via homologous recomb
857.1333	613.53284	0.0089358	NM_026374	-1.42	Ifi2	interleukin enhancer binding factor 2	0006351 // transcription, DNA-templated // not recorded//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006955 // imm
397.5968	283.0752	0.0051039	NM_172746//NM_006507:-1.42		Hirp3	HIRA interacting protein 3	
1083.3943	774.55927	0.0088565	NM_001080129//NM_001-1.42		Tmpo	thymopoeitin	0006355 // regulation of transcription, DNA-templated // inferred from direct assay
180.46896	126.1987	0.0068697	NM_146151//NM_006503:-1.42		Testk2	testis-specific kinase 2	0006468 // protein phosphorylation // not recorded//0007283 // spermatogenesis // inferred from sequence or structural similarity//0007283 // spermatogenesis // infern
199.74016	142.12122	0.0097983	NM_001291105//NM_007-1.41		Ezf1	E2F transcription factor 1	0000077 // DNA damage checkpoint // not recorded//0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // trans
7045.2046	482.664	0.0090404	NM_001166409//NM_001-1.41		Gm15453//Rbm3	predicted gene 15453//RNA binding motif protein 3	0006412 // translation // inferred from direct assay//0006417 // regulation of translation // inferred from direct assay//0009409 // response to cold // inferred from direct
112.97382	80.01478	0.0070836	NM_172453//NM_006510:-1.40		Pif1	Pif1 5'-to-3' DNA helicase homolog (S. cerevisiae)	0000002 // mitochondrial genome maintenance // inferred from electronic annotation//0000002 // mitochondrial genome maintenance // --//0000723 // telomere maint
144.20753	102.839	0.0095304	NM_028115//NM_029839,-1.40		Trub1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	0001522 // pseudouridine synthesis // inferred from electronic annotation//0006396 // RNA processing // inferred from electronic annotation//0006400 // tRNA modificat
995.60706	727.18274	0.0086932	NM_001003898//NM_001-1.39		Tardbp	TAR DNA binding protein	0001933 // negative regulation of protein phosphorylation // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // r
282.16516	203.95131	0.0071624	NM_1980919//NM_006526:-1.39		Cep78	centrosomal protein 78	0007051 // spindle organization // not recorded
50.60283	36.64795	0.0091486	NM_001081099	-1.39	Aurip	aurora kinase A and ninein interacting protein	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006012 // galactose metabolic process // inferred from direct assay//0019388 // gala
375.6049	274.1132	0.0083164	NM_178389//NM_006539:-1.39		Gole	galactose-4-epimerase, UDP	0000216 // microtubule cytoskeleton organization // inferred from mutant phenotype//0003382 // epithelial cell morphogenesis // inferred from mutant phenotype//0008
285.11655	208.1093	0.0096908	NM_001037711//NM_001-1.39		Cgn	cingulin	0007019 // microtubule depolymerization // not recorded//0007052 // mitotic spindle organization // not recorded//0007275 // multicellular organismal developme
4312.385	3039.4275	0.0065291	NM_019641	-1.39	Stmn1	stathmin 1	0016051 // carbohydrate biosynthetic process // inferred from electronic annotation//0030206 // chondroitin sulfate biosynthetic process // not recorded
68.5556	49.480053	0.0085573	NM_0027928	-1.38	Chst13	carbohydrate (chondroitin 4) sulfotransferase 13	0001222 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006357 // regulation of transcription from RNA pol
11146.443	7459.6045	0.0069718	NM_016957	-1.38	Hmgm2	high mobility group nucleosomal binding domain 2	0006378 // mRNA polyadenylation // not recorded//0006379 // mRNA cleavage // not recorded//0006397 // mRNA processing // not recorded//0051262 // protein teta
1340.0198	979.1562	0.0066908	NM_026623	-1.38	Nudt21	NAD15, member RAS oncogene family	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // not recorded//0006904 // vesicle docking involved in exocytosis,
805.3313	597.1891	0.0098942	NM_134050//NM_006515:-1.37		Rab15	RAB15, member RAS oncogene family	0007420 // brain development // not recorded//0008284 // positive regulation of cell proliferation // inferred from direct assay//0022008 // neurogenesis // not recorded//
886.3366	659.2985	0.0089693	NM_133185//NM_011245:-1.37		Rogdi	rogdi homolog (Drosophila)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
356.65585	268.56598	0.0080529	NM_146040//NM_006515:-1.34		Cdca7l	cell division cycle associated 7 like	0016310 // phosphorylation // inferred from electronic annotation
583.1446	404.53812	0.0066908	NM_175400//NM_006497:-1.34		Sephs1	serinephosphatase 1	0006260 // DNA replication // inferred from electronic annotation//0006261 // DNA-dependent DNA replication // not recorded//0006297 // nucleotide-excision repair, DT
550.74396	421.81696	0.0090404	NM_133692//NM_006508:-1.33		Polk3	polymerase (DNA-directed), delta 3, accessory subunit	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//00
59.252865	44.97634	0.0096878	NM_007975//NM_006530:-1.32		Fzr3	coagulation factor II (thrombin) receptor-like 3	0006281 // DNA repair // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred from electronic annotation//0007140 // m
88.51907	66.801544	0.0090012	NM_016925//NM_006530:-1.32		Fanca	Fanconi anemia, complementation group A	0000027 // ribosomal large subunit assembly // --//0006412 // translation // inferred from electronic annotation
8628.585	6220.639	0.0038887	NM_009076//NR_880074-1.31		Rpl12//LOC10263504//Rpl	ribosomal protein L12//60S ribosomal protein L12 pseudogene//ribosomal protein	0007165 // signal transduction // traceable author statement//0008286 // insulin receptor signaling pathway // not recorded//0030178 // negative regulation of Wnt signal
2811.2795	2100.6084	0.0089748	NM_001177629//NM_010-1.31		Grb10	growth factor receptor bound protein 10	0000723 // DNA strand renaturation // not recorded//0006281 // DNA repair // not recorded//0006974 // cellular response to DNA damage stimulus // not recorded//000
76.42907	58.597046	0.0090933	NM_00125945//NM_027-1.30		Zranb3	zinc finger, RAN-binding domain containing 3	0000055 // ribosomal large subunit export from nucleus // inferred from mutant phenotype//0000056 // ribosomal small subunit export from nucleus // inferred from dir
7988.78	5829.5723	0.0079038	NM_001252260//NM_001-1.30		LOC102643093//Npm1//Gn	nucleophosmin pseudogene//nucleophosmin 1//nucleophosmin 1 pseudogene	0006412 // translation // inferred from electronic annotation//0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation//0006425 //
1228.6104	962.49164	0.0038287	NM_001168270//NM_133-1.29		Qars	glutaminyl-tRNA synthetase	0000460 // maturation of 5.8S rRNA // not recorded//0006364 // rRNA processing // inferred from electronic annotation
631.62445	510.6885	0.0084703	NM_026758//NM_011248:-1.26		Mphosph6	M phase phosphoprotein 6	0001841 // neural tube formation // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006913 // nucleocytoplasmic transp
407.2649	331.5466	0.0091756	NM_016714	-1.25	Nup50	nucleoporin 50	0002376 // immune system process // inferred from electronic annotation//0006338 // chromatin remodeling // not recorded//0006351 // transcription, DNA-templated //
59.935574	74.86261	0.0089693	NM_001037909//NM_030-1.25		C130026121Rik//Gm15753//	RIKEN cDNA C130026121 gene//predicted gene 15753//predicted pseudogene 160;	
1265.6335	1602.088	0.0099354	NM_009551//NM_006527:1.27		Zfand5	zinc finger, AN1-type domain 5	0001701 // in utero embryonic development // inferred from mutant phenotype//0001944 // vasculature development // inferred from mutant phenotype//0003016 // re
127.72649	160.53023	0.0089567	NM_010060//NM_006515:1.27		Dnah11	dynein, axonemal, heavy chain 11	0003341 // cilium movement // inferred from mutant phenotype//0003356 // regulation of cilium beat frequency // not recorded//0007018 // microtubule-based move
30.196898	38.96904	0.0086932	NM_001167996	-1.28	1110032F04Rik	RIKEN cDNA 1110032F04 gene	
27.675762	35.937508	0.0089842	NM_001033162//NM_00651-1.29		Shcbl1	Shc SH2-domain binding protein 1-like	0002548 // monocyte chemotaxis // --//0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from electronic ann
43.234664	56.375098	0.0079038	NM_021443//NM_011240:1.29		Cdk1//OC105242483	cyclin dependent kinase 8	
17936.076	22145.688	0.0097741	NM_001289643//NM_001-1.29		Sgpb3a2	spectrocytin, family 3A, member 2	
20.887587	27.605907	0.0075448	NM_020866//NR_045438-1.29		Mospd4	mottle sperm domain containing 4	
100.64475	130.731	0.0065811		1.31	BC038331	cDNA sequence BC038331	
730.721	984.38116	0.008644	NM_009419//NM_006534:1.31		Tps12	protein-tyrosine sulfotransferase 2	0070972 // protein localization to endoplasmic reticulum // inferred from electronic annotation
347.82178	488.0608	0.0080529	NM_175158	1.32	Utp20	UTP20, small subunit (SSU) processome component, homolog (yeast)	0002070 // epithelial cell maturation // inferred from mutant phenotype//0031069 // hair follicle morphogenesis // inferred from mutant phenotype//0042335 // cuticle de
93.94369	123.4245	0.0090494	NM_001159344//NM_027-1.33		Cas2l	casein 2	0006478 // typhoid-tyrosine sulfation // inferred from mutant phenotype//0007342 // fusion of sperm to egg plasma membrane // inferred from mutant phenotype//006
563.8717	767.96265	0.0068788	NM_001109992//NM_011-1.34		Ptpn11	protein tyrosine phosphatase, non-receptor type 11	0006364 // RNA processing // not recorded
88.377	116.905945	0.0097449	NM_001081176	1.34	Polr3g	polymerase (RNA) III (DNA directed) polypeptide G	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
109.69887	145.89856	0.0090626	NM_001161832//NM_013-1.35		Tf	brachyury 2	0000077 // immune system process // inferred from electronic annotation//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006359 // n
44.81647	60.534645	0.0086897	NM_001039537//NM_008-1.35		Lj1	leukemia inhibitory factor	0014028 // notchchord formation // inferred from mutant phenotype
155.65524	209.5741	0.0063393	NM_145132	1.35	Mchr1	melanin-concentrating hormone receptor 1	0001974 // blood vessel remodeling // inferred from genetic interaction//0006955 // immune response // inferred from electronic annotation//0007566 // embryo implant
22.702885	31.012066	0.006795	NM_001163416//NM_026-1.35		Ptx4	pentraxin 4	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // not recorded//0007186 // G-protein coupled r
811.0321	1117.4825	0.0090494	NM_009895//NM_006511:1.35		Cish	cytokine inducible SH2-containing protein	0006469 // negative regulation of protein kinase activity // not recorded//0007205 // protein kinase C-activating G-protein coupled receptor signaling pathway // inferred fr
66.45433	89.63028	0.0084703	NM_138650//NM_006521:1.36		Dgkg	diacylglycerol kinase, gamma	0007205 // protein kinase C

[C3H/HeN][raw]	[Gsr-KO][raw]	p [Corr]	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
1245.1687	1703.9156	0.009277	NM_009546	1.37	Trim25	tripartite motif-containing 25	0002376 // immune system process // inferred from electronic annotation//0006513 // protein monoubiquitination // not recorded//0016567 // protein ubiquitination // r
594.5504	826.9116	0.0090404	NM_029436//NM_006522	1.37	Klh24	kelch-like 24	0016567 // protein ubiquitination // not recorded//2000312 // regulation of kainate selective glutamate receptor activity // inferred from electronic annotation
3685.1448	4951.9624	0.0090933	NM_001311139//NM_021	1.38	Denn25a	DENN/MADD domain containing 5A	0042147 // retrograde transport, endosome to Golgi // not recorded//0043547 // positive regulation of GTPase activity // not recorded//0050982 // detection of mechan
62.927673	86.436516	0.0066193	NM_033373	1.38	Krt23	keratin 23	
563.57434	794.2354	0.0065811	NM_023184//NM_006506	1.38	Klf15	Kruppel-like factor 15	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
17.127337	23.416132	0.0097449	NM_001271548	1.38	Gm715	predicted gene 715	
229.91357	319.22418	0.0085589	NM_011785//NM_006496	1.39	Akt3	thymoma viral proto-oncogene 3	0000002 // mitochondrial genome maintenance // not recorded//0006468 // protein phosphorylation // not recorded//0007165 // signal transduction // not recorded//0
794.88605	1051.2301	0.0085589	NM_173007//NM_006505	1.39	Tspan12	tetraspanin 12	0001525 // angiogenesis // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred from mutant phenotype//0010842 // retina
428.76416	605.016	0.0085912	NM_015774	1.39	Erol1	ER01-like (5. cerevisiae)	0006457 // protein folding // inferred from direct assay//0006457 // protein folding // not recorded//0006810 // transport // inferred from electronic annotation//000691
1174.5762	1631.48	0.0085929	NM_001282037//NM_001	1.39	Sh3gbp1	SH3-domain GRB2-like B1 (endorphin)	0006654 // phosphatidic acid biosynthetic process // inferred from direct assay//0006915 // apoptotic process // not recorded//0007005 // mitochondrion organization //
134.8787	186.56053	0.0071764	NM_001038664//NM_001	1.39	Gngt2	guanine nucleotide binding protein (G-protein), gamma transducing activity polypept	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//00
44.941517	63.028168	0.0068828	NM_008216	1.40	Has2	hyaluronan synthase 2	0001570 // vasculogenesis // inferred from mutant phenotype//0001822 // kidney development // inferred from electronic annotation//0007155 // cell adhesion // not rec
212.50111	301.28427	0.0089693	NM_144835	1.40	Heatr1	HEAT repeat containing 1	0004662 // maturation of SSU-rRNA from tritestic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) // not recorded//0004594 // positive regulation of transcription from
96.12715	133.59744	0.0093601	NM_177003//NM_006506	1.40	Tigrr	Trp53 induced glycolysis regulatory phosphatase	0002931 // response to ischemia // inferred from direct assay//0006003 // fructose 2,6-bisphosphate metabolic process // inferred from mutant phenotype//0006003 // fr
455.28	650.57495	0.0086932	NM_175212//NM_006521	1.41	Tmem65	transmembrane protein 65	0003231 // cardiac ventricle development // inferred from mutant phenotype//1903779 // regulation of cardiac conduction // inferred from mutant phenotype
54.8639	76.7919	0.0097449	NM_175164//NM_006526	1.41	Arhgap26	Rho GTPase activating protein 26	0007165 // signal transduction // inferred from electronic annotation//0003036 // actin cytoskeleton organization // inferred from electronic annotation//0043547 // post
182.2649	256.9377	0.0087842	NM_172594//NM_006517	1.41	Dhx29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	0006396 // RNA processing // not recorded//0006412 // translation // inferred from electronic annotation//0006413 // translational initiation // inferred from electronic an
80.38777	112.50596	0.0066692	NM_023179//NM_006524	1.42	Atp6v1g2	ATPase, H+ transporting, lysosomal V1 subunit G2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015992 // proton transport // inferred fr
650.73926	943.386	0.0088565	NM_001001932//NM_006	1.42	Ecal1	early endosome antigen 1	0006897 // endocytosis // not recorded//0006906 // vesicle fusion // not recorded
57.99307	82.49462	0.0068697	NM_010658	1.43	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annota
3197.828	4456.845	0.0073042	NM_013885	1.43	Clic4	chloride intracellular channel 4 (mitochondrial)	0001525 // angiogenesis // inferred from mutant phenotype//0001886 // endothelial cell morphogenesis // inferred from mutant phenotype//0006749 // glutathione met
116.78553	163.30927	0.0098651		1.43	Al449212	expressed sequence AA49212	
45.295162	65.43218	0.0092128	NM_029662//NM_006503	1.44	Mfsd2a	major facilitator superfamily domain containing 2A	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation//0015908 // fatty acid transport // inferred f
378.74136	554.9958	0.0097449	NM_023245	1.44	Palmd	palmelphin	0008360 // regulation of cell shape // inferred from electronic annotation
248.25574	363.1429	0.0068697	NM_001284410//NM_001	1.44	Bcl2l1	BCL2-like 11 (apoptosis facilitator)	0001701 // in utero embryonic development // inferred from genetic interaction//0001776 // leukocyte homeostasis // inferred from genetic interaction//0001776 // leuk
42.71785	61.716022	0.0074312	NM_001033543//NM_001	1.44	I20rb	interleukin 20 receptor beta	0001808 // negative regulation of type IV hypersensitivity // inferred from mutant phenotype//0002437 // inflammatory response to antigenic stimulus // inferred from mut
179.06792	258.5797	0.0095919	NM_008803	1.44	Pde8a	phosphodiesterase 8A	0006198 // CAP catalytic process // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//
310.81885	455.7374	0.0063393	NM_001081289//NM_011	1.44	Fam217b	family with sequence similarity 217, member B	
197.53992	286.7513	0.0089693	NM_199476//NM_006520	1.44	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	0001822 // kidney development // inferred from mutant phenotype//0003014 // renal system process // inferred from mutant phenotype//0006260 // DNA replication // i
200.43422	289.20087	0.0065811	NM_026189//NM_006510	1.44	Eepd1	endonuclease/exonuclease/phosphatase family domain containing 1	0006281 // DNA repair // inferred from electronic annotation
600.12067	883.69226	0.0066381	NM_001081150	1.45	Lonrf1	LON peptidase N-terminal domain and ring finger 1	0006508 // proteolysis // inferred from electronic annotation
257.24835	374.889	0.0086932	NM_010748//NM_006516	1.45	Lyst	lysosomal trafficking regulator	0002446 // neutrophil mediated immunity // inferred from mutant phenotype//0002456 // T cell mediated immunity // inferred from mutant phenotype//0006644 // phos
93.04892	134.13147	0.0087842	NM_001291044//NM_153	1.45	Nudt6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	0008152 // metabolic process // inferred from electronic annotation
1130.3108	1643.6276	0.0068697	NM_020332	1.45	Ank	progressive ankylosis	0006810 // transport // inferred from electronic annotation//0006817 // phosphate ion transport // inferred from electronic annotation//0003050 // regulation of bone m
233.0611	339.5931	0.0095588	NM_194346//NM_006519	1.45	Rnf31	ring finger protein 31	0002029 // protein polyubiquitination // not recorded//0016567 // protein ubiquitination // inferred from mutant phenotype//0023035 // CD40 signaling pathway // infer
106.98278	152.94997	0.0068697	NM_027268//NM_006506	1.45	Scrn1	sceremin 1	0006508 // proteolysis // inferred from electronic annotation//0006887 // exocytosis // not recorded
543.9085	809.5623	0.0085929	NM_001168304//NM_001	1.45	Cdk19	cyclin-dependent kinase 19	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0043065 // positive regul
641.10004	947.8447	0.0089693	NM_00114328//NM_001	1.45	Ccp1	cell cycle progression 1	0007049 // cell cycle // inferred from electronic annotation//0008284 // positive regulation of cell proliferation // not recorded//0045787 // positive regulation of cell cycle
351.78738	521.0859	0.0071527	NM_016979//NM_006527	1.46	Prkx	protein kinase, X-linked	0001525 // angiogenesis // inferred from mutant phenotype//0001525 // angiogenesis // not recorded//0001935 // endothelial cell proliferation // inferred from mutant pl
894.04285	1319.0879	0.0065467	NM_009230//NM_006496	1.46	Soc11	sterol O acyltransferase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006202 // steroid metabolic process // inferred from electronic annotation//0008203 // chole
73.11238	106.71129	0.008644	NM_001301353//NM_001	1.46	Apod	apolipoprotein D	0003002 // response to reactive oxygen species // inferred from mutant phenotype//0003002 // response to reactive oxygen species // not recorded//0006006 // glucose
18.808596	27.400504	0.0066908	NM_021396//NM_011247	1.46	Ptcd1lg2	programmed cell death 1 ligand 2	0003269 // negative regulation of interferon-gamma production // not recorded//0032693 // negative regulation of interleukin-10 production // not recorded//0042102 //
217.91795	321.52707	0.0093601	NM_199143	1.46	Znf7	zinc and ring finger 2	0016567 // protein ubiquitination // inferred from electronic annotation//0016567 // protein ubiquitination //
1454.3673	2134.1619	0.0075048	NM_008247//NM_008903	1.46	Pfip1	phospholipid phosphatase 1	0006470 // protein dephosphorylation // inferred from direct assay//0006470 // protein dephosphorylation // traceable author statement//0006629 // lipid metabolic pro
196.24185	288.03326	0.0081374	NM_001136260//NM_001	1.47	Slc4a4	solute carrier family 4 (anion exchanger), member 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // infer
384.40848	573.86365	0.0046966	NM_133685	1.47	Rab31	RAB31, member RAS oncogene family	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation//000316
144.78069	210.86339	0.0085929	NM_026159	1.47	Retsat	retinol saturase (all trans retinol 13,14 reductase)	0042572 // retinol metabolic process // inferred from direct assay//0055114 // oxidation-reduction process // inferred from direct assay
2533.167	3620.76	0.0070902	NM_025427	1.47	Rgcc	regulator of cell cycle	0000082 // G1/S transition of mitotic cell cycle // not recorded//0001100 // negative regulation of exit from mitosis // not recorded//0001937 // negative regulation of end
236.28764	350.01755	0.0087842	NM_001001176//NM_001	1.47	Taf9b	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic ann
502.5029	756.82007	0.0083164	NM_001310483//NM_026	1.48	Lmbrd1	LMBR1 domain containing 1	0006810 // transport // inferred from electronic annotation//0038016 // insulin receptor internalization // inferred from mutant phenotype//0043408 // regulation of MAF
16.762423	24.5432	0.0096864	NM_025458	1.48	Tmed6	transmembrane emp24 protein transport domain containing 6	0006810 // transport // inferred from electronic annotation
535.0716	808.76697	0.0070902	NM_001012477//NM_013	1.48	Cxcl12	chemokine (C-X-C motif) ligand 12	0001569 // patterning of blood vessels // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from electronic annotation//0001667 // ameboidal
1185.8323	1744.916	0.0080529	NM_008452	1.48	Klf2	Kruppel-like factor 2 (lung)	0000902 // cell morphogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development // inferred from mutant phenotype//0006351 // transcri
1488.0708	2181.5024	0.0082153	NM_001039390//NM_001	1.48	Plg1	protein kinase inhibitor, gamma	0001022 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0006469 // negative regulation of protein kinase activity // i
127.95897	189.04294	0.0087113	NM_001112288	1.48	Sco2	SCO cytochrome oxidase deficient homolog 2 (yeast)	0001654 // eye development // not recorded//0001701 // in utero embryonic development // inferred from mutant phenotype//0003032 // muscle system process // infer
10182.671	13806.513	0.0079038	NM_008597	1.48	Mgp	matrix gla protein	0001503 // ossification // inferred from electronic annotation//0006461 // protein complex assembly // not recorded//0007275 // multicellular organismal development //
89.49908	132.17178	0.0071653	NM_175638//NM_006534	1.49	Wnk4	WNK lysine deficient protein kinase 4	0006468 // protein phosphorylation // not recorded//0006811 // ion transport // inferred from direct assay//0006821 // chloride transport // inferred from direct assay//
306.64154	464.40405	0.0065811	NM_001173732//NM_033	1.49	Fxyd4	FXD domain-containing ion transport regulator 4	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0071805 // potassium ion transmembrane t
330.3683	501.64032	0.007891	NM_011020//NM_006500	1.49	Hspa4l	heat shock protein 4 like	0006457 // protein folding // not recorded//0006986 // response to unfolded protein // not recorded
147.20726	216.09126	0.0087842	NM_027906//NM_173758	1.49	Vwa8	von Willebrand factor A domain containing 8	0008152 // metabolic process // inferred from electronic annotation
157.34303	233.03777	0.0065464	NM_001136078//NM_008	1.49	Pitpnm1	phosphatidylinositol transfer protein, membrane-associated 1	0006810 // transport // inferred from electronic annotation//0015031 // protein transport // inferred from electronic annotation
14.959984	22.076882	0.0066655	NM_001113323//NM_006	1.50	Gib13	galactosidase, beta 1 like 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
44.868717	67.032845	0.0086897	NM_146063//NM_006520	1.50	Krt79	keratin 79	
243.57065	267.38373	0.0085573	NM_145823//NM_006534	1.50	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation//0007165 // signal transduction // inferred f
254.70616	383.44003	0.008644	NM_183168//NM_006574	1.50	P2yf6	pyrimidineric receptor P2Y, G-protein coupled 6	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//00
2245.095	3252.9995	0.0084703	NM_001159555//NM_001	1.50	Cd36	CD36 antigen	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001676 // long-chain fatty acid metabolic process //
111.92673	164.87944	0.0088565	NM_001163592//NM_173	1.50	Nhs1l	NHS-like 1	
574.3346	878.7723	0.0089296	NM_001014390//NM_006	1.50	Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	0006468 // protein phosphorylation // not recorded//0006915 // apoptotic process // inferred from electronic annotation//0006974 // cellular response to DNA damage st
52.1808	77.96289	0.008644	NM_001304991//NM_001	1.50	Ppp3cc	protein phosphatase 3, catalytic subunit, gamma isoform	0006470 // protein dephosphorylation // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
264.1989	401.71225	0.0065811	NM_001033066//NM_001	1.50	Acs1	acyl-CoA synthetase long-chain family member 3	0001676 // long-chain fatty acid metabolic process // not recorded//0006364 // rRNA processing // inferred from electronic annotation//0006629 // lipid metabolic proces
120.57515	179.29112	0.0055381	NM_0114452	1.51	Serpinc9b	serine (or cysteine) peptidase inhibitor, clade B, member 9b	0010951 // negative regulation of endopeptidase activity // not recorded//00019835 // cytolysis // inferred from direct assay
20.280329	30.786303	0.0090404	NM_177664	1.51	Plpp4r	phospholipid phosphatase related 4	0006470 // protein dephosphorylation // inferred from electronic annotation//0006644 // phospholipid metabolic process // not recorded//0007165 // signal transduction
24.92463	37.962696	0.008843	NM_010846//NR_003520	1.51	Mx1	MX dynamin-like GTPase 1	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009615 // response to
41.053307	62.356464	0.0063993	NM_001261731//NM_007	1.51	Ang	angiogenin, ribonuclease, RNase A family, 5	0001525 // angiogenesis // not recorded//0001666 // response to hypoxia // not recorded//0001878 // response to yeast // inferred from direct assay//0001878 // resp
27.11057	202.8099	0.0089066	NM_006651//NM_006506	1.52	Slc25a26	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 26	0006810 // transport // inferred from electronic annotation//0015805 // S-adenosyl-L-methionine transport // not recorded//0055085 // transmembrane transport // infer
72.89823	108.76453	0.0065464	NM_175510//NM_006496	1.52	Unc80	unc-80 homolog (C. elegans)	
57.70825	87.04559	0.0050895	NM_0016671//NM_011248	1.52	I27ra	interleukin 27 receptor, alpha	0002827 // positive regulation of T-helper 1 type immune response // inferred from mutant phenotype//0002829 // negative regulation of type 2 immune response // infer
309.18314	476.64597	0.0078833	NM_021310	1.52	Jmy	junction-mediating and regulatory protein	0006281 // DNA repair // inferred from electronic annotation//0006357 // regulation of transcription from RNA polymerase II promoter // inferred from direct assay//000
4026.7573	5955.0815	0.0093601	NM_001297747//NM_009	1.52	Btg3//Gm7334	beta cell translocation gene 3//beta-cell translocation gene 3 pseudogene	0045930 // negative regulation of mitotic cell cycle // not recorded
99.91072	149.33043	0.0080529	NM_022413//NM_006506				

[C3H/HeN][raw]	[Gsr-KO][raw]	p [Corr]	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
51.026672	77.96825	0.006897	NM_053217	1.54	Ifit1b12	interferon induced protein with tetratricopeptide repeats 1B like 2	0051607 // defense response to virus // not recorded//0060337 // type I interferon signaling pathway // not recorded
31.62727	49.09779	0.009128	NM_011517	1.54	Sycp3	synaptonemal complex protein 3	000711 // meiotic DNA repair synthesis // inferred from genetic interaction//0007049 // cell cycle // inferred from electronic annotation//0007066 // female meiosis site
260.79916	405.91647	0.008029	NM_029600//NM_006534	1.54	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0006810 // transport // inferred from electronic annotation//0006855 // drug transmembrane transport // not recorded//0008152 // metabolic process // inferred from elc
298.12338	467.93085	0.007042	NM_177644//NM_006496	1.55	Rasa12	RAS protein activator like 2	0007165 // signal transduction // inferred from electronic annotation//0043087 // regulation of GTPase activity // inferred from electronic annotation//0043547 // positive
10228.742	14190.378	0.008963	NM_011402//NM_006503	1.55	Slc34a2	solute carrier family 34 (sodium phosphate), member 2	0001701 // in utero embryonic development // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006811 // ion transport //
114.79747	176.1562	0.0029632	NM_001243857//NM_0061	1.55	Fam124a	family with sequence similarity 124, member A	
598.01666	942.25476	0.0056277	NM_001290475//NM_146	1.55	Tdrd7	tudor domain containing 7	0002089 // lens morphogenesis in camera-type eye // inferred from mutant phenotype//0002089 // lens morphogenesis in camera-type eye // not recorded//0007275 // n
60.331367	92.50227	0.0070902	NM_145700//NM_006511	1.55	Ackr4	atypical chemokine receptor 4	0006988 // receptor-mediated endocytosis // inferred from electronic annotation//0006935 // chemotaxis // inferred from electronic annotation//0007165 // signal tran
179.84302	279.86804	0.0084158	NM_013512//NM_006525	1.56	Epb414a	erythrocyte membrane protein band 4.1 like 4a	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // inferred
702.30115	1117.7863	0.0081374	NM_029415//NM_006535	1.56	Slc10a6	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay//0009968 // negative regulation of signal transduction // inferred from electronic an
53.557236	83.59173	0.0068707	NM_029879//NM_006517	1.56	Rgs7bp	regulator of G-protein signaling 7 binding protein	
45.991867	71.748886	0.0065811	KR_879970//KR_879971	1.56	Tnfrsf130s	tumor necrosis factor (ligand) superfamily, member 13, opposite strand	
256.32257	406.12448	0.0070902	NM_133222	1.56	Adgr4	adhesion G-protein-coupled receptor L4	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0007186
417.68076	607.65866	0.0076866	NM_027045//NM_028407	1.57	Cs2er2	collel-coil serine rich 2	0001578 // microtubule bundle formation // inferred from direct assay
457.5074	731.3009	0.0093543	NM_001159662//NM_153	1.57	Ppp1r16b	protein phosphatase 1, regulatory (inhibitor) subunit 16B	0001938 // positive regulation of endothelial cell proliferation // not recorded//0014066 // regulation of phosphatidylinositol 3-kinase signaling // not recorded//0035307
524.3498	836.8029	0.0071764	NM_001289686//NM_001	1.57	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation//0035556 // intracellular signal transduction // inferred from electronic anc
157.84517	247.81845	0.004449	NM_001113399//NM_001	1.57	Zfp385b	zinc finger protein 385B	0006915 // apoptotic process // inferred from electronic annotation//0072332 // intrinsic apoptotic signaling pathway by p53 class mediator // not recorded
164.14583	255.5532	0.008832	NM_127247//NM_006507	1.57	Kctd13	potassium channel tetramerisation domain containing 13	0006260 // DNA replication // not recorded//0016477 // cell migration // not recorded//0016567 // protein ubiquitination // not recorded//0035024 // negative regulato
66.97553	104.81528	0.0080529	NM_027853	1.58	Mettl7b	methyltransferase like 7B	0008152 // metabolic process // inferred from electronic annotation//0032259 // methylation // not recorded
54.048714	85.03915	0.0080529	NM_001159748//NM_011	1.58	Serpinb8	serine (or cysteine) peptidase inhibitor, clade B, member 8	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded
116.56869	181.12389	0.0056661	NM_145227//NM_006530	1.58	Oas2	2'-5' oligoadenylate synthetase 2	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process // not recorded//0006401 // RNA catabolic;
1460.8104	2282.8374	0.0046966	NM_001111049//NM_001	1.58	Cd151	CD151 antigen	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation
741.03394	1188.6788	0.0080529	NM_025809	1.58	Clec14a	C-type lectin domain family 14, member A	0001656 // metanephros development // inferred from genetic interaction//0001656 // metanephros development // inferred from mutant phenotype//0001822 // kidney
119.15102	189.09705	0.0063393	NM_001038703//NM_030	1.58	Gpr146//D830046C22Rk	G-protein-coupled receptor 146//RIKEN cDNA D830046C22 gene	0006725 // cellular aromatic compound metabolic process // inferred from mutant phenotype//0009636 // response to toxic substance // inferred from electronic annotati
2058.5842	3198.422	0.0079403	NM_001001309//NM_0064	1.58	Itga8	integrin alpha 8	0010224 // response to UV-B // inferred from electronic annotation//0018149 // peptide cross-linking // inferred from electronic annotation//0018153 // isopeptide cross-
520.95087	845.1952	0.0083887	NM_001312918//NM_010	1.58	Ephx1	epoxide hydrolase 1, microsomal	0007517 // muscle organ development // inferred from electronic annotation//0048747 // muscle fiber development // inferred from mutant phenotype//0050513 // card
33.204273	53.26761	0.0046248	NM_008412//NM_006501	1.59	Ivl	involucrin	
673.5006	1087.4612	0.0080202	NM_029620	1.59	Pcalce2	procollagen C-endopeptidase enhancer 2	
73.70373	116.90313	0.0066692	NM_029612//NM_006497	1.59	Slamf9	SLAM family member 9	
305.36475	492.87463	0.0075124	NM_011890	1.59	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	
136.96667	215.83388	0.0099354	NM_026626	1.59	Efcab2	EF-hand calcium binding domain 2	
350.704	567.84186	0.0084664	NM_175518//NM_006537	1.59	Tmem245	transmembrane protein 245	
20.654604	33.078217	0.0065754		1.59	Tcrg-C1//Tcrg-C2	T cell receptor gamma, constant 1//T-cell receptor gamma, constant 2	
1655.2462	2600.2366	0.0071653	NM_001130458//NM_001	1.60	Tcn2	transcobalamin 2	0048873 // homeostasis of number of cells within a tissue // inferred from mutant phenotype
1298.8452	2052.0845	0.0080529	NM_010638	1.60	Klf9	Kruppel-like factor 9	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006824 // cobalt ion transport // inferred fi
568.46454	925.88586	0.0090012	NM_009443//NM_009444	1.60	Tgolin1//Tgolin2	trans-golgi network protein//trans-golgi network protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//000
282.7969	1336.2534	0.0090404	NM_001039562//NM_0061	1.60	Ankrd37	ankyrin repeat domain 37	0006895 // Golgi to endosome transport // not recorded
2382.7917	3764.5945	0.0088671	NM_001013296//NM_013	1.60	Hacd1	3-hydroxyacyl-CoA dehydrogenase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatt
136.20184	214.4599	0.0058589	NM_008105//NM_023887	1.60	Gcn2c	glucosaminyl (N-acetyl) transferase 2, I-branched enzyme	0005486 // protein glycosylation // not recorded//0007179 // transforming growth factor beta receptor signaling pathway // inferred from mutant phenotype//0007179 //
129.9166	204.78058	0.0066908	NM_008381	1.60	Inhbb	inhibin beta-B	0001654 // eye development // traceable author statement//000287 // cellular response to starvation // inferred from expression pattern//0009612 // response to mech.
84.38545	132.56483	0.0058111	NM_019510//NM_006535	1.60	Tp3c	transient receptor potential cation channel, subfamily C, member 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // inferre
1063.3546	1711.0933	0.009452	NM_00116420//NM_013	1.61	Vldlr	very low density lipoprotein receptor	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from elec
44.73098	71.795074	0.003657	NM_021334//NR_378219	1.61	ItgaX	integrin alpha X	0007155 // cell adhesion // inferred from electronic annotation//0007229 // integrin-mediated signaling pathway // inferred from electronic annotation//0034113 // heter
103.922424	165.2464	0.0062819	NM_001289740//NM_001	1.62	Mturm	maturnin, neural progenitor differentiation regulator homolog (Xenopus)	0007275 // multicellular organismal development // inferred from electronic annotation//0048666 // neuron development // inferred from sequence or structural simil
1211.821	1947.1868	0.0084354	NM_007520//NM_006522	1.62	Bach1	BTB and CNC homology 1	0000083 // regulation of transcription involved in G1/S transition of mitotic cell cycle // not recorded//0000117 // regulation of transcription involved in G2/M transition of
3585.2346	5610.445	0.0097449	NM_001289782//NM_001	1.62	Cryab	crystallin, alpha B	0001666 // response to hypoxia // inferred from mutant phenotype//0002088 // lens development // inferred from genetic interaction//0006457 // prc
255.14734	418.67978	0.006897	NM_172689	1.62	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0002230 // positive regulation of defense response to virus by host // not recorded//0002376 // immune system process // inferred from electronic annotation//0008152 //
671.4385	1107.8151	0.0086932	NM_009320//NM_006505	1.63	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	0001762 // beta-alanine transport // inferred from direct assay//0006810 // transport // inferred from electronic annotation//0006836 // neurotransmitter transport // inf
326.3001	537.4946	0.0085208	NM_028421//NM_028864	1.63	Zc3hav1	zinc finger CCHC type, antiviral 1	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009615 // response to
152.39314	245.42938	0.0096878	NM_001145978//KR_3831	1.63	Parp4	poly (ADP-ribose) polymerase family, member 4	0006464 // cell cycle protein modification process // not recorded//0006471 // protein ADP-ribosylation // inferred from electronic annotation//0006954 // inflammatory re
1952.652	3163.9395	0.0084323	NM_001287256//NM_011	1.64	Prmp	prion protein	0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype//0006139 // nucleobase-containing compound metabolic process // traceabl
309.9866	513.1897	0.0075737	NM_008580//NM_006512	1.64	Map3k5	mitogen-activated protein kinase kinase kinase 5	0000165 // MAPK cascade // not recorded//0000186 // activation of MAPK activity // not recorded//0000187 // activation of MAPK activity // inferred from direct assay,
806.08704	1336.9982	0.0030131	NM_028757//NM_006497	1.64	Nebi	nebulin	0071691 // cardiac muscle thin filament assembly // inferred from sequence or structural similarity
1660.4001	2668.2544	0.0066692	NM_011326//NM_006507	1.64	Scnn1g	sodium channel, nonvoltage-gated J gamma	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // inferre
32.117317	53.55617	0.0065276	NM_177304//NM_006509	1.65	Enpp6	ectonucleotide pyrophosphatase/phosphodiesterase 6	0006629 // lipid metabolic process // not recorded//0008152 // metabolic process // inferred from electronic annotation//0016042 // lipid catabolic process // inferred fr
319.5472	531.4907	0.0095588	NM_025831//NM_006516	1.65	Pxd1	Px domain containing 1	
93.669235	151.5203	0.0093601	NM_001024478//NM_0061	1.65	Cdhr3	cadherin-related family member 3	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from electronic
159.03163	260.33548	0.0075048	NM_001177571//NM_001	1.65	Ccdc162	collel-coil domain containing 162	
987.3046	1643.0605	0.0098684	NM_001291190//NM_177	1.65	Ssh2	slingshot homolog 2 (Drosophila)	0006470 // protein dephosphorylation // not recorded//0008064 // regulation of actin polymerization or depolymerization // not recorded//0010591 // regulation of lame
707.95465	1193.0107	0.0080529	NM_133897//NM_006534	1.65	Lrrc8c	leucine rich repeat containing 8 family, member C	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0005444 // fat cell differentiation // inferred
44.343937	73.260445	0.0080529	NM_133868	1.65	Lrrc4	leucine rich repeat containing 4	0005087 // regulation of synapse organization // inferred from mutant phenotype//0005088 // synapse organization // inferred from direct assay//0097119 // postsynapti
147.0674	239.3405	0.0096679	NM_029094//NM_006511	1.65	Plk3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide	0001935 // endothelial cell proliferation // inferred from mutant phenotype//0001952 // regulation of cell-matrix adhesion // inferred from mutant phenotype//0001952 //
118.88309	192.06656	0.0096878	NM_027629//NM_006508	1.65	Pgm2l1	phosphoglucomutase 2-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005978 // glycogen biosynthetic process // --//0006006 // glucose metabolic proces
759.157	1269.0675	0.0088671	NM_010234	1.65	Fos	FBJ osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//000631
2042.41571	3322.41139	0.0066908	NM_001159518//NM_008	1.65	Igf1bp7	insulin-like growth factor binding protein 7	0001558 // regulation of cell growth // inferred from electronic annotation//0007155 // cell adhesion // not recorded//004839 // inner ear development // inferred from
28.98437	48.55488	0.0097449	NM_001136181//NM_0061	1.66	Hsbp11	heat shock factor binding protein 1-like 1	
1176.2095	1945.0859	0.0075984	NM_001039175//NM_001	1.66	Elov1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatt
31.653519	52.989143	0.0070902	NM_001271716//NM_001	1.66	Mct2	monocarboxylate 2 receptor	0001890 // placenta development // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein cou
59.853203	98.29669	0.004326	NM_001272239//NM_177	1.66	Zmat4	zinc finger, matrix type 4	0072332 // intrinsic apoptotic signaling pathway by p53 class mediator // not recorded
393.0927	665.1955	0.0029632	NM_025833	1.66	Balap2l1	BAL-associated protein 2-like 1	0007009 // plasma membrane organization // inferred from electronic annotation//0008286 // insulin receptor signaling pathway // not recorded//0009617 // response to
493.04117	834.1128	0.0064729	NM_001160018//NM_001	1.66	Tor1aip1	TOR1A interacting protein 1	0032781 // positive regulation of ATPase activity // not recorded//0034504 // protein localization to nucleus // inferred from mutant phenotype//0071763 // nuclear mem
1778.2186	2918.9375	0.0059002	NM_175930//NM_006515	1.67	Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation//0003556 // intracellular signal transduction // inferred from electronic annot
291.30316	494.9083	0.0058111	NM_001302376//NM_001	1.67	Ccr12	chemokine (C-C motif) receptor-like 2	0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred from direct assay//0007165 // signal transduction // inferre
83.08191	135.89091	0.008149	NM_001033443//NM_0061	1.67	Cdk1k	cyclin-dependent kinase-like 4	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0051726 // regulation of c
34.206284	57.88053	0.0081374	NM_001033922//NM_001	1.68	Trem14	triggering receptor expressed on myeloid cells-like 4	002457 // T cell antigen processing and presentation // inferred from mutant phenotype//0006911 // phagocytosis, engulfment // inferred from direct assay
58.479546	97.6004	0.0065754	NM_0010131741	1.68	Ddn	dendrin	0045944 // positive regulation of transcription from RNA polymerase II promoter // not recorded
255.40147	432.5907	0.0065464	NM_001033348//NM_0061	1.68	Ralgapa2	Ral GTPase activating protein, alpha subunit 2 (catalytic)	0032484 // Ral protein signal transduction // inferred from mutant phenotype//0032880 // regulation of protein localization // inferred from mutant phenotype//0051056
104.67884	171.46066	0.0098942	NM_001177503//NM_0061	1.68	Plekhd1	pleckstrin homolog domain containing, family D (with collel-coil domains) member 1	
134.11865	223.32632	0.0070842	NM_126166//NM_006509	1.68	Trl3	tol-like receptor 3	0001774 // microglial cell activation // not recorded//0001819 // positive regulation of cytokine production // inferred from electronic annotation//0001934 // positive reg
18.742228	31.431572	0.0091756	NM_145467//NM_006518	1.69	Itgbl1	integrin, beta-like 1	</

[C3H/HeN][raw]	[Gsr-KO][raw]	p [Corr]	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
226.32802	386.1712	0.0092225	NM_027288//NM_0065006	1.70	Mamba	mannosidase, beta A, lysosomal	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006516 // glycoprotein catabolic process // inferred from direct assay//0008152 // m
249.0405	427.8245	0.0051715	NM_001271356//NM_001	1.70	Fln	follistatin	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0000122 // negative regulation of transcription from
130.01054	218.65361	0.0068697	NM_001122635//NM_177	1.70	Cdhr4	cadherin-related family member 4	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from electronic
25.975962	44.556644	0.0045517	XR_390980//XR_390981//	1.70	LOC102631977	uncharacterized LOC102631977	
111.1445	188.18314	0.0093097	NM_023044	1.70	Slc15a3	solute carrier family 15, member 3	0006810 // transport // inferred from electronic annotation//0006857 // oligopeptide transport // inferred from electronic annotation//0015031 // protein transport // inf
155.87709	267.8136	0.0096864	NM_01033149//NM_006	1.71	Tct9	tetratricopeptide repeat domain 9	0000413 // protein peptidyl-prolyl isomerization // not recorded//0006107 // chaperone-mediated protein folding // not recorded
172.39857	294.61115	0.0065276	NM_009841	1.71	Cd14	CD14 antigen	0002237 // response to molecule of bacterial origin // inferred from direct assay//0002376 // immune system process // inferred from electronic annotation//0006898 // r
1419.1439	2382.3271	0.008644	NM_0103671	1.71	Sod2	superoxide dismutase 2, mitochondrial	0000302 // response to reactive oxygen species // inferred from mutant phenotype//0000303 // response to superoxide // inferred from mutant phenotype//0000303 // r
186.20483	317.71875	0.0095919	XR_387233//XR_387234//	1.72	Gm29538	predicted gene 29538	
321.45078	560.8739	0.003657	NM_001286062//NM_009	1.72	Angpt1	angiopoietin 1	0001525 // angiogenesis // inferred from direct assay//0001525 // angiogenesis // inferred from mutant phenotype//0001541 // ovarian follicle development // not rec
141.70741	241.15158	0.0079092	NM_001005740//NM_001	1.72	Phcrt1//Cst11	phosphatase and actin regulator 1//carbohydrate sulfotransferase 11	0031032 // actomyosin structure organization // inferred from mutant phenotype//0031032 // actomyosin structure organization // not recorded//0031532 // actin cytos
451.15045	787.47424	0.0065464	NM_029508//NM_006527	1.72	Pcgf5	polycomb group ring finger 5	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
88.48398	147.9736	0.0097449	NM_011033156//NM_001	1.72	Steap2	six transmembrane epithelial antigen of prostate 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006893 // Golgi to plasma membrane tran
287.14225	502.43848	0.0052567	NM_001167860//NM_001	1.72	Wipf3	WAS/WASL interacting protein family, member 3	0000147 // actin cortical patch assembly // --//0006897 // endocytosis // --//0007275 // multicellular organismal development // inferred from electronic annotation//D
482.09055	853.3207	0.0089693	NM_001039181//NM_001	1.73	Npr3	natriuretic peptide receptor 3	0001501 // skeletal system development // inferred from direct assay//0001501 // skeletal system development // inferred from mutant phenotype//0002158 // osteoclas
7493.454	12037.867	0.0071126	NM_025378	1.73	Ifitm3	interferon induced transmembrane protein 3	0002376 // immune system process // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from mutant phenotype//0008285 // ne
245.71704	428.8852	0.0079038	NM_01024139//NM_006	1.73	Adamts15	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1	0006508 // proteolysis // inferred from electronic annotation
181.65309	314.36923	0.008368	NM_001146342//NM_001	1.73	Rnk	renalin, FAD-dependent amine oxidase	0002931 // response to ischemia // inferred from electronic annotation//0003073 // regulation of systemic arterial blood pressure // inferred from mutant phenotype//000
236.38373	412.7049	0.0057397	NM_001033213//NM_006	1.73	Tct7b	tetratricopeptide repeat domain 7B	
305.4366	536.0349	0.0075335	NM_023755//NM_006529	1.73	Tfcp2l1	transcription factor CP2-like 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000902 // cell morphogenesis // inferred from mutant phe
131.37415	225.08957	0.0086932	NM_001289588//NM_001	1.74	Radi1	Ras association and Dbl domains	0007155 // cell adhesion // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0007275 // multicellular organism
95.03452	161.67819	0.0075048	NM_177855//NM_006501	1.75	Med12l	mediator complex subunit 12-like	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
58.401875	102.86504	0.0085573	NM_026955//NM_011242	1.75	Vstm5	V-set and transmembrane domain containing 5	
104.39475	177.79718	0.0097449	NM_021439//NM_006513	1.75	Cst11//Phcrt1	carbohydrate sulfotransferase 11//phosphatase and actin regulator 1	0002063 // chondrocyte development // inferred from mutant phenotype//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0007585 //
578.948	1033.826	0.0051039	NM_001134191//NM_001	1.76	Gm21949//Schip1	predicted gene, 21949//schwannomin interacting protein 1	0001553 // uterine invagination // inferred from genetic interaction//0001822 // kidney development // inferred from mutant phenotype//0006807 // nitrogen compound metab
43.128742	75.84508	0.0065464	NM_178908	1.76	Fam26e	family with sequence similarity 26, member E	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // --//003422X
73.797386	129.19374	0.0086932	NM_181748	1.77	Ffar4	free fatty acid receptor 4	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay//0007186 //
177.39967	309.7365	0.0096878	NM_008987	1.77	Ptx3	pentraxin related gene	0001878 // response to yeast // inferred from mutant phenotype//0008228 // opsonization // inferred from mutant phenotype//0044869 // negative regulation by host of
35.71676	64.05593	0.0089296	NM_009375//NM_006520	1.77	Tg	thyroglobulin	0006590 // thyroid hormone generation // not recorded//0009268 // response to pH // not recorded//0015705 // iodide transport // inferred from mutant phenotype//D
87.682724	152.86406	0.0075124	NM_009759	1.77	Bmx	BMX non-receptor tyrosine kinase	0002250 // adaptive immune response // not recorded//0006468 // protein phosphorylation // inferred from electronic annotation//0006915 // apoptotic process // infer
841.7611	1492.6134	0.0098942	NM_138751	1.77	Tmem47	transmembrane protein 47	0098609 // cell-cell adhesion // not recorded
206.18208	365.76892	0.0067139	NM_001029838//NM_148	1.78	Pknox2	Pbx/knotted 1 homeobox 2	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 // regulation of transcription from RNA polymerase II promoter // ir
260.15036	469.4192	0.0091756	NR_028300	1.78	Dubr	Dppa2 upstream binding RNA	
405.07373	739.9634	0.0055381	NM_001002031//NM_008	1.79	Hspa2	heat shock protein 2	0001934 // positive regulation of protein phosphorylation // inferred from mutant phenotype//0007140 // male meiosis // inferred from mutant phenotype//0007141 // r
168.69484	301.58395	0.0096782	NM_01162957	1.79	Rsph4a	radial spoke head 4 homolog A (Chlamydomonas)	0003341 // cilium movement // not recorded//0035082 // axonemal assembly // not recorded
84.0419	147.38301	0.0079637	NM_021427	1.79	Fam181b	family with sequence similarity 181, member B	
600.61676	1099.8865	0.0089693	NM_011498	1.79	Bhhel40	basic helix-loop-helix family, member 40	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic ann
240.95113	436.5521	0.0065811	NM_025807//NM_006513	1.79	Slc16a9	solute carrier family 16 (monocarboxylic acid transporters), member 9	0006810 // transport // inferred from electronic annotation//0015718 // monocarboxylic acid transport // --//0034220 // ion transmembrane transport // not recorded//
1329.6221	2393.8083	0.0096679	NM_019738	1.80	Nupr1	nucleolar protein transcription regulatory 1	0005226 // acute inflammatory response // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
32.173088	57.879307	0.0052021	NM_001142959//NM_001	1.80	Bcl2l15	BCL2-like 15	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // traceable author statement//0006886 // intracellular protein tra
140.03128	251.22546	0.0086319	NM_145523	1.80	Gcc	granulin C	0006508 // proteolysis // not recorded
81.45403	143.87514	0.0066908	NM_175522//NM_006504	1.80	Elfn1	leucine rich repeat and fibronectin type III, extracellular 1	0010923 // negative regulation of phosphatase activity // not recorded//005808 // synapse organization // inferred from mutant phenotype
78.42289	140.94006	0.0086426	NM_026358//NR_028121	1.80	Mgap9	mitochondrial localized glutamic acid rich protein	0006626 // protein targeting to mitochondrion // inferred from direct assay//0008089 // anterograde axon cargo transport // inferred from mutant phenotype//0008090 //
705.3691	1285.108	0.0085573	NM_177715	1.81	Kctd12	potassium channel tetramerization domain containing 12	0008277 // regulation of G-protein coupled receptor protein signaling pathway // inferred from genetic interaction//0051260 // protein homooligomerization // inferred fro
3539.897	6248.1313	0.0088655	NM_009160	1.82	Sftpd	surfactant associated protein D	0002376 // immune system process // inferred from electronic annotation//0007585 // respiratory gaseous exchange // inferred from electronic annotation//0008228 // o
124.19299	226.99611	0.0085929	NM_001254747//NM_008	1.82	Il15	interleukin 15	0001779 // natural killer cell differentiation // inferred from genetic interaction//0001866 // NK T cell proliferation // inferred from mutant phenotype//0006954 // inflamm
463.41934	865.88745	0.0078742	NM_001281819//NM_009	1.83	Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	0001822 // kidney development // inferred from mutant phenotype//0001822 // kidney development // not recorded//0002446 // neutrophil mediated immunity // infer
114.420746	205.82428	0.0071764	NM_001190490//NM_001	1.83	Dmpk	dyostrophin myotonic-protein kinase	0000082 // G1/S transition of mitotic cell cycle // --//0002028 // regulation of sodium ion transport // inferred from mutant phenotype//0006468 // protein phosphorylat
1092.0975	1994.2253	0.004449	NM_001134191//NM_001	1.83	Gm21949//Schip1	predicted gene, 21949//schwannomin interacting protein 1	0001553 // uterine invagination // inferred from genetic interaction//0001822 // kidney development // inferred from mutant phenotype//0006807 // nitrogen compound metab
165.57332	303.71582	0.0058281	NM_001037221//NM_001	1.84	Samd4	sterile alpha motif domain containing 4	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006417 // regulation of translation // inferred from electronic annotation//
81.79255	146.99629	0.008644	NM_008032//NM_006527	1.84	Afp2	A1/FMR2 family, member 2	0006397 // mRNA processing // inferred from electronic annotation//0007611 // learning or memory // inferred from mutant phenotype//0008380 // RNA splicing // infer
27.299326	50.68959	0.0080529	NM_001081642//NM_001	1.84	Xlr4a//Xlr4b//Xlr4c	X-linked lymphocyte-regulated 4A//X-linked lymphocyte-regulated 4B//X-linked lyr	0007286 // spermatid development // not recorded//0051965 // positive regulation of synapse assembly // inferred from mutant phenotype//00061003 // positive regulati
157.13287	286.29163	0.0097449	NM_181073//NM_006515	1.85	Plekhh1	pleckstrin homology domain containing, family H (with MyTH domain) member 1	
84.94911	154.22983	0.0070842	NM_144810//NM_006529	1.85	Klhdc8a	kelch domain containing 8A	0042787 // protein ubiquitination involved in ubiquitin-dependent protein catabolic process // not recorded
58.70021	109.41725	0.0096679	NM_003150	1.85	Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58	0002376 // immune system process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0009615 // response to
65.54396	119.71974	0.0089693	NM_001083906//NM_006	1.85	Nr3c2	nuclear receptor subfamily 3, group C, member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annot
832.7405	1534.192	0.0086932	NM_010156//NM_177590	1.85	Samd9l	sterile alpha motif domain containing 9-like	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//0017145 // stem cell division // inferred from mutant phenotype//0034058 //
195.23616	363.6839	0.0016791	NM_008846//NM_006526	1.85	Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	0016310 // phosphorylation // inferred from electronic annotation//0046488 // phosphatidylinositol metabolic process // inferred from direct assay//0046484 // phosphat
469.6203	884.9181	0.0091547	NM_026163	1.85	Pkp2	p plakophilin 2	0002159 // desmosome assembly // not recorded//0007507 // heart development // inferred from mutant phenotype//0008285 // negative regulation of cell proliferation
905.9772	1689.2041	0.0088871	NM_0194142//NM_198048	1.85	Prx	perixin	0019226 // transmission of nerve impulse // inferred from mutant phenotype//0019233 // sensory perception of pain // inferred from mutant phenotype//0032287 // peri
45.013584	83.33225	0.0079038	NM_001161837//NM_001	1.86	Ptprr	protein tyrosine phosphatase, receptor type, R	0001701 // in utero embryonic development // inferred from sequence or structural similarity//0001701 // in utero embryonic development // inferred from electronic ann
570.0356	1069.675	0.0080529	NM_011909	1.86	Usp18	UBR3 regulatory peptidase 18	0006508 // proteolysis // inferred from electronic annotation//0006511 // ubiquitin-dependent protein catabolic process // inferred from electronic annotation//0016579 //
247.34767	466.3572	0.0022089	NM_029870//NM_006525	1.87	Crefb1	CREB3 regulatory factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic ann
493.22305	934.52826	0.0065464	NM_008591//NM_006504	1.87	Mct	met proto-oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0000187 // activation of MAPK activity // inferred from physical interacti
1139.4884	2124.53	0.0066692	NM_001040005//NM_006	1.87	Rnf213	ring finger protein 213	0008152 // metabolic process // inferred from electronic annotation//0016567 // protein ubiquitination // not recorded//0051865 // protein autoubiquitination // not rec
1570.9651	2895.2432	0.0065464	NM_175386	1.87	Lhfp	lipian HMGIC fusion partner	
155.73012	293.67978	0.0089296	NM_010266//NM_006526	1.87	Gda	guanine deaminase	0006147 // guanine catabolic process // inferred from electronic annotation//0031116 // positive regulation of microtubule polymerization // not recorded//0040698 // gu
78.21652	143.29047	0.0093601	NM_021560	1.88	Bhhle22	basic helix-loop-helix family, member e22	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annot
31.886229	60.065887	0.0097449	NM_001035042//NM_001	1.88	Spef2	spERM tagellar 2	0002520 // immune system development // inferred from mutant phenotype//0007283 // spermatogenesis // inferred from mutant phenotype//0009566 // fertilization //
271.8951	514.67596	0.0086932	NM_001025379//NM_006	1.88	Sema3g	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphor	0001755 // neural crest cell migration // not recorded//0003035 // positive regulation of cell migration // not recorded//0048843 // negative regulation of axon extensi
58.09308	108.905464	0.003657	NM_028048//NM_006534	1.88	Slc25a35	solute carrier family 25, member 35	0006810 // transport // inferred from electronic annotation
160.99495	299.06546	0.0063393	NM_0118801//NM_173067	1.88	Syt7	synaptotagmin VII	0001778 // plasma membrane repair // inferred from direct assay//0006887 // exocytosis // inferred from electronic annotation//0006906 // vesicle fusion // --//001607
422.0928	808.178	0.0098942	NM_001289462//NM_001	1.89	Mme	mannose metallo endopeptidase	0001822 // kidney development // inferred from sequence or structural similarity//0001822 // kidney development // inferred from electronic annotation//0006508 // pr
391.24072	751.61505	0.0051039	NM_178772//NM_011249	1.89	Nche1	neutral cholesterol ester hydrolase 1	0006470 // protein dephosphorylation // inferred from direct assay//0006629 // lipid metabolic process // inferred from electronic annotation//0006805 // xenobiotic met
440.41406	847.1742	0.0091756	NM_207237//NM_006538	1.89	Man1c1	mannosidase, alpha, class 1C, member 1	0006013 // mannose metabolic process // not recorded//0006491 // N-glycan processing // not recorded//0008152 // metabolic process // inferred from electronic annot
1695.592	3142.9358	0.003657	NM_026432	1.89	Saraf	store-operated calcium entry-associated regulatory factor	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // infer
129.56706	243.19618	0.0085589	NM_001316678//NM_001	1.89	Ptprc	protein tyrosine phosphatase, receptor type, E	0006470 // protein dephosphorylation // inferred from electronic annotation//0007185 // transmembrane receptor protein tyrosine phosphatase signaling pathway // infer
1264.7797	2382.2705	0.0071527	NM_001135149//NM_001	1.90	Slc39a8	solute carrier family 39 (metal ion transporter), member 8	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006829 // zinc II ion transport // not rec
171.44202	323.4576	0.0091557	NM_009744	1.90	Bcl6	B cell leukemia/lymphoma 6	0000060 // protein import into nucleus, translocation

[C3H/HeN][raw]	[Gsr-KO][raw]	p [Corr]	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
183.5103	352.99823	0.0075048	NM_001085501	1.93	Ppp1r3d	protein phosphatase 1, regulatory subunit 3D	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0005977 // glycogen metabolic process // inferred from electronic annotation//0005977
957.9298	1837.1918	0.0053533	NM_0052347	1.93	Bmper	BMP-binding endothelial regulator	0001657 // ureteric bud development // inferred from expression pattern//0002043 // blood vessel endothelial cell proliferation involved in sprouting angiogenesis // not rec
316.13116	618.3344	0.0066381	NM_001042605//NM_010_1.93		Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II anti	0000187 // activation of MAPK activity // not recorded//0001516 // prostaglandin biosynthesis process // not recorded//0001961 // positive regulation of cytokine-mediat
199.3179	388.6029	0.0070571	NM_001290814//NM_010_1.93		Aff3	A4/FMR2 family, member 3	0006351 // transcription, DNA-templated // traceable author statement//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006351
7611.6143	13720.644	0.0029632	NM_013590	1.94	Lyz1	lysozyme 1	0008152 // metabolic process // inferred from electronic annotation//0019835 // cytolysis // inferred from electronic annotation//0042742 // defense response to bacteri
143.35594	278.46924	0.0064052	NM_144547//XXM_006520_1.95		Amlr2	anti-Mullerian hormone type 2 receptor	0006468 // metallophosphorylation // inferred from electronic annotation//0007165 // signal transduction // not recorded//0007178 // transmembrane receptor protein: /
170.1078	334.28027	0.0063393	NM_001253872//NM_001_1.96		Itgal	integrin alpha L	0002291 // T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell // not recorded//0007155 // cell adhesion // inferred /
218.2756	431.7685	0.0093601	NM_001291071//NM_019_1.97		Pfkap	phosphofuroctokinase, platelet	0006002 // fructose 6-phosphate metabolic process // not recorded//0006096 // glycolytic process // not recorded//0006096 // metabolic process // inferred from electro
183.34116	360.3573	0.0062819	NM_025285	1.97	Stmn2	stathmin-like 2	0007230 // microtubule depolymerization // not recorded//0007026 // negative regulation of microtubule depolymerization // not recorded//0010976 // positive regulati
570.3194	1147.4928	0.0068707	NM_013743	1.98	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	0000219 // positive regulation of defense response to virus by host // not recorded//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0002122 //
123.05497	239.6657	0.0065811	NM_001127330//NM_001_1.98		Pparg	peroxisome proliferator activated receptor gamma	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA p
166.21759	324.85428	0.0065811	NM_0010109//NM_0207654_1.98		EfnA5	ephrin A5	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//,
835.683	1664.1372	0.009206	NM_010821//NM_006526_1.99		Mpeg1	macrophage expressed gene 1	0006725 // cellular aromatic compound metabolic process // not recorded//0018879 // biphenyl metabolic process // not recorded//0018917 // fluorene metabolic proces
862.0359	1742.0831	0.0054206	NM_007823	1.99	Cyp4b1	cytochrome P450, family 4, subfamily b, polypeptide 1	0006725 // cellular aromatic compound metabolic process // not recorded//0018879 // biphenyl metabolic process // not recorded//0018917 // fluorene metabolic proces
346.9916	702.69035	0.0051039	NM_001081369//XXM_006_2.00		Cxcl15	colled-coil domain containing 153	0006725 // cellular aromatic compound metabolic process // not recorded//0018879 // biphenyl metabolic process // not recorded//0018917 // fluorene metabolic proces
110.81851	217.79674	0.0071292	NM_026346	2.00	Fbxo32	F-box protein 32	0014878 // response to electrical stimulus involved in regulation of muscle adaptation // not recorded//0014889 // muscle atrophy // not recorded//0014894 // response t
205.68527	413.8293	0.0059714	NM_146017//NM_006514_2.00		Gabbr	gamma-aminobutyric acid (GABA) A receptor, pi	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006821 // chloride transport // inferred fro
44.236576	87.78764	0.0066908	NM_183187//NM_006518_2.00		Fam107a	family with sequence similarity 107, member A	0001558 // regulation of cell growth // not recorded
513.9294	1058.8928	0.0087842	NM_008481//NM_006512_2.02		Lama2	laminin, alpha 2	0007155 // cell adhesion // inferred from electronic annotation//0007411 // axon guidance // inferred from genetic interaction//0022011 // myelination in peripheral nerv
262.12515	531.6998	0.0066908	NM_183180//NM_006499_2.02		Tspan18	tetraspanin 18	0007166 // cell surface receptor signaling pathway // not recorded
1361.3677	2712.8774	0.0029159	NM_001034851//NM_001_2.02		Fam134b	family with sequence similarity 134, member B	0006914 // autophagy // inferred from electronic annotation//0019233 // sensory perception of pain // not recorded//0043524 // negative regulation of neuronal apoptotic
670.5195	1381.5487	0.0051039	NM_001177980//NM_001_2.03		Pde4b	phosphodiesterase 4B, cAMP specific	0001780 // neurotrophin homeostasis // inferred from mutant phenotype//0006198 // cAMP catabolic process // inferred from direct assay//0006198 // cAMP catabolic proc
282.0061	580.5407	0.0068997	NM_139200//XXM_006498_2.03		Cytip	cytohesin 1 interacting protein	0030155 // regulation of cell adhesion // not recorded
564.5124	1168.4445	0.0089693	NM_001020927//XXM_006_2.03		Penk	preproenkephalin	0001662 // behavioral fear response // inferred from mutant phenotype//0001964 // startle response // inferred from mutant phenotype//0002118 // aggressive behavior
269.2509	550.75854	0.0087842	NR_02845	2.04	Copg2os2	coatamer protein complex, subunit gamma 2, opposite strand 2	
72.43213	143.86687	0.0080529	NM_177388//NM_006513_2.04		Slc41a2	solute carrier family 41, member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from
102.79859	206.82564	0.0098162	NM_009676//XXM_006495_2.04		Aox1	aldehyde oxidase 1	0055114 // oxidation-reduction process // inferred from electronic annotation
243.65027	502.38266	0.0080529	NM_025658	2.04	Ms4d4d	membrane-spanning 4-domains, subfamily A, member 4D	
234.50768	483.66772	0.0097449	NM_172771//XXM_006511_2.05		Dmx12	Dmx-like 2	
126.23253	255.52855	0.0080091	NM_001284189//NM_011_2.05		Home1	homeo homolog 1 (Drosophila)	0003009 // skeletal muscle contraction // inferred from mutant phenotype//0007216 // G-protein coupled glutamate receptor signaling pathway // not recorded//0007216
197.83577	408.99017	0.0085589	NM_133969	2.05	Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	0006629 // lipid metabolic process // inferred from electronic annotation//0010430 // fatty acid omega-oxidation // not recorded//0055114 // oxidation-reduction proces
8346.263	15851.749	0.0028223	NM_011339	2.06	Cxcl15	chemokine (C-X-C motif) ligand 15	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006935 // chemotaxis // inferred from direct assay//0006954 // inflammatory response // infer
112.669655	227.2316	0.0039361	NM_001033336//NM_001_2.06		Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	0006810 // transport // inferred from electronic annotation//0006855 // drug transmembrane transport // traceable author statement//0008152 // metabolic process // infer
553.1897	1158.5629	0.0074508	NM_001038917//NM_001_2.06		Scn3b	sodium channel, voltage-gated, type III, beta	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006814 // sodium ion transport // not reco
272.63644	568.39166	0.0085634	NM_145158//XXM_006524_2.07		Emilin2	elastin microfibril interactor 2	0007155 // cell adhesion // inferred from electronic annotation
6952.505	13050.141	0.0098162	NM_017372	2.07	Lyz2	lysozyme 2	0008152 // metabolic process // inferred from electronic annotation//0019835 // cytolysis // inferred from electronic annotation//0042742 // defense response to bacteri
1783.7448	3611.0603	0.0075737	NM_021475	2.07	Adamde1	ADAM-like, decysin 1	0006508 // proteolysis // inferred from electronic annotation
215.27951	446.15735	0.0088655	NM_011104//XXM_006523_2.07		Prkce	protein kinase C, epsilon	0002281 // macrophage activation involved in immune response // inferred from mutant phenotype//0002376 // immune system process // inferred from electronic annot
540.2403	1132.3718	0.0096782	NM_001130479//NM_016_2.08		Nucb2	nucleobindin 2	0006874 // cellular calcium ion homeostasis // traceable author statement//0009749 // response to glucose // inferred from electronic annotation//0030818 // negative re
201.31445	418.7091	0.0057594	NM_178890	2.08	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	0009737 // cellular response to toxic substance // inferred from mutant phenotype
120.35099	248.19347	0.0029632	NM_011395	2.08	Slc22a3	solute carrier family 22 (organic cation transporter), member 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0015695 // organic cation transport // infer
141.80731	292.08832	0.0075124	NM_175460//NM_006529_2.08		Nnma12	nicotianamide nucleotide adenyltransferase 2	0006767 // water-soluble vitamin metabolic process // not recorded//0009058 // biosynthesis process // inferred from electronic annotation//0009425 // NAD biosynthesi
141.44603	291.13028	0.0045517	NM_172887//NM_18781_2.08		Fry	furry homolog (Drosophila)	0000902 // cell morphogenesis // not recorded//0031175 // neuron projection development // not recorded//0043086 // negative regulation of catalytic activity // infer
47.727184	98.83141	0.0075335	NM_001039094//NM_177_2.08		Negr1	neuronal growth regulator 1	0007155 // cell adhesion // inferred from electronic annotation//0007626 // locomotory behavior // inferred from mutant phenotype//0007631 // feeding behavior // infer
403.36682	859.81635	0.0065754	NM_001159485//NM_001_2.09		Mcf2l	mcf2 transforming sequence-like	0007266 // Rho protein signal transduction // inferred from direct assay//0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation//C
25.09648	53.149937	0.0066381	NM_145838//XXM_006497_2.09		St8sia6	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 6	0001574 // ganglioside biosynthesis process // inferred from direct assay//0006486 // protein glycosylation // inferred from electronic annotation//0006493 // protein O-li
82.79159	171.69635	0.0068697	NM_009808//NM_006509_2.11		Casp12	caspace 12	0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from reviewed computational analysis//0006915 // apoptotic process // inferred from direct ass
104.49214	217.39034	0.0058241	NM_001164441//NM_026_2.12		Ankrd33b	ankyrin repeat domain 33B	
3200.7126	6525.588	0.0029632	NM_019759	2.12	Dpt	dermatopontin	0007155 // cell adhesion // inferred from electronic annotation//0008285 // negative regulation of cell proliferation // inferred from direct assay//0030199 // collagen fibri
84.07279	173.98712	0.0089693	NM_001159583//NM_027_2.12		Fam219a	family with sequence similarity 219, member A	
1165.376	2492.3284	0.0085589	NM_010171	2.13	F3	coagulation factor III	0001938 // positive regulation of endothelial cell proliferation // not recorded//0002541 // activation of plasma proteins involved in acute inflammatory response // not rec
140.26965	294.8461	0.0059002	NM_177708//XXM_006533_2.13		Rtn4r1l	reticulon 4 receptor-like 1	0031103 // axon regeneration // traceable author statement
39.341496	83.005196	0.0080529	NM_006543141//NM_012_2.13		Gm626	predicted gene 626	
311.07205	674.5031	0.0053533	NM_008332//XXM_006526_2.14		Ifit2	interferon-induced protein with tetratricopeptide repeats 2	0002376 // immune system process // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation//0006915 // response to v
77.038185	162.28484	0.0054667	NM_010474	2.14	H3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	0008152 // metabolic process // inferred from electronic annotation
499.13605	1098.2954	0.0096782	NM_008343//XXM_011243_2.16		lgfbp3	insulin-like growth factor binding protein 3	0001588 // regulation of cell growth // inferred from genetic interaction//0001649 // osteoblast differentiation // inferred from expression pattern//0001933 // negative re
146.05898	313.95056	0.0045556	NM_001001179	2.18	BC048546	cDNA sequence BC048546	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // inferred from electr
65.58282	141.8646	0.003657	NM_007413	2.18	Adora2b	adenosine A2b receptor	0001973 // adenosine receptor signaling pathway // inferred from electronic annotation//0002882 // positive regulation of chronic inflammatory response to non-antigenic
143.07633	313.9796	0.0085929	NM_197986//XXM_006506_2.18		Tmem140	transmembrane protein 140	
105.139244	225.87843	0.0093601	NM_001143776//NM_001_2.18		Fam13c	family with sequence similarity 13, member C	
1925.8959	4058.4963	0.0098878	NM_001267695//NM_021_2.19		Cts5	cathepsin S	0002250 // adaptive immune response // inferred from electronic annotation//0006508 // proteolysis // inferred from direct assay//0006508 // proteolysis // not recordec
505.31128	1128.7517	0.0091692	NM_001252578//NM_001_2.19		Sulf2	sulfatase 2	0001822 // kidney development // inferred from genetic interaction//0002063 // chondrocyte development // inferred from mutant phenotype//0003094 // glomerular fil
277.31012	612.9941	0.0065811	NM_011107//NM_006530_2.19		Plg2g1b	phospholipase A2, group IB, pancreas	0002227 // innate immune response in mucosa // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006633 // fatty acid biosynthe
71.52299	155.01794	0.0068697	NM_001163161//NM_010_2.20		Clec4d	cell-type lectin domain family 4, member d	0002250 // adaptive immune response // inferred from mutant phenotype//0002292 // T cell differentiation involved in immune response // inferred from mutant phenoty
82.66568	181.7305	0.0086841	NM_001164059//NM_011_2.20		Seif	selectin, lymphocyte	0007155 // cell adhesion // inferred from electronic annotation//0033198 // response to ATP // inferred from direct assay//0034201 // response to oleic acid // inferred fr
2931.3572	6099.77	0.0075737	NM_021472//NM_201239_2.20		Rnase4	ribonuclease, RNase A family 4	0001525 // angiogenesis // inferred from electronic annotation//0001525 // angiogenesis // inferred from sequence or structural similarity//
65.77799	143.27281	0.0065726	NM_00104867//XXM_006_2.20		Pm20d2	peptidase M20 domain containing 2	0008152 // metabolic process // inferred from electronic annotation
412.89944	925.6845	0.0080529	NM_172471//NM_006497_2.21		Ith5	inter-alpha (globulin) inhibitor h5	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // inferred from electr
922.0197	2029.1315	0.0063393	NM_001290549//NM_001_2.21		Tsk	endothelial-specific receptor tyrosine kinase	0001525 // angiogenesis // inferred from mutant phenotype//0001525 // angiogenesis // traceable author statement//0001569 // patterning of blood vessels // infer
221.3412	490.21185	0.0068707	NM_028135//XXM_011248_2.21		Tmem163	transmembrane protein 163	
156.42018	340.83166	0.0089693	NM_178405	2.22	Atp1a2	ATPase, Na(+)/K(+)-transporting, alpha 2 polypeptide	0001504 // neurotransmitter uptake // inferred from mutant phenotype//0002026 // regulation of the force of heart contraction // inferred from mutant phenotype//0002
108.42433	239.35023	0.0016929	NM_001025074//NM_001_2.22		Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	0001570 // vasculogenesis // inferred from mutant phenotype//0001764 // neuron migration // inferred from mutant phenotype//0006468 // protein phosphorylation // i
2165.2852	4642.895	0.0058241	NM_010406	2.23	Hc	hemolytic complement	0001701 // in utero embryonic development // inferred from genetic interaction//0002376 // immune system process // inferred from electronic annotation//0006954 // i
174.98154	389.37378	0.0036447	NM_009062	2.23	Rgs4	regulator of G-protein signaling 4	0007186 // G-protein coupled receptor signaling pathway // traceable author statement//0009968 // negative regulation of signal transduction // inferred from electronic ar
303.26843	685.24176	0.0066555	NM_001285833//NM_001_2.23		Nox4	NADPH oxidase 4	0009092 // cell morphogenesis // inferred from mutant phenotype//0001666 // response to hypoxia // inferred from electronic annotation//0006801 // superoxide metab
274.38187	616.9132	0.0065644	NM_0019588//XXM_006527_2.23		Plice1	phospholipase C, epsilon 1	0000187 // activation of MAPK activity // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0007165 // signal transduction // infer
206.79994	465.12817	0.0056277	NM_001005422	2.24	Stmn1	stathmin domain containing 1	0007019 // microtubule depolymerization // not recorded//0031110 // regulation of microtubule polymerization or depolymerization // inferred from electronic annotati
3339.0195	7139.971	0.0056422	NM_023134//XXM_011244_2.24		Sftoa1	surfactant associated protein A1	0001666 // response to hypoxia // inferred from electronic annotation//0007623 // circadian rhythm // inferred from electronic annotation//0009725 // response to horm
261.6693	595.74915	0.008644	NM_008013	2.24	Fgl2	fibrinogen-like protein 2	0019835 // cytolysis // inferred from electronic annotation
46.226135	105.49858	0.0087756	NM_001190869//NM_001_2.24		Kcnc3	potassium voltage-gated channel, Isk-related subfamily, gene 3	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // infer

[C3H/HeN][raw]	[Gsr-KO][raw]	p [Corr]	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
248.62372	565.4211	0.0097449	NM_001080707//NM_001_2.27	2.28	Gpr155	G protein-coupled receptor 155	0035556 // intracellular signal transduction // inferred from electronic annotation//0050890 // cognition // not recorded//0055085 // transmembrane transport // inferred
66.32563	147.98506	0.0075737	NM_0195177//NM_006523C_1.28	2.27	Bace2	beta-site APP-cleaving enzyme 2	0006508 // proteolysis // inferred from electronic annotation//0006509 // membrane protein ectodomain proteolysis // not recorded//0030163 // protein catabolic process
299.9457	689.37805	0.0063393	NM_0110566//NM_006517L_1.28	2.28	Pde4d	phosphodiesterase 4D, cAMP specific	0002027 // regulation of heart rate // inferred from mutant phenotype//0006198 // cAMP catabolic process // inferred from direct assay//0006198 // cAMP catabolic process
1120.0814	2564.8206	0.0070842	NM_029928//NM_006513C_1.28	2.28	Ptpnb	protein tyrosine phosphatase, receptor type, B	0001525 // angiogenesis // inferred from direct assay//0001525 // angiogenesis // inferred from mutant phenotype//0006470 // protein dephosphorylation // inferred from
170.89438	391.39023	0.0093457	NM_177629	2.29	Fam216b	family with sequence similarity 216, member B	
89.581764	207.10336	0.0081374	NM_010350//NM_006532C_1.28	2.29	Grin2c	glutamate receptor, ionotropic, NMDA2C (epsilon 3)	0001964 // startle response // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation
71.34034	159.94627	0.0079020	NM_001024474//NM_006_2.31	2.31	Diras2	DIRAS family, GTP-binding RAS-like 2	0007165 // signal transduction // inferred from electronic annotation//0007264 // small GTPase mediated signal transduction // inferred from electronic annotation
277.63974	649.59906	0.0030958	NM_008926//NM_006534C_1.28	2.31	Prkg2	protein kinase, cGMP-dependent, type II	0006468 // protein phosphorylation // inferred from electronic annotation//0007623 // circadian rhythm // inferred from mutant phenotype//0016310 // phosphorylation
100.182076	229.4005	0.003839	NM_013875//NM_006512C_1.28	2.31	Pde7b	phosphodiesterase 7B	0006198 // cAMP catabolic process // inferred from electronic annotation//0007165 // signal transduction // inferred from electronic annotation//0008152 // metabolic p
220.03156	514.675	0.0065754	NM_001010937//NM_001_2.32	2.32	Gjb6	gap junction protein, beta 6	0006915 // apoptotic process // inferred from electronic annotation//0007154 // cell communication // inferred from electronic annotation//0007568 // aging // inferred f
75.645226	172.8547	0.0083164	NM_001163645//NM_027_2.32	2.32	Osbp13	oxysterol binding protein-like 3	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation
130.28003	298.87988	0.0063393	NM_198612//NM_006506C_1.28	2.32	Gxylt2	glucosyl xylosyltransferase 2	0016266 // O-glycan processing // not recorded
118.558075	280.851	0.0068697	NM_029796	2.33	Lrg1	leucine-rich alpha-2-glycoprotein 1	0001938 // positive regulation of endothelial cell proliferation // inferred from mutant phenotype//0030511 // positive regulation of transforming growth factor beta recept
84.71815	195.9373	0.0066692	NM_007609//NM_006508L_1.28	2.34	Casp4	caspace-4, apoptosis-related cysteine peptidase	0006508 // proteolysis // inferred from reviewed computational analysis//0006915 // apoptotic process // not recorded//0007015 // actin filament organization // traceab
125.147896	289.6305	0.0068697	NM_001039530//NM_006_2.34	2.34	Panp14	pankayin domain 29	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
78.07248	178.92007	0.0084158	NM_001190371	2.34	Ankrd29	ankyrin repeat domain 29	
270.6297	645.497	0.003657	NM_011584	2.35	Nr1d2	nuclear receptor subfamily 1, group D, member 2	0006355 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from direct assay//001
46.896732	109.975426	0.0088565	NM_182839//NM_006517L_1.28	2.36	Tppp	tubulin polymerization promoting protein	0001578 // microtubule bundle formation // not recorded//0031334 // positive regulation of protein complex assembly // inferred from sequence or structural similarity//0
1191.6819	2793.941	0.0057397	NM_001081178//NM_006_2.37	2.37	Adgrf5	adhesion G-protein-coupled receptor F5	0006112 // energy reserve metabolic process // inferred from mutant phenotype//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation
62.762768	147.30373	0.0040505	NM_139134//NM_006523C_1.28	2.38	Chodl	chondrolectin	0010975 // regulation of neuron projection development // inferred from genetic interaction
367.12323	891.27124	0.003657	NM_001037713//NM_001_2.39	2.39	Xaf1	XIAP associated factor 1	0006915 // apoptotic process // inferred from electronic annotation//0031333 // negative regulation of protein complex assembly // not recorded//0035456 // response t
12435.358	26707.742	0.002626	NM_011681	2.39	Scgb1a1	secretoglobin, family 1A, member 1 (uteroglobin)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA p
52.192047	126.30348	0.0029632	NM_001291903//NM_009_2.41	2.41	Adcy8	adenylyl cyclase 8	0006171 // cAMP biosynthetic process // not recorded//007189 // adenylyl cyclase-activating G-protein coupled receptor signaling pathway // not recorded//0007193
146.92699	350.37753	0.0063393	NM_001113198//NM_001_2.42	2.42	Mitf	microphthalmia-associated transcription factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic ann
59.913155	143.71056	0.0030958	NM_00121297	2.42	Tlr4	tolllike receptor 4	0000187 // activation of MAPK activity // inferred from mutant phenotype//0001774 // microglial cell activation // not recorded//0002218 // activation of innate immune
816.94666	1980.6986	0.0066908	NM_001164724//NM_133_2.43	2.43	Il33	interleukin 33	0002686 // negative regulation of leukocyte migration // inferred from genetic interaction//0002826 // negative regulation of T-helper 1 type immune response // inferred f
19.55856	47.740593	0.0079038	NM_00121718	2.44	Ms4d4b	membrane-spanning 4-domains, subfamily A, member 4B	
399.34976	976.8734	0.0079038	NM_020509	2.44	Retna	resistin like alpha	
447.8262	1111.3579	0.0063393	NM_001145886//NM_001_2.45	2.45	Tiam1	T cell lymphoma invasion and metastasis 1	0003300 // cardiac muscle hypertrophy // not recorded//0007160 // cell-matrix adhesion // not recorded//0007165 // signal transduction // inferred from electronic anno
46.329746	114.348724	0.0029632	NM_009381	2.45	Thrsp	thyroid hormone responsive	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
3121.7246	7459.5205	0.0028223	NM_009127	2.47	Scd1	sterol Coenzyme A desaturase 1	0006629 // lipid metabolic process // inferred from electronic annotation//0006631 // fatty acid metabolic process // inferred from electronic annotation//0006633 // fatt
187.52766	466.9856	7.89E-04	NM_172892	2.48	Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4	0006814 // sodium ion transport // inferred from electronic annotation//0008272 // sulfate transport // --//0035725 // sodium ion transmembrane transport // --//0055
249.69566	623.3437	0.0054644	NM_001098799//NM_006_2.48	2.48	Tox2	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
36.784607	90.86002	0.0055381	NM_001012324	2.50	Ecm2	extracellular matrix protein 2, female organ and adipocyte specific	0007409 // xenogenesis // not recorded//0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay//0030198 // extracellular matrix organiza
63.79858	159.57997	0.007891	NM_144559	2.51	Fcgr4	Fc receptor, IgG, low affinity IV	0001866 // NK T cell proliferation // not recorded//0051930 // regulation of sensory perception of pain // not recorded//0071222 // cellular response to lipopolysaccharid
15.575886	37.80726	0.0099337		2.51	Igic2//Ilgc3//Iglv1	immunoglobulin lambda constant 2//immunoglobulin lambda constant 3//immun	0006898 // receptor-mediated endocytosis // not recorded//0006910 // phagocytosis, recognition // not recorded//0006911 // phagocytosis, engulfment // not recorded//
579.46643	1448.4227	0.0065464	NM_023386//NM_006522C_1.28	2.51	Rtp4	receptor transporter protein 4	0001580 // detection of chemical stimulus involved in sensory perception of bitter taste // not recorded//0006612 // protein targeting to membrane // not recorded//0051
282.9635	726.5134	0.0029632	NR_045305	2.55	AU049972	expressed sequence AU049972	
313.8854	804.7225	0.0068697	NM_011446	2.55	Sox7	SRY (sex determining region Y)-box 7	0007306 // endoderm formation // not recorded//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription,
264.44065	689.82953	0.0055381	NM_007592	2.57	Car8	carbonic anhydrase 8	0006730 // one-carbon metabolic process // inferred from electronic annotation//0048015 // phosphatidylinositol-mediated signaling // inferred from direct assay
88.28486	226.24412	0.0070842	NM_001020898//NM_001_2.58	2.58	LOC10038947//Sirp1a1	Sigal-regulatory protein beta 1-like//signal-regulatory protein beta 1A//signal-regu	0035556 // intracellular signal transduction // inferred from direct assay//0005766 // positive regulation of phagocytosis // inferred from direct assay
78.65452	201.84773	0.0056277	NM_001101605//NM_001_2.59	2.59	Ifi1b1	interferon induced protein with tetratricopeptide repeats 1B like 1	0051607 // defense response to virus // not recorded//0002337 // type I interferon signaling pathway // not recorded
155.10568	399.486	0.0048754	NM_001308641//NM_001_2.59	2.59	Aqp4	aquaporin 4	0006810 // transport // inferred from electronic annotation//0006833 // water transport // inferred from mutant phenotype//0006833 // water transport // not recorded/
476.5647	1249.7941	0.0055381	NM_007734	2.60	Col4a3	collagen, type IV, alpha 3	0006919 // activation of cysteine-type endopeptidase activity involved in apoptotic process // not recorded//0007155 // cell adhesion // inferred from electronic annotation/
43.79667	111.05094	0.0029632	NM_001034874//NM_006_2.60	2.60	Shis6	shisa family member 6	0048172 // regulation of short-term neuronal synaptic plasticity // not recorded
169.33844	446.06946	0.0043221	NM_001164437//NM_006_2.60	2.60	Tmem212	transmembrane protein 212	
53.896458	142.30481	0.001878	NM_001081088	2.64	Lrp2	low density lipoprotein receptor-related protein 2	0003281 // ventricular septum development // inferred from mutant phenotype//0006766 // vitamin metabolic process // inferred from mutant phenotype//0006897 // ei
115.617325	305.10468	0.002626	NM_153576	2.64	Cxcl17	chemokine (C-X-C motif) ligand 17	0001525 // negative regulation of septum development // inferred from electronic annotation//0006935 // chemotaxis // inferred from electronic annotation//0007275 // multicellular organismal dev
133.59479	355.50977	0.0066381	NM_0118874	2.65	Pnliprp1	pancreatic lipase related protein 1	0006629 // lipid metabolic process // inferred from electronic annotation
110.56271	295.46518	0.0038113	NM_001033450//NM_001_2.65	2.65	Ifi204//Ifi205//Mnda//Mm	interferon activated gene 204//interferon activated gene 205//myeloid cell nuclear	0000122 // negative regulation of transcription from RNA polymerase II promoter // --//0006351 // transcription, DNA-templated // inferred from electronic annotation//0
73.1712	196.85178	0.0068697	NM_010780	2.67	Cma1	chymase 1, mast cell	0006508 // proteolysis // not recorded//0006518 // peptide metabolic process // inferred from electronic annotation//0016485 // protein processing // not recorded//00
1158.1539	3081.4294	0.0030958	NM_0019634//NM_006527C_1.28	2.69	Tspan7	tetraspanin 7	0007166 // cell surface receptor signaling pathway // not recorded
115.40602	416.12753	0.003657	NM_00121320	2.69	Ntn4	netrin 4	0016322 // neuron remodeling // inferred from direct assay//0006668 // regulation of branching involved in salivary gland morphogenesis by extracellular matrix-epithelial
219.98262	592.2917	0.0017344	NM_0023850//NM_006500C_1.28	2.69	Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006012 // galactose metabolic process // not recorded//0006790 // sulfur compound
271.42337	734.7937	0.0038505	NM_001276719//NM_021_2.69	2.69	Acr2	atypical chemokine receptor 2	0006898 // receptor-mediated endocytosis // not recorded//0006935 // chemotaxis // inferred from electronic annotation//0006954 // inflammatory response // inferred
83.36129	224.26677	0.003657	NM_001313712//NM_001_2.72	2.72	Sp100	nuclear antigen Sp100	0000723 // telomere maintenance // inferred from sequence or structural similarity//0006338 // chromatin remodeling // not recorded//0006351 // transcription, DNA-tem
59.955883	163.16252	0.0083164	NM_001316716//NM_001_2.72	2.72	Ddo	D-aspartate oxidase	0006531 // aspartate metabolic process // inferred from mutant phenotype//0006533 // aspartate catabolic process // not recorded//0007320 // insemination // inferred
26.73941	73.40502	0.0071527	NM_001081215//NM_001_2.72	2.72	Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	0008152 // metabolic process // inferred from electronic annotation//0009615 // response to virus // not recorded//0051607 // defense response to virus // inferred from
273.74947	637.3048	0.0084664	NM_016808//NM_198091_1.28	2.72	Usp2	ubiquitin specific peptidase 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006355 // regulation of transcription, DNA-templated // not recorded//
87.42301	238.32614	0.0038113	NM_001033450//NM_001_2.72	2.72	Ifi204//Ifi205//Mnda//Mm	interferon activated gene 204//interferon activated gene 205//myeloid cell nuclear	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotat
22.355173	62.1911	0.0058428	NM_021451	2.81	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1	0001836 // release of cytochrome c from mitochondria // inferred from direct assay//0001836 // release of cytochrome c from mitochondria // inferred from mutant phen
179.624	509.33017	0.003945	NM_001122899//NM_010_2.82	2.82	Lepc	leptin receptor	0001525 // angiogenesis // not recorded//0007165 // signal transduction // traceable author statement//0007186 // G-protein coupled receptor signaling pathway // not r
127.14587	362.2733	0.0071527	NM_007753//NM_006535C_1.28	2.86	Cpa3	carboxypeptidase A3, mast cell	0002002 // regulation of angiotensin levels in blood // inferred from genetic interaction//0002230 // positive regulation of defense response to virus by host // not r
72.75436	207.88339	0.0070571	NM_00103671//NM_001_2.89	2.89	Pcdha11//Pcdha10//Pcdha1	protocadherin alpha 11//protocadherin alpha 10//protocadherin alpha 11//protoc	0007155 // cell adhesion // inferred from electronic annotation//0007155 // cell adhesion // traceable author statement//0007156 // homophilic cell adhesion via plasma r
338.25473	1145.30774	0.002629	NM_026433//NM_006534C_1.28	2.93	Tmem100	transmembrane protein 100	0001525 // angiogenesis // inferred from mutant phenotype//0001570 // vasculogenesis // inferred from mutant phenotype//0001701 // in utero embryonic development
294.21704	873.9351	0.0056464	NM_181579//NM_006528C_1.28	2.95	Pof1b	premature ovarian failure 1B	
47.54183	140.87915	0.0010672	NM_010720//NM_006525C_1.28	2.95	Lipg	lipase, endothelial	0006629 // lipid metabolic process // inferred from electronic annotation//0007584 // response to nutrient // inferred from electronic annotation//0008152 // metabolic p
49.676265	204.17834	0.0070571	NM_00103671//NM_001_2.97	2.97	Pcdha11//Pcdha10//Pcdha1	protocadherin alpha 11//protocadherin alpha 10//protocadherin alpha 11//protoc	0007155 // cell adhesion // inferred from electronic annotation//0007155 // cell adhesion // traceable author statement//0007156 // homophilic cell adhesion via plasma r
278.57547	843.65344	0.00442	NM_001170851//NM_006_3.02	3.02	Mnda//Ifi204//Ifi205//Mm	myeloid nuclear differentiation antigen like//interferon activated gene 204//interfe	0000122 // negative regulation of transcription from RNA polymerase II promoter // --//0030308 // negative regulation of cell growth // inferred from mutant phenotype//
343.45944	1063.4453	0.0017344	NM_001290541//NM_001_3.07	3.07	Acer2	alkaline ceramidase 2	0001953 // negative regulation of cell-matrix adhesion // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006672 // ceramide m
82.15428	253.48254	0.0059793	NM_029499//NM_006527C_1.30	3.09	Ms4a4c	membrane-spanning 4-domains, subfamily A, member 4C	
21.08036	64.9102	0.0085634	NM_001081642//NM_001_3.09	3.09	Xlr4a//Xlr4b//Xlr4c	X-linked lymphocyte-regulated 4A//X-linked lymphocyte-regulated 4B//X-linked lrr	0007286 // spermatid development // not recorded//0051965 // positive regulation of synapse assembly // inferred from mutant phenotype//0061003 // positive regulati
293.97482	932.5208	0.008644	NM_00892//NM_145126C_1.14	3.14	Chil3//Chil4	chitinase-like 3//chitinase-like 4	0000272 // polysaccharide catabolic process // inferred from electronic annotation//0005975 // carbohydrate metabolic process // inferred from electronic annotation//0k
24.66331	67.95044	0.0063393	NM_001281830//NM_029_3.15	3.15	Ifi272a	interferon, alpha-inducible protein 27 like 2A	0007568 // aging // inferred from direct assay//0009615 // response to virus // inferred from direct assay
84.34006	264.42447	0.0068697	NM_00103671//NM_001_3.15	3.15	Pcdha11//Pcdha10//Pcdha1	protocadherin alpha 11//protocadherin alpha 10//protocadherin alpha 11//protoc	0007155 // cell adhesion // inferred from electronic annotation//0007155 // cell adhesion // traceable author statement//0007156 // homophilic cell adhesion via plasma r
363.27496	1157.218	0.0017358	NM_007607//NM_006532C_1.15	3.15	Car4	carbonic anhydrase 4	0006730 // one-carbon metabolic process // inferred from electronic annotation//0006885 // regulation of pH // inferred by curator//0008152 // metabolic process

[C3H/HeN][raw]	[Gsr-KO][raw]	p (Corr)	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
148.76588	525.8434	0.0017344	NM_001045481//NM_001:3.51	3.51	Gm16340	interferon-activable protein 203-like//interferon activated gene 203//interferon-act	0000122 // negative regulation of transcription from RNA polymerase II promoter // ---//0030308 // negative regulation of cell growth // inferred from mutant phenotype//
148.76588	525.8434	0.0017344	NM_001045481//NM_001:3.51	3.51	Gm16340	interferon-activable protein 203-like//interferon activated gene 203//interferon-act	0000122 // negative regulation of transcription from RNA polymerase II promoter // ---//0030308 // negative regulation of cell growth // inferred from mutant phenotype//
122.42584	440.06717	0.0093457	NM_001302559//NM_011:3.54	3.54	Sjfn4	schlafen 4//schlafen 3	0008285 // negative regulation of cell proliferation // inferred from direct assay
77.33128	277.4902	0.0044089	NM_009978//XM_0064988:3.59	3.59	Cst8	cystatin 8 (cystatin-related epididymal spermatogenic)	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // inferred from electr
19.270977	69.53402	0.0090404	NM_0080847//XM_006505:3.59	3.59	Asb15	ankyrin repeat and SOCS box-containing 15	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // intracellular signal transduction // inferred from electronic annotation
250.2713	918.66266	5.12E-04	NM_028765//XM_006500:3.63	3.63	Acox1	acyl-Coenzyme A oxidase-like	0006631 // fatty acid metabolic process // inferred from electronic annotation//0006635 // fatty acid beta-oxidation // inferred from electronic annotation//0008152 // m
248.67621	911.01575	0.0026157	NM_028770//XM_006521:3.65	3.65	Krt80	keratin 80	
311.6158	1145.917	0.0034655	NM_133871//XM_006502:3.66	3.66	Ifi44	interferon-induced protein 44	
117.619316	433.94168	0.0028847	NM_007689	3.70	Chad	chondroadherin	0001502 // cartilage condensation // inferred from electronic annotation//0060348 // bone development // inferred from mutant phenotype//1900155 // negative regulat
68.84327	254.50429	0.0089772	XR_389090//XR_393604//	3.71	Gm11716	predicted gene 11716	
109.76887	399.0587	0.0096679	NM_008744	3.71	Ntn1	netrin 1	0001764 // neuron migration // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0006930 // substrate-dependent c
127.171875	498.67465	0.0022089	NM_010501//XM_011247:3.88	3.88	Ifi13	interferon-induced protein with tetratricopeptide repeats 3	0002376 // immune system process // inferred from electronic annotation//0008285 // negative regulation of cell proliferation // inferred from sequence or structural simil
240.64757	932.2404	0.0040953	NM_011854//XM_006530:3.89	3.89	Oasl2	2'-5' oligoadenylate synthetase-like 2	0002376 // immune system process // inferred from electronic annotation//0006164 // purine nucleotide biosynthetic process // inferred from direct assay//0006955 // in
21.40042	83.14979	0.0079632	NM_198192	3.95	Orfp1	pyroglutamylated RFamide peptide receptor	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not recorded//0007218 // neuropeptid
81.53489	330.30823	0.0080529	NM_027491	4.11	Rragd	Ras-related GTP binding D	0009267 // cellular response to starvation // not recorded//0010506 // regulation of autophagy // not recorded//0032008 // positive regulation of TOR signaling // not rec
24.4407	99.06813	0.0089693	NM_001081180//XM_0064:4.18	4.18	Spink5	serine peptidase inhibitor, Kazal type 5	0002787 // negative regulation of antibacterial peptide production // inferred from mutant phenotype//0009913 // epidermal cell differentiation // not recorded//0010951
1292.4209	5602.4985	0.0029632	NM_001099217//NM_001:4.35	4.35	Ly6c1	lymphocyte antigen 6 complex, locus C1//lymphocyte antigen 6 complex, locus C2	
284.9526	1298.0779	0.0058237	NM_001039160//NM_001:4.52	4.52	Gm4070	predicted gene 4070//GTPase, very large interferon inducible 1	
97.2642	456.6046	0.0059002	NM_001204201//NM_001:4.62	4.62	Spp1	secreted phosphoprotein 1	0001503 // ossification // inferred from electronic annotation//0001649 // osteoblast differentiation // not recorded//0006954 // inflammatory response // inferred from c
1081.0643	5144.0933	8.76E-04	NM_009349	4.83	Inmt	indolethylamine N-methyltransferase	0009308 // amine metabolic process // not recorded//0009636 // response to toxic substance // inferred from electronic annotation//0032259 // methylation // not recon
105.83715	517.7283	0.0016929	NM_001004173//XM_0064:4.91	4.91	Sgpp2	sphingosine-1-phosphate phosphatase 2	0006470 // protein dephosphorylation // ---//0006470 // protein dephosphorylation // inferred from electronic annotation//0006670 // sphingosine metabolic process // n
732.7444	3666.9175	0.0010806	NM_007695//XM_006529:5.00	5.00	Chit1	chitinase-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006032 // chitin catabolic process // inferred from electronic annotation//0006915 //
75.53567	381.17316	0.0022352	NM_022983	5.03	Lpar3	lysophosphatidic acid receptor 3	0000187 // activation of MAPK activity // inferred from direct assay//0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled
335.8451	1698.0586	7.20E-05	NM_001081346//NM_133:5.07	5.07	Rtkn2	receptor tyrosine kinase 2	0008284 // positive regulation of cell proliferation // inferred from direct assay//0030097 // hemopoiesis // inferred from direct assay
39.824207	215.54616	0.0089693	NM_024435//XM_006513:5.38	5.38	Nts	neurotensin	0001889 // liver development // inferred from electronic annotation//0001975 // response to amphetamine // inferred from electronic annotation//0006972 // hyperosm
1546.6343	8505.589	8.76E-04	NM_001271416//NM_001:5.65	5.65	Ly6a	lymphocyte antigen 6 complex, locus A	
285.31845	1651.0138	0.0053407	NM_001289492//NM_001:5.86	5.86	Gbp3	guanylate binding protein 3	0008152 // metabolic process // inferred from electronic annotation//0035458 // cellular response to interferon-beta // inferred from direct assay//0042832 // defense res
113.93021	760.41766	0.003657	NM_008331	6.73	Ifi11	interferon-induced protein with tetratricopeptide repeats 1	0002376 // immune system process // inferred from electronic annotation//0009615 // response to virus // inferred from mutant phenotype//0035457 // cellular response