Table S2. Lung genes (n=448) significantly different between wild-type (*Gsr* -WT) and glutathione reductase-deficient (*Gsr* -KO) mouse neonates at PND5 (moderated t-test, p < 0.01).

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

p (Corr)	[C3H/HeN, P5](raw)	[Gsr-KO, P5](raw)	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.008322	816.4111	20.499601	NM_001252569///NM_	-39.83	***Serpina1a///Serpina1d***	serine (or cysteine) peptidase inhibitor, clade A, member 1A///serine (or cysteine) peptidase inhibi	0001701 // in utero embryonic development // inferred from mutant phenotype///0006487 // protein N-linked glycosyl
0.007904	1212.1318	31.046421	NM_001111048///NM_	-39.04	***Fga***	fibrinogen alpha chain	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // i
0.007904	3976.5908	111.966354	NM_007423	-35.52	***Afp***	alpha fetoprotein	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype///0001889 // liver development // inferre
0.007904	10688.147	387.60977	NM_009654	-27.57	***Alb***	albumin	0001895 // retina homeostasis // inferred from electronic annotation///0006810 // transport // inferred from electronic
0.007904	2191.248	93.23511	NM_013697	-23.50	***Ttr***	transthyretin	0006810 // transport // inferred from electronic annotation///0042572 // retinol metabolic process // not recorded///0
0.007904	1061.1097	49.17563	NM_009245	-21.58	***Serpina1c***	serine (or cysteine) peptidase inhibitor, clade A, member 1C	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regula
0.009035	769.831	35.87392	NM_009244///XM_0065	-21.46	***Serpina1b///Serpina1e***	serine (or cysteine) preptidase inhibitor, clade A, member 1B///serine (or cysteine) peptidase inhib	0001701 // in utero embryonic development // inferred from mutant phenotype///0006487 // protein N-linked glycosyl
0.007904	1290.831	66.092	NM_001317105///NM_	-19.53	***Fgg***	fibrinogen gamma chain	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // i
0.007904	848.1587	45.2978	NM_181849	-18.72	***Fgb***	fibrinogen beta chain	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // i
0.007904	1642.4264	98.6514	NM_009692	-16.65	***Apoa1***	apolipoprotein A-I	0001932 // regulation of protein phosphorylation // inferred from direct assay///0001935 // endothelial cell proliferatio
0.007904	716.4201	51.838066	NM_001080809///XM_	-13.82	***Cps1***	carbamoyl-phosphate synthetase 1	0000050 // urea cycle // not recorded///0000050 // urea cycle // inferred by curator///0001889 // liver development //
0.008322	375.42416	34.417618	NM_008096	-10.91	***Gc***	group specific component	0006810 // transport // inferred from electronic annotation///0007565 // female pregnancy // inferred from electronic
0.009035	359.7782	36.298824	NM_001102411///NM_	-9.91	***Kng1***	kininogen 1	0006954 // inflammatory response // inferred from electronic annotation///0007204 // positive regulation of cytosolic
0.008322	377.97778	38.284813	NM_007376	-9.87	***Pzp***	pregnancy zone protein	0007566 // embryo implantation // inferred from genetic interaction///0010466 // negative regulation of peptidase acti
0.009035	803.4665	85.73314	NM_001276449///NM_	-9.37	***Ahsg***	alpha-2-HS-glycoprotein	0001503 // ossification // inferred from direct assay///0006461 // protein complex assembly // not recorded///0006953
0.009035	589.5441	63.61869	NM_016668	-9.27	***Bhmt***	betaine-homocysteine methyltransferase	0006479 // protein methylation // not recorded///0006577 // amino-acid betaine metabolic process // not recorded///
0.007904	415.43906	45.725254	NM_008407///XM_0065	-9.09	***Itih3***	inter-alpha trypsin inhibitor, heavy chain 3	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regula
0.009539	376.79904	42.170784	NM_008341	-8.94	***Igfbp1***	insulin-like growth factor binding protein 1	0001558 // regulation of cell growth // inferred from electronic annotation///0008286 // insulin receptor signaling path
0.008514	410.85446	46.395454	NM_133997	-8.86	***Apof***	apolipoprotein F	0006629 // lipid metabolic process // inferred from electronic annotation///0006641 // triglyceride metabolic process //
0.00824	321.74286	36.345715	NM_080844///XM_0064	-8.85	***Serpinc1***	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	0007584 // response to nutrient // not recorded///0007596 // blood coagulation // inferred from electronic annotation
0.008579	677.73535	76.81403	NM_008877	-8.82	***Plg***	plasminogen	0006508 // proteolysis // inferred from electronic annotation///0007596 // blood coagulation // not recorded///00075
0.007904	931.0161	106.86725	NM_001305549///NM_	-8.71	***Apoa2***	apolipoprotein A-II	0002526 // acute inflammatory response // inferred from electronic annotation///0002740 // negative regulation of cyt
0.007904	784.26904	90.57742	NM_019395///XM_0112	-8.66	***Fbp1***	fructose bisphosphatase 1	0005975 // carbohydrate metabolic process // not recorded///0006002 // fructose 6-phosphate metabolic process // n
0.008295	354.58105	41.410778	NM_017399	-8.56	***Fabp1***	fatty acid binding protein 1, liver	0002230 // positive regulation of defense response to virus by host // not recorded///0006810 // transport // inferred f
0.009035	460.40594	54.565132	NM_007443	-8.44	***Ambp***	alpha 1 microglobulin/bikunin	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regula
0.009035	364.10437	44.204582	NM_175628///XM_0112	-8.24	***A2m***	alpha-2-macroglobulin	0001869 // negative regulation of complement activation, lectin pathway // not recorded///0007565 // female pregnan
0.007904	117.096016	14.251434	NM_029562///XM_0065	-8.22	***Cyp2d26***	cytochrome P450, family 2, subfamily d, polypeptide 26	0006805 // xenobiotic metabolic process // not recorded///0007565 // female pregnancy // inferred from electronic an
0.009035	569.55914	72.32811	NM_013475///XM_0065	-7.87	***Apoh***	apolipoprotein H	0001937 // negative regulation of endothelial cell proliferation // not recorded///0006641 // triglyceride metabolic proc
0.008933	297.7368	42.9369	NM_001039555///XM_	-6.93	***Cyp2c68***	cytochrome P450, family 2, subfamily c, polypeptide 68	0006805 // xenobiotic metabolic process // not recorded///0019373 // epoxygenase P450 pathway // not recorded///0
0.009515	530.3659	79.21489	NM_144903	-6.70	***Aldob***	aldolase B, fructose-bisphosphate	0001889 // liver development // inferred from electronic annotation///0006000 // fructose metabolic process // not rec
0.009035	107.0329	16.240175	NM_001150749///NM_	-6.59	***Rdh7***	retinol dehydrogenase 7	0008152 // metabolic process // inferred from electronic annotation///0042572 // retinol metabolic process // inferred
0.008933	101.333954	16.885468	NM_031164///XM_0065	-6.00	***F13b***	coagulation factor XIII, beta subunit	0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electroni
0.00121	567.4212	95.492805	NM_010344	-5.94	***Gsr***	glutathione reductase	0006749 // glutathione metabolic process // inferred by curator///0006749 // glutathione metabolic process // not reco
0.009035	123.63873	21.02113	NM_019775	-5.88	***Cpb2***	carboxypeptidase B2 (plasma)	0003331 // positive regulation of extracellular matrix constituent secretion // not recorded///0006508 // proteolysis //
0.009515	115.26279	20.11462	NM_008777	-5.73	***Pah***	phenylalanine hydroxylase	0006558 // L-phenylalanine metabolic process // not recorded///0006559 // L-phenylalanine catabolic process // inferre
0.007904	323.92343	60.301983	NM_053149///XM_0112	-5.37	***Hemgn***	hemogen	0007275 // multicellular organismal development // inferred from electronic annotation///0030154 // cell differentiatio
0.009035	97.145935	21.40032	NM_001277944///NM_	-4.54	***Apoc2///Apoc4-apoc2***	apolipoprotein C-II///Apoc4-Apoc2 readthrough	0006629 // lipid metabolic process // inferred from electronic annotation///0006810 // transport // inferred from electr
0.009035	97.145935	21.40032	NM_001277944///NM_	-4.54	***Apoc2///Apoc4-apoc2***	apolipoprotein C-II///Apoc4-Apoc2 readthrough	0006629 // lipid metabolic process // inferred from electronic annotation///0006810 // transport // inferred from electr
0.009362	275.06216	60.65339	NM_011318	-4.53	***Apcs***	serum amyloid P-component	0006461 // protein complex assembly // not recorded///0044869 // negative regulation by host of viral exo-alpha-sialid
0.009035	205.81808	48.39711	NM_009474	-4.25	***Uox***	urate oxidase	0006144 // purine nucleobase metabolic process // traceable author statement///0019628 // urate catabolic process //
0.009035	366.01755	88.19856	NM_007686///XM_0065	-4.15	***Cfi***	complement component factor i	0002376 // immune system process // inferred from electronic annotation///0006508 // proteolysis // inferred from ele
0.009035	369.15646	89.358025	NM_017371	-4.13	***Hpx***	hemopexin	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype///0002925 // positive
0.009393	79.1952	19.251146	NM_007768	-4.11	***Crp***	C-reactive protein, pentraxin-related	0006953 // acute-phase response // inferred from electronic annotation///0006958 // complement activation, classical
0.009539	46.109886	11.378008	NM_022884	-4.05	***Bhmt2***	betaine-homocysteine methyltransferase 2	0009086 // methionine biosynthetic process // not recorded///0032259 // methylation // inferred from electronic anno
0.009539	79.056564	20.695496	NM_009258	-3.82	***Spink1***	serine peptidase inhibitor, Kazal type 1	0010466 // negative regulation of peptidase activity // inferred from direct assay///0010751 // negative regulation of ni
0.009838	94.33337	24.844864	NM_008277	-3.80	***Hpd***	4-hydroxyphenylpyruvic acid dioxygenase	0006559 // L-phenylalanine catabolic process // inferred from electronic annotation///0006572 // tyrosine catabolic pro
0.009035	76.63665	20.551262	NM_031197	-3.73	***Slc2a2***	solute carrier family 2 (facilitated glucose transporter), member 2	0006810 // transport // inferred from electronic annotation///0008643 // carbohydrate transport // traceable author st
0.009539	266.90024	73.43783	NM_009060///XM_0065	-3.63	***Rgn***	regucalcin	0001822 // kidney development // inferred from electronic annotation///0001889 // liver development // inferred from
0.009035	328.84247	91.71179	NM_010582	-3.59	***Itih2***	inter-alpha trypsin inhibitor, heavy chain 2	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regula
0.009035	103.575714	29.131329	NM_013913	-3.56	***Angptl3***	angiopoietin-like 3	0006071 // glycerol metabolic process // not recorded///0006631 // fatty acid metabolic process // not recorded///000
0.009838	59.324883	17.908747	NM_008769///XM_0112	-3.31	***Otc***	ornithine transcarbamylase	0000050 // urea cycle // not recorded///0001889 // liver development // inferred from electronic annotation///00065
0.007904	1182.6617	361.0509	NM_009921	-3.28	***Camp***	cathelicidin antimicrobial peptide	0001878 // response to yeast // not recorded///0001934 // positive regulation of protein phosphorylation // not record
0.008579	210.20525	66.2185	NM_010391///XM_0112	-3.17	***H2-Q10***	histocompatibility 2, Q region locus 10	0002376 // immune system process // inferred from electronic annotation///0002474 // antigen processing and present
0.008322	680.87775	216.48624	NM_008522	-3.15	***Ltf***	lactotransferrin	0001503 // ossification // inferred from electronic annotation///0001817 // regulation of cytokine production // not rec
0.009515	132.50206	43.66293	NM_145499///XM_0112	-3.03	***Cyp2c70***	cytochrome P450, family 2, subfamily c, polypeptide 70	0006805 // xenobiotic metabolic process // not recorded///0019373 // epoxygenase P450 pathway // not recorded///0
0.008322	46.314484	15.829743	NM_153598	-2.93	***Ugt2b34***	UDP glucuronosyltransferase 2 family, polypeptide B34	0008152 // metabolic process // inferred from electronic annotation///0009813 // flavonoid biosynthetic process // not
0.008322	35.96051	12.506638	NM_009244///NM_009	-2.88	***Serpina1b///Serpina1e***	serine (or cysteine) preptidase inhibitor, clade A, member 1B///serine (or cysteine) peptidase inhib	0001701 // in utero embryonic development // inferred from mutant phenotype///0006487 // protein N-linked glycosyl
0.009515	1939.3445	687.6849	NM_008694	-2.82	***Ngp***	neutrophilic granule protein	0006952 // defense response // inferred from electronic annotation///0010466 // negative regulation of peptidase activ
0.009539	152.1246	58.687115	NM_009693///XM_0065	-2.59	***Apob***	apolipoprotein B	0001701 // in utero embryonic development // inferred from mutant phenotype///0006629 // lipid metabolic process //
0.008514	4169.445	1656.9628	NM_001281852///NM_	-2.52	***S100a9***	S100 calcium binding protein A9 (calgranulin B)	0002376 // immune system process // inferred from electronic annotation///0002523 // leukocyte migration involved in
0.00948	51.676186	20.722546	NM_001174170///NM_	-2.49	***Serpinb2***	serine (or cysteine) peptidase inhibitor, clade B, member 2	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regula
0.009515	36.6129	15.245841		-2.40	***AI195470***	expressed sequence AI195470	
0.009035	2648.2278	1103.3864	NM_025288///NM_001	-2.40	***Stfa3///BC100530///Stfa1***	stefin A3///cDNA sequence BC100530///stefin A1	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regula
0.008322	3385.8508	1448.3231	NM_001082543///NM_	-2.34	***BC100530///Stfa1///Stfa3***	cDNA sequence BC100530///stefin A1///stefin A3	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regula
0.009515	463.5324	198.47755	NM_001030294///XM_	-2.34	***Olfm4***	olfactomedin 4	0007155 // cell adhesion // inferred from electronic annotation///0043124 // negative regulation of I-kappaB kinase/NF
0.009515	29.197231	12.557258	NM_009467	-2.33	***Ugt2b5***	UDP glucuronosyltransferase 2 family, polypeptide B5	0008152 // metabolic process // inferred from electronic annotation///0009813 // flavonoid biosynthetic process // not
0.009539	130.07101	56.527664	NM_010824///XM_0065	-2.30	***Mpo***	myeloperoxidase	0001878 // response to yeast // inferred from mutant phenotype///0002149 // hypochlorous acid biosynthetic process
0.009539	68.18764	29.641487		-2.30	***9430047L24Rik***	RIKEN cDNA 9430047L24 gene	
0.009035	38.63272	17.025496	NM_020495///NM_178	-2.27	***Slco1b2***	solute carrier organic anion transporter family, member 1b2	0001889 // liver development // inferred from electronic annotation///0006810 // transport // inferred from electronic
0.009035	213.84431	95.23019	NM_026414	-2.25	***Asprv1***	aspartic peptidase, retroviral-like 1	0006508 // proteolysis // inferred from electronic annotation///0016485 // protein processing // inferred from direct as
0.009035	380.6708	171.54848	NM_001159299///NM_	-2.22	***Itih4***	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation///0010466 // negative regulation of peptidase
0.009539	821.34784	370.5598	NM_001159487///NM_	-2.22	***Rbp4***	retinol binding protein 4, plasma	0001654 // eye development // inferred from mutant phenotype///0001654 // eye development // not recorded///000
0.009539	109.62054	49.707043	NM_001042767///NM_	-2.21	***Proc***	protein C	0006508 // proteolysis // inferred from electronic annotation///0007596 // blood coagulation // inferred from electroni
0.009035	85.57101	40.139442	NM_030611///XM_0065	-2.13	***Akr1c6***	aldo-keto reductase family 1, member C6	0006629 // lipid metabolic process // inferred from electronic annotation///0006694 // steroid biosynthetic process // i

p (Corr)	[C3H/HeN, P5](raw)	[Gsr-KO, P5](raw)	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.009035	6512.8364	3080.731	NM_013650	-2.11	***S100a8***	S100 calcium binding protein A8 (calgranulin A)	0002376 // immune system process // inferred from electronic annotation///0002523 // leukocyte migration involved in
0.009539	91.161674	43.631207	NM_001083904///NM_	-2.09	***Fetub***	fetuin beta	0007338 // single fertilization // inferred from mutant phenotype///0007339 // binding of sperm to zona pellucida // inf
0.007904	45.47442	22.273838	NM_001291131///NM_	-2.04	***Asgr1***	asialoglycoprotein receptor 1	0006897 // endocytosis // inferred from electronic annotation///0006898 // receptor-mediated endocytosis // not recor
0.00931	161.25824	79.039925	NM_008572///XM_0065	-2.04	***Mcpt8***	mast cell protease 8	0006508 // proteolysis // inferred from electronic annotation///0006955 // immune response // not recorded///001648
0.009539	72.10932	35.654472	NM_027427///XM_0065	-2.02	***Taf15***	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	
0.009515	34.55852	17.145666	NM_010001	-2.02	***Cyp2c37***	cytochrome P450, family 2. subfamily c, polypeptide 37	0006805 // xenobiotic metabolic process // not recorded///0019373 // epoxygenase P450 pathway // not recorded///0
0.009035	142.16702	70.81732	NM_133653///XM_0065	-2.01	***Mat1a***	methionine adenosyltransferase I, alpha	0006556 // S-adenosylmethionine biosynthetic process // not recorded///0006730 // one-carbon metabolic process // i
0.009539	88.50968	44.16997	NM_001302496///NM_	-2.00	***Gjb1***	gap junction protein, beta 1	0007154 // cell communication // inferred from electronic annotation///0015868 // purine ribonucleotide transport //
0.008514	114.84889	57.78398	NM_001301404///NM_	-1.99	***Serpina10***	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electroni
0.009035	170.41675	88.12699	NM_011575	-1.93	***Tff3***	trefoil factor 3, intestinal	0010906 // regulation of glucose metabolic process // inferred from direct assay
0.007958	369.59058	191.68193	NM_001159564///NM_	-1.93	***Itgb6***	integrin beta 6	0006954 // inflammatory response // inferred from mutant phenotype///0007155 // cell adhesion // inferred from elect
0.007904	115.297844	60.250324	NM_020504	-1.91	***Cldn13***	claudin 13	
0.009035	74.39093	39.278843	NM_019447///XM_0065	-1.89	***Hgfac***	hepatocyte growth factor activator	0006508 // proteolysis // inferred from electronic annotation
0.009035	203.5702	107.778244	NM_001142706///NM_	-1.89	***Cfb***	complement factor B	0002376 // immune system process // inferred from electronic annotation///0006508 // proteolysis // inferred from ele
0.007904	469.32083	251.78458	NM_029784///XM_0065	-1.86	***Fam81a***	family with sequence similarity 81, member A	
0.009515	74.15848	39.8889	NM_145146	-1.86	***Afm***	afamin	0006810 // transport // inferred from electronic annotation///0051180 // vitamin transport // not recorded
0.009035	82.129814	46.073097	NM_001082960///NM_	-1.78	***Itgam***	integrin alpha M	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant phenotype///0006412 // tra
0.008322	287.88992	161.85806	NM_008256	-1.78	***Hmgcs2***	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	0001822 // kidney development // inferred from electronic annotation///0001889 // liver development // inferred from
0.009515	121.671135	69.7707	NM_001122683///NM_	-1.74	***Bdh1***	3-hydroxybutyrate dehydrogenase, type 1	0008152 // metabolic process // inferred from electronic annotation///0055114 // oxidation-reduction process // not re
0.009035	109.09615	62.895817	NM_032540///XM_0065	-1.73	***Kel***	Kell blood group	0006508 // proteolysis // inferred from electronic annotation///0006874 // cellular calcium ion homeostasis // inferred
0.004229	111.313835	64.34137	NM_001168515///NM_	-1.73	***Rpgrip1***	retinitis pigmentosa GTPase regulator interacting protein 1	0007601 // visual perception // inferred from mutant phenotype///0042462 // eye photoreceptor cell development // i
0.009035	20.140684	11.720101	NM_015787	-1.72	***Hist1h1e***	histone cluster 1, H1e	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction///
0.009838	85.03456	49.78549	NM_001271777///NM_	-1.71	***C8g***	complement component 8, gamma polypeptide	0002376 // immune system process // inferred from electronic annotation///0006957 // complement activation, alterna
0.009539	265.6635	156.26965	NM_001110827///NM_	-1.70	***Rbfox2***	RNA binding protein, fox-1 homolog (C. elegans) 2	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from genetic interaction///0000381 // re
0.009838	71.19826	42.00909	NM_001276710///NM_	-1.69	***Agxt***	alanine-glyoxylate aminotransferase	0007219 // Notch signaling pathway // inferred from direct assay///0008152 // metabolic process // inferred from electr
0.00948	32.087597	18.967062	NM_001289755///NM_	-1.69	***Apoc3***	apolipoprotein C-III	0006629 // lipid metabolic process // inferred from electronic annotation///0006641 // triglyceride metabolic process //
0.009757	82.98969	49.437355	XR_380276///XR_39286	-1.68	***Gm33916***	predicted gene, 33916	
0.009515	521.6738	311.00317	NM_016966///NR_0335	-1.68	***Gm8096///Phgdh///Gm675***	3-phosphoglycerate dehydrogenase pseudogene///3-phosphoglycerate dehydrogenase	0006541 // glutamine metabolic process // inferred from mutant phenotype///0006544 // glycine metabolic process // i
0.007904	209.88908	125.27118	NM_010635	-1.68	***Klf1***	Kruppel-like factor 1 (erythroid)	0001701 // in utero embryonic development // inferred from mutant phenotype///0001889 // liver development // infe
0.008322	31.614925	19.28061	NM_001290645///NM_	-1.64	***C8a***	complement component 8, alpha polypeptide	0002376 // immune system process // inferred from electronic annotation///0006955 // immune response // inferred fr
0.009161	68.87866	42.34007	NM_009398	-1.63	***Tnfaip6***	tumor necrosis factor alpha induced protein 6	0007155 // cell adhesion // inferred from electronic annotation///0030335 // positive regulation of cell migration // not
0.008933	163.9482	101.6475	NM_011270	-1.61	***Rhd***	Rh blood group, D antigen	0015696 // ammonium transport // inferred from mutant phenotype///0048821 // erythrocyte development // inferre
0.009035	146.27252	91.4925	NM_009690	-1.60	***Cd5l***	CD5 antigen-like	0006898 // receptor-mediated endocytosis // inferred from electronic annotation///0006915 // apoptotic process // inf
0.009539	318.34985	200.75731	NM_008638///XM_0065	-1.59	***Mthfd2***	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohy	0006730 // one-carbon metabolic process // not recorded///0008152 // metabolic process // inferred from electronic ar
0.009035	182.09444	114.99019	NM_177271	-1.58	***Samd5***	sterile alpha motif domain containing 5	
0.008322	203.05083	128.72978		-1.58	***Gm10401***	predicted gene 10401	
0.00824	1346.5383	856.39703	NM_133243///XR_0023	-1.57	***AY036118***	cDNA sequence AY036118	
0.007904	432.43604	275.88815	NM_027711///XM_011	-1.57	***Iqgap2***	IQ motif containing GTPase activating protein 2	0007165 // signal transduction // inferred from electronic annotation///0007264 // small GTPase mediated signal transd
0.009515	159.25708	102.108574	NM_007976	-1.56	***F5***	coagulation factor V	0007596 // blood coagulation // inferred from direct assay///0007596 // blood coagulation // inferred from mutant phe
0.009539	49.777195	31.949018	XM_011243805	-1.56	***Gm40824***	predicted gene, 40824	
0.009539	404.84216	260.87363	NM_028013	-1.55	***Endod1***	endonuclease domain containing 1	0008152 // metabolic process // inferred from electronic annotation///0090305 // nucleic acid phosphodiester bond hy
0.009539	107.88894	69.59727	NM_198414	-1.55	***Paqr9***	progestin and adipoQ receptor family member IX	
0.009515	75.23336	48.9117	NM_010024///XM_0065	-1.54	***Dct***	dopachrome tautomerase	0002052 // positive regulation of neuroblast proliferation // inferred from mutant phenotype///0006583 // melanin bio
0.009657	71.39743	46.500046	NM_023530///XM_0065	-1.54	***Pla2g12b***	phospholipase A2, group XIIB	0016042 // lipid catabolic process // inferred from electronic annotation///0042632 // cholesterol homeostasis // inferr
0.009539	327.16165	213.19955	NR_015519	-1.53	***AI662270***	expressed sequence AI662270	
0.009515	380.11133	251.04103	NM_010369///XM_0065	-1.51	***Gypa***	glycophorin A	0007016 // cytoskeletal anchoring at plasma membrane // inferred from mutant phenotype///0047484 // regulation of
0.009539	231.7885	153.44604	NM_015767///XM_011	-1.51	***Ttpa***	tocopherol (alpha) transfer protein	0001890 // placenta development // inferred from mutant phenotype///0001892 // embryonic placenta development /
0.007904	149.97658	99.34097	NM_001289507///NM_	-1.51	***Tfr2***	transferrin receptor 2	0006879 // cellular iron ion homeostasis // traceable author statement///0006898 // receptor-mediated endocytosis //
0.009035	99.47614	66.52702	NM_027903///XM_0065	-1.50	***Dhdh***	dihydrodiol dehydrogenase (dimeric)	0042843 // D-xylose catabolic process // inferred from direct assay///0055114 // oxidation-reduction process // inferred
0.009035	50.317238	33.86893	NM_008952///XM_011	-1.49	***Pipox***	pipecolic acid oxidase	0033514 // L-lysine catabolic process to acetyl-CoA via L-pipecolate // not recorded///0033514 // L-lysine catabolic proc
0.009141	174.4411	117.53102	NM_007788///XM_006	-1.48	***Csnk2a1///Gm10031***	casein kinase 2, alpha 1 polypeptide///predicted pseudogene 10031	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcriptio
0.009161	60.244728	40.656837	NM_145539	-1.48	***Tm4sf4***	transmembrane 4 superfamily member 4	0042246 // tissue regeneration // inferred from electronic annotation
0.009035	146.79344	99.46615	NM_007994	-1.48	***Fbp2***	fructose bisphosphatase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006094 // gluconeogenesis // not
0.009515	307.14972	209.08922	NM_027457	-1.47	***Tmem242***	transmembrane protein 242	
0.009035	50.580288	34.443153	NM_008061	-1.47	***G6pc***	glucose-6-phosphatase, catalytic	0005977 // glycogen metabolic process // inferred from mutant phenotype///0005980 // glycogen catabolic process // i
0.009515	192.03654	130.93428	NM_001161667///NM_	-1.47	***Acox2***	acyl-Coenzyme A oxidase 2, branched chain	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid metabolic process // i
0.009838	294.8808	201.16042	NM_007633	-1.47	***Ccne1***	cyclin E1	0000082 // G1/S transition of mitotic cell cycle // inferred from electronic annotation///0001547 // antral ovarian follicle
0.007904	136.62427	93.20229	NM_025310	-1.47	***Ftsj3***	FtsJ homolog 3 (E. coli)	0000453 // enzyme-directed rRNA 2'-O-methylation // inferred from electronic annotation///0000463 // maturation of
0.009035	47.06415	32.44323	NR_040338	-1.45	***Redrum***	Redrum, erythroid developmental long intergenic non-protein coding transcript	
0.008933	872.99396	606.62067	NM_001110251///NM_	-1.44	***Hmbs***	hydroxymethylbilane synthase	0001666 // response to hypoxia // inferred from electronic annotation///0006779 // porphyrin-containing compound bi
0.009539	5428.973	3773.0076	NM_001048061///NM_	-1.44	***Hnrnpab***	heterogeneous nuclear ribonucleoprotein A/B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction///
0.009035	78.971115	54.98317	NM_026085///NM_026	-1.44	***Pbld1///Pbld2***	phenazine biosynthesis-like protein domain containing 1///phenazine biosynthesis-like protein do	0009058 // biosynthetic process // inferred from electronic annotation///0010633 // negative regulation of epithelial ce
0.009035	109.25326	76.39132	NM_178931///XM_0065	-1.43	***Tnfrsf14***	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	0002741 // positive regulation of cytokine secretion involved in immune response // inferred from mutant phenotype//
0.009539	62.149387	44.175636	NM_001136237///NM_	-1.41	***Slc39a5***	solute carrier family 39 (metal ion transporter), member 5	0001654 // eye development // not recorded///0006810 // transport // inferred from electronic annotation///0006811
0.009035	279.50458	198.9557	NM_008698///XM_0065	-1.40	***Nipsnap1***	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	0019233 // sensory perception of pain // inferred from mutant phenotype
0.009035	1414.5854	1008.10645	NM_001313723///NM_	-1.40	***Tuba4a***	tubulin, alpha 4A	0007017 // microtubule-based process // inferred from electronic annotation///0008152 // metabolic process // inferre
0.009838	555.4557	398.02176	NM_001024945///NM_	-1.40	***Qsox1***	quiescin Q6 sulfhydryl oxidase 1	0006457 // protein folding // not recorded///0016242 // negative regulation of macroautophagy // not recorded///004
0.008953	2961.0923	2127.6135	NM_011239	-1.39	***Ranbp1***	RAN binding protein 1	0007051 // spindle organization // inferred from direct assay///0010976 // positive regulation of neuron projection deve
0.009539	48.109287	34.59443	XR_880475///XR_88855	-1.39	***Gm42127***	predicted gene, 42127	
0.009539	638.3205	459.50595	NM_010104	-1.39	***Edn1***	endothelin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001501 // skeletal
0.009515	26.50757	19.083727	NM_172881	-1.39	***Ugt2b35***	UDP glucuronosyltransferase 2 family, polypeptide B35	0008152 // metabolic process // inferred from electronic annotation///0009813 // flavonoid biosynthetic process // not
0.009647	20.862589	15.07787	NM_001195596	-1.38	***Smlr1***	small leucine-rich protein 1	
0.009838	575.3545	415.9078	NM_027421///XM_0065	-1.38	***Ints2***	integrator complex subunit 2	0016180 // snRNA processing // not recorded
0.009539	81.67399	59.150433	NM_013754	-1.38	***Insl6***	insulin-like 6	0007283 // spermatogenesis // inferred from mutant phenotype///0007286 // spermatid development // inferred from
0.009539	178.88324	130.4749	NM_010792///XM_0065	-1.37	***Mettl1***	methyltransferase like 1	0006400 // tRNA modification // not recorded///0008033 // tRNA processing // inferred from electronic annotation///0
0.009035	1982.2194	1451.1311	NM_177730	-1.37	***Impad1***	inositol monophosphatase domain containing 1	0001501 // skeletal system development // inferred from mutant phenotype///0001958 // endochondral ossification //

p (Corr)	[C3H/HeN, P5](raw)	[Gsr-KO, P5](raw)	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.009035	96.40056	70.88627	NM_001161515///NM_	-1.36	***Dctd***	dCMP deaminase	0006220 // pyrimidine nucleotide metabolic process // inferred from electronic annotation///0008152 // metabolic proc
0.009393	145.70305	107.20567	NM_020591///NR_0278	-1.36	***Chd3os***	chromodomain helicase DNA binding protein 3, opposite strand	
0.009539	248.24391	183.27887	NM_028228///XM_0065	-1.35	***Pinx1***	PIN2/TERF1 interacting, telomerase inhibitor 1	0007004 // telomere maintenance via telomerase // inferred from direct assay///0007080 // mitotic metaphase plate co
0.009317	1118.0834	826.66895	NM_146229	-1.35	***Dync1li1***	dynein cytoplasmic 1 light intermediate chain 1	0006810 // transport // inferred from electronic annotation///0007018 // microtubule-based movement // inferred fro
0.007904	422.27673	312.24203	NM_007682	-1.35	***Cenpb***	centromere protein B	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
0.009539	828.747	613.9402	NM_024193///XM_0065	-1.35	***Nop56***	NOP56 ribonucleoprotein	0000154 // rRNA modification // not recorded///0042254 // ribosome biogenesis // inferred from electronic annotation
0.009539	194.61078	144.35522		-1.35	***Tes3-ps***	testis derived transcript 3, pseudogene	
0.009515	115.65555	85.826584	NM_054094///XM_0065	-1.35	***Acsm1***	acyl-CoA synthetase medium-chain family member 1	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid metabolic process // i
0.009393	197.96646	146.96428	NM_001102404///NM_	-1.35	***Acp5***	acid phosphatase 5, tartrate resistant	0006470 // protein dephosphorylation // inferred from electronic annotation///0016311 // dephosphorylation // inferr
0.009393	82.71533	61.67905	NR_003964///NM_0237	-1.34	***Tubb2a-ps2///Tubb2b***	tubulin, beta 2a, pseudogene 2///tubulin, beta 2B class IIB	0001764 // neuron migration // not recorded///0007017 // microtubule-based process // inferred from electronic anno
0.009035	416.94724	312.54208	NM_001127233///NM_	-1.33	***Trp53***	transformation related protein 53	0000060 // protein import into nucleus, translocation // inferred from direct assay///0000122 // negative regulation of
0.009539	2649.8318	1989.797	NM_001252476///NM_	-1.33	***Prmt1***	protein arginine N-methyltransferase 1	0001701 // in utero embryonic development // inferred from mutant phenotype///0006355 // regulation of transcriptio
0.009539	225.13934	169.49669	NM_019547///XM_0064	-1.33	***Rbm38***	RNA binding motif protein 38	0006397 // mRNA processing // inferred from electronic annotation///0006977 // DNA damage response, signal transdu
0.009539	343.71655	259.67032	NM_010478	-1.32	***Hspa1b***	heat shock protein 1B	0007339 // binding of sperm to zona pellucida // inferred from direct assay///0009408 // response to heat // inferred fr
0.009539	634.3614	479.27847	NM_001290667///NM_	-1.32	***Chac2***	ChaC, cation transport regulator 2	0008152 // metabolic process // inferred from electronic annotation
0.007904	782.0202	591.61865	NM_025954	-1.32	***Pgp***	phosphoglycolate phosphatase	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0008152 // metabolic process // in
0.009838	676.9084	515.1457	NM_015800///XM_0065	-1.31	***Crim1***	cysteine rich transmembrane BMP regulator 1 (chordin like)	0001558 // regulation of cell growth // inferred from electronic annotation///0010951 // negative regulation of endope
0.009515	138.16159	105.437546	NM_001202445///NM_	-1.31	***Mapk8ip1***	mitogen-activated protein kinase 8 interacting protein 1	0006355 // regulation of transcription, DNA-templated // inferred from direct assay///0007165 // signal transduction //
0.00948	151.6453	115.771126	NM_008396	-1.31	***Itga2***	integrin alpha 2	0002687 // positive regulation of leukocyte migration // not recorded///0006929 // substrate-dependent cell migration
0.009035	514.3032	393.19016	NM_009266	-1.31	***Sephs2***	selenophosphate synthetase 2	0001887 // selenium compound metabolic process // inferred from direct assay///0001887 // selenium compound meta
0.009035	857.5765	656.29474	NM_001030307///XM_	-1.31	***Dkc1***	dyskeratosis congenita 1, dyskerin	0000154 // rRNA modification // not recorded///0000495 // box H/ACA snoRNA 3'-end processing // not recorded///00
0.009539	85.157585	65.53217	NM_009400///NM_021	-1.30	***Tnfrsf18***	tumor necrosis factor receptor superfamily, member 18	0002687 // positive regulation of leukocyte migration // not recorded///0006915 // apoptotic process // inferred from e
0.009539	454.66617	351.08884	NM_001291128///NM_	-1.30	***Nnat***	neuronatin	0007275 // multicellular organismal development // inferred from electronic annotation///0007420 // brain developme
0.009515	1189.5702	919.7363	NM_025584	-1.29	***Cd99***	CD99 antigen	0001773 // myeloid dendritic cell activation // inferred from direct assay
0.009657	1411.8641	1096.1992	NM_018868///XM_0064	-1.29	***Nop58***	NOP58 ribonucleoprotein	0000154 // rRNA modification // not recorded///0006608 // snRNP protein import into nucleus // not recorded///00422
0.009515	698.4649	542.6236	NM_001001493///XM_	-1.29	***Gm2573///Wdr83os***	predicted gene 2573///WD repeat domain 83 opposite strand	
0.009515	785.9864	613.72473	NM_001033536///XM_	-1.28	***Rfx7***	regulatory factor X, 7	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006357 // regulation o
0.009539	1795.9786	1406.2979	NM_026027	-1.28	***Pfdn1***	prefoldin 1	0006457 // protein folding // inferred from electronic annotation///0021537 // telencephalon development // inferred
0.009539	1325.4642	1038.1267	NM_026122///NM_175	-1.28	***Hmgn3***	high mobility group nucleosomal binding domain 3	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0016568
0.009035	572.92474	451.67682	NM_023203	-1.27	***Dctpp1***	dCTP pyrophosphatase 1	0009143 // nucleoside triphosphate catabolic process // inferred from direct assay///0051289 // protein homotetrameri
0.009539	663.1274	525.63696	NM_026845	-1.26	***Ppil1***	peptidylprolyl isomerase (cyclophilin)-like 1	0000413 // protein peptidyl-prolyl isomerization // not recorded///0006397 // mRNA processing // inferred from electr
0.009539	589.9028	467.6986	NM_001302163///NM_	-1.26	***Acsl1***	acyl-CoA synthetase long-chain family member 1	0001676 // long-chain fatty acid metabolic process // not recorded///0006629 // lipid metabolic process // inferred fro
0.009035	1009.2893	804.79645	NM_010411///XR_3859	-1.25	***Hdac3***	histone deacetylase 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction///
0.009515	259.44144	206.95248	NM_027297///XM_0065	-1.25	***Prpf4***	PRP4 pre-mRNA processing factor 4 homolog (yeast)	0000398 // mRNA splicing, via spliceosome // not recorded///0006397 // mRNA processing // inferred from electronic a
0.009035	453.9274	362.5217	NM_019816///XM_0065	-1.25	***Aatf***	apoptosis antagonizing transcription factor	0006357 // regulation of transcription from RNA polymerase II promoter // not recorded///0006974 // cellular response
0.009515	687.4245	549.7506	NM_001252450///NM_	-1.25	***Cldnd1***	claudin domain containing 1	
0.009539	1186.0769	950.7319	NM_025507	-1.25	***Snw1***	SNW domain containing 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0000398 // mRNA s
0.009539	695.9858	558.87134	NM_026742	-1.25	***Ndufaf4***	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	0008284 // positive regulation of cell proliferation // not recorded///0010257 // NADH dehydrogenase complex assemb
0.009515	963.01416	774.43896	NM_025544	-1.24	***Mrps15***	mitochondrial ribosomal protein S15	0006412 // translation // inferred from electronic annotation///0032543 // mitochondrial translation // inferred from s
0.009539	1239.7227	997.7482	NM_019657	-1.24	***Hsd17b12***	hydroxysteroid (17-beta) dehydrogenase 12	0006629 // lipid metabolic process // inferred from electronic annotation///0006633 // fatty acid biosynthetic process /
0.009035	871.2057	701.7155	NM_001035228///NM_	-1.24	***St3gal5***	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0001574 // ganglioside biosynthetic process // not recorded///0006486 // protein glycosylation // inferred from electro
0.009393	1185.0565	954.66797	NM_001003913///NM_	-1.24	***Mars***	methionine-tRNA synthetase	0006412 // translation // inferred from electronic annotation///0006418 // tRNA aminoacylation for protein translation
0.009515	334.53293	269.49628	NM_025903///XM_011	-1.24	***Ifrd2***	interferon-related developmental regulator 2	
0.009393	337.53903	272.58347	NM_016856///XM_0065	-1.24	***Cpsf2***	cleavage and polyadenylation specific factor 2	0006378 // mRNA polyadenylation // inferred from electronic annotation///0006379 // mRNA cleavage // inferred from
0.009539	64.897865	52.419785	NM_001312906///NM_	-1.24	***Hnf4a***	hepatic nuclear factor 4, alpha	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcriptio
0.009539	503.20862	406.62573	NM_019553	-1.24	***Ddx21***	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	0001649 // osteoblast differentiation // not recorded///0006351 // transcription, DNA-templated // inferred from elect
0.009515	909.7652	738.1548	NM_001033966///NM_	-1.23	***Ak2***	adenylate kinase 2	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation///0006172 // A
0.009838	159.77129	129.77583	NM_080457///NM_183	-1.23	***Muc4***	mucin 4	0001953 // negative regulation of cell-matrix adhesion // not recorded///0002244 // hematopoietic progenitor cell diffe
0.009539	285.77148	232.21115	NM_027242///XM_0065	-1.23	***Ppp1r35***	protein phosphatase 1, regulatory subunit 35	0010923 // negative regulation of phosphatase activity // not recorded
0.009838	64.23175	52.348244	NM_001077514///NM_	-1.23	***Slc1a2***	solute carrier family 1 (glial high affinity glutamate transporter), member 2	0006810 // transport // inferred from electronic annotation///0006835 // dicarboxylic acid transport // inferred from el
0.009539	266.27518	217.09465	NM_001163283///NM_	-1.23	***Zbtb5***	zinc finger and BTB domain containing 5	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcriptio
0.009515	429.2057	350.48245	NM_001085390	-1.22	***Dusp5***	dual specificity phosphatase 5	0000188 // inactivation of MAPK activity // not recorded///0001706 // endoderm formation // not recorded///0006470
0.009539	231.37968	189.52222	NM_033573	-1.22	***Prcc***	papillary renal cell carcinoma (translocation-associated)	0007093 // mitotic cell cycle checkpoint // not recorded
0.009515	1644.7557	1353.1824	NM_001304528///NM_	-1.22	***Ahcy///Gm4737***	S-adenosylhomocysteine hydrolase///predicted gene 4737	0002439 // chronic inflammatory response to antigenic stimulus // not recorded///0006730 // one-carbon metabolic pr
0.009755	432.92596	357.80963	NM_026660///XM_0065	-1.21	***Mfsd10***	major facilitator superfamily domain containing 10	0006810 // transport // inferred from electronic annotation///0006915 // apoptotic process // inferred from electronic
0.009539	235.79848	194.93832	NM_145365///XM_011	-1.21	***Creb3l3***	cAMP responsive element binding protein 3-like 3	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcriptio
0.009515	439.4294	364.59235	NM_001038230///NM_	-1.21	***Anapc11***	anaphase promoting complex subunit 11	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear division // inferred from electr
0.009539	510.38306	424.5472	NM_010817	-1.20	***Psmd7***	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	0043161 // proteasome-mediated ubiquitin-dependent protein catabolic process // not recorded
0.009539	2587.43	2155.1052	NM_144784	-1.20	***Acat1***	acetyl-Coenzyme A acetyltransferase 1	0001889 // liver development // inferred from electronic annotation///0007420 // brain development // inferred from
0.009539	328.1385	275.55862	NM_028428	-1.19	***Fut11***	fucosyltransferase 11	0006486 // protein glycosylation // inferred from electronic annotation///0036065 // fucosylation // inferred from elect
0.009539	551.38324	464.7824	NM_025840///XM_0065	-1.19	***Bzw2***	basic leucine zipper and W2 domains 2	0007275 // multicellular organismal development // inferred from electronic annotation///0007399 // nervous system
0.009515	15.254267	17.774426	NM_008671	1.17	***Nap1l2***	nucleosome assembly protein 1-like 2	0006334 // nucleosome assembly // inferred from electronic annotation///0035066 // positive regulation of histone ace
0.009393	15.830147	18.650099	NM_011023	1.18	***Otx1***	orthodenticle homolog 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006357 // regulation o
0.009539	44.71552	53.331398	NM_001177366///NM_	1.19	***Fut7***	fucosyltransferase 7	0002361 // CD4-positive, CD25-positive, alpha-beta regulatory T cell differentiation // inferred from mutant phenotype/
0.009838	98.30729	117.45883	NM_001024700	1.19	***Igh-VJ558///Igha***	immunoglobulin heavy chain (J558 family)///immunoglobulin heavy constant alpha	0002385 // mucosal immune response // inferred from direct assay///0002455 // humoral immune response mediated
0.009539	25.095377	30.028923	NR_110482	1.20	***Gm38403***	predicted gene, 38403	
0.009838	71.126236	85.54989	NM_176987///XM_0065	1.20	***Simc1***	SUMO-interacting motifs containing 1	
0.009539	20.03472	24.266289	NM_176848///XM_0065	1.21	***Fbxo2***	F-box protein 2	0006511 // ubiquitin-dependent protein catabolic process // inferred from direct assay///0006516 // glycoprotein catab
0.009539	90.46158	109.88717	NM_053255///XM_011	1.21	***Elac1***	elaC homolog 1 (E. coli)	0008033 // tRNA processing // inferred from electronic annotation///0034414 // tRNA 3'-trailer cleavage, endonucleoly
0.009838	177.27383	216.18193	NM_023750	1.22	***Zfp84***	zinc finger protein 84	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
0.009539	34.521523	42.238297	NR_033221	1.22	***BC031361***	cDNA sequence BC031361	
0.009515	40.641575	49.79235	NM_001079873///NM_	1.23	***Brdt***	bromodomain, testis-specific	0001207 // histone displacement // inferred from mutant phenotype///0006338 // chromatin remodeling // inferred fr
0.009515	81.076225	99.432945	NM_013904	1.23	***Hey2***	hairy/enhancer-of-split related with YRPW motif 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///00001
0.009515	40.186634	49.31	NM_010341	1.23	***Nmur1***	neuromedin U receptor 1	0006816 // calcium ion transport // not recorded///0006821 // chloride transport // not recorded///0006939 // smooth
0.009539	41.73369	51.33612	NM_145603///NR_0337	1.23	***Ces2c///Ces2d-ps***	carboxylesterase 2C///carboxylesterase 2D, pseudogene	0001101 // response to acid chemical // inferred from direct assay///0008152 // metabolic process // inferred from elec
0.009515	117.33529	145.04886	NM_025943///NR_1307	1.24	***Dzip1***	DAZ interacting protein 1	0007224 // smoothened signaling pathway // inferred from mutant phenotype///0007275 // multicellular organismal d

p (Corr)	[C3H/HeN, P5](raw)	[Gsr-KO, P5](raw)	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.009539	68.9773	85.47465	NM_001243741///NM_	1.24	***C87436///Gm38849***	expressed sequence C87436///predicted gene, 38849	
0.009838	666.24347	826.46735	NM_020625///XM_0065	1.24	***Zbtb22***	zinc finger and BTB domain containing 22	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription
0.009838	9509.946	11800.324	NM_013755///XM_0065	1.24	***Gyg***	glycogenin	0005978 // glycogen biosynthetic process // not recorded///0008152 // metabolic process // inferred from electronic an
0.009838	329.86398	409.743	NM_145151///NR_0734	1.24	***Crebzf***	CREB/ATF bZIP transcription factor	0006351 // transcription, DNA-templated // not recorded///0006355 // regulation of transcription, DNA-templated // in
0.009539	62.271606	77.42998	XR_377689///XR_40338	1.24	***Gm16499***	predicted gene 16499	
0.009393	118.81321	147.82677	NM_130882///XM_0065	1.24	***Cyp4f13***	cytochrome P450, family 4, subfamily f, polypeptide 13	0006691 // leukotriene metabolic process // not recorded///0055114 // oxidation-reduction process // inferred from ele
0.009539	115.48705	143.71123	NM_001168564///NM_	1.24	***Kcns3***	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic anno
0.009539	244.16508	304.57812	NM_194346///XM_0065	1.25	***Rnf31***	ring finger protein 31	0000209 // protein polyubiquitination // not recorded///0016567 // protein ubiquitination // inferred from mutant phe
0.009838	2020.9365	2524.2908	NM_001163635///XM_	1.25	***Tnks2***	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	0000209 // protein polyubiquitination // not recorded///0000723 // telomere maintenance // inferred from mutant phe
0.009539	8101.5117	10130.0625	NM_009932	1.25	***Col4a2***	collagen, type IV, alpha 2	0001525 // angiogenesis // inferred from electronic annotation///0006351 // transcription, DNA-templated // inferred f
0.009539	1276.4156	1596.5925	NM_001081364///NM_	1.25	***Arhgap21***	Rho GTPase activating protein 21	0007030 // Golgi organization // not recorded///0007165 // signal transduction // inferred from electronic annotation//
0.009515	37.730293	47.209244	NM_175514///XM_0064	1.25	***Fam171b***	family with sequence similarity 171, member B	
0.009539	1140.678	1428.8904	NM_019767	1.25	***Arpc1a***	actin related protein 2/3 complex, subunit 1A	0030833 // regulation of actin filament polymerization // inferred from electronic annotation///0034314 // Arp2/3 com
0.009838	27.220903	34.211407	NM_001272057///NM_	1.26	***Adam5***	a disintegrin and metallopeptidase domain 5	0006508 // proteolysis // inferred from electronic annotation
0.009838	328.1849	412.80176	NM_001110253///NM_	1.26	***Fyco1***	FYVE and coiled-coil domain containing 1	0006810 // transport // inferred from electronic annotation///0072383 // plus-end-directed vesicle transport along micr
0.009539	33.495815	42.134575	NM_053250///NM_181	1.26	***Crip3***	cysteine-rich protein 3	0042098 // T cell proliferation // inferred from mutant phenotype
0.009838	360.62012	453.7087	NM_017378	1.26	***Pcdh12***	protocadherin 12	0005977 // glycogen metabolic process // inferred from mutant phenotype///0007155 // cell adhesion // inferred from
0.009539	70.070786	88.25277	NM_001136496///NM_	1.26	***Zfp935***	zinc finger protein 935	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
0.009582	192.0062	241.86015	NM_173865	1.26	***Slc41a1***	solute carrier family 41, member 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic anno
0.009035	132.09906	166.5039	NM_027007///XM_0065	1.26	***Zfp397***	zinc finger protein 397	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription
0.009838	760.297	961.42017	NM_001081241///XM_	1.26	***Fam65a***	family with sequence similarity 65, member A	
0.009721	1276.3322	1616.231	NM_010761///XM_0064	1.27	***Ccndbp1***	cyclin D-type binding-protein 1	0007049 // cell cycle // inferred from electronic annotation///0051726 // regulation of cell cycle // inferred from electro
0.009539	133.90605	169.81232	XM_006517803///XM_	1.27	***D130037M23Rik***	RIKEN cDNA D130037M23 gene	
0.009393	435.22348	552.22626	NM_029788	1.27	***Rnft1***	ring finger protein, transmembrane 1	
0.009801	165.18332	210.24138	NM_001039951///NM_	1.27	***Zfp606***	zinc finger protein 606	0006355 // regulation of transcription, DNA-templated // not recorded
0.009539	37.738472	48.03753	NM_001005232	1.27	***Dbx1***	developing brain homeobox 1	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006357 // regulation o
0.009515	30.937084	39.39259	NM_001101482///NM_	1.27	***Mrap2***	melanocortin 2 receptor accessory protein 2	0006112 // energy reserve metabolic process // inferred from mutant phenotype///0007631 // feeding behavior // infer
0.009035	98.88922	126.10651	NM_025981///XM_0065	1.28	***2810416G20Rik///LOC10264***	RIKEN cDNA 2810416G20 gene///uncharacterized LOC102642487	
0.009515	56.52688	72.152306	NR_045164	1.28	***Slc2a4rg-ps***	Slc2a4 regulator, pseudogene	
0.009539	357.88156	456.92197	NM_007772///XM_0065	1.28	***Hivep1***	human immunodeficiency virus type I enhancer binding protein 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///000012
0.009035	23.108797	29.550993	NM_010846///NR_0035	1.28	***Mx1***	MX dynamin-like GTPase 1	0002376 // immune system process // inferred from electronic annotation///0008152 // metabolic process // inferred fr
0.009515	155.8945	199.79364	NM_001311069///NM_	1.28	***Dixdc1***	DIX domain containing 1	0007049 // cell cycle // inferred from mutant phenotype///0007275 // multicellular organismal development // inferred
0.009539	27.122637	34.801304	NM_198621	1.28	***Cct8l1***	chaperonin containing TCP1, subunit 8 (theta)-like 1	0006457 // protein folding // inferred from electronic annotation
0.009515	389.0285	499.26144	NM_001164056///NM_	1.28	***Pld1***	phospholipase D1	0006629 // lipid metabolic process // inferred from electronic annotation///0006643 // membrane lipid metabolic proce
0.009539	126.22039	162.15186	NM_001291047///NM_	1.28	***Ypel1***	yippee-like 1 (Drosophila)	
0.009515	3079.7148	3961.3894	NM_024473	1.29	***BC005537***	cDNA sequence BC005537	
0.009035	153.61166	197.64618	NM_001290720///NM_	1.29	***Tsga10***	testis specific 10	0030031 // cell projection assembly // inferred from mutant phenotype
0.009515	561.0085	723.5869	NM_001163475///XM_	1.29	***Zfp746***	zinc finger protein 746	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///000012
0.009539	1456.5138	1881.6926	NM_175134///XM_0065	1.29	***Ankrd46***	ankyrin repeat domain 46	
0.009515	64.59649	83.649956	NM_001146046///NM_	1.29	***Lrrc49***	leucine rich repeat containing 49	
0.009539	125.48795	162.6137	NM_001159317///NM_	1.30	***Il1rap***	interleukin 1 receptor accessory protein	0002376 // immune system process // inferred from electronic annotation///0006954 // inflammatory response // infer
0.009515	234.31003	303.73087	NM_001113333///NM_	1.30	***Cry2***	cryptochrome 2 (photolyase-like)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006281 // DNA rep
0.009539	308.44458	399.93097	NM_001195633///XM_	1.30	***Epg5***	ectopic P-granules autophagy protein 5 homolog (C. elegans)	0006914 // autophagy // inferred from mutant phenotype///0032456 // endocytic recycling // inferred from mutant ph
0.009394	585.879	760.092	NM_001098233///NM_	1.30	***Purg***	purine-rich element binding protein G	
0.009539	626.092	812.32465	NM_133821	1.30	***Phlpp1***	PH domain and leucine rich repeat protein phosphatase 1	0001932 // regulation of protein phosphorylation // not recorded///0002667 // regulation of T cell anergy // inferred fro
0.009515	484.48434	628.6416	NM_009811	1.30	***Casp6***	caspase 6	0002525 // acute inflammatory response to non-antigenic stimulus // not recorded///0006508 // proteolysis // not reco
0.009539	603.2058	782.78564	NM_018869///XM_0065	1.30	***Grk5***	G protein-coupled receptor kinase 5	0002029 // desensitization of G-protein coupled receptor protein signaling pathway // not recorded///0006468 // protei
0.009539	296.29507	384.67972	NM_172689	1.30	***Ddx58***	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0002230 // positive regulation of defense response to virus by host // not recorded///0002376 // immune system proce
0.009539	329.23483	428.31912	NM_177732///XM_0065	1.30	***Slc35d1***	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), memb	0015781 // pyrimidine nucleotide-sugar transport // inferred from direct assay///0030206 // chondroitin sulfate biosynt
0.009539	418.5663	546.51855	NM_030253///XM_0065	1.31	***Parp9***	poly (ADP-ribose) polymerase family, member 9	0006281 // DNA repair // inferred from electronic annotation///0006302 // double-strand break repair // not recorded/
0.009539	770.3314	1006.33606	NM_001161817///NM_	1.31	***Myo1b***	myosin IB	0006892 // post-Golgi vesicle-mediated transport // not recorded///0007015 // actin filament organization // not recor
0.009539	36.510136	47.803246	NM_009509///XM_0112	1.31	***Vil1***	villin 1	0001951 // intestinal D-glucose absorption // inferred from genetic interaction///0006915 // apoptotic process // inferre
0.009035	41.369984	54.34814	XR_106421///XR_10756	1.31	***Gm17501***	predicted gene, 17501	
0.009515	136.4876	180.40723	NM_172919///XM_0065	1.32	***Zfp846***	zinc finger protein 846	0006355 // regulation of transcription, DNA-templated // not recorded
0.009539	171.21489	226.58789	NM_001164792///NM_	1.32	***Tpbg***	trophoblast glycoprotein	0051965 // positive regulation of synapse assembly // inferred from direct assay
0.009539	220.0344	291.39944	NM_009180///XR_3883	1.32	***St6galnac2***	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialylt	0001574 // ganglioside biosynthetic process // not recorded///0006486 // protein glycosylation // inferred from electro
0.009035	208.12044	275.67743	NM_008137	1.32	***Gna14***	guanine nucleotide binding protein, alpha 14	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor signaling
0.009515	62.23488	82.47314	NM_020262///XM_0065	1.33	***Zfp109***	zinc finger protein 109	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
0.009539	755.15295	1001.0058	NM_010332	1.33	***Ednra***	endothelin receptor type A	0001569 // patterning of blood vessels // inferred from genetic interaction///0001666 // response to hypoxia // inferred
0.009515	525.23474	697.06226	NM_001033217///XM_	1.33	***Prickle1***	prickle homolog 1 (Drosophila)	0001843 // neural tube closure // not recorded///0006606 // protein import into nucleus // not recorded///0031398 //
0.009831	64.66972	85.87017	NM_001200023	1.33	***Zfp963***	zinc finger protein 963	0006355 // regulation of transcription, DNA-templated // not recorded
0.009141	175.53862	233.50746	NM_153782///XM_0065	1.33	***Fam20a***	family with sequence similarity 20, member A	0001934 // positive regulation of protein phosphorylation // inferred from direct assay///0001934 // positive regulation
0.009515	138.31209	184.2994	NM_001177752///NM_	1.33	***Pfkfb3***	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	0006000 // fructose metabolic process // inferred from electronic annotation///0006003 // fructose 2,6-bisphosphate m
0.009539	204.77612	273.3012	NM_030168///XM_0065	1.33	***Rictor***	RPTOR independent companion of MTOR, complex 2	0001932 // regulation of protein phosphorylation // inferred from mutant phenotype///0001938 // positive regulation
0.009539	417.60373	557.38226	NM_001164289///NM_	1.33	***Phf11c///Phf11d***	PHD finger protein 11C///PHD finger protein 11D	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription
0.00985	93.8642	125.77775	NM_183254///XM_0065	1.34	***Fam229b***	family with sequence similarity 229, member B	
0.009035	1969.3298	2662.9504	NM_001199186///NM_	1.35	***Slc44a2***	solute carrier family 44, member 2	0006810 // transport // inferred from electronic annotation///0007165 // signal transduction // not recorded///004312
0.009035	579.5005	787.2598	NM_001113386///NM_	1.36	***Lifr***	leukemia inhibitory factor receptor	0008284 // positive regulation of cell proliferation // inferred from genetic interaction///0008284 // positive regulation
0.009539	27.542223	37.46456	NM_175532	1.36	***Nlrp10***	NLR family, pyrin domain containing 10	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // i
0.009539	452.46844	615.86365	NM_001243908///XM_	1.36	***Zfp383***	zinc finger protein 383	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
0.009539	979.5401	1336.2693	NM_001290659///NM_	1.36	***Tanc1***	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	0007520 // myoblast fusion // inferred from mutant phenotype///0008542 // visual learning // inferred from mutant ph
0.009539	186.42381	254.51581	NM_001199048///NR_0	1.37	***Zfp942***	zinc finger protein 942	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
0.009035	194.84016	266.33487	NM_144873///XM_0065	1.37	***Uhrf2***	ubiquitin-like, containing PHD and RING finger domains 2	0006511 // ubiquitin-dependent protein catabolic process // not recorded///0006511 // ubiquitin-dependent protein ca
0.009515	2735.611	3748.7139	NM_001243199///NM_	1.37	***Gimap4***	GTPase, IMAP family member 4	
0.009035	280.86273	385.044	NM_013881///XM_0065	1.37	***Ulk2***	unc-51 like kinase 2	0000045 // autophagosome assembly // not recorded///0006468 // protein phosphorylation // inferred from electronic
0.009515	26.97145	37.005226	NR_038032	1.37	***Gm15663***	predicted gene 15663	

p (Corr)	[C3H/HeN, P5](raw)	[Gsr-KO, P5](raw)	RefSeq Transcript ID	FD	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.008771	97.42562	134.67738	NM_007911///XM_0065	1.38	***Efnb3***	ephrin B3	0007275 // multicellular organismal development // inferred from electronic annotation///0007399 // nervous system d
0.009035	356.06174	495.6695	NM_001033851///NM_	1.39	***Cpne8***	copine VIII	
0.009515	35.75946	49.786163	NM_001081084	1.39	***Cubn***	cubilin (intrinsic factor-cobalamin receptor)	0001701 // in utero embryonic development // not recorded///0006629 // lipid metabolic process // inferred from elect
0.009035	98.064575	137.12593	NM_001143776///NM_	1.40	***Fam13c***	family with sequence similarity 13, member C	
0.007904	101.20299	141.52968	XR_870188///XR_87018	1.40	***Gm29782***	predicted gene, 29782	
0.009515	119.81094	168.41316	NM_001039530///XM_	1.41	***Parp14***	poly (ADP-ribose) polymerase family, member 14	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcriptio
0.009838	241.15141	341.40613	NM_175460///XM_0065	1.42	***Nmnat2***	nicotinamide nucleotide adenylyltransferase 2	0006767 // water-soluble vitamin metabolic process // not recorded///0009058 // biosynthetic process // inferred from
0.009035	32.524933	46.156807	NM_001045550///NM_	1.42	***Gm2083///Gm21320///Mup***	major urinary protein LOC100048885///predicted gene, 21320///major urinary protein 1///major	0006112 // energy reserve metabolic process // inferred from sequence or structural similarity///0006112 // energy rese
0.009838	438.85696	624.98376	NM_001276719///NM_	1.42	***Ackr2***	atypical chemokine receptor 2	0006898 // receptor-mediated endocytosis // not recorded///0006935 // chemotaxis // inferred from electronic annota
0.009515	87.13523	124.178055	NM_027560///XM_0112	1.43	***Arrdc2***	arrestin domain containing 2	0007165 // signal transduction // inferred from electronic annotation
0.009035	1273.1368	1817.7776	NR_002321///NR_00232	1.43	***Tug1***	taurine upregulated gene 1	0042461 // photoreceptor cell development // inferred from mutant phenotype
0.009539	564.8375	806.9806	NM_001310534///NM_	1.43	***Txndc16***	thioredoxin domain containing 16	0045454 // cell redox homeostasis // inferred from electronic annotation
0.009539	241.2777	347.8312	NM_001033633	1.44	***Slc2a13***	solute carrier family 2 (facilitated glucose transporter), member 13	0006810 // transport // inferred from electronic annotation///0008643 // carbohydrate transport // inferred from elect
0.009539	111.349304	160.87154	NM_001164573///NM_	1.44	***Myo1h***	myosin 1H	0008152 // metabolic process // inferred from electronic annotation
0.009515	78.335976	114.08768	NM_175140///XM_0065	1.46	***Chst8***	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006790 // sulfur compound meta
0.009035	230.2688	339.45102	NM_008987	1.47	***Ptx3***	pentraxin related gene	0001878 // response to yeast // inferred from mutant phenotype///0008228 // opsonization // inferred from mutant ph
0.009035	93.00372	137.63376	NM_001012324	1.48	***Ecm2***	extracellular matrix protein 2, female organ and adipocyte specific	0007409 // axonogenesis // not recorded///0010811 // positive regulation of cell-substrate adhesion // inferred from d
0.009582	53.519703	79.219284	NM_001164374///XM_	1.48	***Gm17455***	predicted gene, 17455	
0.009035	816.0237	1209.8616	NM_020052	1.48	***Scube2***	signal peptide, CUB domain, EGF-like 2	
0.009539	783.3385	1162.6428	NR_002840///NR_02854	1.48	***Gas5///Snord47***	growth arrest specific 5///small nucleolar RNA, C/D box 47	
0.009539	664.98114	992.8802	NR_002896///NR_00444	1.49	***Snhg1///Snord22***	small nucleolar RNA host gene 1///small nucleolar RNA, C/D box 22	
0.009539	1330.5524	1999.7644	NM_053109///XM_0065	1.50	***Clec2d***	C-type lectin domain family 2, member d	0006968 // cellular defense response // traceable author statement///0007165 // signal transduction // inferred from se
0.007904	98.97489	153.05981	NM_001289740///NM_	1.55	***Mturn***	maturin, neural progenitor differentiation regulator homolog (Xenopus)	0007275 // multicellular organismal development // inferred from electronic annotation///0048666 // neuron develop
0.009035	489.15015	765.87396	NM_008326///XM_0065	1.57	***Irgm1***	immunity-related GTPase family M member 1	0002376 // immune system process // inferred from electronic annotation///0006914 // autophagy // inferred from ele
0.009515	313.42593	493.61218	NR_029656	1.57	***Mirlet7d***	microRNA let7d	0007566 // embryo implantation // inferred from direct assay///0030509 // BMP signaling pathway // inferred from dire
0.009838	238.08238	376.7505	NM_019440	1.58	***Irgm2***	immunity-related GTPase family M member 2	0034341 // response to interferon-gamma // inferred from direct assay///0034341 // response to interferon-gamma // i
0.009838	432.136	687.02563	NM_001289492///NM_	1.59	***Gbp3***	guanylate binding protein 3	0008152 // metabolic process // inferred from electronic annotation///0035458 // cellular response to interferon-beta /
0.009539	305.10446	503.60126	NM_001316729///NM_	1.65	***Qpct***	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	0017186 // peptidyl-pyroglutamic acid biosynthetic process, using glutaminyl-peptide cyclotransferase // not recorded
0.009515	142.237	236.04419	NM_010114///NM_010	1.66	***Klk1b22///Klk1b9***	kallikrein 1-related peptidase b22///kallikrein 1-related peptidase b9	0002526 // acute inflammatory response // ---///0003073 // regulation of systemic arterial blood pressure // ---///0006
0.009515	142.237	236.04419	NM_010114///NM_010	1.66	***Klk1b22///Klk1b9***	kallikrein 1-related peptidase b22///kallikrein 1-related peptidase b9	0002526 // acute inflammatory response // ---///0003073 // regulation of systemic arterial blood pressure // ---///0006
0.009539	23.49422	39.586937	NM_027770///XM_0065	1.68	***Col24a1***	collagen, type XXIV, alpha 1	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype
0.009539	305.28564	521.377	NM_016704///XM_0065	1.71	***C6***	complement component 6	0001701 // in utero embryonic development // inferred from genetic interaction///0001970 // positive regulation of act
0.009539	551.9062	970.214	NM_001177980///NM_	1.76	***Pde4b***	phosphodiesterase 4B, cAMP specific	0001780 // neutrophil homeostasis // inferred from mutant phenotype///0006198 // cAMP catabolic process // inferre
0.009515	191.56723	340.33087	NM_194336///XM_0065	1.78	***Gbp6***	guanylate binding protein 6	0006955 // immune response // inferred from mutant phenotype///0008152 // metabolic process // inferred from elect
0.003126	1671.4963	3212.4534	NM_026432	1.92	***Saraf***	store-operated calcium entry-associated regulatory factor	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic anno
0.009515	198.83435	450.50763	NM_011854///XM_0065	2.27	***Oasl2***	2'-5' oligoadenylate synthetase-like 2	0002376 // immune system process // inferred from electronic annotation///0006164 // purine nucleotide biosynthetic
0.009035	214.45288	1245.4403	NM_010861///XM_0065	5.81	***Myl2***	myosin, light polypeptide 2, regulatory, cardiac, slow	0002026 // regulation of the force of heart contraction // not recorded///0003007 // heart morphogenesis // inferred fr
0.008933	92.58727	1654.6576	NM_008725	17.87	***Nppa***	natriuretic peptide type A	0001666 // response to hypoxia // inferred from electronic annotation///0003085 // negative regulation of systemic art