Table S5. Lung genes (n=1033) significantly changed by hyperoxia (O2) in wild-type (*Gsr* -WT) mouse neonates at PND5 (moderated t-test, p < 0.01).

Blue(-): fold decreased by O2. Red : fold increased by O2.

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	RefSeq Transcript ID	p	FC (Air:O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
37.38233	123.414505	NM_008036///XM_006	5.84E-04	3.30	***Fosb***	FBJ osteosarcoma oncogene B	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006357 // regulation of transcription from RNA polymerase II promoter // inferred from electronic a
77.99382	231.76727	NM_009704	0.005845343	2.97	***Areg***	amphiregulin	0007173 // epidermal growth factor receptor signaling pathway // not recorded///0007186 // G-protein coupled receptor signaling pathway // not recorded///0008284 // positive regulation of cell
152.11726	409.09592	NM_011198	0.005421948	2.69	***Ptgs2***	prostaglandin-endoperoxide synthase 2	0001516 // prostaglandin biosynthetic process // inferred from direct assay///0001516 // prostaglandin biosynthetic process // not recorded///0001525 // angiogenesis // not recorded///0006629
813.2235	1995.0363	NM_010234	6.40E-04	2.45	***Fos***	FBJ osteosarcoma oncogene	0001661 // conditioned taste aversion // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from direct assay///0006355 // regulation of trans
140.6054	339.85855	NM_139134///XM_006	0.001574421	2.42	***Chodl***	chondrolectin	0010975 // regulation of neuron projection development // inferred from genetic interaction
980.0045	2356.3657	NM_010444///XM_006	2.86E-04	2.40	***Nr4a1***	nuclear receptor subfamily 4, group A, member 1	0001938 // positive regulation of endothelial cell proliferation // not recorded///0002042 // cell migration involved in sprouting angiogenesis // not recorded///0006351 // transcription, DNA-templ
1424.2338	3373.7683	NM_007913	1.86E-05	2.37	***Egr1***	early growth response 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001975 // response to amphetamine // inferred from electronic annotation///000
439.88135	960.6826	NM_008871	0.001247915	2.18	***Serpine1***	serine (or cysteine) peptidase inhibitor, clade E, member 1	0001300 // chronological cell aging // inferred from electronic annotation///0001525 // angiogenesis // inferred from electronic annotation///0001890 // placenta development // inferred from mu
26.472225	56.36958	NM_011990///XM_006	0.001099438	2.13	***Slc7a11***	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	0003333 // amino acid transmembrane transport // inferred from electronic annotation///0006810 // transport // inferred from electronic annotation///0006865 // amino acid transport // inferred
162.3565	328.37933	NM_001099774	0.001789968	2.02	***Krtap17-1***	keratin associated protein 17-1	
54.131863	105.7784		0.002377528	1.95	***AA407107***	expressed sequence AA407107	
1931.0345	3541.622	NM_019738	0.001172722	1.83	***Nupr1***	nuclear protein transcription regulator 1	0002526 // acute inflammatory response // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcript
479.9306	879.5057	NM_001291892///NM_	0.002088835	1.83	***Lilr4b///Lilrb4a***	leukocyte immunoglobulin-like receptor, subfamily B, member 4B///leukocyte immunog	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // inferred from electronic annotation
3730.86	6707.5347	NM_053247	0.005618611	1.80	***Lyve1***	lymphatic vessel endothelial hyaluronan receptor 1	0006027 // glycosaminoglycan catabolic process // inferred from direct assay///0006810 // transport // inferred from electronic annotation///0007155 // cell adhesion // inferred from electronic ar
1112.6222	1998.9093	NM_010295///XM_006	0.005294423	1.80	***Gclc***	glutamate-cysteine ligase, catalytic subunit	0006534 // cysteine metabolic process // not recorded///0006536 // glutamate metabolic process // not recorded///0006749 // glutathione metabolic process // inferred from mutant phenotype//
796.40405	1414.1843	NM_153127	0.008906208	1.78	***Mmrn2***	multimerin 2	0001525 // angiogenesis // inferred from electronic annotation///0030948 // negative regulation of vascular endothelial growth factor receptor signaling pathway // not recorded///0090051 // neg
272.83313	481.5459	NM_001083894///NM_	0.006772685	1.76	***Liph***	lipase, member H	0006629 // lipid metabolic process // inferred from electronic annotation///0016042 // lipid catabolic process // not recorded
1284.7445	2238.7104	NM_009349	0.003307177	1.74	***Inmt***	indolethylamine N-methyltransferase	0009308 // amine metabolic process // not recorded///0009636 // response to toxic substance // inferred from electronic annotation///0032259 // methylation // not recorded
336.0312	577.17	NM_008416	5.02E-04	1.72	***Junb***	jun B proto-oncogene	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001570 // vasculogenesis // inferred from mutant phenotype///0001649 // osteoblast different
29.427765	49.945538	NM_144555///NR_1104	0.002754394	1.70	***Lncpint***	long non-protein coding RNA, Trp53 induced transcript	0035264 // multicellular organism growth // inferred from mutant phenotype
29.029982	49.20545	NM_173777///XM_006	0.002880002	1.69	***Olfm2***	olfactomedin 2	0007601 // visual perception // inferred from mutant phenotype///0007626 // locomotory behavior // inferred from mutant phenotype///0009306 // protein secretion // not recorded///0051152 /
2131.7495	3607.0237	NM_013642	0.003945669	1.69	***Dusp1***	dual specificity phosphatase 1	0000188 // inactivation of MAPK activity // inferred from sequence or structural similarity///0000188 // inactivation of MAPK activity // inferred from electronic annotation///0001706 // endoderm
194.57767	328.3086	NM_001169153///NM_	0.006524343	1.69	***Cd300lf***	CD300 antigen like family member F	0002376 // immune system process // inferred from electronic annotation///0030316 // osteoclast differentiation // inferred from direct assay
268.94742	450.1406	NM_029415///XM_006	0.003441845	1.67	***Slc10a6***	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006814 // sodium ion transport // inferred from electronic annotat
112.42752	187.63474	NM_001289925///NM_	4.54E-04	1.67	***Egr3***	early growth response 3	0001938 // positive regulation of endothelial cell proliferation // not recorded///0002042 // cell migration involved in sprouting angiogenesis // not recorded///0006351 // transcription, DNA-templ
1042.2667	1726.719	NM_010516	5.67E-04	1.66	***Cyr61***	cysteine rich protein 61	0001558 // regulation of cell growth // inferred from electronic annotation///0001649 // osteoblast differentiation // inferred from genetic interaction///0001934 // positive regulation of protein pl
1421.7599	2333.789	NR_003513///NR_1312	5.60E-04	1.64	***Neat1***	nuclear paraspeckle assembly transcript 1 (non-protein coding)	0030575 // nuclear body organization // inferred from mutant phenotype///0043954 // cellular component maintenance // inferred from direct assay///0043954 // cellular component maintenance
94.76352	155.50803	NR_045032	0.004866363	1.64	***Gdap10***	ganglioside-induced differentiation-associated-protein 10	
310.55615	507.42877	NM_001127382///NM_	6.97E-04	1.63	***Rbm47***	RNA binding motif protein 47	0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype///0016554 // cytidine to uridine editing // inferred from genetic interaction
337.13852	540.21277	NM_145839///NM_181	1.97E-04	1.60	***Rasgef1b***	RasGEF domain family, member 1B	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///0043547 // positive regulation of GTPase activity // inferred from electronic annotation
4063.339	6472.9634	NM_010406	0.007343931	1.59	***Hc***	hemolytic complement	0001701 // in utero embryonic development // inferred from genetic interaction///0002376 // immune system process // inferred from electronic annotation///0006954 // inflammatory response /
42.479637	67.51076	NM_007950	0.005589217	1.59	***Ereg***	epiregulin	0000187 // activation of MAPK activity // not recorded///0001525 // angiogenesis // inferred from electronic annotation///0001550 // ovarian cumulus expansion // not recorded///0001556 // ooc
389.20187	616.508	NM_001167860///NM_	1.63E-04	1.58	***Wipf3***	WAS/WASL interacting protein family, member 3	0000147 // actin cortical patch assembly // ---///0006897 // endocytosis // ---///0007275 // multicellular organismal development // inferred from electronic annotation///0007283 // spermatogen
207.88284	328.71164	NM_010062///NR_1034	0.006640752	1.58	***Dnase2a///Gm38426***	deoxyribonuclease II alpha///predicted gene, 38426	0000737 // DNA catabolic process, endonucleolytic // inferred from mutant phenotype///0006259 // DNA metabolic process // inferred from electronic annotation///0006308 // DNA catabolic proc
384.6075	603.5137	NM_001159564///NM_	0.00216116	1.57	***Itgb6***	integrin beta 6	0006954 // inflammatory response // inferred from mutant phenotype///0007155 // cell adhesion // inferred from electronic annotation///0007160 // cell-matrix adhesion // inferred from electron
219.49326	343.87042	NM_175437///XM_006	0.006792043	1.57	***Gsap***	gamma-secretase activating protein	0030162 // regulation of proteolysis // not recorded///1902004 // positive regulation of beta-amyloid formation // inferred from direct assay///1902004 // positive regulation of beta-amyloid forma
329.97717	514.5321	NM_023755///XM_006	5.74E-04	1.56	***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 phenotype///0002070 // ep
273.58063	422.76328	NM_011391///XM_006	0.007875001	1.55	***Slc16a7***	solute carrier family 16 (monocarboxylic acid transporters), member 7	0006810 // transport // inferred from electronic annotation///0015718 // monocarboxylic acid transport // inferred from electronic annotation///0035873 // lactate transmembrane transport // no
607.5148	936.553	NM_178772///XM_011	0.00530027	1.54	***Nceh1***	neutral cholesterol ester hydrolase 1	0006470 // protein dephosphorylation // inferred from direct assay///0006629 // lipid metabolic process // inferred from electronic annotation///0006805 // xenobiotic metabolic process // inferre
136.17421	209.46509	NM_175388///XM_006	0.001734492	1.54	***Rnf169***	ring finger protein 169	0006974 // cellular response to DNA damage stimulus // not recorded///0016567 // protein ubiquitination // inferred from electronic annotation///2000780 // negative regulation of double-strand
214.55724	328.51874	NM_001190400///NM_	0.001119591	1.53	***Bend7***	BEN domain containing 7	
202.60489	309.27942	NM_007498	0.008897428	1.53	***Atf3***	activating transcription factor 3	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000122 // negative regulation of transcription from RNA polymerase II promoter //
961.6649	1450.4319	NM_001038999///NM_	0.006759967	1.51	***Atp8a1***	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic annotation///0007612 // learning // inferred from mutant phenotype///000815
474.25955	713.40125	NM_175518///XM_006	0.001134578	1.50	***Tmem245***	transmembrane protein 245	
57.834538	86.04273	NM_001034874///XM_	0.002429239	1.49	***Shisa6***	shisa family member 6	0048172 // regulation of short-term neuronal synaptic plasticity // not recorded
249.06627	367.32254	NM_177628///XM_006	0.002632302	1.47	***Fam167a***	family with sequence similarity 167, member A	
47.12992	69.1932		0.003396256	1.47	***C77648***	expressed sequence C77648	
187.11278	273.19156	NM_001039056///NM_	6.02E-04	1.46	***Kcnj15***	potassium inwardly-rectifying channel, subfamily J, member 15	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006813 // potassium ion transport // inferred from direct assay///
2036.5303	2967.486	NM_010664	0.003392058	1.46	***Krt18***	keratin 18	0033209 // tumor necrosis factor-mediated signaling pathway // inferred from genetic interaction///0043000 // Golgi to plasma membrane CFTR protein transport // not recorded///0043066 // neg
706.1365	1028.7281	NM_010573	0.009133884	1.46	***Irx1***	Iroquois related homeobox 1 (Drosophila)	0001656 // metanephros development // inferred from expression pattern///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0072086 // specificatio
31.268293	45.464844	NM_001110506///NM_	0.003066656	1.45	***Efcab12***	EF-hand calcium binding domain 12	
825.2685	1199.2144	NM_011324	3.66E-04	1.45	***Scnn1a***	sodium channel, nonvoltage-gated 1 alpha	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006814 // sodium ion transport // inferred from direct assay///000
271.50986	394.1254	NM_177604	0.009171831	1.45	***AA986860***	expressed sequence AA986860	
257.6483	372.8141	NM_001033348///XM_	5.02E-04	1.45	***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 // regulation of small G
297.86356	430.55035	NM_001033258///XM_	0.001747617	1.45	***Arfgef3***	ARFGEF family member 3	0010923 // negative regulation of phosphatase activity // not recorded///0016192 // vesicle-mediated transport // not recorded///0032012 // regulation of ARF protein signal transduction // inferr
433.51276	621.4129	NM_001159367///NM_	0.00828187	1.43	***Per1***	period circadian clock 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000122 // negative regulation of transcription from RNA polymerase II promoter //
604.45593	862.96747	NM_008037	7.55E-04	1.43	***Fosl2***	fos-like antigen 2	0001666 // response to hypoxia // not recorded///0003334 // keratinocyte development // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred from electronic a
233.05194	332.2972	NM_008381	0.005944416	1.43	***Inhbb***	inhibin beta-B	0001654 // eye development // traceable author statement///0009267 // cellular response to starvation // inferred from expression pattern///0009612 // response to mechanical stimulus // not rec
103.16504	146.81528	NM_001033324///XM_	0.008637991	1.42	***Zbtb16***	zinc finger and BTB domain containing 16	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001501 // skeletal system development // inferred from mutant phenotype///0001823 // meso
281.4342	399.89764	NM_001037937///NM_	0.001361269	1.42	***Deptor***	DEP domain containing MTOR-interacting protein	0006469 // negative regulation of protein kinase activity // not recorded///0032007 // negative regulation of TOR signaling // not recorded///0035556 // intracellular signal transduction // inferred
293.3034	415.9969	NM_009886///XM_006	1.86E-04	1.42	***Celsr1***	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	0001702 // gastrulation with mouth forming second // non-traceable author statement///0001736 // establishment of planar polarity // inferred from mutant phenotype///0001764 // neuron migra
234.63474	332.48288	NM_144848	0.002238819	1.42	***Eppk1***	epiplakin 1	
906.28265	1284.151	NM_010019///XM_006	0.005420953	1.42	***Dapk2***	death-associated protein kinase 2	0006468 // protein phosphorylation // not recorded///0006468 // protein phosphorylation // inferred from sequence or structural similarity///0006915 // apoptotic process // inferred from electro
520.8303	737.6758	NM_010574///XM_006	0.002051145	1.42	***Irx2***	Iroquois related homeobox 2 (Drosophila)	0001656 // metanephros development // inferred from expression pattern///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0072086 // specificatio
511.498	723.33057	NM_007707///XM_011	0.001083782	1.41	***Socs3***	suppressor of cytokine signaling 3	0001666 // response to hypoxia // inferred from electronic annotation///0001932 // regulation of protein phosphorylation // inferred from direct assay///0006469 // negative regulation of protein
746.323	1051.2252	NM_001024602///XM_	0.00270068	1.41	***Cep170b***	centrosomal protein 170B	
146.90018	206.62756	NM_001103156///NM_	0.007301306	1.41	***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 transport // not recorded///
371.51614	521.9512	NM_007885	4.17E-04	1.40	***Slc26a2***	solute carrier family 26 (sulfate transporter), member 2	0001503 // ossification // not recorded///0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0008272 // sulfate transp
3949.0017	5530.3354	NM_009721	0.002821305	1.40	***Atp1b1***	ATPase, Na+/K+ transporting, beta 1 polypeptide	0001666 // response to hypoxia // not recorded///0001824 // blastocyst development // inferred from mutant phenotype///0002230 // positive regulation of defense response to virus by host // no
3267.633	4573.598	NM_001271538///NM_	6.07E-04	1.40	***Myh14***	myosin, heavy polypeptide 14	0003009 // skeletal muscle contraction // not recorded///0007519 // skeletal muscle tissue development // not recorded///0007605 // sensory perception of sound // not recorded///0008152 // m
420.33865	586.3509	NM_010831	0.007045759	1.39	***Sik1***	salt inducible kinase 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0002028 // regulation of sodium ion transport // not recorded///0006468 // protein phosphoryl
74.23192	103.38791	XM_001477212	0.00285816	1.39	***Gm3556***	predicted gene 3556	
407.57462	567.2956	NM_183029///XM_011	0.001714329	1.39	***Igf2bp2***	insulin-like growth factor 2 mRNA binding protein 2	0006417 // regulation of translation // inferred from electronic annotation///0006810 // transport // inferred from electronic annotation///0051028 // mRNA transport // inferred from electronic a
161.55202	224.64705	NM_178061///XM_006	0.002905194	1.39	***Mob3b***	MOB kinase activator 3B	
527.1077	731.84546	NM_009670///NM_146	0.002743318	1.39	***Ank3***	ankyrin 3, epithelial	0000281 // mitotic cytokinesis // not recorded///0007009 // plasma membrane organization // not recorded///0007165 // signal transduction // inferred from electronic annotation///0007409 // a
260.91122	361.30063	NM_008587///XM_006	0.009244863	1.38	***Mertk***	c-mer proto-oncogene tyrosine kinase	0001779 // natural killer cell differentiation // inferred from genetic interaction///0006468 // protein phosphorylation // not recorded///0006909 // phagocytosis // not recorded///0007283 // sper
286.37833	396.26074	NM_027652	0.009675908	1.38	***Ept1***	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	0006629 // lipid metabolic process // inferred from electronic annotation///0006646 // phosphatidylethanolamine biosynthetic process // not recorded///0008654 // phospholipid biosynthetic proc
1069.7924	1480.2643	NM_011436	0.00361779	1.38	***Sorl1***	sortilin-related receptor, LDLR class A repeats-containing	0000042 // protein targeting to Golgi // not recorded///0006605 // protein targeting // not recorded///0006622 // protein targeting to lysosome // not recorded///0006629 // lipid metabolic proce
378.49936	523.6387	NM_001304830///NM_	0.002964168	1.38	***Maff***	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	0001701 // in utero embryonic development // inferred from genetic interaction///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of trans
297.13788	410.64188	NM_011068///XM_006	0.009212852	1.38	***Pex11a***	peroxisomal biogenesis factor 11 alpha	0007031 // peroxisome organization // not recorded///0007165 // signal transduction // not recorded///0016557 // peroxisome membrane biogenesis // not recorded///0016559 // peroxisome fis
554.0281	765.62036	NM_001114098///NM_	6.27E-04	1.38	***Mtcl1***	microtubule crosslinking factor 1	0001578 // microtubule bundle formation // inferred from direct assay///0010506 // regulation of autophagy // inferred from electronic annotation///0045197 // establishment or maintenance of
427.99307	590.8284	NM_175268///NM_212	0.001597076	1.38	***Fam53b***	family with sequence similarity 53, member B	
825.0809	1138.714	NM_001081322///XM_	0.001779136	1.38	***Myo5c***	myosin VC	0008152 // metabolic process // inferred from electronic annotation///0032254 // establishment of secretory granule localization // not recorded
1250.9496	1726.2533	NM_007570	0.001452931	1.38	***Btg2***	B cell translocation gene 2, anti-proliferative	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // re
854.95184	1173.1329	NM_001276292///NM_	0.001814497	1.37	***Wwp1***	WW domain containing E3 ubiquitin protein ligase 1	0016567 // protein ubiquitination // inferred from direct assay///0016567 // protein ubiquitination // traceable author statement///0030217 // T cell differentiation // traceable author statement//
248.01494	339.4977	NM_001171000///NM_	3.70E-04	1.37	***Ahcyl2***	S-adenosylhomocysteine hydrolase-like 2	0006730 // one-carbon metabolic process // inferred from electronic annotation///0033353 // S-adenosylmethionine cycle // not recorded
816.7312	1117.2758	NM_010139///XM_006	0.002238735	1.37	***Epha2***	Eph receptor A2	0001501 // skeletal system development // inferred from mutant phenotype///0001525 // angiogenesis // inferred from electronic annotation///0001568 // blood vessel development // inferred fro
522.75397	714.48865	NM_001114312///NM_	0.001940249	1.37	***Shtn1***	shootin 1	0006930 // substrate-dependent cell migration, cell extension // not recorded///0007265 // Ras protein signal transduction // not recorded///0007275 // multicellular organismal development // in
305.2689	417.1623	NM_012026///XM_006	0.007140057	1.37	***Arhgef28***	Rho guanine nucleotide exchange factor (GEF) 28	0021955 // central nervous system neuron axonogenesis // inferred from mutant phenotype///0030154 // cell differentiation // inferred from electronic annotation///0035023 // regulation of Rho
501.2641	682.9445	NM_018824///XM_006	0.001719914	1.36	***Slc23a2***	solute carrier family 23 (nucleobase transporters), member 2	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006814 // sodium ion transport // inferred from electronic annotat
43.390915	59.055687	NM_023140///NR_0336	0.002062244	1.36	***Glrx3///Gm12669***	glutaredoxin 3///glutaredoxin 3 pseudogene	0002026 // regulation of the force of heart contraction // inferred from mutant phenotype///0010614 // negative regulation of cardiac muscle hypertrophy // inferred from mutant phenotype///004
2056.078	2793.2964	NM_001081066///XM_	0.007665182	1.36	***Dennd3***	DENN/MADD domain containing 3	0008333 // endosome to lysosome transport // inferred from genetic interaction///0043547 // positive regulation of GTPase activity // not recorded///0044257 // cellular protein catabolic process

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	RefSeq Transcript ID	p	FC (Air:O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
407.10663	553.0156	NM_001033287///NM_	0.003309002	1.36	***Ptpn14***	protein tyrosine phosphatase, non-receptor type 14	0001946 // lymphangiogenesis // inferred from mutant phenotype///0001946 // lymphangiogenesis // not recorded///0006351 // transcription, DNA-templated // inferred from electronic annotati
383.62408	520.78455	NM_001025566///NM_	0.001913004	1.36	***Chka***	choline kinase alpha	0006580 // ethanolamine metabolic process // not recorded///0006629 // lipid metabolic process // inferred from electronic annotation///0006646 // phosphatidylethanolamine biosynthetic proce
520.5742	706.25085	NM_029166///XM_006	0.00143661	1.36	***Uhrf1bp1l***	UHRF1 (ICBP90) binding protein 1-like	
121.745514	164.69046	NM_001001737///NM_	0.003053795	1.35	***Zfp950***	zinc finger protein 950	0001570 // vasculogenesis // inferred from mutant phenotype///0001822 // kidney development // inferred from mutant phenotype///0006355 // regulation of transcription, DNA-templated // infe
20.843884	28.191956	XR_864485///XR_86448	0.009262349	1.35	***Gm38639***	predicted gene, 38639	
101.050804	136.6212		0.009754658	1.35	***W91776***	expressed sequence W91776	
348.197	469.72803	NM_010266///XM_006	0.003637469	1.35	***Gda***	guanine deaminase	0006147 // guanine catabolic process // inferred from electronic annotation///0031116 // positive regulation of microtubule polymerization // not recorded///0046098 // guanine metabolic proces
370.55664	498.78146	NR_002853///NR_0277	0.007353815	1.35	***Airn***	antisense Igf2r RNA	0006349 // regulation of gene expression by genetic imprinting // inferred from mutant phenotype///0051570 // regulation of histone H3-K9 methylation // inferred from mutant phenotype
68.51983	92.09903	NM_001195617///NM_	0.006191571	1.34	***Dcdc2a***	doublecortin domain containing 2a	0001764 // neuron migration // inferred from genetic interaction///0001764 // neuron migration // not recorded///0007399 // nervous system development // inferred from electronic annotation/
438.96487	589.52893	NM_011897///XM_006	0.002410484	1.34	***Spry2***	sprouty homolog 2 (Drosophila)	0000132 // establishment of mitotic spindle orientation // inferred from genetic interaction///0007275 // multicellular organismal development // inferred from electronic annotation///0007605 //
117.457664	157.44104	NM_001033443///XM_	0.008349649	1.34	***Cdkl4***	cyclin-dependent kinase-like 4	0006468 // protein phosphorylation // inferred from electronic annotation///0016310 // phosphorylation // inferred from electronic annotation///0051726 // regulation of cell cycle // inferred fro
1129.9148	1513.6592	NM_001099288///NM_	0.007812132	1.34	***Arhgap44***	Rho GTPase activating protein 44	0007165 // signal transduction // inferred from electronic annotation///0043547 // positive regulation of GTPase activity // inferred from electronic annotation
558.0418	747.2911	NM_133829///NM_178	0.001811663	1.34	***Mfsd6***	major facilitator superfamily domain containing 6	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // inferred from electronic annotation///0055085 // transmembrane transport /
210.15689	280.93292	NM_001166633///NM_	0.006577869	1.34	***Gyltl1b***	glycosyltransferase-like 1B	0006486 // protein glycosylation // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation///0035269 // protein O-linked mannosylation // infer
197.9558	264.5334	NM_001177995///NM_	0.007480026	1.34	***Prdm16***	PR domain containing 16	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0000122 // negative regulation of transcription from RNA polymerase II prom
670.2252	894.3502	NM_144847///XM_006	0.001185593	1.33	***Nrbp2***	nuclear receptor binding protein 2	0006468 // protein phosphorylation // inferred from electronic annotation///0007399 // nervous system development // inferred from electronic annotation///0016242 // negative regulation of ma
27.39146	36.466972		0.007256189	1.33	***AU015536***	expressed sequence AU015536	
356.23785	474.22256	NM_001316678///NM_	0.001601126	1.33	***Ptpre***	protein tyrosine phosphatase, receptor type, E	0006470 // protein dephosphorylation // inferred from electronic annotation///0007185 // transmembrane receptor protein tyrosine phosphatase signaling pathway // inferred from direct assay///
256.62045	341.09824	NM_001109040///NM_	0.003957991	1.33	***Kif21a***	kinesin family member 21A	0007018 // microtubule-based movement // not recorded///0008152 // metabolic process // inferred from electronic annotation
356.75464	473.79205	NM_178726///XM_006	0.002081727	1.33	***Ppm1l***	protein phosphatase 1 (formerly 2C)-like	0000165 // MAPK cascade // inferred from physical interaction///0006470 // protein dephosphorylation // inferred from electronic annotation///0007178 // transmembrane receptor protein serine
1518.4796	2014.3811	NM_001252653///NM_	0.003598545	1.33	***Ecm1***	extracellular matrix protein 1	0001503 // ossification // inferred from electronic annotation///0001525 // angiogenesis // inferred from electronic annotation///0001938 // positive regulation of endothelial cell proliferation // n
398.76205	528.15375	NM_001035531///NM_	0.004632358	1.32	***Adrbk2***	adrenergic receptor kinase, beta 2	0001934 // positive regulation of protein phosphorylation // not recorded///0002029 // desensitization of G-protein coupled receptor protein signaling pathway // not recorded///0006468 // protei
64.08077	84.69259	NM_008719///XM_011	0.007165891	1.32	***Npas2***	neuronal PAS domain protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006974 // cellula
810.3151	1070.7461	NM_170779	0.001997171	1.32	***Wwc1***	WW, C2 and coiled-coil domain containing 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // re
4760.889	6282.781	NM_001081286///XM_	0.004660445	1.32	***Fat1***	FAT tumor suppressor homolog 1 (Drosophila)	0007015 // actin filament organization // inferred from mutant phenotype///0007155 // cell adhesion // inferred from electronic annotation///0007156 // homophilic cell adhesion via plasma mem
203.83978	268.46323	NM_008105///NM_023	0.001016067	1.32	***Gcnt2***	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	0006486 // protein glycosylation // not recorded///0007179 // transforming growth factor beta receptor signaling pathway // inferred from mutant phenotype///0007179 // transforming growth fa
2637.189	3470.8955	NM_007735///XM_011	0.009288732	1.32	***Col4a4***	collagen, type IV, alpha 4	0032836 // glomerular basement membrane development // inferred from mutant phenotype///0032836 // glomerular basement membrane development // not recorded
983.2645	1293.6791	NM_001077403///NM_	0.009066818	1.32	***Nrp2***	neuropilin 2	0001525 // angiogenesis // inferred from electronic annotation///0001755 // neural crest cell migration // inferred from mutant phenotype///0001764 // neuron migration // inferred from mutant
167.76083	220.68974	NM_010441///XM_006	0.007354527	1.32	***Hmga2***	high mobility group AT-hook 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001837 // epithelial to mesenchymal transition // inferred from sequence or structural similarit
985.9826	1295.6543	NM_001242419///NM_	0.009746431	1.31	***Susd6***	sushi domain containing 6	0006974 // cellular response to DNA damage stimulus // not recorded///0008219 // cell death // not recorded
322.6954	423.25653	NM_019427///XM_006	0.003100493	1.31	***Epb41l4b***	erythrocyte membrane protein band 4.1 like 4b	0010628 // positive regulation of gene expression // not recorded///0031032 // actomyosin structure organization // not recorded///0042060 // wound healing // not recorded///0045785 // positiv
131.23123	172.09679	NM_001290733///NM_	0.006146731	1.31	***Osbpl6***	oxysterol binding protein-like 6	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic annotation
500.67035	656.1234	NM_010756	0.004497939	1.31	***Mafg***	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	0001701 // in utero embryonic development // inferred from genetic interaction///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of trans
132.92372	173.78185	NM_178639///XM_006	0.004554516	1.31	***Sfxn5***	sideroflexin 5	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0015746 // citrate transport // not recorded///0034220 // ion trans
6080.784	7945.0317	NM_023134///XM_011	0.00609484	1.31	***Sftpa1***	surfactant associated protein A1	0001666 // response to hypoxia // inferred from electronic annotation///0007623 // circadian rhythm // inferred from electronic annotation///0009725 // response to hormone // inferred from ele
221.80902	289.80542	NM_207202	0.004484124	1.31	***Ccdc120***	coiled-coil domain containing 120	
2083.3118	2720.7524	NM_001293667///NM_	0.001472981	1.31	***Atp11a***	ATPase, class VI, type 11A	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotati
437.01465	570.61316	NM_001005784///NM_	0.005564036	1.31	***Inadl***	InaD-like (Drosophila)	
335.82	438.40463	NM_008478///XM_006	0.0074249	1.31	***L1cam***	L1 cell adhesion molecule	0007155 // cell adhesion // inferred from electronic annotation///0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from mutant phenotype///0007157 // h
250.2933	326.36548	NM_177271	0.007636873	1.30	***Samd5***	sterile alpha motif domain containing 5	
107.44085	140.06169	NM_001291268///NM_	0.008189959	1.30	***Hnf1b***	HNF1 homeobox B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001706 // endoderm formation // not recorded///0001714 // endodermal cell fate
230.51567	300.45352	NM_001110218///NM_	0.008262175	1.30	***Ppm1h***	protein phosphatase 1H (PP2C domain containing)	0006470 // protein dephosphorylation // inferred from electronic annotation
1509.2809	1961.9949	NM_008259///XM_006	0.005939459	1.30	***Foxa1***	forkhead box A1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0000122 // negative regulation of transcription from RNA polymerase II prom
401.71042	521.77765	NM_001122759///NM_	0.003972929	1.30	***Pde7a***	phosphodiesterase 7A	0006198 // cAMP catabolic process // inferred from electronic annotation///0007165 // signal transduction // inferred from electronic annotation///0008152 // metabolic process // inferred from e
287.88727	373.5391	NM_001081155///NM_	0.008889131	1.30	***Rap1gap***	Rap1 GTPase-activating protein	0022409 // positive regulation of cell-cell adhesion // inferred from mutant phenotype///0043087 // regulation of GTPase activity // not recorded///0043547 // positive regulation of GTPase activity
408.59457	529.0231	NM_001195025///NM_	0.003851789	1.29	***Nuak2***	NUAK family, SNF1-like kinase, 2	0006468 // protein phosphorylation // not recorded///0006915 // apoptotic process // inferred from electronic annotation///0016310 // phosphorylation // inferred from electronic annotation///0
939.82996	1216.3804	NM_001123382///NM_	0.002127687	1.29	***Il1r1***	interleukin 1 receptor, type I	0007165 // signal transduction // inferred from electronic annotation///0009314 // response to radiation // not recorded///0010286 // heat acclimation // not recorded///0019221 // cytokine-med
1528.3687	1977.9941	NM_001168333///NM_	0.002030536	1.29	***Tinagl1***	tubulointerstitial nephritis antigen-like 1	0006508 // proteolysis // inferred from electronic annotation///0006898 // receptor-mediated endocytosis // inferred from electronic annotation///0006955 // immune response // inferred from el
361.6311	468.00662	NM_001081355///NM_	0.003970692	1.29	***Prdm2***	PR domain containing 2, with ZNF domain	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0008340 // determination of adult lifespan // inferred from mutant phenotype///0032355 // respons
185.50215	239.77614	NM_001024617///NM_	0.007355195	1.29	***Inpp4b***	inositol polyphosphate-4-phosphatase, type II	0006874 // cellular calcium ion homeostasis // inferred from genetic interaction///0036092 // phosphatidylinositol-3-phosphate biosynthetic process // not recorded///0045671 // negative regulati
1603.2427	2070.9624	NM_001291065///NM_	0.007149878	1.29	***Foxa2***	forkhead box A2	0000432 // positive regulation of transcription from RNA polymerase II promoter by glucose // inferred from direct assay///0000433 // negative regulation of transcription from RNA polymerase II p
1710.4757	2207.7852	NM_001025250///NM_	0.002878465	1.29	***Vegfa***	vascular endothelial growth factor A	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001525 // angiogenesis // inferred from direct assay///0001525 // angiogenesis // inferred fro
592.0897	763.7925	NM_001024624	0.00146201	1.29	***Cdkl5***	cyclin-dependent kinase-like 5	0001764 // neuron migration // not recorded///0006468 // protein phosphorylation // inferred from electronic annotation///0016310 // phosphorylation // inferred from electronic annotation///0
466.96338	602.07007	NM_010153	0.003649187	1.29	***Erbb3***	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	0003197 // endocardial cushion development // inferred from mutant phenotype///0006468 // protein phosphorylation // inferred from electronic annotation///0007162 // negative regulation of c
945.8543	1218.3705	NM_011756	0.001165486	1.29	***Zfp36***	zinc finger protein 36	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0000122 // negative regulation of transcription from RNA polymerase II prom
28.196205	36.272247		0.007101238	1.29	***D7Ertd558e***	DNA segment, Chr 7, ERATO Doi 558, expressed	
2222.579	2858.4988	NM_008808///XM_006	0.001829359	1.29	***Pdgfa***	platelet derived growth factor, alpha	0001525 // angiogenesis // inferred from direct assay///0001942 // hair follicle development // inferred from mutant phenotype///0002053 // positive regulation of mesenchymal cell proliferation
330.54477	424.83102	NM_001242427///NM_	0.001493512	1.29	***Slc37a1***	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	0006810 // transport // inferred from electronic annotation///0006820 // anion transport // not recorded///0035435 // phosphate ion transmembrane transport // ---///0055062 // phosphate ion
1006.2722	1292.6781	NM_018881///XM_006	0.004505317	1.28	***Fmo2***	flavin containing monooxygenase 2	0006082 // organic acid metabolic process // not recorded///0006739 // NADP metabolic process // not recorded///0006805 // xenobiotic metabolic process // not recorded///0009404 // toxin me
278.695	357.85294	NM_009523	0.002435394	1.28	***Wnt4***	wingless-type MMTV integration site family, member 4	0001656 // metanephros development // inferred from mutant phenotype///0001656 // metanephros development // traceable author statement///0001658 // branching involved in ureteric bud
2445.0894	3135.405	NM_009655///XM_006	0.006525636	1.28	***Alcam***	activated leukocyte cell adhesion molecule	0007155 // cell adhesion // inferred from electronic annotation///0007157 // heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules // inferred from sequence or structural si
292.50104	374.82904	NM_146013///XM_006	0.004768179	1.28	***Sec14l4***	SEC14-like lipid binding 4	0006810 // transport // inferred from electronic annotation
1497.366	1916.3384	NM_001285870///NM_	0.004520725	1.28	***Trim3***	tripartite motif-containing 3	0006810 // transport // inferred from electronic annotation///0015031 // protein transport // inferred from electronic annotation///0016567 // protein ubiquitination // inferred from direct assay
210.75037	269.5759	NM_001204931///NM_	0.003295566	1.28	***Reep6***	receptor accessory protein 6	0032386 // regulation of intracellular transport // inferred from direct assay
166.97786	213.40076	XR_379375///XR_40567	0.004812483	1.28	***Gm32819***	predicted gene, 32819	
1200.5897	1533.7145	NM_001172160///NM_	0.001586058	1.28	***Flrt3***	fibronectin leucine rich transmembrane protein 3	0003345 // proepicardium cell migration involved in pericardium morphogenesis // inferred from mutant phenotype///0007155 // cell adhesion // inferred from electronic annotation///0007275 //
32.180107	41.09088	NM_023852///XM_006	0.007803954	1.28	***Rab3c***	RAB3C, member RAS oncogene family	0006810 // transport // inferred from electronic annotation///0006886 // intracellular protein transport // not recorded///0006904 // vesicle docking involved in exocytosis // not recorded///0007
1913.2311	2440.413	NM_181444///XM_006	0.002394067	1.28	***Gprc5a***	G protein-coupled receptor, family C, group 5, member A	0007165 // signal transduction // inferred from electronic annotation///0007175 // negative regulation of epidermal growth factor-activated receptor activity // inferred from mutant phenotype///
41.73875	53.2297	NM_008412///XM_006	0.004702997	1.28	***Ivl***	involucrin	0010224 // response to UV-B // inferred from electronic annotation///0018149 // peptide cross-linking // inferred from electronic annotation///0018153 // isopeptide cross-linking via N6-(L-isoglut
846.31726	1077.7935	NM_001243132///NM_	0.003912692	1.27	***Tspan2***	tetraspanin 2	0006954 // inflammatory response // inferred from genetic interaction///0007166 // cell surface receptor signaling pathway // not recorded///0007420 // brain development // inferred from electr
62.270107	79.17364	NM_001174107///NM_	0.006408958	1.27	***Map3k9***	mitogen-activated protein kinase kinase kinase 9	0000165 // MAPK cascade // inferred from electronic annotation///0000186 // activation of MAPKK activity // inferred from electronic annotation///0006351 // transcription, DNA-templated // inf
2057.0906	2611.735	NM_201529///XM_006	0.002841721	1.27	***Lmo7***	LIM domain only 7	0016337 // single organismal cell-cell adhesion // not recorded///0023051 // regulation of signaling // inferred from electronic annotation///0030155 // regulation of cell adhesion // inferred from
1569.542	1992.6072	NM_001034851///NM_	0.003107579	1.27	***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 neuron apoptotic process // inferred from
57.509842	73.00801	NM_001162970///XM_	0.002583854	1.27	***Aim1l***	absent in melanoma 1-like	
730.0157	925.0214	NM_173038///XM_006	0.003904908	1.27	***Tbcel***	tubulin folding cofactor E-like	
632.7603	801.61237	NM_001199059///NM_	0.006329605	1.27	***Rabgef1***	RAB guanine nucleotide exchange factor (GEF) 1	0001933 // negative regulation of protein phosphorylation // inferred from mutant phenotype///0002686 // negative regulation of leukocyte migration // inferred from mutant phenotype///000661
2006.9261	2542.1685	NM_001162532	0.00548018	1.27	***Fam174b***	family with sequence similarity 174, member B	
1663.2024	2104.5557	NM_001081071///NM_	0.009691878	1.27	***Lclat1***	lysocardiolipin acyltransferase 1	0006629 // lipid metabolic process // inferred from electronic annotation///0007275 // multicellular organismal development // inferred from electronic annotation///0008152 // metabolic process
363.9186	459.78488	NM_176838///XM_006	0.009630457	1.26	***Esrp2***	epithelial splicing regulatory protein 2	0006397 // mRNA processing // inferred from electronic annotation///0008380 // RNA splicing // inferred from electronic annotation///0043484 // regulation of RNA splicing // not recorded
535.15436	675.91174	NM_031380	0.002322349	1.26	***Fstl3***	follistatin-like 3	0001503 // ossification // inferred from electronic annotation///0001822 // kidney development // inferred from electronic annotation///0002244 // hematopoietic progenitor cell differentiation //
533.65405	673.4432	NM_008576///XM_006	0.002280301	1.26	***Abcc1***	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	0006810 // transport // inferred from electronic annotation///0006855 // drug transmembrane transport // not recorded///0006979 // response to oxidative stress // not recorded///0008152 // m
1558.4786	1965.2582	NM_177305	0.005111118	1.26	***Arl4c***	ADP-ribosylation factor-like 4C	0006810 // transport // inferred from electronic annotation///0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///0032456 // endocytic recycling // not
573.0028	722.34814	NM_010415	0.006871689	1.26	***Hbegf***	heparin-binding EGF-like growth factor	0001525 // angiogenesis // non-traceable author statement///0001832 // blastocyst growth // traceable author statement///0007173 // epidermal growth factor receptor signaling pathway // infer
50.744976	63.899475	NM_001110513///NM_	0.00520535	1.26	***Ebf4***	early B cell factor 4	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from direct assay///0006366 // transcription fr
331.0545	416.33224	NM_001085495///XM_	0.006623237	1.26	***Arfgef2***	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	0001881 // receptor recycling // not recorded///0006810 // transport // inferred from electronic annotation///0006887 // exocytosis // not recorded///0006893 // Golgi to plasma membrane trans
597.7092	751.471	NM_133757///XM_011	0.005876104	1.26	***Pgs1***	phosphatidylglycerophosphate synthase 1	0006629 // lipid metabolic process // inferred from electronic annotation///0006655 // phosphatidylglycerol biosynthetic process // inferred from sequence or structural similarity///0006655 // ph
345.78284	434.64417	NM_172501	0.00750721	1.26	***Nhlrc3***	NHL repeat containing 3	
381.70642	479.68195	NM_001109975///NM_	0.007157282	1.26	***Synpo***	synaptopodin	0030865 // cortical cytoskeleton organization // non-traceable author statement///0032233 // positive regulation of actin filament bundle assembly // inferred from direct assay///0051492 // regul
601.21063	753.78296	NM_181595///XM_006	0.007148996	1.25	***Ppp1r9a***	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0007015 // actin filament organization // inferred from physical interaction///0010976 // positive regulation of neuron projection development // not recorded///0019722 // calcium-mediated sign
1137.0524	1424.2941	NM_001111073///NM_	0.009344352	1.25	***Fxyd5***	FXYD domain-containing ion transport regulator 5	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0034220 // ion transmembrane transport // inferred from electroni
75.04911	93.89852	NM_175480///XM_006	0.0070803	1.25	***Zfp612***	zinc finger protein 612	0006355 // regulation of transcription, DNA-templated // not recorded
4107.917	5132.2495	NM_010493	0.005632566	1.25	***Icam1***	intercellular adhesion molecule 1	0001541 // ovarian follicle development // inferred from electronic annotation///0001666 // response to hypoxia // inferred from electronic annotation///0001975 // response to amphetamine // i
2838.922	3546.394	NM_009194///XM_006	0.003173459	1.25	***Slc12a2***	solute carrier family 12, member 2	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006813 // potassium ion transport // not recorded///0006814 // s
749.2429	935.74603	NM_001165253///NM_	0.00274639	1.25	***Ctage5***	CTAGE family, member 5	

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	RefSeq Transcript ID	p	FC (Air:O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
789.1126	985.4984	NM_008654	0.005799206	1.25	***Ppp1r15a***	protein phosphatase 1, regulatory (inhibitor) subunit 15A	0006417 // regulation of translation // inferred from electronic annotation///0006915 // apoptotic process // inferred from electronic annotation///0010628 // positive regulation of gene expressio
950.3166	1186.4846	NM_001038643///NM_	0.002910278	1.25	***Slco3a1***	solute carrier organic anion transporter family, member 3a1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006857 // oligopeptide transport // not recorded///0015711 // org
8145.351	10165.925	NM_001029937///XM_	0.009392737	1.25	***Sec14l3***	SEC14-like lipid binding 3	0006810 // transport // inferred from electronic annotation
275.76782	343.7545	NM_029291///XM_0065	0.006149239	1.25	***Ascc2***	activating signal cointegrator 1 complex subunit 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
452.89276	564.2718	NM_001034030///NM_	0.008969214	1.25	***Limk2***	LIM motif-containing protein kinase 2	0006468 // protein phosphorylation // inferred from mutant phenotype///0006468 // protein phosphorylation // not recorded///0007283 // spermatogenesis // inferred from mutant phenotype///
218.59479	272.117	NM_183183///XM_0065	0.006962176	1.24	***Gprin3***	GPRIN family member 3	
1687.3281	2099.2078	NM_001293622///NM_	0.005596881	1.24	***Ppp3ca***	protein phosphatase 3, catalytic subunit, alpha isoform	0000082 // G1/S transition of mitotic cell cycle // inferred from mutant phenotype///0001975 // response to amphetamine // inferred from electronic annotation///0006470 // protein dephosphory
1279.319	1591.5577	NM_001285917///NM_	0.005087391	1.24	***Dapk1***	death associated protein kinase 1	0006417 // regulation of translation // inferred from electronic annotation///0006468 // protein phosphorylation // inferred from direct assay///0006468 // protein phosphorylation // not recorde
248.21167	308.5953	NM_053169///XM_0065	0.006915159	1.24	***Trim16***	tripartite motif-containing 16	0043966 // histone H3 acetylation // not recorded///0043967 // histone H4 acetylation // not recorded///0045618 // positive regulation of keratinocyte differentiation // not recorded///0045893 /
3122.544	3877.6018	NM_011595	0.007898194	1.24	***Timp3***	tissue inhibitor of metalloproteinase 3	0007417 // central nervous system development // inferred from electronic annotation///0007568 // aging // inferred from electronic annotation///0009612 // response to mechanical stimulus // i
338.4052	420.1267	NM_027514	0.006594795	1.24	***Pvr***	poliovirus receptor	0002860 // positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target // ---///0007156 // homophilic cell adhesion via plasma membrane adhesion molecules //
548.4758	680.0645	NM_001039181///NM_	0.006998207	1.24	***Npr3***	natriuretic peptide receptor 3	0001501 // skeletal system development // inferred from direct assay///0001501 // skeletal system development // inferred from mutant phenotype///0002158 // osteoclast proliferation // inferre
3529.805	4353.9326	NM_001305440///NM_	0.009659083	1.23	***Spry1***	sprouty homolog 1 (Drosophila)	0000132 // establishment of mitotic spindle orientation // inferred from genetic interaction///0001656 // metanephros development // inferred from genetic interaction///0001657 // ureteric bud
400.33698	493.3685	NM_007865///XM_0112	0.008344945	1.23	***Dll1***	delta-like 1 (Drosophila)	0001701 // in utero embryonic development // non-traceable author statement///0001756 // somitogenesis // inferred from genetic interaction///0001756 // somitogenesis // inferred from mutan
1782.3717	2194.9504	NM_001004468///NM_	0.003032173	1.23	***Tacc2***	transforming, acidic coiled-coil containing protein 2	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype///0008283 // cell proliferation // inferred from mutant phenotype///0021987 // cerebral cortex development
381.49026	469.6352	NM_001253386///NM_	0.008596059	1.23	***Serinc2***	serine incorporator 2	0006658 // phosphatidylserine metabolic process // not recorded///0006665 // sphingolipid metabolic process // inferred from electronic annotation///0015825 // L-serine transport // not recorde
184.15356	225.44762	NM_001163749///NM_	0.00960717	1.22	***Camsap3***	calmodulin regulated spectrin-associated protein family, member 3	0000226 // microtubule cytoskeleton organization // not recorded///0010923 // negative regulation of phosphatase activity // not recorded///0031175 // neuron projection development // inferre
71.19115	87.00874	NM_175666	0.008873613	1.22	***Hist2h2bb***	histone cluster 2, H2bb	0006334 // nucleosome assembly // not recorded
503.03867	613.9215	NM_007711///NM_173	0.005255878	1.22	***Clcn3***	chloride channel, voltage-sensitive 3	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // not recorded///0006821 // chloride transport // not recorded///0006911 // phagocytosis, engulfment // i
2445.0586	2974.7217	NM_001161413///NM_	0.006944822	1.22	***Slc3a2***	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006810 // transport // inferred from electronic annotation///0006865 // amino acid transport // inferred from
1279.4628	1555.5134	NM_001287514///NM_	0.006531842	1.22	***Cebpa***	CCAAT/enhancer binding protein (C/EBP), alpha	0000050 // urea cycle // inferred from direct assay///0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001889 // liver development
429.69196	521.97565	NM_001162375///NM_	0.007404229	1.21	***Fam73a***	family with sequence similarity 73, member A	
1259.9539	1529.7999	NM_011803	0.006202603	1.21	***Klf6***	Kruppel-like factor 6	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0019221 // cytoki
1826.7445	2217.0193	NM_001081274///NM_	0.00647463	1.21	***Pgd***	phosphogluconate dehydrogenase	0005975 // carbohydrate metabolic process // not recorded///0006098 // pentose-phosphate shunt // not recorded///0006739 // NADP metabolic process // not recorded///0009051 // pentose-ph
1324.7793	1603.9137	NM_007734	0.007148852	1.21	***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///0007166 // cell surfa
555.607	672.00195	NM_029508///XM_0065	0.007366358	1.21	***Pcgf5***	polycomb group ring finger 5	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0045944 // positi
142.42418	172.15913	NM_031880///XM_0065	0.007749506	1.21	***Tnk1***	tyrosine kinase, non-receptor, 1	0006468 // protein phosphorylation // inferred from electronic annotation///0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // not recorded///0016310 // phosphor
33.161358	40.02322	NM_001164767///NM_	0.008009913	1.21	***Robo3***	roundabout homolog 3 (Drosophila)	0001764 // neuron migration // inferred from mutant phenotype///0006935 // chemotaxis // inferred from electronic annotation///0007275 // multicellular organismal development // inferred fro
471.20993	568.0679	NM_001313918///NM_	0.004545672	1.21	***Eif2ak3***	eukaryotic translation initiation factor 2 alpha kinase 3	0001501 // skeletal system development // inferred from mutant phenotype///0001503 // ossification // not recorded///0001525 // angiogenesis // not recorded///0002063 // chondrocyte develo
927.7281	1112.0266	NM_153389///NR_0039	0.006121195	1.20	***Atp10d***	ATPase, class V, type 10D	0006810 // transport // inferred from electronic annotation///0006812 // cation transport // non-traceable author statement///0006869 // lipid transport // inferred from electronic annotation///
437.2646	523.69025	NM_001159394///NM_	0.008714629	1.20	***Nfkbiz***	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006357 // regula
1793.3213	2147.0642	NM_001166408///NM_	0.008957124	1.20	***Rai14***	retinoic acid induced 14	
474.6698	567.26447	NM_001038602///NM_	0.007153812	1.20	***Marveld2***	MARVEL (membrane-associating) domain containing 2	0007605 // sensory perception of sound // inferred from mutant phenotype///0007605 // sensory perception of sound // not recorded///0045216 // cell-cell junction organization // inferred from
4808.496	5742.4917	NM_033073	0.007291713	1.19	***Krt7***	keratin 7	
2655.6184	3164.502	NM_010637	0.00802799	1.19	***Klf4***	Kruppel-like factor 4 (gut)	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006351 // transcription, DNA-templated // inferred from mutant phenotype///0006355 // regul
2308.3855	2740.9998	NM_010581///XM_0065	0.007570742	1.19	***Cd47***	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	0007155 // cell adhesion // inferred from electronic annotation///0007165 // signal transduction // inferred from electronic annotation///0007165 // signal transduction // ---///0007229 // integrin
1005.0988	1191.934	NM_133791	0.009684668	1.19	***Wwc2***	WW, C2 and coiled-coil domain containing 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0035331 // negative regulation of hippo signaling // not recorded///0046621 // negative regulat
20.939976	24.808792	XR_865726	0.004247976	1.18	***LOC105244007***	uncharacterized LOC105244007	
233.1591	205.92485	NM_001163511///NM_	0.009366385	-1.13	***Spata5***	spermatogenesis associated 5	0007275 // multicellular organismal development // inferred from electronic annotation///0007283 // spermatogenesis // inferred from electronic annotation///0030154 // cell differentiation // in
147.00795	129.42291	NM_007726///XM_0065	0.009855953	-1.14	***Cnr1***	cannabinoid receptor 1 (brain)	0002866 // positive regulation of acute inflammatory response to antigenic stimulus // not recorded///0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein
252.76439	220.22298	NM_133677///NR_0279	0.008649599	-1.15	***Zbtb11os1***	zinc finger and BTB domain containing 11, opposite strand 1	
248.4654	216.06413	NM_033175	0.006386783	-1.15	***Lce3c***	late cornified envelope 3C	0008544 // epidermis development // inferred from electronic annotation///0018149 // peptide cross-linking // not recorded///0030216 // keratinocyte differentiation // not recorded
184.01167	159.92508	NM_023844///XM_0065	0.007789469	-1.15	***Jam2***	junction adhesion molecule 2	0007162 // negative regulation of cell adhesion // inferred from genetic interaction
115.64928	100.45263	NM_009936///XM_0065	0.009519205	-1.15	***Col9a3***	collagen, type IX, alpha 3	0008584 // male gonad development // inferred from expression pattern///0008585 // female gonad development // inferred from expression pattern
186.73788	161.4204	NM_011764///XM_0065	0.009554279	-1.16	***Zfp90***	zinc finger protein 90	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0006351 // transcription, DNA-templated // inferred from electronic annotation///
178.89636	154.15787	NM_010835	0.005008502	-1.16	***Msx1***	msh homeobox 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000122 // negative regulation of transcription from RNA polymerase II promoter //
263.56796	226.98973	NM_177857///XM_0065	0.009853996	-1.16	***Dennd2c***	DENN/MADD domain containing 2C	0043547 // positive regulation of GTPase activity // not recorded
395.6713	340.30524	NM_009013///XM_0065	0.006633704	-1.16	***Rad51ap1***	RAD51 associated protein 1	0006281 // DNA repair // inferred from electronic annotation///0006310 // DNA recombination // inferred from physical interaction///0006974 // cellular response to DNA damage stimulus // infer
298.2584	255.43314	NM_010381///XM_0036	0.00880283	-1.17	***H2-Ea-ps***	histocompatibility 2, class II antigen E alpha, pseudogene	0002376 // immune system process // inferred from electronic annotation///0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC class II // inferred from el
124.185074	106.27043	NM_173365///XM_0065	0.006449269	-1.17	***Gpr20***	G protein-coupled receptor 20	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor signaling pathway // not recorded
270.6594	231.2604	NM_001252568///NM_	0.003521152	-1.17	***Phyhd1***	phytanoyl-CoA dioxygenase domain containing 1	0002329 // pre-B cell differentiation // inferred from mutant phenotype///0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annota
740.3509	632.4095	NM_028977	0.008449008	-1.17	***Lrrc17***	leucine rich repeat containing 17	0001503 // ossification // inferred from electronic annotation///0001649 // osteoblast differentiation // inferred from direct assay///0033687 // osteoblast proliferation // inferred from direct assa
345.43604	294.9927	NM_145492///XM_0065	0.007478691	-1.17	***Zfp521***	zinc finger protein 521	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0007275 // multic
157.20836	133.80429	NM_008101///XM_0065	0.006889852	-1.17	***Gcgr***	glucagon receptor	0006887 // exocytosis // not recorded///0007165 // signal transduction // inferred from electronic annotation///0007166 // cell surface receptor signaling pathway // inferred from electronic anno
110.431564	93.89231	NM_019508///XM_0065	0.009051858	-1.18	***Il17b***	interleukin 17B	0006954 // inflammatory response // inferred from electronic annotation///0007166 // cell surface receptor signaling pathway // not recorded///0030593 // neutrophil chemotaxis // not recorded/
234.96635	199.74162	NM_009204///XM_0065	0.008736748	-1.18	***Slc2a4***	solute carrier family 2 (facilitated glucose transporter), member 4	0006810 // transport // inferred from electronic annotation///0008643 // carbohydrate transport // inferred from electronic annotation///0010021 // amylopectin biosynthetic process // inferred f
165.90924	141.00389	NM_177391///XM_0065	0.006563343	-1.18	***Fam109b***	family with sequence similarity 109, member B	0001881 // receptor recycling // not recorded///0007032 // endosome organization // not recorded///0042147 // retrograde transport, endosome to Golgi // not recorded
399.10037	339.0597	NM_010811///XM_0112	0.006226222	-1.18	***Ndst2***	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	0002002 // regulation of angiotensin levels in blood // inferred from mutant phenotype///0006024 // glycosaminoglycan biosynthetic process // traceable author statement///0008152 // metabolic
269.62973	228.8949	NM_023637///XM_0065	0.008344904	-1.18	***Sars2***	seryl-aminoacyl-tRNA synthetase 2	0006412 // translation // inferred from electronic annotation///0006418 // tRNA aminoacylation for protein translation // inferred from electronic annotation///0006434 // seryl-tRNA aminoacylati
410.7646	348.21103	NM_172705///XM_0112	0.004020016	-1.18	***Phf13***	PHD finger protein 13	0000278 // mitotic cell cycle // not recorded///0007049 // cell cycle // inferred from electronic annotation///0007059 // chromosome segregation // not recorded///0007067 // mitotic nuclear divi
164.69235	139.53923	NM_001286005///NM_	0.003508852	-1.18	***Abcg8***	ATP-binding cassette, sub-family G (WHITE), member 8	0006810 // transport // inferred from electronic annotation///0007584 // response to nutrient // inferred from electronic annotation///0007588 // excretion // inferred from mutant phenotype///
280.2898	237.42984	NM_016911	0.00668865	-1.18	***Srpx***	sushi-repeat-containing protein	0001845 // phagolysosome assembly // inferred from mutant phenotype///0006914 // autophagy // inferred from mutant phenotype///0034976 // response to endoplasmic reticulum stress // infe
292.75888	247.92036	NM_007440///XM_0112	0.009580907	-1.18	***Alox12***	arachidonate 12-lipoxygenase	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid metabolic process // inferred from electronic annotation///0006928 // movement of cell or subcell
4018.3362	3389.8147	NM_010494///XM_0065	0.0060007	-1.19	***Icam2***	intercellular adhesion molecule 2	0007155 // cell adhesion // not recorded///0016337 // single organismal cell-cell adhesion // inferred from electronic annotation
459.4756	387.014	NM_028306///XM_0065	0.008276964	-1.19	***Hspa12b***	heat shock protein 12B	
2760.5708	2323.3743	NM_029938	0.007700698	-1.19	***H2afv***	H2A histone family, member V	0006325 // chromatin organization // not recorded///0006342 // chromatin silencing // not recorded
60.661728	51.03382	XM_011251757	0.009236917	-1.19	***LOC102641619***	uncharacterized LOC102641619	
549.53625	462.12872	NM_145974///XM_0065	0.007414868	-1.19	***N4bp3***	NEDD4 binding protein 3	
163.50677	137.46042	NR_131182///XR_8617	0.009725694	-1.19	***Hoxaas2***	Hoxa cluster antisense RNA 2	
423.30942	355.19946	NM_024257	0.007082052	-1.19	***Hdhd3***	haloacid dehalogenase-like hydrolase domain containing 3	0008152 // metabolic process // inferred from electronic annotation
149.3137	125.25706	NM_175525///XM_0065	0.006019953	-1.19	***Ssu2***	ssu-2 homolog (C. elegans)	
90.77547	76.14254	NM_130453	0.00757058	-1.19	***Gpha2***	glycoprotein hormone alpha 2	1903955 // positive regulation of protein targeting to mitochondrion // not recorded
119.92948	100.5592	NM_031872	0.003996673	-1.19	***Tas1r3***	taste receptor, type 1, member 3	0001582 // detection of chemical stimulus involved in sensory perception of sweet taste // not recorded///0007165 // signal transduction // inferred from electronic annotation///0007186 // G-prot
1076.8334	900.75024	NM_001166377///NM_	0.007503269	-1.20	***Armcx1***	armadillo repeat containing, X-linked 1	
121.83629	101.76613	NM_144534///XM_0065	0.006453248	-1.20	***Tmem38a***	transmembrane protein 38A	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006813 // potassium ion transport // inferred from electronic anno
140.64401	117.248604	NM_177909	0.005808052	-1.20	***Slc9a9***	solute carrier family 9 (sodium/hydrogen exchanger), member 9	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006812 // cation transport // inferred from electronic annotation//
495.43036	412.74908	NM_001291156///NM_	0.003544553	-1.20	***Tlcd2***	TLC domain containing 2	
120.04116	99.97108	NM_026956///XM_0065	0.003495034	-1.20	***Cd209f***	CD209f antigen	
215.91557	179.81009	NM_009620	0.005197522	-1.20	***Adam4***	a disintegrin and metallopeptidase domain 4	0006508 // proteolysis // inferred from electronic annotation///0007229 // integrin-mediated signaling pathway // inferred from electronic annotation
78.285034	65.11406	NM_001048179///NM_	0.008547667	-1.20	***Ccl27a///Ccl27b///Gm***	chemokine (C-C motif) ligand 27A///chemokine (C-C motif) ligand 27b///predicted gene	0006955 // immune response // inferred from electronic annotation///0010820 // positive regulation of T cell chemotaxis // inferred from direct assay///0060326 // cell chemotaxis // inferred from
89.300865	74.22726	NM_001159374///NM_	0.009093158	-1.20	***Krt32***	keratin 32	
631.2004	524.2385	NM_025455///XM_0112	0.006142978	-1.20	***Ccdc28b***	coiled coil domain containing 28B	0030030 // cell projection organization // inferred from electronic annotation///0042384 // cilium assembly // not recorded
48.21261	40.032413	NM_001001454///NM_	0.009646241	-1.20	***Ttyh1***	tweety homolog 1 (Drosophila)	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006821 // chloride transport // not recorded///0007067 // mitotic
1212.1976	1004.6385	NM_173784///XM_0112	0.00724278	-1.21	***Ubtd2***	ubiquitin domain containing 2	
147.2023	121.91758	NM_001145949///NM_	0.005839225	-1.21	***Dlgap5***	discs, large (Drosophila) homolog-associated protein 5	0006470 // protein dephosphorylation // not recorded///0007049 // cell cycle // inferred from electronic annotation///0016311 // dephosphorylation // ---///0023052 // signaling // inferred from
1522.8271	1261.2205	NM_026439///XM_0065	0.004581366	-1.21	***Ccdc80***	coiled-coil domain containing 80	0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay///0030198 // extracellular matrix organization // inferred from direct assay
56.49337	46.752335	NM_031169///XM_0065	0.006119187	-1.21	***Kcnmb1***	potassium large conductance calcium-activated channel, subfamily M, beta member 1	0005513 // detection of calcium ion // not recorded///0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006813 //
2096.8682	1734.5073	NM_009870///XM_0065	0.004701736	-1.21	***Cdk4///LOC102641469***	cyclin-dependent kinase 4///cyclin-dependent kinase 4 pseudogene	0000082 // G1/S transition of mitotic cell cycle // not recorded///0002088 // lens development in camera-type eye // inferred from electronic annotation///0006468 // protein phosphorylation // in
519.0911	429.05222	NM_011581	0.005584574	-1.21	***Thbs2***	thrombospondin 2	0007155 // cell adhesion // inferred from electronic annotation///0016525 // negative regulation of angiogenesis // inferred from mutant phenotype///0016525 // negative regulation of angiogene
337.86295	279.24713	NM_016933	0.004568804	-1.21	***Ptprcap***	protein tyrosine phosphatase, receptor type, C polypeptide-associated protein	0006468 // protein phosphorylation // inferred from direct assay///0006468 // protein phosphorylation // inferred from electronic annotation///0006952 // defense response // not recorded///001
826.1582	682.6295	NM_020618///XM_0065	0.009607514	-1.21	***Smarce1***	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	0006337 // nucleosome disassembly // not recorded///0006338 // chromatin remodeling // not recorded///0006355 // regulation of transcription, DNA-templated // not recorded///0007399 // ne
77.884514	64.33711	NM_026235	0.00832781	-1.21	***Larp6***	La ribonucleoprotein domain family, member 6	0006396 // RNA processing // inferred from electronic annotation///0006417 // regulation of translation // inferred from electronic annotation
126.36181	104.2588	NM_025681///XM_0065	0.009621933	-1.21	***Gm11578///Lix1***	predicted gene 11578///limb expression 1 homolog (chicken)	0006914 // autophagy // not recorded///0097352 // autophagosome maturation // not recorded
126.36181	104.2588	NM_025681///XM_0065	0.009621933	-1.21	***Gm11578///Lix1***	predicted gene 11578///limb expression 1 homolog (chicken)	0006914 // autophagy // not recorded///0097352 // autophagosome maturation // not recorded

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	RefSeq Transcript ID	p	FC (Air:O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
3894.6462	3212.9739	NM_019791	0.008886055	-1.21	***Maged1***	melanoma antigen, family D, 1	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0032922 // circadian regulation of gene expression // inferred from mutant phenotype///004
157.40665	129.81396	NM_019517///XM_0065	0.004557086	-1.21	***Bace2***	beta-site APP-cleaving enzyme 2	0006508 // proteolysis // inferred from electronic annotation///0006509 // membrane protein ectodomain proteolysis // not recorded///0030163 // protein catabolic process // not recorded///004
165.3509	136.11333	NM_011270	0.002415653	-1.21	***Rhd***	Rh blood group, D antigen	0015696 // ammonium transport // inferred from mutant phenotype///0048821 // erythrocyte development // inferred from mutant phenotype///0060586 // multicellular organismal iron ion hom
120.91733	99.494255	NM_001081085///NM_	0.008117654	-1.22	***Sapcd2***	suppressor APC domain containing 2	
123.108345	101.29558	NM_012012///XM_0064	0.004761875	-1.22	***Exo1***	exonuclease 1	0002376 // immune system process // inferred from electronic annotation///0002455 // humoral immune response mediated by circulating immunoglobulin // inferred from mutant phenotype///00
1126.6392	926.2342	NM_080595///XM_0065	0.005510762	-1.22	***Emid1***	EMI domain containing 1	
434.79102	357.31918	NM_011923///XM_0064	0.009071883	-1.22	***Angptl2***	angiopoietin-like 2	
105.528404	86.61554	NM_001034013///NM_	0.001849715	-1.22	***Asic2***	acid-sensing (proton-gated) ion channel 2	0003026 // regulation of systemic arterial blood pressure by aortic arch baroreceptor feedback // inferred from mutant phenotype///0006810 // transport // inferred from electronic annotation///0
82.37563	67.54325	NM_001159647///NM_	0.003497345	-1.22	***Cntn1***	contactin 1	0007155 // cell adhesion // inferred from electronic annotation///0007219 // Notch signaling pathway // inferred from electronic annotation///0010628 // positive regulation of gene expression //
3520.0674	2883.6455	NM_172145///XM_0065	0.00823294	-1.22	***Eva1b***	eva-1 homolog B (C. elegans)	0098779 // mitophagy in response to mitochondrial depolarization // not recorded
78.22164	64.045876	NM_001164593///NM_	0.009711746	-1.22	***Pdzrn4***	PDZ domain containing RING finger 4	0016567 // protein ubiquitination // not recorded
234.00603	191.51558	NM_001040435///NM_	0.006618717	-1.22	***Tacc3***	transforming, acidic coiled-coil containing protein 3	0000226 // microtubule cytoskeleton organization // inferred from mutant phenotype///0001666 // response to hypoxia // inferred from direct assay///0008283 // cell proliferation // inferred from
179.36557	146.73427	NM_025864	0.002896201	-1.22	***Tmem206***	transmembrane protein 206	
1759.6533	1438.8083	NM_009870///XM_0065	0.003139645	-1.22	***Cdk4///LOC102641469***	cyclin-dependent kinase 4///cyclin-dependent kinase 4 pseudogene	0000082 // G1/S transition of mitotic cell cycle // not recorded///0002088 // lens development in camera-type eye // inferred from electronic annotation///0006468 // protein phosphorylation // in
302.26154	246.94635	NM_010112///XM_0065	0.001418271	-1.22	***Efs***	embryonal Fyn-associated substrate	0007155 // cell adhesion // inferred from electronic annotation
112.30793	91.74245	NM_178203///NM_178	0.006230252	-1.22	***Hist1h3b///Hist1h3h//***	histone cluster 1, H3b///histone cluster 1, H3h///histone cluster 1, H3e///histone cluste	0000183 // chromatin silencing at rDNA // traceable author statement///0002230 // positive regulation of defense response to virus by host // not recorded///0006334 // nucleosome assembly // n
1504.2819	1228.171	NM_001161796///NM_	0.00726586	-1.22	***Gucy1b3***	guanylate cyclase 1, soluble, beta 3	0006182 // cGMP biosynthetic process // not recorded///0007165 // signal transduction // not recorded///0007263 // nitric oxide mediated signal transduction // not recorded///0009190 // cyclic
178.15102	145.41344	NM_033612	0.006900379	-1.23	***Cela1***	chymotrypsin-like elastase family, member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0006508 // proteolysis // not recorded///0006954 // inflammatory response
1165.879	951.409	NM_010828///XM_0065	0.002410609	-1.23	***Cited2***	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001568 // blood vessel development // inferred from mutant phenotype///0001570 // vasculog
168.69127	137.65018	NM_021272	0.006308482	-1.23	***Fabp7***	fatty acid binding protein 7, brain	0001964 // startle response // inferred from mutant phenotype///0006810 // transport // inferred from electronic annotation///0021846 // cell proliferation in forebrain // inferred from mutant ph
25.05572	20.440367	NM_001031811///XM_	0.006049808	-1.23	***Kcnh8***	potassium voltage-gated channel, subfamily H (eag-related), member 8	0000160 // phosphorelay signal transduction system // inferred from electronic annotation///0006357 // regulation of transcription from RNA polymerase II promoter // not recorded///0006810 //
199.40442	162.62015	NM_001290761///NM_	0.007195685	-1.23	***Nmral1***	NmrA-like family domain containing 1	
1141.8058	930.5608	NM_001110211///NM_	0.004933062	-1.23	***Anxa6***	annexin A6	0006816 // calcium ion transport // inferred from mutant phenotype///0006937 // regulation of muscle contraction // inferred from mutant phenotype///0034220 // ion transmembrane transport
162.4499	132.36917	NM_013552///XM_0065	0.003965737	-1.23	***Hmmr***	hyaluronan mediated motility receptor (RHAMM)	
209.94354	170.96625	NM_009161///XM_011	0.006019118	-1.23	***Sgca***	sarcoglycan, alpha (dystrophin-associated glycoprotein)	0061024 // membrane organization // traceable author statement
763.05566	621.2856	NM_026979///XM_0065	0.007130411	-1.23	***C1qtnf2***	C1q and tumor necrosis factor related protein 2	0000187 // activation of MAPK activity // inferred from direct assay///0045725 // positive regulation of glycogen biosynthetic process // inferred from direct assay///0046321 // positive regulation
173.4144	141.13445	NM_013603	0.003342803	-1.23	***Mt3***	metallothionein 3	0000060 // protein import into nucleus, translocation // inferred from sequence or structural similarity///0000060 // protein import into nucleus, translocation // inferred from electronic annotatio
199.74557	162.40637	NM_022424///XM_0065	0.005735806	-1.23	***Fndc4***	fibronectin type III domain containing 4	
231.36537	187.96097	NM_001291184///NM_	0.009709475	-1.23	***Pcsk6***	proprotein convertase subtilisin/kexin type 6	0006508 // proteolysis // inferred from electronic annotation///0007354 // zygotic determination of anterior/posterior axis, embryo // inferred from genetic interaction///0007354 // zygotic deter
1120.4635	910.1688	NM_027506///NM_028	0.00898608	-1.23	***Gulp1***	GULP, engulfment adaptor PTB domain containing 1	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic annotation///0006909 // phagocytosis // inferred from electronic annotation///
71.93179	58.412685	NM_001113350///NM_	0.007871632	-1.23	***Xkr5***	X Kell blood group precursor-related family, member 5	
162.05418	131.52913	NM_145433	0.003521578	-1.23	***Mrm1***	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	0000453 // enzyme-directed rRNA 2'-O-methylation // not recorded///0001510 // RNA methylation // inferred from electronic annotation///0006364 // rRNA processing // inferred from electronic
236.60751	191.93196	NM_145365///XM_011	0.002053089	-1.23	***Creb3l3***	cAMP responsive element binding protein 3-like 3	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006366 // transc
835.90674	677.3797	NM_007683///XM_0065	0.004972493	-1.23	***Cenpc1***	centromere protein C1	0000278 // mitotic cell cycle // not recorded///0007049 // cell cycle // inferred from electronic annotation///0007059 // chromosome segregation // not recorded///0007067 // mitotic nuclear divi
129.92197	105.20876	NM_001081324///XM_	0.005411779	-1.23	***Neto2***	neuropilin (NRP) and tolloid (TLL)-like 2	2000312 // regulation of kainate selective glutamate receptor activity // inferred from electronic annotation///2000463 // positive regulation of excitatory postsynaptic potential // inferred from mu
146.57736	118.57673	NM_001163640///NM_	0.008687629	-1.24	***Chn2***	chimerin 2	0007165 // signal transduction // inferred from electronic annotation///0035556 // intracellular signal transduction // inferred from electronic annotation///0043547 // positive regulation of GTPas
521.4635	420.9284	NM_011224	0.004262141	-1.24	***Pygm***	muscle glycogen phosphorylase	0001666 // response to hypoxia // not recorded///0005975 // carbohydrate metabolic process // inferred from electronic annotation///0005977 // glycogen metabolic process // not recorded///00
156.9178	126.60256	NM_016785///XM_0065	0.002678498	-1.24	***Tpmt***	thiopurine methyltransferase	0032259 // methylation // inferred from electronic annotation
58.700928	47.33114	NR_045285	0.008167155	-1.24	***Gm5083***	predicted gene 5083	
307.48026	247.69774	NM_001289449///NM_	8.93E-04	-1.24	***Cd1d2***	CD1d2 antigen	0001916 // positive regulation of T cell mediated cytotoxicity // inferred from direct assay///0002376 // immune system process // inferred from electronic annotation///0006955 // immune respon
146.17296	117.70024	NM_028130///XM_0065	0.001462864	-1.24	***Zfp157***	zinc finger protein 157	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0010453 // regulation of cell fate commitment // inferred from mutant phenotype///0048286 // lung
310.52414	249.93759	NM_010102	0.002593054	-1.24	***S1pr4***	sphingosine-1-phosphate receptor 4	0003376 // sphingosine-1-phosphate signaling pathway // inferred from electronic annotation///0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupl
113.496895	91.350426	NM_027366///XM_0065	0.004248321	-1.24	***Ly6g6e***	lymphocyte antigen 6 complex, locus G6E	0007178 // transmembrane receptor protein serine/threonine kinase signaling pathway // inferred from electronic annotation
1908.5068	1533.0668	NM_026383///XM_0065	0.006344339	-1.24	***Pnrc2***	proline-rich nuclear receptor coactivator 2	0000184 // nuclear-transcribed mRNA catabolic process, nonsense-mediated decay // not recorded///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 //
108.16065	86.85006	NM_175481///XM_0065	0.005358766	-1.25	***Grik4***	glutamate receptor, ionotropic, kainate 4	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0034220 // ion transmembrane transport // not recorded///003523
344.2607	276.11166	NM_001135172///NM_	0.004451839	-1.25	***C1qtnf7***	C1q and tumor necrosis factor related protein 7	0051260 // protein homooligomerization // inferred from direct assay
420.3556	336.66663	NM_025566	0.004248937	-1.25	***Tnfaip8l1***	tumor necrosis factor, alpha-induced protein 8-like 1	0032007 // negative regulation of TOR signaling // inferred from direct assay
72.204575	57.821598	NM_138628///XM_011	0.004294118	-1.25	***Txlnb***	taxilin beta	
68.0685	54.434032	NM_021332	0.009419181	-1.25	***Glp1r***	glucagon-like peptide 1 receptor	0006950 // response to stress // inferred from mutant phenotype///0007165 // signal transduction // inferred from electronic annotation///0007166 // cell surface receptor signaling pathway // inf
32.126408	25.638657	NM_001170638///NM_	0.004712476	-1.25	***Slc17a1***	solute carrier family 17 (sodium phosphate), member 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006814 // sodium ion transport // inferred from electronic annotat
64.95869	51.835857	NM_054055///XM_0064	0.003842996	-1.25	***Slc13a3***	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006814 // sodium ion transport // inferred from electronic annotat
135.13045	107.78611	NM_001291047///NM_	0.003001194	-1.25	***Ypel1***	yippee-like 1 (Drosophila)	
173.65616	138.50116	NM_001252533///NM_	0.004528096	-1.25	***Cacnb2***	calcium channel, voltage-dependent, beta 2 subunit	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006816 // calcium ion transport // inferred from electronic annota
231.69582	184.74803	NM_027902///XM_0065	0.002832194	-1.25	***Tmprss6***	transmembrane serine protease 6	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype///0006508 // proteolysis // not recorded///0006879 // cellular iron ion homeo
1367.8923	1090.0197	NM_010681	0.004500225	-1.25	***Lama4***	laminin, alpha 4	0001568 // blood vessel development // inferred from mutant phenotype///0007155 // cell adhesion // inferred from electronic annotation///0030155 // regulation of cell adhesion // inferred from
98.0148	77.9567	NM_001012324	0.001502775	-1.26	***Ecm2***	extracellular matrix protein 2, female organ and adipocyte specific	0007409 // axonogenesis // not recorded///0010811 // positive regulation of cell-substrate adhesion // inferred from direct assay///0030198 // extracellular matrix organization // inferred from dir
376.96872	299.1337	NM_001033851///NM_	0.001489248	-1.26	***Cpne8***	copine VIII	
203.5593	161.52213	NM_134033	0.008473804	-1.26	***Ccdc117***	coiled-coil domain containing 117	
785.8378	622.2642	NM_022814	0.007763727	-1.26	***Svep1***	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	0007155 // cell adhesion // inferred from electronic annotation
237.64087	187.9672		0.004709999	-1.26	***Trav9d-3***	T cell receptor alpha variable 9D-3	0050852 // T cell receptor signaling pathway // ---
450.01117	355.61835	NM_026230///NM_207	0.005697807	-1.27	***H2afy2///H2afy3***	H2A histone family, member Y2///H2A histone family, member Y3	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006325 // chromatin organization // not recorded///0006334 // nucleosome assembly // infer
1104.0846	872.0527	NM_053267	0.003130646	-1.27	***Selm***	selenoprotein M	0010269 // response to selenium ion // inferred from mutant phenotype///0035264 // multicellular organism growth // inferred from mutant phenotype///0035934 // corticosterone secretion // in
637.42365	502.56302	NM_001042652///NM_	0.004579736	-1.27	***Nusap1***	nucleolar and spindle associated protein 1	0000070 // mitotic sister chromatid segregation // not recorded///0000226 // microtubule cytoskeleton organization // inferred from electronic annotation///0000281 // mitotic cytokinesis // not r
127.485916	100.50268	NM_013548///NM_145	0.004428218	-1.27	***Hist1h3e///Hist1h3f//***	histone cluster 1, H3e///histone cluster 1, H3f///histone cluster 1, H3g///histone cluster	0000183 // chromatin silencing at rDNA // traceable author statement///0002230 // positive regulation of defense response to virus by host // not recorded///0006334 // nucleosome assembly // n
83.30711	65.626595	NM_001271353///NM_	0.006300421	-1.27	***Cbs***	cystathionine beta-synthase	0001958 // endochondral ossification // inferred from mutant phenotype///0001974 // blood vessel remodeling // inferred from mutant phenotype///0006535 // cysteine biosynthetic process from
131.15137	103.31002	NM_009690	0.006858509	-1.27	***Cd5l***	CD5 antigen-like	0006898 // receptor-mediated endocytosis // inferred from electronic annotation///0006915 // apoptotic process // inferred from electronic annotation
211.4427	166.54738	NM_178149///XM_0065	0.001424259	-1.27	***Pik3ip1***	phosphoinositide-3-kinase interacting protein 1	0006508 // proteolysis // ---///0014067 // negative regulation of phosphatidylinositol 3-kinase signaling // inferred from direct assay///0014067 // negative regulation of phosphatidylinositol 3-kina
69.00866	54.334633	NM_134005	0.003741802	-1.27	***Enpp3***	ectonucleotide pyrophosphatase/phosphodiesterase 3	0006796 // phosphate-containing compound metabolic process // not recorded///0006898 // receptor-mediated endocytosis // inferred from electronic annotation///0006955 // immune response
109.32402	86.06967	NM_001081220///NM_	9.26E-04	-1.27	***Gpr179***	G protein-coupled receptor 179	0007186 // G-protein coupled receptor signaling pathway // not recorded///0007601 // visual perception // not recorded///0072659 // protein localization to plasma membrane // inferred from dir
1648.8358	1298.0487	NM_026555///XM_0065	0.00471824	-1.27	***Rcn3***	reticulocalbin 3, EF-hand calcium binding domain	
96.8686	76.1616	NM_009116///XM_0064	0.004773809	-1.27	***Prrx2***	paired related homeobox 2	0002053 // positive regulation of mesenchymal cell proliferation // inferred from genetic interaction///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
83.95897	65.996284	NM_001007154///NM_	0.007098455	-1.27	***Phactr3***	phosphatase and actin regulator 3	0043086 // negative regulation of catalytic activity // inferred from electronic annotation///0050790 // regulation of catalytic activity // inferred from electronic annotation
166.86436	131.09906	NM_178203///NM_178	0.003795846	-1.27	***Hist1h3b///Hist1h3h//***	histone cluster 1, H3b///histone cluster 1, H3h///histone cluster 1, H3a///histone cluste	0000183 // chromatin silencing at rDNA // traceable author statement///0002230 // positive regulation of defense response to virus by host // not recorded///0006334 // nucleosome assembly // n
84.0216	65.99552	NM_145137///XM_0065	0.002617206	-1.27	***Mgl2***	macrophage galactose N-acetyl-galactosamine specific lectin 2	
4035.5056	3165.879	NM_019564	0.003472995	-1.27	***Htra1***	HtrA serine peptidase 1	0001558 // regulation of cell growth // inferred from electronic annotation///0001890 // placenta development // inferred from mutant phenotype///0006508 // proteolysis // inferred from direct
300.4559	235.66049	NM_028279///XM_0065	0.002791497	-1.27	***Naalad2***	N-acetylated alpha-linked acidic dipeptidase 2	0006508 // proteolysis // inferred from direct assay///0008152 // metabolic process // inferred from electronic annotation///0042135 // neurotransmitter catabolic process // inferred from direct a
43.86145	34.402218	NM_001033212	0.00551926	-1.27	***Rprml***	reprimo-like	
252.82756	198.27364	NM_001146328///NM_	0.005611274	-1.28	***Rbm46***	RNA binding motif protein 46	
620.39014	485.6454	NM_008269///XM_0065	0.005754388	-1.28	***Hoxb6***	homeobox B6	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0007275 // multic
145.04219	113.5134	XM_486441	0.001710996	-1.28	***Zfp125***	zinc finger protein 125	
157.08028	122.92062	NM_001289507///NM_	0.00765966	-1.28	***Tfr2***	transferrin receptor 2	0006879 // cellular iron ion homeostasis // traceable author statement///0006898 // receptor-mediated endocytosis // not recorded///0010039 // response to iron ion // not recorded///0033572 /
564.74493	441.35162	NM_001164212///NM_	0.003301167	-1.28	***Rerg***	RAS-like, estrogen-regulated, growth-inhibitor	0007165 // signal transduction // inferred from electronic annotation///0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///0008152 // metabolic proces
1227.2369	958.799	NM_001033208	0.008436082	-1.28	***Myzap***	myocardial zonula adherens protein	0035556 // intracellular signal transduction // inferred from direct assay
276.39545	215.2929	NM_031863	0.003918182	-1.28	***Cenpq***	centromere protein Q	
713.83057	555.33307	NM_015776///XM_0065	0.002159361	-1.29	***Mfap5***	microfibrillar associated protein 5	0043206 // extracellular fibril organization // inferred from direct assay///0060216 // definitive hemopoiesis // inferred from mutant phenotype
166.80812	129.68823	NM_013548///NM_145	0.002798203	-1.29	***Hist1h3e///Hist1h3f//***	histone cluster 1, H3e///histone cluster 1, H3f///histone cluster 1, H3g///histone cluster	0000183 // chromatin silencing at rDNA // traceable author statement///0002230 // positive regulation of defense response to virus by host // not recorded///0006334 // nucleosome assembly // n
2530.8538	1964.3698	NM_001293623///NM_	0.00414198	-1.29	***Hmgb3***	high mobility group box 3	0006338 // chromatin remodeling // not recorded///0006355 // regulation of transcription, DNA-templated // not recorded///0032392 // DNA geometric change // inferred from sequence or struct
28.127428	21.814392	NM_053231///NM_134	0.001656757	-1.29	***Vmn1r10///Vmn1r9***	vomeronasal 1 receptor 10///vomeronasal 1 receptor 9	0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation///0007606 // sensory perception of chemical stimulus // traceable author statement///0019236 //
118.10794	91.582634	NM_016674	0.009746971	-1.29	***Cldn1***	claudin 1	0016338 // calcium-independent cell-cell adhesion via plasma membrane cell-adhesion molecules // inferred from direct assay///0045216 // cell-cell junction organization // not recorded///005126
411.07642	318.33344	NM_001098789///XM_	8.61E-04	-1.29	***Ndufa4l2***	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	
72.51477	56.10015	NM_010883	0.009754487	-1.29	***Ndp***	Norrie disease (pseudoglioma) (human)	0001890 // placenta development // inferred from mutant phenotype///0016055 // Wnt signaling pathway // not recorded///0035426 // extracellular matrix-cell signaling // inferred from direct as
1499.8722	1159.5144	NM_139198///XM_011	0.008212882	-1.29	***Plac8***	placenta-specific 8	0008284 // positive regulation of cell proliferation // inferred from direct assay///0009409 // response to cold // inferred from mutant phenotype///0040015 // negative regulation of multicellular
39.31469	30.351803	NM_027132///XM_0065	0.006227751	-1.30	***Otop3***	otopetrin 3	
339.25275	261.87836	NM_001170855///NM_	0.006811719	-1.30	***Trim36***	tripartite motif-containing 36	0007340 // acrosome reaction // inferred from mutant phenotype///0008152 // metabolic process // inferred from electronic annotation///0016567 // protein ubiquitination // inferred from electr

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	RefSeq Transcript ID	p	FC (Air:O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
189.0283	145.87575	XM_977361	0.00339819	-1.30	***LOC665506///Trbc2///***	T-cell receptor beta-2 chain C region-like///T cell receptor beta, constant 2///T cell receptor beta, joining region///T cell receptor beta, constant region 1///T cell receptor beta, variable 26	
168.86008	130.30035	NM_027402///XM_006	0.002589407	-1.30	***Fndc5***	fibronectin type III domain containing 5	0014850 // response to muscle activity // inferred from direct assay///0090336 // positive regulation of brown fat cell differentiation // inferred from direct assay
166.71684	128.41515	NM_001311062///NM_	0.001128667	-1.30	***Nnmt***	nicotinamide N-methyltransferase	0010243 // response to organonitrogen compound // inferred from electronic annotation///0031100 // organ regeneration // inferred from electronic annotation///0032259 // methylation // infer
198.5534	152.48564	NM_001024712///NM_	0.009332348	-1.30	***Gm10406///Gm2897//***	predicted gene 10406///predicted gene 2897///predicted gene 2956///predicted gene	0001933 // negative regulation of protein phosphorylation // inferred from direct assay///0007416 // synapse assembly // inferred from direct assay///0007416 // synapse assembly // inferred fro
329.91806	253.34778	NM_001289546///NM_	0.005966243	-1.30	***Amph***	amphiphysin	0007612 // learning // inferred from mutant phenotype///0048488 // synaptic vesicle endocytosis // inferred from mutant phenotype
524.87134	402.7077	NM_145741	0.00458889	-1.30	***Gdf10***	growth differentiation factor 10	0001503 // ossification // inferred from electronic annotation///0001649 // osteoblast differentiation // inferred from electronic annotation///0010862 // positive regulation of pathway-restricted
198.95648	152.63681	NR_040286	0.003659848	-1.30	***Gm11627***	predicted gene 11627	
27.77665	21.307734	NM_007608	0.007950821	-1.30	***Car5a***	carbonic anhydrase 5a, mitochondrial	0006094 // gluconeogenesis // traceable author statement///0006730 // one-carbon metabolic process // inferred from electronic annotation
33.694782	25.831835	NM_001033638///NM_	0.005751124	-1.30	***Crxos***	cone-rod homeobox, opposite strand	
536.22095	411.02426	NM_011133///XM_006	0.007355692	-1.30	***Pole2***	polymerase (DNA directed), epsilon 2 (p59 subunit)	0006260 // DNA replication // inferred from electronic annotation///0006261 // DNA-dependent DNA replication // not recorded///0042276 // error-prone translesion synthesis // not recorded
303.46637	232.39465	NM_016662///XR_8734	0.005481401	-1.31	***Mxd3***	Max dimerization protein 3	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0045892 // negati
581.682	444.82303	NM_001195006///NM_	0.005888755	-1.31	***Ndrg4***	N-myc downstream regulated gene 4	0007165 // signal transduction // not recorded///0007420 // brain development // not recorded///0008542 // visual learning // inferred from mutant phenotype///0010642 // negative regulation
133.30725	101.9239	NM_030152///XM_006	0.002449113	-1.31	***Nol3***	nucleolar protein 3 (apoptosis repressor with CARD domain)	0001666 // response to hypoxia // inferred from mutant phenotype///0001974 // blood vessel remodeling // inferred from mutant phenotype///0002931 // response to ischemia // inferred from m
130.15642	99.43262	NM_009937///NM_019	0.008873645	-1.31	***Colq///Hacl1///LOC10***	collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinestera	0001561 // fatty acid alpha-oxidation // not recorded///0006629 // lipid metabolic process // inferred from direct assay///0006631 // fatty acid metabolic process // inferred from electronic annota
102.21879	77.979485	NM_001039162///NM_	0.007885421	-1.31	***Clip2***	CAP-GLY domain containing linker protein 2	
61.568314	46.96607	XR_384910///XR_38491	0.001723066	-1.31	***4930461C15Rik***	RIKEN cDNA 4930461C15 gene	
142.44415	108.65357	NM_009115	4.22E-04	-1.31	***S100b***	S100 protein, beta polypeptide, neural	0006112 // energy reserve metabolic process // non-traceable author statement///0006874 // cellular calcium ion homeostasis // non-traceable author statement///0007611 // learning or memory
221.69476	169.01898	XM_977361	0.004189276	-1.31	***LOC665506///Trbc2///***	T-cell receptor beta-2 chain C region-like///T cell receptor beta, constant 2///T cell receptor beta, joining region///T cell receptor beta, constant region 1	
87.57351	66.657104	NM_178713	0.00657037	-1.31	***Aldh8a1***	aldehyde dehydrogenase 8 family, member A1	0008152 // metabolic process // inferred from electronic annotation///0042573 // retinoic acid metabolic process // not recorded///0042574 // retinal metabolic process // inferred by curator///0
230.88373	175.68396	NM_022019///XM_006	0.006243027	-1.31	***Dusp10***	dual specificity phosphatase 10	0000188 // inactivation of MAPK activity // not recorded///0002819 // regulation of adaptive immune response // inferred from mutant phenotype///0006470 // protein dephosphorylation // not r
64.342	48.907772	NM_011993///XM_006	0.002126675	-1.32	***Dpysl4***	dihydropyrimidinase-like 4	0008152 // metabolic process // inferred from electronic annotation///0048666 // neuron development // inferred from electronic annotation///0070997 // neuron death // inferred from electroni
299.22507	227.40921	NM_009413///XM_006	0.009858822	-1.32	***Tpd52l1***	tumor protein D52-like 1	0000086 // G2/M transition of mitotic cell cycle // not recorded///0043406 // positive regulation of MAP kinase activity // not recorded///0046330 // positive regulation of JNK cascade // not recor
49.027687	37.258095	NM_008952///XM_011	0.007652541	-1.32	***Pipox***	pipecolic acid oxidase	0033514 // L-lysine catabolic process to acetyl-CoA via L-pipecolate // not recorded///0033514 // L-lysine catabolic process to acetyl-CoA via L-pipecolate // inferred from sequence or structural sim
417.5129	317.1652	NM_010255///XM_006	0.008407558	-1.32	***Gamt***	guanidinoacetate methyltransferase	0006601 // creatine biosynthetic process // inferred from mutant phenotype///0006601 // creatine biosynthetic process // not recorded///0007283 // spermatogenesis // inferred from mutant phe
44.394897	33.69496	NM_008260	0.004690303	-1.32	***Foxa3***	forkhead box A3	0001678 // cellular glucose homeostasis // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcripti
187.39413	141.80872	NM_001113246///NM_	0.003131317	-1.32	***Chn1***	chimerin 1	0007165 // signal transduction // inferred from electronic annotation///0007399 // nervous system development // inferred from electronic annotation///0008045 // motor neuron axon guidance /
157.94553	119.45468	NM_145073///NM_178	0.002822057	-1.32	***Hist1h3d///Hist1h3e//***	histone cluster 1, H3d///histone cluster 1, H3e///histone cluster 1, H3g///histone cluste	0000183 // chromatin silencing at rDNA // traceable author statement///0002230 // positive regulation of defense response to virus by host // not recorded///0006334 // nucleosome assembly // n
79.55031	60.10018	NM_013874///XM_006	8.19E-04	-1.32	***Dpf1***	D4, zinc and double PHD fingers family 1	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0007399 // nervo
97.258385	73.2427	XR_105414///XR_10653	0.005115876	-1.33	***BB319198***	expressed sequence BB319198	
2538.4473	1909.0544	NM_001172481///NM_	9.91E-04	-1.33	***Aspn***	asporin	0030282 // bone mineralization // not recorded///0030512 // negative regulation of transforming growth factor beta receptor signaling pathway // inferred from direct assay///0030512 // negative
572.80664	430.55405	NM_009943	0.006414854	-1.33	***Cox6a2***	cytochrome c oxidase subunit VIa polypeptide 2	1902600 // hydrogen ion transmembrane transport // inferred from electronic annotation
130.62384	97.848526	NM_023893///NR_0282	0.008215139	-1.33	***Sapcd1***	suppressor APC domain containing 1	
663.5716	496.89578	NM_001285792///NM_	0.001184061	-1.34	***Wnt11***	wingless-type MMTV integration site family, member 11	0001649 // osteoblast differentiation // inferred from genetic interaction///0001822 // kidney development // inferred from direct assay///0001837 // epithelial to mesenchymal transition // infer
380.6026	284.77222	NM_011766///XM_006	0.003777881	-1.34	***Zfpm2***	zinc finger protein, multitype 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0001570 // vasculogenesis // inferred from direct assay///0001570 // vasculogenes
484.0141	361.22134	NM_026507///XR_3794	0.009592122	-1.34	***Zwilch***	zwilch kinetochore protein	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear division // inferred from electronic annotation///0007093 // mitotic cell cycle checkpoint // not recorded//
521.67694	389.01385	NM_172301///XM_011	0.004115058	-1.34	***Ccnb1///Gm5593***	cyclin B1///predicted gene 5593	0000278 // mitotic cell cycle // inferred from electronic annotation///0001556 // oocyte maturation // not recorded///0001701 // in utero embryonic development // inferred from mutant phenoty
341.2712	254.4048	NM_177157	0.009672785	-1.34	***Gchfr***	GTP cyclohydrolase I feedback regulator	0006461 // protein complex assembly // not recorded///0008152 // metabolic process // inferred from electronic annotation///0009890 // negative regulation of biosynthetic process // inferred fr
88.97832	66.2403	NM_178870	0.008170303	-1.34	***Hs3st3a1***	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	0008152 // metabolic process // inferred from electronic annotation
1094.1049	813.5031	NM_007630	0.009631392	-1.34	***Ccnb2***	cyclin B2	0001701 // in utero embryonic development // inferred from mutant phenotype///0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear division // inferred from
42.91121	31.889149	NM_001113323///XM_	0.009625666	-1.35	***Glb1l3***	galactosidase, beta 1 like 3	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation
56.909023	42.254776	NM_172951///XM_006	0.001329307	-1.35	***Sntg2***	syntrophin, gamma 2	
54.56656	40.49965	NM_007870///XM_006	0.001472945	-1.35	***Dnase1l3***	deoxyribonuclease 1-like 3	0006308 // DNA catabolic process // inferred from electronic annotation///0006309 // apoptotic DNA fragmentation // inferred from direct assay///0006915 // apoptotic process // inferred from el
148.58667	110.250305	NM_133657	0.003541715	-1.35	***Cyp2a12***	cytochrome P450, family 2, subfamily a, polypeptide 12	0006805 // xenobiotic metabolic process // not recorded///0009804 // coumarin metabolic process // not recorded///0019373 // epoxygenase P450 pathway // not recorded///0042738 // exogen
209.61296	155.32094	NM_026272	0.005431102	-1.35	***Narf***	nuclear prelamin A recognition factor	0016226 // iron-sulfur cluster assembly // ---
41.305496	30.594374	NM_001305451///NM_	0.007885694	-1.35	***Plppr5***	phospholipid phosphatase related 5	0006644 // phospholipid metabolic process // not recorded///0007165 // signal transduction // not recorded///0008152 // metabolic process // inferred from electronic annotation///0046839 // p
1479.3536	1095.6038	NM_029620	0.004882235	-1.35	***Pcolce2***	procollagen C-endopeptidase enhancer 2	0010952 // positive regulation of peptidase activity // not recorded
83.97234	62.180065	NM_019538///XM_006	5.95E-04	-1.35	***Plac1***	placental specific protein 1	0001890 // placenta development // inferred from expression pattern///0001890 // placenta development // inferred from electronic annotation///0007275 // multicellular organismal developme
476.18713	351.8902	NM_023785	0.00398311	-1.35	***Ppbp***	pro-platelet basic protein	0002523 // leukocyte migration involved in inflammatory response // inferred from mutant phenotype///0002690 // positive regulation of leukocyte chemotaxis // not recorded///0006954 // infla
114.962105	84.890724	NM_001012306///NM_	0.004329782	-1.35	***Hsd3b3///Hsd3b2///H***	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3///hydrox	0006694 // steroid biosynthetic process // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation///0055114 // oxidation-reduction process // in
354.41446	261.4442	NM_001190733///NM_	0.002693217	-1.36	***Dcun1d4***	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	0045116 // protein neddylation // not recorded///0051443 // positive regulation of ubiquitin-protein transferase activity // not recorded
186.93636	137.77863	NM_054077///XM_006	4.42E-04	-1.36	***Prelp***	proline arginine-rich end leucine-rich repeat	0007409 // axonogenesis // ---///0007569 // cell aging // inferred from direct assay///0018146 // keratan sulfate biosynthetic process // not recorded///0042340 // keratan sulfate catabolic proces
267.04495	196.74127	NM_013548///NM_013	0.001963066	-1.36	***Hist1h3a///Hist1h3b//***	histone cluster 1, H3a///histone cluster 1, H3b///histone cluster 1, H3c///histone cluste	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000183 // chromatin silencing at rDNA // traceable author statement///0002230 /
99.37821	73.2093	NM_001177600///NM_	0.001856598	-1.36	***Adam23***	a disintegrin and metallopeptidase domain 23	0006508 // proteolysis // inferred from electronic annotation///0007155 // cell adhesion // inferred from electronic annotation
425.58768	313.09772	NM_011496///XM_006	0.009358098	-1.36	***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 recorded///0006468 // protein
309.18173	227.28185	NM_053091	0.001594854	-1.36	***Cox4i2***	cytochrome c oxidase subunit IV isoform 2	0006123 // mitochondrial electron transport, cytochrome c to oxygen // ---///0009060 // aerobic respiration // ---///1902600 // hydrogen ion transmembrane transport // not recorded
546.4507	401.47784	NM_001253808///NM_	0.006395718	-1.36	***Racgap1***	Rac GTPase-activating protein 1	0000281 // mitotic cytokinesis // not recorded///0000915 // actomyosin contractile ring assembly // not recorded///0006810 // transport // inferred from electronic annotation///0006811 // ion tr
189.68596	139.26758	XM_977361	0.004157001	-1.36	***LOC665506///Tcrb-J//***	T-cell receptor beta-2 chain C region-like///T cell receptor beta, joining region///T cell receptor beta, constant region 1///T cell receptor beta, constant 2	
101.73936	74.69284	NM_023729///XM_006	0.009742639	-1.36	***Asz1***	ankyrin repeat, SAM and basic leucine zipper domain containing 1	0007140 // male meiosis // inferred from mutant phenotype///0007165 // signal transduction // non-traceable author statement///0007275 // multicellular organismal development // inferred fro
2704.9768	1983.0739	NM_021896///XM_006	0.007983006	-1.36	***Gucy1a3***	guanylate cyclase 1, soluble, alpha 3	0006182 // cGMP biosynthetic process // inferred from mutant phenotype///0006182 // cGMP biosynthetic process // not recorded///0007165 // signal transduction // not recorded///0007263 //
85.47547	62.541897	NM_024237///XM_006	0.002771269	-1.37	***Fbln7***	fibulin 7	0007155 // cell adhesion // inferred from electronic annotation
29.10569	21.294611	NM_172881	0.008575853	-1.37	***Ugt2b35***	UDP glucuronosyltransferase 2 family, polypeptide B35	0008152 // metabolic process // inferred from electronic annotation///0009813 // flavonoid biosynthetic process // not recorded///0032870 // cellular response to hormone stimulus // not recorde
284.58817	208.11089	NM_010615	0.00702277	-1.37	***Kif11***	kinesin family member 11	0007018 // microtubule-based movement // not recorded///0007049 // cell cycle // inferred from electronic annotation///0007051 // spindle organization // not recorded///0007059 // chromoso
290.49033	212.24098	NM_023294	0.002954948	-1.37	***Ndc80***	NDC80 homolog, kinetochore complex component (S. cerevisiae)	0000070 // mitotic sister chromatid segregation // not recorded///0000132 // establishment of mitotic spindle orientation // not recorded///0007049 // cell cycle // inferred from electronic annota
410.01532	298.67725	NM_001291185///NM_	0.006405784	-1.37	***Aurka***	aurora kinase A	0000212 // meiotic spindle organization // inferred from mutant phenotype///0000226 // microtubule cytoskeleton organization // inferred from genetic interaction///0000278 // mitotic cell cycle
61.556835	44.793827	NM_013485	0.004343597	-1.37	***C9***	complement component 9	0002376 // immune system process // inferred from electronic annotation///0006955 // immune response // inferred from electronic annotation///0006957 // complement activation, alternative p
78.32104	56.97495	NM_001163098	0.001417046	-1.37	***Tchh***	trichohyalin	0045109 // intermediate filament organization // inferred from direct assay
62.649708	45.51216	NM_001033767///XM_	0.003623473	-1.38	***Gm4951***	predicted gene 4951	0035458 // cellular response to interferon-beta // inferred from direct assay
614.2503	445.8619	NM_028804	5.30E-04	-1.38	***Ccdc3***	coiled-coil domain containing 3	
47.90137	34.766285	NM_009136	0.002315223	-1.38	***Scrg1***	scrapie responsive gene 1	
2094.4548	1516.0364	NM_001199246///NM_	0.007841181	-1.38	***Maged2***	melanoma antigen, family D, 2	
1380.936	996.51764	NM_175366	0.004224809	-1.39	***Mex3b***	mex3 homolog B (C. elegans)	0022409 // positive regulation of cell-cell adhesion // inferred from mutant phenotype///0043547 // positive regulation of GTPase activity // inferred from genetic interaction///0050766 // positive
109.644966	79.04609	NM_138673	0.008710697	-1.39	***Stab2***	stabilin 2	0006897 // endocytosis // not recorded///0006898 // receptor-mediated endocytosis // ---///0006898 // receptor-mediated endocytosis // inferred from electronic annotation///0007155 // cell ad
296.8485	213.867	NM_172604	0.007994882	-1.39	***Scara3***	scavenger receptor class A, member 3	
169.95557	122.22284	NM_008156///XM_011	0.009890824	-1.39	***Gpld1***	glycosylphosphatidylinositol specific phospholipase D1	0001503 // ossification // inferred from expression pattern///0002042 // cell migration involved in sprouting angiogenesis // not recorded///0002062 // chondrocyte differentiation // inferred from
410.84442	295.23694	NM_010225	0.006406569	-1.39	***Foxf2***	forkhead box F2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0006366 // transc
71.83726	51.516804	NM_001035509///NM_	9.12E-04	-1.39	***Zcchc18***	zinc finger, CCHC domain containing 18	0030509 // BMP signaling pathway // not recorded
91.50224	65.607895	NM_009860///XM_006	0.003694366	-1.39	***Cdc25c***	cell division cycle 25C	0000086 // G2/M transition of mitotic cell cycle // not recorded///0000087 // mitotic M phase // inferred from electronic annotation///0006470 // protein dephosphorylation // inferred from electr
97.47271	69.76567	NM_001166350///NM_	0.008467481	-1.40	***Serpina11***	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of endopeptidase activity // not recorded
752.6646	538.115	NM_001081416///XM_	0.001052963	-1.40	***Fndc1***	fibronectin type III domain containing 1	0001934 // positive regulation of protein phosphorylation // not recorded///0010666 // positive regulation of cardiac muscle cell apoptotic process // not recorded///0051223 // regulation of prote
497.83148	355.8448	NM_026385	0.001096431	-1.40	***Pllp***	plasma membrane proteolipid	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // not recorded///0009611 // response to wounding // inferred from electronic annotation///0042552 // my
80.462364	57.460537	NM_029723	0.00257242	-1.40	***Dapl1***	death associated protein-like 1	0006915 // apoptotic process // inferred from electronic annotation///0010507 // negative regulation of autophagy // ---///0030154 // cell differentiation // inferred from electronic annotation///0
1424.6067	1016.99713	NM_001195431///NM_	7.23E-04	-1.40	***Islr***	immunoglobulin superfamily containing leucine-rich repeat	
80.059006	56.922134	NM_175434///XM_006	0.004644504	-1.41	***Slc35f3***	solute carrier family 35, member F3	0006810 // transport // inferred from electronic annotation///0015888 // thiamine transport // not recorded
46.44406	33.006096	NM_001033264///NM_	0.008242777	-1.41	***Gls2***	glutaminase 2 (liver, mitochondrial)	0006537 // glutamate biosynthetic process // not recorded///0006541 // glutamine metabolic process // inferred from electronic annotation///0006543 // glutamine catabolic process // not record
267.6193	189.9617	NM_021282	0.003753417	-1.41	***Cyp2e1***	cytochrome P450, family 2, subfamily e, polypeptide 1	0006641 // triglyceride metabolic process // not recorded///0006805 // xenobiotic metabolic process // not recorded///0008202 // steroid metabolic process // not recorded///0010193 // respons
397.64203	281.84546	NM_001164426///NM_	4.89E-04	-1.41	***Kcnk13***	potassium channel, subfamily K, member 13	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006813 // potassium ion transport // inferred from electronic ann
126.7755	89.77814	NM_130452///XM_006	0.004810722	-1.41	***Bbox1***	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxyl	0045329 // carnitine biosynthetic process // not recorded///0055114 // oxidation-reduction process // inferred from electronic annotation
1460.7573	1032.9121	NM_016798///XM_006	0.003958494	-1.41	***Pdlim3***	PDZ and LIM domain 3	0007015 // actin filament organization // inferred from direct assay///0007507 // heart development // inferred from mutant phenotype///0007519 // skeletal muscle tissue development // inferr
565.3833	399.50952	NM_001302129///NM_	0.002444359	-1.42	***Cenpa***	centromere protein A	0000132 // establishment of mitotic spindle orientation // not recorded///0051382 // kinetochore assembly // not recorded///0071459 // protein localization to chromosome, centromeric region //
880.3293	620.35565	NM_001177371///NM_	0.004298807	-1.42	***Dbn1***	drebrin 1	0007015 // actin filament organization // inferred from direct assay///0007275 // multicellular organismal development // inferred from electronic annotation///0007399 // nervous system develo
55.713825	39.16976	NM_001166631///NM_	0.006620586	-1.42	***Havcr1***	hepatitis A virus cellular receptor 1	0006911 // phagocytosis, engulfment // inferred from electronic annotation///0007584 // response to nutrient // inferred from electronic annotation///0010046 // response to mycotoxin // inferr
748.9963	522.2766	NM_133903///XM_006	0.001809416	-1.43	***Spon2***	spondin 2, extracellular matrix protein	0002376 // immune system process // inferred from electronic annotation///0002448 // mast cell mediated immunity // inferred from mutant phenotype///0007155 // cell adhesion // not recorded
75.06238	52.0902	NM_010024///XM_006	0.006654876	-1.44	***Dct***	dopachrome tautomerase	0002052 // positive regulation of neuroblast proliferation // inferred from mutant phenotype///0006583 // melanin biosynthetic process from tyrosine // inferred from direct assay///0008152 // m
87.36746	60.526245	NM_175140///XM_006	0.001207483	-1.44	***Chst8***	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006790 // sulfur compound metabolic process // not recorded///0016051 // carbohydrate biosynthetic proces

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	RefSeq Transcript ID	p	FC (Air:O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
168.01364	115.862076	NM_025495///XM_006	0.001110381	-1.45	***Cenpp***	centromere protein P	0034080 // CENP-A containing nucleosome assembly // inferred from electronic annotation
705.95074	486.16928	NM_019696	0.009535124	-1.45	***Cpxm1***	carboxypeptidase X 1 (M14 family)	0006508 // proteolysis // inferred from direct assay///0006518 // peptide metabolic process // ---///0008152 // metabolic process // inferred from electronic annotation///0016485 // protein proc
39.764717	27.36691	NM_009512	0.002683119	-1.45	***Slc27a5***	solute carrier family 27 (fatty acid transporter), member 5	0000038 // very long-chain fatty acid metabolic process // not recorded///0001676 // long-chain fatty acid metabolic process // traceable author statement///0006629 // lipid metabolic process //
325.86383	224.15471	NM_001316729///NM_	0.001639707	-1.45	***Qpct***	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	0017186 // peptidyl-pyroglutamic acid biosynthetic process, using glutaminyl-peptide cyclotransferase // not recorded
452.6234	310.10916	NM_175013	1.00E-03	-1.46	***Pgm5***	phosphoglucomutase 5	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0005978 // glycogen biosynthetic process // ---///0006006 // glucose metabolic process // inferred from electro
110.27305	75.11504	NM_001312905///NM_	0.001569709	-1.47	***Kcnn2***	potassium intermediate/small conductance calcium-activated channel, subfamily N, mer	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from direct assay///0006813 // potassium ion transport // not recorded///0048168 // regulation
151.9871	103.295204	NM_146052///XM_006	0.004232128	-1.47	***Lrrc3b***	leucine rich repeat containing 3B	
1404.9125	952.4901	NM_001164171///NM_	0.008740387	-1.47	***Myh6///Myh7***	myosin, heavy polypeptide 6, cardiac muscle, alpha///myosin, heavy polypeptide 7, card	0001701 // in utero embryonic development // inferred from mutant phenotype///0002026 // regulation of the force of heart contraction // inferred from mutant phenotype///0002026 // regulatio
107.102325	72.08221	NM_029797///XM_006	0.0012578	-1.49	***Mnd1***	meiotic nuclear divisions 1 homolog (S. cerevisiae)	0006310 // DNA recombination // inferred from electronic annotation///0051321 // meiotic cell cycle // inferred from electronic annotation
64.475334	43.38813	NM_001081389///NM_	0.00379618	-1.49	***Nlrp6***	NLR family, pyrin domain containing 6	0002376 // immune system process // inferred from electronic annotation///0002862 // negative regulation of inflammatory response to antigenic stimulus // inferred from mutant phenotype///00
381.5137	256.4819	NM_178890	0.002984563	-1.49	***Abtb2***	ankyrin repeat and BTB (POZ) domain containing 2	0097237 // cellular response to toxic substance // inferred from mutant phenotype
105.643845	70.97993	NM_001113515///NM_	0.007456162	-1.49	***Col2a1***	collagen, type II, alpha 1	0001501 // skeletal system development // not recorded///0001502 // cartilage condensation // inferred from mutant phenotype///0001503 // ossification // inferred from expression pattern///00
178.5613	119.7702	NM_001040689///XM_	0.00688414	-1.49	***Rspo4***	R-spondin 4	0016055 // Wnt signaling pathway // inferred from electronic annotation///0050896 // response to stimulus // inferred from electronic annotation///0090263 // positive regulation of canonical Wn
303.3703	202.81453	NM_013811///XM_006	0.003096877	-1.50	***Dnah8***	dynein, axonemal, heavy chain 8	0007018 // microtubule-based movement // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation
70.02316	46.791542	NM_019546///XM_006	0.00173966	-1.50	***Prodh2***	proline dehydrogenase (oxidase) 2	0006560 // proline metabolic process // inferred from electronic annotation///0006562 // proline catabolic process // inferred from electronic annotation///0010133 // proline catabolic process to
120.38198	80.08182	NM_001308327///NM_	0.008247933	-1.50	***Enpp1***	ectonucleotide pyrophosphatase/phosphodiesterase 1	0006091 // generation of precursor metabolites and energy // not recorded///0006796 // phosphate-containing compound metabolic process // not recorded///0006898 // receptor-mediated endo
277.09024	182.36577	NM_001166406///NM_	0.004344233	-1.52	***Kif20a***	kinesin family member 20A	0000281 // mitotic cytokinesis // not recorded///0000910 // cytokinesis // not recorded///0000920 // cell separation after cytokinesis // not recorded///0001578 // microtubule bundle formation /
185.80823	121.88865	NM_011797///XM_006	0.00236166	-1.52	***Car14***	carbonic anhydrase 14	0006885 // regulation of pH // inferred by curator///0008152 // metabolic process // inferred from electronic annotation///0015670 // carbon dioxide transport // inferred by curator
43.59563	28.55314	NM_001081567///NM_	0.007358679	-1.53	***Mapk10***	mitogen-activated protein kinase 10	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0000165 // MAPK cascade // inferred from electronic annotation///0006468 // protein phospho
169.51477	110.84661	NM_144869///XM_006	0.003293102	-1.53	***BC021614***	cDNA sequence BC021614	0008152 // metabolic process // inferred from electronic annotation
171.438	111.85506	NM_001242368///NM_	0.004170349	-1.53	***F10***	coagulation factor X	0006508 // proteolysis // inferred from electronic annotation///0007596 // blood coagulation // not recorded///0007599 // hemostasis // inferred from electronic annotation///0030335 // positive
86.33238	56.16087	NM_008243///XM_006	0.001163503	-1.54	***Mst1***	macrophage stimulating 1 (hepatocyte growth factor-like)	0006508 // proteolysis // inferred from electronic annotation///0007283 // spermatogenesis // inferred from electronic annotation///0007566 // embryo implantation // inferred from direct assay/
223.27997	144.00882	NM_172301///XM_011	0.004021784	-1.55	***Ccnb1///Gm5593***	cyclin B1///predicted gene 5593	0000278 // mitotic cell cycle // inferred from electronic annotation///0001556 // oocyte maturation // not recorded///0001701 // in utero embryonic development // inferred from mutant phenoty
344.83237	221.29279	NM_019662///XM_006	9.33E-04	-1.56	***Rrad***	Ras-related associated with diabetes	0007165 // signal transduction // inferred from electronic annotation///0007264 // small GTPase mediated signal transduction // inferred from electronic annotation///0030308 // negative regulati
23.84237	15.212607	NM_001195596	0.004552898	-1.57	***Smlr1***	small leucine-rich protein 1	
64.28954	40.688522	NM_145539	8.39E-04	-1.58	***Tm4sf4***	transmembrane 4 superfamily member 4	0042246 // tissue regeneration // inferred from electronic annotation
80.29109	50.800438	NM_001276710///NM_	0.005120005	-1.58	***Agxt***	alanine-glyoxylate aminotransferase	0007219 // Notch signaling pathway // inferred from direct assay///0008152 // metabolic process // inferred from electronic annotation///0009436 // glyoxylate catabolic process // not recorded//
169.34901	107.0099	NM_007385	0.008169087	-1.58	***Apoc4***	apolipoprotein C-IV	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic annotation///0010890 // positive regulation of sequestering of triglyceride // no
121.737144	76.915276	NM_001301404///NM_	0.008417004	-1.58	***Serpina10***	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), me	0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electronic annotation///0010466 // negative regulation of peptidase activity // inferre
49.80333	31.42588	NM_008280///XM_006	0.005906464	-1.58	***Lipc***	lipase, hepatic	0006629 // lipid metabolic process // inferred from electronic annotation///0006631 // fatty acid metabolic process // not recorded///0006633 // fatty acid biosynthetic process // not recorded///0
47.997456	30.27916	NM_001081361///NM_	0.009827971	-1.59	***1-Mar***	mitochondrial amidoxime reducing component 1	0042126 // nitrate metabolic process // not recorded///0055114 // oxidation-reduction process // not recorded
248.65813	156.40622	NM_001271402///NM_	3.46E-05	-1.59	***Ephx2***	epoxide hydrolase 2, cytoplasmic	0002539 // prostaglandin production involved in inflammatory response // not recorded///0006470 // protein dephosphorylation // inferred from electronic annotation///0006629 // lipid metaboli
259.05347	161.85078	NM_028222///XM_006	0.00168719	-1.60	***Cdkn3***	cyclin-dependent kinase inhibitor 3	0000082 // G1/S transition of mitotic cell cycle // not recorded///0006470 // protein dephosphorylation // not recorded///0006974 // cellular response to DNA damage stimulus // not recorded///0
162.89772	101.10014	NM_026183///XM_006	8.68E-04	-1.61	***Slc47a1***	solute carrier family 47, member 1	0006810 // transport // inferred from electronic annotation///0006855 // drug transmembrane transport // not recorded///0015695 // organic cation transport // not recorded///0015893 // drug
195.3091	121.179985	NM_001170978///NM_	5.77E-04	-1.61	***Abat***	4-aminobutyrate aminotransferase	0001666 // response to hypoxia // not recorded///0007568 // aging // not recorded///0007620 // copulation // not recorded///0007626 // locomotory behavior // not recorded///0009448 // gam
91.19781	55.703423	NM_001033415	5.08E-04	-1.64	***Shisa3***	shisa family member 3	0007275 // multicellular organismal development // inferred from electronic annotation
123.40443	73.35719	NM_001003914///NM_	0.007634766	-1.68	***Obscn***	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	0006468 // protein phosphorylation // inferred from electronic annotation///0007275 // multicellular organismal development // inferred from electronic annotation///0016310 // phosphorylation
184.62808	109.56841	NM_011978	0.007060659	-1.69	***Slc27a2***	solute carrier family 27 (fatty acid transporter), member 2	0000038 // very long-chain fatty acid metabolic process // inferred from direct assay///0001561 // fatty acid alpha-oxidation // not recorded///0001676 // long-chain fatty acid metabolic process //
2611.0825	1545.8308	NM_008120	0.001223628	-1.69	***Gja4***	gap junction protein, alpha 4	0001568 // blood vessel development // inferred from mutant phenotype///0003158 // endothelium development // inferred from electronic annotation///0006816 // calcium ion transport // not r
1094.1165	645.82526	NM_018870	0.004460862	-1.69	***Pgam2***	phosphoglycerate mutase 2	0006094 // gluconeogenesis // not recorded///0006096 // glycolytic process // inferred from direct assay///0006096 // glycolytic process // not recorded///0006470 // protein dephosphorylation /
67.583115	38.96788	NM_145146	0.00150004	-1.73	***Afm***	afamin	0006810 // transport // inferred from electronic annotation///0051180 // vitamin transport // not recorded
94.460754	54.41995	NM_001271777///NM_	0.002884099	-1.74	***C8g***	complement component 8, gamma polypeptide	0002376 // immune system process // inferred from electronic annotation///0006957 // complement activation, alternative pathway // inferred from electronic annotation///0006958 // compleme
106.256775	60.01181	NM_011658	3.16E-04	-1.77	***Twist1***	twist basic helix-loop-helix transcription factor 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0000122 // negative regulation of transcription from RNA polymerase II promoter //
135.0162	76.13907	NM_001126338///NM_	0.004004287	-1.77	***Prn///Prnd***	prion protein gene complex///prion protein dublet	0006878 // cellular copper ion homeostasis // inferred from direct assay///0051260 // protein homooligomerization // inferred from electronic annotation
78.03546	43.725334	NM_027150///XM_006	0.00345755	-1.78	***Mlip***	muscular LMNA-interacting protein	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction///0010614 // negative regulation of cardiac muscle hypertrophy // inferred fro
123.09304	68.45728	NM_028270	0.002694023	-1.80	***Aldh1b1***	aldehyde dehydrogenase 1 family, member B1	0006068 // ethanol catabolic process // inferred from electronic annotation///0008152 // metabolic process // inferred from electronic annotation///0055114 // oxidation-reduction process // infe
154.93188	84.98652	NM_054063	0.001426787	-1.82	***Psg28***	pregnancy-specific glycoprotein 28	0007565 // female pregnancy // inferred from electronic annotation
75.622925	40.378742	NM_019447///XM_006	0.00456328	-1.87	***Hgfac***	hepatocyte growth factor activator	0006508 // proteolysis // inferred from electronic annotation
700.61145	367.42453	NM_010174	9.61E-04	-1.91	***Fabp3***	fatty acid binding protein 3, muscle and heart	0006810 // transport // inferred from electronic annotation///0007507 // heart development // inferred from electronic annotation///0015909 // long-chain fatty acid transport // not recorded///0
1290.3738	666.3822	NM_009406	0.002053409	-1.94	***Tnni3***	troponin I, cardiac 3	0001570 // vasculogenesis // inferred from direct assay///0001980 // regulation of systemic arterial blood pressure by ischemic conditions // inferred from mutant phenotype///0003009 // skeletal
120.92352	62.355164	NM_008223///XM_006	0.001383099	-1.94	***Serpind1***	serine (or cysteine) peptidase inhibitor, clade D, member 1	0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electronic annotation///0010466 // negative regulation of peptidase activity // inferre
414.36502	211.73636	NM_001159299///NM_	0.006469854	-1.96	***Itih4***	inter alpha-trypsin inhibitor, heavy chain 4	0006953 // acute-phase response // inferred from electronic annotation///0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulati
317.9818	161.72597	NM_010321///XM_006	0.009760449	-1.97	***Gnmt***	glycine N-methyltransferase	0005977 // glycogen metabolic process // inferred from mutant phenotype///0006111 // regulation of gluconeogenesis // inferred from mutant phenotype///0006555 // methionine metabolic proc
280.64297	141.34807	NM_144944///XM_011	0.006621049	-1.99	***Prokr2***	prokineticin receptor 2	0007165 // signal transduction // inferred from electronic annotation///0007166 // cell surface receptor signaling pathway // not recorded///0007186 // G-protein coupled receptor signaling path
132.63043	64.94063	NM_153529///XM_006	0.00952198	-2.04	***Nrn1***	neuritin 1	0007399 // nervous system development // not recorded///0007409 // axonogenesis // not recorded///1990138 // neuron projection extension // inferred from direct assay
1089.3699	522.68	NM_001198841///NM_	0.002625942	-2.08	***Csrp3***	cysteine and glycine-rich protein 3	0001974 // blood vessel remodeling // inferred from electronic annotation///0002026 // regulation of the force of heart contraction // inferred from genetic interaction///0003300 // cardiac muscl
178.5191	85.29722	NM_011575	0.003150318	-2.09	***Tff3***	trefoil factor 3, intestinal	0010906 // regulation of glucose metabolic process // inferred from direct assay
489.41696	231.00311	NM_175499///XM_006	6.75E-04	-2.12	***Slitrk6***	SLIT and NTRK-like family, member 6	0001964 // startle response // inferred from mutant phenotype///0002088 // lens development in camera-type eye // inferred from mutant phenotype///0002093 // auditory receptor cell morphog
148.86583	69.325676	NM_001013013	0.004717326	-2.15	***Dhrs7c***	dehydrogenase/reductase (SDR family) member 7C	0008152 // metabolic process // inferred from electronic annotation///0010880 // regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum // inferred from direct ass
1250.5642	582.11584	NM_178738///XM_006	0.002778543	-2.15	***Prss35***	protease, serine 35	0006508 // proteolysis // inferred from electronic annotation
112.65766	52.04719	NM_001042767///NM_	0.009778603	-2.16	***Proc***	protein C	0006508 // proteolysis // inferred from electronic annotation///0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electronic annotation
906.5109	408.92502	NM_007428	7.77E-04	-2.22	***Agt***	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	0001543 // ovarian follicle rupture // inferred from mutant phenotype///0001568 // blood vessel development // inferred from mutant phenotype///0001658 // branching involved in ureteric bud
5186.2637	2266.7493	NM_133977	0.003465162	-2.29	***Trf***	transferrin	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotation///0006826 // iron ion transport // inferred from mutant phenotype///
158.87906	69.040665	NM_018816	0.008245284	-2.30	***Apom***	apolipoprotein M	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic annotation///0009749 // response to glucose // inferred from electronic annotat
270.94098	117.547455	NM_008878	0.007576522	-2.30	***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///0010033 // response
1008.33905	436.82083	NM_001159487///NM_	0.006665224	-2.31	***Rbp4***	retinol binding protein 4, plasma	0001654 // eye development // inferred from mutant phenotype///0001654 // eye development // not recorded///0006094 // gluconeogenesis // inferred from mutant phenotype///0006094 // glu
38.062843	16.056923	NM_010001	0.001597849	-2.37	***Cyp2c37***	cytochrome P450, family 2. subfamily c, polypeptide 37	0006805 // xenobiotic metabolic process // not recorded///0019373 // epoxygenase P450 pathway // not recorded///0042738 // exogenous drug catabolic process // not recorded///0055114 // oxi
41.417965	17.426592	NM_020495///NM_178	0.00423561	-2.38	***Slco1b2***	solute carrier organic anion transporter family, member 1b2	0001889 // liver development // inferred from electronic annotation///0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic annotatio
80.86726	32.44042	NM_023383	0.008065633	-2.49	***Aadac***	arylacetamide deacetylase (esterase)	0008152 // metabolic process // inferred from electronic annotation///0010898 // positive regulation of triglyceride catabolic process // inferred from direct assay
34.048435	13.5257		0.001319491	-2.52	***AI195470***	expressed sequence AI195470	
61.97208	24.148952	NM_007818	0.006114157	-2.57	***Cyp3a11***	cytochrome P450, family 3, subfamily a, polypeptide 11	0055114 // oxidation-reduction process // inferred from electronic annotation
400.89282	155.4179	NM_010859	2.95E-04	-2.58	***Myl3***	myosin, light polypeptide 3	0002026 // regulation of the force of heart contraction // not recorded///0006942 // regulation of striated muscle contraction // not recorded///0007519 // skeletal muscle tissue development // in
48.445793	18.405342	NM_153598	0.002529251	-2.63	***Ugt2b34***	UDP glucuronosyltransferase 2 family, polypeptide B34	0008152 // metabolic process // inferred from electronic annotation///0009813 // flavonoid biosynthetic process // not recorded///0032870 // cellular response to hormone stimulus // not recorde
27.27758	10.32527	NM_009467	0.004846289	-2.64	***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 stimulus // not recorde
372.8114	140.45026	NM_001284507///NM_	1.43E-04	-2.65	***Crabp1***	cellular retinoic acid binding protein I	0006810 // transport // inferred from electronic annotation///0034653 // retinoic acid catabolic process // inferred from electronic annotation
170.55814	62.199368	NM_009693///XM_006	0.004176184	-2.74	***Apob***	apolipoprotein B	0001701 // in utero embryonic development // inferred from mutant phenotype///0006629 // lipid metabolic process // inferred from direct assay///0006629 // lipid metabolic process // inferred f
257.30023	93.65552	NM_010391///XM_011	0.006669458	-2.75	***H2-Q10***	histocompatibility 2, Q region locus 10	0002376 // immune system process // inferred from electronic annotation///0002474 // antigen processing and presentation of peptide antigen via MHC class I // not recorded///0006955 // immun
369.06665	126.889275	NM_007686///XM_006	0.00641572	-2.91	***Cfi***	complement component factor i	0002376 // immune system process // inferred from electronic annotation///0006508 // proteolysis // inferred from electronic annotation///0006898 // receptor-mediated endocytosis // inferred f
329.0414	110.15066	NM_001164047///NM_	5.69E-04	-2.99	***Mb***	myoglobin	0001666 // response to hypoxia // inferred from mutant phenotype///0006810 // transport // inferred from electronic annotation///0007507 // heart development // inferred from mutant phenoty
137.58159	45.46429	NM_145499///XM_011	0.007513497	-3.03	***Cyp2c70***	cytochrome P450, family 2, subfamily c, polypeptide 70	0006805 // xenobiotic metabolic process // not recorded///0019373 // epoxygenase P450 pathway // not recorded///0042738 // exogenous drug catabolic process // not recorded///0055114 // oxi
453.09998	145.50194	NM_010582	0.004667306	-3.11	***Itih2***	inter-alpha trypsin inhibitor, heavy chain 2	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation///0030
394.8125	121.338135	NM_017371	0.004478756	-3.25	***Hpx***	hemopexin	0002639 // positive regulation of immunoglobulin production // inferred from mutant phenotype///0002925 // positive regulation of humoral immune response mediated by circulating immunoglo
112.559555	33.580326	NM_013913	0.004016636	-3.35	***Angptl3***	angiopoietin-like 3	0006071 // glycerol metabolic process // not recorded///0006631 // fatty acid metabolic process // not recorded///0006641 // triglyceride metabolic process // non-traceable author statement///0
88.85538	24.32654	NM_007768	0.006075835	-3.65	***Crp***	C-reactive protein, pentraxin-related	0006953 // acute-phase response // inferred from electronic annotation///0006958 // complement activation, classical pathway // not recorded///0010628 // positive regulation of gene expression
95.151535	25.68433	NM_009258	0.00569038	-3.70	***Spink1***	serine peptidase inhibitor, Kazal type 1	0010466 // negative regulation of peptidase activity // inferred from direct assay///0010751 // negative regulation of nitric oxide mediated signal transduction // inferred from direct assay///00507
316.10275	84.599594	NM_009060///XM_006	0.003667172	-3.74	***Rgn***	regucalcin	0001822 // kidney development // inferred from electronic annotation///0001889 // liver development // inferred from electronic annotation///0001933 // negative regulation of protein phosphor
46.088512	12.1416025	NM_022884	0.009378723	-3.80	***Bhmt2***	betaine-homocysteine methyltransferase 2	0009086 // methionine biosynthetic process // not recorded///0032259 // methylation // inferred from electronic annotation///0033477 // S-methylmethionine metabolic process // not recorded//
334.7225	86.187035	NM_011318	0.003468372	-3.88	***Apcs***	serum amyloid P-component	0006461 // protein complex assembly // not recorded///0044869 // negative regulation by host of viral exo-alpha-sialidase activity // not recorded///0044871 // negative regulation by host of viral
344.85083	86.67087	NM_011707	0.004099859	-3.98	***Vtn***	vitronectin	0006898 // receptor-mediated endocytosis // inferred from electronic annotation///0006955 // immune response // inferred from electronic annotation///0007155 // cell adhesion // inferred from
256.84567	60.272255	NM_009474	0.00185618	-4.26	***Uox***	urate oxidase	0006144 // purine nucleobase metabolic process // traceable author statement///0019628 // urate catabolic process // inferred from electronic annotation///0055114 // oxidation-reduction proce
327.87958	69.54179	NM_001039555///XM_	0.0047942	-4.71	***Cyp2c68***	cytochrome P450, family 2, subfamily c, polypeptide 68	0006805 // xenobiotic metabolic process // not recorded///0019373 // epoxygenase P450 pathway // not recorded///0042738 // exogenous drug catabolic process // not recorded///0055114 // oxi
107.377945	22.473856	NM_031164///XM_006	0.003138581	-4.78	***F13b***	coagulation factor XIII, beta subunit	0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electronic annotation
143.05722	28.310953	NM_001150749///NM_	0.002709184	-5.05	***Rdh7***	retinol dehydrogenase 7	0008152 // metabolic process // inferred from electronic annotation///0042572 // retinol metabolic process // inferred from electronic annotation///0055114 // oxidation-reduction process // infe
125.10741	24.347816	NM_008777	0.006246509	-5.14	***Pah***	phenylalanine hydroxylase	0006558 // L-phenylalanine metabolic process // not recorded///0006559 // L-phenylalanine catabolic process // inferred from electronic annotation///0006571 // tyrosine biosynthetic process //

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	RefSeq Transcript ID	p	FC (Air:O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
511.79596	97.485985	NM_007443	0.005793012	-5.25	***Ambp***	alpha 1 microglobulin/bikunin	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of endopeptidase activity // not recorded///0018298 // protein-chromo
129.119	23.872452	NM_019775	0.006770643	-5.41	***Cpb2***	carboxypeptidase B2 (plasma)	0003331 // positive regulation of extracellular matrix constituent secretion // not recorded///0006508 // proteolysis // not recorded///0007596 // blood coagulation // inferred from electronic anno
736.41583	134.9244	NM_019395///XM_0112	0.003684547	-5.46	***Fbp1***	fructose bisphosphatase 1	0005975 // carbohydrate metabolic process // not recorded///0006002 // fructose 6-phosphate metabolic process // not recorded///0006094 // gluconeogenesis // not recorded///0006111 // regu
449.72153	80.4534	NM_008407///XM_0065	0.003136996	-5.59	***Itih3***	inter-alpha trypsin inhibitor, heavy chain 3	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation///0030
615.0215	109.01663	NM_013475///XM_0065	0.0020096	-5.64	***Apoh***	apolipoprotein H	0001937 // negative regulation of endothelial cell proliferation // not recorded///0006641 // triglyceride metabolic process // not recorded///0007596 // blood coagulation // not recorded///00075
5225.318	858.9625	NM_007423	0.001240295	-6.08	***Afp***	alpha fetoprotein	0001542 // ovulation from ovarian follicle // inferred from mutant phenotype///0001889 // liver development // inferred from electronic annotation///0006810 // transport // inferred from electro
1068.612	174.232	NM_001305549///NM_0	0.001337639	-6.13	***Apoa2***	apolipoprotein A-II	0002526 // acute inflammatory response // inferred from electronic annotation///0002740 // negative regulation of cytokine secretion involved in immune response // not recorded///0006457 // p
128.37373	20.784555	NM_029562///XM_0065	0.001377294	-6.18	***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 process // not recorded///0
408.96286	63.600693	NM_080844///XM_0064	0.001862161	-6.43	***Serpinc1***	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	0007584 // response to nutrient // not recorded///0007596 // blood coagulation // inferred from electronic annotation///0007599 // hemostasis // inferred from electronic annotation///0010466 /
758.61774	117.43251	NM_008877	0.001870046	-6.46	***Plg***	plasminogen	0006508 // proteolysis // inferred from electronic annotation///0007596 // blood coagulation // not recorded///0007599 // hemostasis // inferred from electronic annotation///0010812 // negativ
399.31967	61.641228	NM_175628///XM_0112	0.002430989	-6.48	***A2m***	alpha-2-macroglobulin	0001869 // negative regulation of complement activation, lectin pathway // not recorded///0007565 // female pregnancy // inferred from electronic annotation///0010466 // negative regulation of
611.8743	92.97415	NM_016668	0.0029433	-6.58	***Bhmt***	betaine-homocysteine methyltransferase	0006479 // protein methylation // not recorded///0006577 // amino-acid betaine metabolic process // not recorded///0006579 // amino-acid betaine catabolic process // inferred from electronic a
10772.42	1635.3412	NM_009654	0.002354565	-6.59	***Alb***	albumin	0001895 // retina homeostasis // inferred from electronic annotation///0006810 // transport // inferred from electronic annotation///0009267 // cellular response to starvation // not recorded///0
484.14145	72.10355	NM_144903	0.003056649	-6.71	***Aldob***	aldolase B, fructose-bisphosphate	0001889 // liver development // inferred from electronic annotation///0006000 // fructose metabolic process // not recorded///0006096 // glycolytic process // not recorded///0006116 // NADH o
394.76944	58.08626	NM_008341	0.002247223	-6.80	***Igfbp1***	insulin-like growth factor binding protein 1	0001558 // regulation of cell growth // inferred from electronic annotation///0008286 // insulin receptor signaling pathway // inferred from electronic annotation///0030307 // positive regulation
335.13254	49.025208	NM_133997	0.001651755	-6.84	***Apof***	apolipoprotein F	0006629 // lipid metabolic process // inferred from electronic annotation///0006641 // triglyceride metabolic process // inferred from mutant phenotype///0006810 // transport // inferred from ele
489.39594	69.592	NM_008096	9.97E-04	-7.03	***Gc***	group specific component	0006810 // transport // inferred from electronic annotation///0007565 // female pregnancy // inferred from electronic annotation///0007595 // lactation // inferred from electronic annotation///0
392.33728	54.011658	NM_001102411///NM_0	0.00232564	-7.26	***Kng1***	kininogen 1	0006954 // inflammatory response // inferred from electronic annotation///0007204 // positive regulation of cytosolic calcium ion concentration // ---///0007596 // blood coagulation // inferred fro
763.2383	98.7395	NM_001080809///XM_0	0.002999039	-7.73	***Cps1***	carbamoyl-phosphate synthetase 1	0000050 // urea cycle // not recorded///0000050 // urea cycle // inferred by curator///0001889 // liver development // inferred from electronic annotation///0005980 // glycogen catabolic process
861.95667	109.99669	NM_001276449///NM_0	0.002829061	-7.84	***Ahsg***	alpha-2-HS-glycoprotein	0001503 // ossification // inferred from direct assay///0006461 // protein complex assembly // not recorded///0006953 // acute-phase response // not recorded///0008584 // male gonad develop
421.03027	47.93317	NM_017399	0.001678601	-8.78	***Fabp1***	fatty acid binding protein 1, liver	0002230 // positive regulation of defense response to virus by host // not recorded///0006810 // transport // inferred from electronic annotation///0008284 // positive regulation of cell proliferati
1738.2124	195.41092	NM_009692	0.001586324	-8.90	***Apoa1***	apolipoprotein A-I	0001932 // regulation of protein phosphorylation // inferred from direct assay///0001935 // endothelial cell proliferation // inferred from mutant phenotype///0002740 // negative regulation of cyt
2337.167	257.77368	NM_013697	0.001559754	-9.07	***Ttr***	transthyretin	0006810 // transport // inferred from electronic annotation///0042572 // retinol metabolic process // not recorded///0070327 // thyroid hormone transport // inferred from electronic annotation
1634.0963	177.98416	NM_001317105///NM_	0.002402098	-9.18	***Fgg***	fibrinogen gamma chain	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // inferred from electronic annotation///0007160 // cell-matrix adhesion // not r
481.74808	49.186993	NM_007376	0.001039365	-9.79	***Pzp***	pregnancy zone protein	0007566 // embryo implantation // inferred from genetic interaction///0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation
1225.3838	123.2816	NM_009245	0.001811876	-9.94	***Serpina1c***	serine (or cysteine) peptidase inhibitor, clade A, member 1C	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative regulation of endopeptidase activity // not recorded///0034097 // response to cyto
981.44305	97.02705	NM_181849	0.001676218	-10.12	***Fgb***	fibrinogen beta chain	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // inferred from electronic annotation///0007160 // cell-matrix adhesion // not r
892.4763	87.18443	NM_009244///XM_0065	0.001580199	-10.24	***Serpina1b///Serpina1e***	serine (or cysteine) preptidase inhibitor, clade A, member 1B///serine (or cysteine) pepti	0001701 // in utero embryonic development // inferred from mutant phenotype///0006487 // protein N-linked glycosylation // inferred from direct assay///0006953 // acute-phase response // infe
1249.6205	121.73912	NM_001111048///NM_0	0.002412222	-10.26	***Fga***	fibrinogen alpha chain	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process // inferred from electronic annotation///0006461 // protein complex assembly //
892.4203	63.98877	NM_001252569///NM_0	0.001010352	-13.95	***Serpina1a///Serpina1d***	serine (or cysteine) peptidase inhibitor, clade A, member 1A///serine (or cysteine) peptic	0001701 // in utero embryonic development // inferred from mutant phenotype///0006487 // protein N-linked glycosylation // inferred from direct assay///0006953 // acute-phase response // infe