

Table S6. Lung genes (n=567) significantly changed by hyperoxia (O2) in glutathione reductase-deficient (Gsr-KO) mouse neonates at PND5 (moderated t-test, p < 0.01).

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

[Gsr-KO, Air][raw]	[Gsr-KO, O2][raw]	RefSeq	Transcript ID	p	FC (Air: O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
76.9784	4483.964	NM_009394		4.85E-06	57.44	<b>Tnnc2</b>	troponin C2, fast	0003009 // skeletal muscle contraction // not recorded
58.468548	2832.6384	NM_177369		3.90E-08	47.75	<b>Myh8</b>	myosin, heavy polypeptide 8, skeletal muscle, perinatal	0003009 // skeletal muscle contraction // not recorded//0006936 // muscle contraction // ---//0008152 // metabolic process // inferred from electronic annotation//0014
24.953693	863.6152	NM_001313949//NM_		2.90E-07	34.24	<b>Krt13</b>	keratin 13	0007010 // cytoskeleton organization // not recorded//0009314 // response to radiation // inferred from electronic annotation//0043587 // tongue morphogenesis // infe
95.823166	3093.5344	NM_016754//XM_0061		1.85E-04	32.25	<b>Myh1f</b>	myosin light chain, phosphorylatable, fast skeletal muscle	0006955 // immune response // inferred from electronic annotation//0007519 // skeletal muscle tissue development // inferred from mutant phenotype
50.705944	1179.135	NM_001163664//NM_		7.71E-06	22.80	<b>Tnnt3</b>	troponin T3, skeletal, fast	0003009 // skeletal muscle contraction // not recorded//0006937 // regulation of muscle contraction // inferred from electronic annotation//0006942 // regulation of stri
338.56406	7321.125	NM_001272041//NM_		3.16E-06	21.43	<b>Acta1</b>	actin, alpha 1, skeletal muscle	0009612 // response to mechanical stimulus // inferred from electronic annotation//0009991 // response to extracellular stimulus // inferred from electronic annotation//
203.46117	4223.8726	NM_001113387//NM_		3.68E-04	20.41	<b>Myl1</b>	myosin, light polypeptide 1	0006936 // muscle contraction // not recorded//0060048 // cardiac muscle contraction // not recorded
92.97833	1910.9205	NM_008475		1.66E-06	20.20	<b>Krt4</b>	keratin 4	0007010 // cytoskeleton organization // not recorded//0009790 // embryo development // traceable author statement//0030855 // epithelial cell differentiation // infer
66.04276	1225.579	NM_001099635//XM_0061		0.003312	18.38	<b>Myh3</b>	myosin, heavy polypeptide 3, skeletal muscle, embryonic	0003009 // skeletal muscle contraction // not recorded//0046034 // ATP metabolic process // not recorded
22.856401	396.6772	NM_010889//XM_0061		6.74E-06	16.71	<b>Neb</b>	nebulin	0030832 // regulation of actin filament length // traceable author statement//0045214 // sarcomere organization // traceable author statement
17.903265	310.30438	NM_001290389//NM_		2.30E-06	16.26	<b>Atp1b4</b>	ATPase, (Na+K+) transporting, beta 4 polypeptide	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not recorded//0006810 // tran
26.560461	388.2157	NM_030679//NM_010		9.14E-07	14.45	<b>Myh11//Myh4</b>	myosin, heavy polypeptide 1, skeletal muscle, adult//my	0006936 // muscle contraction // not recorded//0008152 // metabolic process // inferred from electronic annotation//0003009 // skeletal muscle contraction // inferred f
21.769707	228.27621	NM_001033621//XM_0061		7.52E-06	10.39	<b>Myot</b>	myotilin	
111.290146	1123.4584	NM_009405//XM_0061		7.68E-06	9.88	<b>Tnni2</b>	troponin I, skeletal, fast 2	0003009 // skeletal muscle contraction // not recorded//0006937 // regulation of muscle contraction // not recorded//0045893 // positive regulation of transcription, DN
30.852324	274.40927	NM_001121769//XM_0061		7.87E-04	8.76	<b>Tceal7</b>	transcription elongation factor A (SII)-like 7	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annota
17.78789	143.10919	NM_001081123//XM_0061		1.79E-06	7.66	<b>Arhgap36</b>	Rho GTPase activating protein 36	0007165 // signal transduction // inferred from electronic annotation//0043547 // positive regulation of GTPase activity // inferred from electronic annotation
66.22598	523.25354	NM_027416		1.13E-04	7.66	<b>Calml3</b>	calmodulin-like 3	
115.31618	804.8055	NM_007606//XM_011		0.001421	6.87	<b>Car3</b>	carbonic anhydrase 3	0006470 // protein dephosphorylation // inferred from electronic annotation//0006730 // one-carbon metabolic process // inferred from electronic annotation//0006979
49.759773	345.17355	NM_013456		1.54E-05	6.78	<b>Actn3</b>	actinin alpha 3	0001649 // osteoblast differentiation // inferred from mutant phenotype//0006936 // muscle contraction // inferred from direct assay//0014728 // regulation of the force
44.184513	279.04303	NM_001252372//NM_		1.89E-06	6.20	<b>Mybp1c</b>	myosin binding protein C, slow-type	0006936 // muscle contraction // inferred from direct assay//1903955 // positive regulation of protein targeting to mitochondrion // not recorded
59.477646	348.76804	NM_031189		0.003989	6.20	<b>Myog</b>	myogenin	0001503 // ossification // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of tra
12.981329	72.490616	NM_001033239		7.87E-05	5.49	<b>Csta1</b>	cystatin A1	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // ---//0010951 // ne
306.33025	1702.0999	NM_008469		0.004839	5.46	<b>Krt15</b>	keratin 15	0098779 // mitophagy in response to mitochondrial depolarization // not recorded
32.838654	160.28629	NM_029569//XM_0061		1.35E-05	4.89	<b>Asb5</b>	ankyrin repeat and SOCS box-containing 5	0016567 // protein ubiquitination // inferred from electronic annotation//0035556 // intracellular signal transduction // inferred from electronic annotation
17.86937	696.1657	NM_007504//XM_0061		2.25E-06	4.87	<b>Atp2a1</b>	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // not rec
62.09625	308.34082	NM_001081087		0.004885	4.81	<b>Klhl41</b>	kelch-like 41	0016567 // protein ubiquitination // not recorded//0030239 // myofibril assembly // inferred from mutant phenotype//0031275 // regulation of lateral pseudopodium ass
56.34639	260.24808	NM_009141		0.003056	4.54	<b>Cxcl5</b>	chemokine (C-X-C motif) ligand 5	0001776 // leukocyte homeostasis // inferred from mutant phenotype//0001816 // cytokine production // not recorded//0002690 // positive regulation of leukocyte chem
71.152824	321.5579	NM_028216		5.67E-04	4.41	<b>Psc</b>	prostate stem cell antigen	
32.55182	141.47806	NM_007582		1.32E-04	4.36	<b>Cacng1</b>	calcium channel, voltage-dependent, gamma subunit 1	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // inferred
258.07495	1131.0095	NM_001164787//NM_		1.07E-04	4.28	<b>Sprr2a1//Sprr2a2</b>	small proline-rich protein 2A1//small proline-rich protein	0008360 // regulation of cell shape // traceable author statement//0008544 // epidermis development // non-traceable author statement//0018149 // peptide cross-linki
118.66843	514.4448	NM_001101605//NM_		0.001112	4.17	<b>Ifit1b1</b>	interferon induced protein with tetratricopeptide repeats	0051607 // defense response to virus // not recorded//0060337 // tyrosine kinase signaling pathway // not recorded
44.905346	188.82568	NM_028798		1.54E-04	4.14	<b>Crc1</b>	cysteine-rich C-terminal 1	0018149 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiation // not recorded
52.8892	217.84296	NM_001199556//NM_		3.08E-04	4.03	<b>AWS51984</b>	expressed sequence AWS51984	0055007 // cardiac muscle cell differentiation // inferred from mutant phenotype//0060923 // cardiac muscle cell fate commitment // inferred from genetic interaction
30.585264	118.26599	NM_008651//XM_0061		7.45E-05	3.89	<b>Myf6</b>	myogenic factor 6	0001756 // somitogenesis // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation//0006357 //
28.39306	108.52695	NM_009109//XM_0061		2.89E-05	3.86	<b>Ryr1</b>	ryanodine receptor 1, skeletal muscle	0001666 // response to hypoxia // not recorded//0003151 // outflow tract morphogenesis // inferred from mutant phenotype//0006810 // transport // inferred from elec
76.60803	288.5503	NM_008476		1.10E-04	3.67	<b>Krt6a</b>	keratin 6A	0002009 // morphogenesis of an epithelium // inferred from genetic interaction//0002009 // morphogenesis of an epithelium // inferred from mutant phenotype//00160
57.28121	213.16151	NM_021508		8.82E-06	3.63	<b>Myoz1</b>	myozenin 1	
43.795063	158.04631	NM_173385		0.006373	3.59	<b>Clp</b>	cartilage intermediate layer protein, nucleotide pyrophos	0043569 // negative regulation of insulin-like growth factor receptor signaling pathway // not recorded
107.61155	400.9013	NM_026841		6.13E-05	3.58	<b>Prr32</b>	proline rich 32	
38.48617	136.62178	NM_013505//XM_0061		3.40E-05	3.53	<b>Dsc2</b>	desmocollin 2	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // inferred from electroni
60.9142	196.92682	NM_016749//XM_0061		0.003253	3.17	<b>Mybph</b>	myosin binding protein H	0007155 // cell adhesion // inferred from electronic annotation
45.98375	143.36182	NM_007812//NM_009		1.09E-04	3.10	<b>Cyp2a4//Cyp2a5</b>	cytochrome P450, family 2, subfamily a, polypeptide 4//c	0006805 // xenobiotic metabolic process // not recorded//0009804 // coumarin metabolic process // not recorded//0019373 // epoxygenase P450 pathway // not record
131.00752	412.9011	NM_013712//XM_011		7.68E-04	3.06	<b>Itgb1bp2</b>	integrin beta 1 binding protein 2	
97.62915	308.56287	NM_139134//XM_0061		1.67E-04	3.05	<b>Chodl</b>	chondrolectin	0010975 // regulation of neuron projection development // inferred from genetic interaction
199.118	612.06366	NM_008522		5.29E-04	2.97	<b>Ltf</b>	lactotransferrin	0001503 // ossification // inferred from electronic annotation//0001817 // regulation of cytokine production // not recorded//0001895 // retina homeostasis // inferred fr
62.484314	188.89784	NM_001081375//NM_		8.48E-04	2.97	<b>Cnfn</b>	cornifelin	0031424 // keratinization // inferred from electronic annotation
26.90576	78.44409	NM_001033131		2.15E-05	2.96	<b>Krtadp</b>	keratinocyte differentiation associated protein	0008544 // epidermis development // not recorded//0030154 // cell differentiation // inferred from electronic annotation
25.22052	73.11003	NM_001174170//NM_		6.30E-05	2.96	<b>Serpinc2</b>	serine (or cysteine) peptidase inhibitor, clade B, member	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded//004
29.133148	82.44814	NM_001081157//XM_0061		0.001746	2.87	<b>Lmod3</b>	leiomodin 3 (fetal)	0006936 // muscle contraction // not recorded//0007015 // actin filament organization // not recorded//0030239 // myofibril assembly // not recorded//0051694 // poin
16.71076	47.89749	NM_011472		0.006858	2.80	<b>Sprr2f</b>	small proline-rich protein 2F	0008544 // epidermis development // non-traceable author statement//0018149 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiation // not r
51.451138	141.78748	NM_028202//XM_0061		2.46E-04	2.73	<b>Klhl40</b>	kelch-like 40	0007275 // multicellular organismal development // inferred from electronic annotation//0016567 // protein ubiquitination // ---//0031397 // negative regulation of prote
128.54233	363.57333	NM_026414		2.55E-04	2.71	<b>Asprv1</b>	aspartic peptidase, retroviral-like 1	0006508 // proteolysis // inferred from electronic annotation//0016485 // protein processing // inferred from direct assay//0016485 // protein processing // not recorded
250.01558	683.995	NM_009813		2.24E-04	2.68	<b>Casq1</b>	calsequestrin 1	0006937 // regulation of muscle contraction // traceable author statement//0007029 // endoplasmic reticulum organization // inferred from mutant phenotype//0007515
58.277485	158.10065	NM_001007580//XM_0061		9.18E-04	2.67	<b>Fndc3c1</b>	fibronectin type III domain containing 3C1	
62.840107	167.70041	NM_146189//XM_0061		2.34E-04	2.62	<b>Mybp2c</b>	myosin binding protein C, fast-type 2	0006936 // muscle contraction // inferred from direct assay//0007155 // cell adhesion // inferred from electronic annotation
21.105312	53.855396	NM_025867		8.91E-05	2.55	<b>Serpinc1</b>	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin)	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded
67.41971	173.87897	NM_009264		0.00237	2.53	<b>Sprr1a</b>	small proline-rich protein 1A	0018149 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiation // not recorded//0031424 // keratinization // inferred from electronic annotatio
12.686517	32.053776	NM_001033233//XM_0061		5.09E-04	2.40	<b>Tmprss11a</b>	transmembrane protease, serine 11a	0006508 // proteolysis // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation
246.73846	604.106	NM_009694		0.009031	2.39	<b>Apobec2</b>	apolipoprotein B mRNA editing enzyme, catalytic polypep	0006397 // mRNA processing // inferred from electronic annotation//0016556 // mRNA modification // inferred from mutant phenotype//0008111 // DNA demethylation
528.7196	1264.5781	NM_009922//XM_0061		0.001964	2.39	<b>Cnn1</b>	calponin 1	0031032 // actomyosin structure organization // inferred from electronic annotation
48.584885	115.7181	NM_001313701//NM_		2.17E-04	2.38	<b>Pkp1</b>	plakophilin 1	0007155 // cell adhesion // inferred from electronic annotation//0016337 // single organismal cell-cell adhesion // inferred from electronic annotation//0045110 // interr
24.725973	57.088352	NM_001081023//NM_		0.004491	2.37	<b>Cacna1s</b>	calcium channel, voltage-dependent, L type, alpha 1S sub	0001501 // skeletal system development // inferred from mutant phenotype//0002074 // extracellular skeletal muscle development // inferred from mutant phenotype//00
48.330772	113.52331	NM_001033303//XM_0061		7.24E-05	2.35	<b>Ampd1</b>	adenosine monophosphate deaminase 1	0009117 // nucleotide metabolic process // inferred from electronic annotation//0009168 // purine ribonucleoside monophosphate biosynthetic process // inferred from e
112.7098	271.40237	NM_027011		1.87E-05	2.31	<b>Krt5</b>	keratin 5	
65.316025	152.30411	NM_027126//XM_0061		2.64E-04	2.30	<b>Hfe2</b>	hemochromatosis type 2 (juvenile) (human homolog)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0006879 // cellular iron ion homeostasis // inferred
65.18649	150.86432	NM_001204427//NM_		0.002307	2.29	<b>Sprr3</b>	small proline-rich protein 3	0018149 // peptide cross-linking // not recorded//0030216 // keratinocyte differentiation // not recorded//0031424 // keratinization // inferred from electronic annotatio
44.50794	100.58403	NM_007389		0.001612	2.26	<b>Chrn4</b>	cholinergic receptor, nicotinic, alpha polypeptide 1 (mus	0003009 // skeletal muscle contraction // not recorded//0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic
78.13614	179.08975	NM_001122683//NM_		2.00E-04	2.25	<b>Bdh1</b>	3-hydroxybutyrate dehydrogenase, type 1	0008152 // metabolic process // inferred from electronic annotation//005114 // oxidation-reduction process // not recorded
2106.3872	4656.372	NM_002094		0.002094	2.18	<b>Gsto1</b>	glutathione S-transferase omega 1	0006749 // glutathione metabolic process // not recorded//0008152 // metabolic process // inferred from electronic annotation//0010880 // regulation of release of sequ
24.626236	53.256237	NM_153179//XM_0061		0.008783	2.16	<b>Phkd1</b>	polycystic kidney and hepatic disease 1	0001822 // kidney development // inferred from direct assay//0006874 // cellular calcium ion homeostasis // not recorded//0008284 // positive regulation of cell prolifer
50.64267	108.13938	XR_861642//XR_86895		0.004749	2.14	<b>Gm38785</b>	predicted gene, 38785	
75.6316	162.59714	NM_016689		0.001552	2.11	<b>Aqp3</b>	aquaporin 3	0002684 // positive regulation of immune system process // not recorded//0006810 // transport // inferred from electronic annotation//0006833 // water transport // inf
17.868435	38.00067	NM_009251//XM_0061		4.79E-04	2.11	<b>Serpinc5</b>	serine (or cysteine) peptidase inhibitor, clade B, member	0002009 // morphogenesis of an epithelium // inferred from mutant phenotype//0010951 // negative regulation of endopeptidase activity // not recorded//0030198 // e
29.245455	59.957985	NM_133743		4.09E-06	2.10	<b>Lypd3</b>	Ly6/Plaur domain containing 3	0006928 // movement of cell or subcellular component // not recorded//0007160 // cell-matrix adhesion // not recorded
24.89903	50.04128	NM_175440//XM_011		0.002686	2.08	<b>Prss27</b>	protease, serine 27	0006508 // proteolysis // inferred from electronic annotation
151.80606	326.8504	NM_001005423//XM_0061		0.007568	2.06	<b>Mreg</b>	melanoregulin	0030318 // melanocyte differentiation // inferred from mutant phenotype//0032402 // melanosome transport // inferred from direct assay//0042640 // anagen // infer
53.20544	108.66783	NM_001080995//NM_		0.008147	2.04	<b>Ddias</b>	DNA damage-induced apoptosis suppressor	0006915 // apoptotic process // inferred from electronic annotation//0006974 // cellular response to DNA damage stimulus // inferred from mutant phenotype//0007049

Gene Symbol	Gene Title	Gene Ontology Biological Process
<b>2.01 Trp63</b>	transformation related protein 63	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA polymerase II promoter
<b>1.98 Krt6b</b>	keratin 6B	0002009 // morphogenesis of an epithelium // inferred from genetic interaction//00031424 // keratinization // inferred from genetic interaction//00045109 // intermediate
<b>1.98 Mylk4</b>	myosin light chain kinase family, member 4	0006468 // protein phosphorylation // inferred from electronic annotation//00016310 // phosphorylation // inferred from electronic annotation
<b>1.90 Eno3</b>	enolase 3, beta subunit	0006095 // glycolytic process // inferred from electronic annotation//0007568 // aging // inferred from electronic annotation//00042493 // response to drug // inferred from
<b>1.96 Gm12300</b>	predicted gene 12300	
<b>1.94 Gatm</b>	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0006601 // creatine biosynthetic process // not recorded//0006979 // response to oxidative stress // inferred from electronic annotation//0007584 // response to nutrient
<b>1.91 Tcaal3//Tcaals5</b>	transcription elongation factor A (SII)-like 3//transcription	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
<b>1.90 Pitx1</b>	forkhead-like homeodomain transcription factor 1	0001501 // skeletal system development // inferred from mutant phenotype//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 //
<b>1.87 Fst</b>	follicistatin	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001501 // skeletal system development // inferred from genetic interaction
<b>1.85 Vip</b>	vasoactive intestinal polypeptide	0001878 // response to yeast // not recorded//0001938 // positive regulation of endothelial cell proliferation // not recorded//0007611 // learning or memory // not recorded
<b>1.85 Crym</b>	crystallin, mu	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006839 // mitochondrial transport // not recorded//0007605 // sense
<b>1.83 Myod1</b>	myogenic differentiation 1	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from direct assay//0000381 // regulation of alternative mRNA splicing, via spliceosome // in
<b>1.81 Alox15</b>	arachidonate 15-lipoxygenase	0001503 // ossification // inferred from mutant phenotype//0002820 // negative regulation of adaptive immune response // inferred from mutant phenotype//0006629 //
<b>1.81 Rhov</b>	ras homolog gene family, member V	0007165 // signal transduction // not recorded//0007264 // small GTPase mediated signal transduction // inferred from electronic annotation
<b>1.80 Ky</b>	kyphoscoliosis septidase	0006508 // proteolysis // inferred from electronic annotation//0007517 // muscle organ development // inferred from mutant phenotype//0007528 // neuromuscular junction
<b>1.80 Col8a1</b>	collagen, type VIII, alpha 1	0001525 // angiogenesis // inferred from electronic annotation//0007155 // cell adhesion // inferred from electronic annotation//0010811 // positive regulation of cell-cell
<b>1.76 Fbp2</b>	fructose biphosphatase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation//0006094 // gluconeogenesis // not recorded//0006470 // protein dephosphorylation //
<b>1.75 Ecm1</b>	extracellular matrix protein 1	0001503 // ossification // inferred from electronic annotation//0001525 // angiogenesis // inferred from electronic annotation//0001938 // positive regulation of endothelial
<b>1.69 Pdlim4</b>	PDZ and LIM domain 4	0030036 // actin cytoskeleton organization // not recorded
<b>1.68 Dck1</b>	doublecortin-like kinase 1	0001764 // neuron migration // inferred from genetic interaction//0006468 // protein phosphorylation // inferred from electronic annotation//0007275 // multicellular or
<b>1.68 Hlr2</b>	interleukin 1 receptor, type II	0019221 // cytokine-mediated signaling pathway // inferred from electronic annotation
<b>1.68 Grh3</b>	grainyhead-like 3 (Drosophila)	0001736 // establishment of planar polarity // inferred from genetic interaction//0001843 // neural tube closure // inferred from mutant phenotype//0006351 // transcrit
<b>1.67 Rrp12</b>	ribosomal RNA processing 12 homolog (S. cerevisiae)	
<b>1.66 Sostd1</b>	serothionin domain containing 1	0007389 // pattern specification process // inferred from mutant phenotype//0010454 // negative regulation of cell fate commitment // inferred from mutant phenotype//
<b>1.66 Dapl1</b>	death associated protein-like 1	0006915 // apoptotic process // inferred from electronic annotation//0010507 // negative regulation of autophagy // --//0030154 // cell differentiation // inferred from e
<b>1.66 Hs6st2</b>	heparan sulfate 6-O-sulfotransferase 2	0015015 // heparan sulfate proteoglycan biosynthetic process, enzymatic modification // inferred from direct assay
<b>1.65 Hspa1b</b>	heat shock protein 1B	0007339 // binding of sperm to zona pellucida // inferred from direct assay//0009408 // response to heat // inferred from direct assay//0043066 // negative regulation of
<b>1.64 Krt14//Krt17</b>	keratin 14//keratin 17	0007568 // aging // not recorded//0010043 // response to zinc ion // inferred from electronic annotation//0010212 // response to ionizing radiation // inferred from elect
<b>1.63 Arpp21</b>	cyclic AMP-regulated phosphoprotein, 21	0034605 // cellular response to heat // inferred from direct assay
<b>1.62 Ache</b>	acetylcholinesterase	0001919 // regulation of receptor recycling // inferred from mutant phenotype//0002076 // osteoblast development // inferred from electronic annotation//0006581 // in
<b>1.61 Sim2</b>	single-minded homolog 2 (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0006351 // transcription, DNA-templated // inferred
<b>1.60 Muc4</b>	mucin 4	0001953 // negative regulation of cell-matrix adhesion // not recorded//0002244 // hematopoietic progenitor cell differentiation // inferred from mutant phenotype//000
<b>1.58 Lgi2</b>	leucine-rich repeat LGI family, member 2	
<b>1.53 Trim29</b>	tripartite motif-containing 29	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//1900181 // negative regulation of protein localizat
<b>1.52 Serpinb1a</b>	serine (or cysteine) peptidase inhibitor, clade B, member	0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010951 // negative regulation of endopeptidase activity // not recorded//00
<b>1.52 Pad1</b>	peptidyl arginine deiminase, type I	0018101 // protein cullination // not recorded
<b>1.52 Synpo2</b>	synaptopodin 2	
<b>1.51 Gm94</b>	predicted gene 94	
<b>1.51 Barx2</b>	BarH-like homeobox 2	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001502 // cartilage condensation // inferred from direct a
<b>1.51 Upk3bl</b>	uropaklin 3B-like	0006979 // response to oxidative stress // inferred from electronic annotation//0005114 // oxidation-reduction process // inferred from electronic annotation
<b>1.49 Gm8096//Phgdh</b>	3-phosphoglycerate dehydrogenase pseudogene//3-pho	0006541 // glutamine metabolic process // inferred from mutant phenotype//0006544 // glycine metabolic process // inferred from mutant phenotype//0006563 // L-seri
<b>1.49 Mall</b>	mal, T cell differentiation protein-like	
<b>1.49 Myom3</b>	myomesin family, member 3	
<b>1.49 Des</b>	desmin	0007517 // muscle organ development // traceable author statement
<b>1.48 Art1</b>	ADP-ribosyltransferase 1	0006471 // protein ADP-ribosylation // inferred from direct assay
<b>1.47 Calcr</b>	calcitonin receptor	0007165 // signal transduction // inferred from electronic annotation//0007166 // cell surface receptor signaling pathway // inferred from electronic annotation//0007181
<b>1.47 Cadm4</b>	cell adhesion molecule 4	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // --//0007157 // hetero
<b>1.46 Dnph1</b>	2'-deoxy nucleoside 5'-phosphate N-hydrolase 1	0008152 // metabolic process // inferred from electronic annotation//0009116 // nucleoside metabolic process // inferred from electronic annotation//0009117 // nucleo
<b>1.45 Dmrt2</b>	doublesex and mab-3 related transcription factor like fam	0002052 // positive regulation of neuroblast proliferation // inferred from mutant phenotype//0006355 // regulation of transcription, DNA-templated // inferred from elec
<b>1.44 Olr1</b>	oxidized low density lipoprotein (lectin-like) receptor 1	0002376 // immune system process // inferred from electronic annotation//0006898 // receptor-mediated endocytosis // inferred from direct assay//0006954 // inflam
<b>1.44 Slc30a2</b>	solute carrier family 30 (zinc transporter), member 2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006812 // cation transport // inferred from
<b>1.44 Tgm3</b>	transglutaminase 3, E polypeptide	0008544 // epidermis development // traceable author statement//0018149 // peptide cross-linking // not recorded//0018149 // peptide cross-linking // traceable author
<b>1.44 Trim54</b>	tripartite motif-containing 54	0007026 // negative regulation of microtubule depolymerization // inferred from direct assay//0007275 // multicellular organismal development // inferred from electroni
<b>1.43 Gpr87</b>	G-protein-coupled receptor 87	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not recorded//0007194 // negative reg
<b>1.43 Sbn</b>	suprabasin	
<b>1.43 Scg2</b>	secretogranin II	0000165 // MAPK cascade // not recorded//0000165 // MAPK cascade // inferred from sequence or structural similarity//0001525 // angiogenesis // inferred from direct i
<b>1.42 Osr1</b>	odd-skipped related 1 (Drosophila)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interaction//0001655 // urogenital system development // inferi
<b>1.42 Six1</b>	sine oculis-related homeobox 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0001657 // uterine bud development // inferred from gen
<b>1.41 Entpd2</b>	ectonucleoside triphosphate diphosphohydrolase 2	0007186 // G-protein coupled receptor signaling pathway // inferred from direct assay//0009181 // purine ribonucleoside diphosphate catabolic process // inferred from d
<b>1.41 Tmem121</b>	transmembrane protein 121	
<b>1.41 Gm41224</b>	predicted gene, 41224	
<b>1.40 Atp6v0e2</b>	ATPase, H <sup>+</sup> transporting, lysosomal VO subunit E2	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0008152 // metabolic process // inferred fr
<b>1.40 Pkrag3</b>	protein kinase, AMP-activated, gamma 3 non-catalytic su	0005978 // glycogen biosynthetic process // inferred from mutant phenotype//0006468 // protein phosphorylation // not recorded//0006629 // lipid metabolic process //
<b>1.40 Bin1</b>	bridging integrator 1	0006897 // endocytosis // inferred from electronic annotation//0007275 // multicellular organismal development // inferred from electronic annotation//00030100 // regu
<b>1.39 Igcc4</b>	immunoglobulin superfamily, DCC subclass, member 4	
<b>1.38 Psoap</b>	prosaposin	0006629 // lipid metabolic process // inferred from electronic annotation//0006665 // sphingolipid metabolic process // inferred from electronic annotation//0006687 // i
<b>1.37 Flnc</b>	filamin C, gamma	0030029 // actin filament-based process // traceable author statement//0048747 // muscle fiber development // inferred from direct assay
<b>1.36 Cenpb</b>	centromere protein B	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation
<b>1.35 D16Ert6e</b>	DNA segment, Chr 16, ERATO Doi 6, expressed	
<b>1.35 Csnk2a1//Gm1003</b>	casein kinase 2, alpha 1 polypeptide//predicted pseudog	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annota
<b>1.35 Thsd4</b>	thrombospondin, type 1, domain containing 4	0006508 // proteolysis // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation//0048251 // elastic fiber assembly // i
<b>1.34 Gjb2</b>	gap junction protein, beta 2	0007154 // cell communication // inferred from electronic annotation//0007267 // cell-cell signaling // inferred from direct assay//0007565 // female pregnancy // inferre
<b>1.34 Tub</b>	tubby candidate gene	0006909 // phagocytosis // inferred from electronic annotation//0006910 // phagocytosis, recognition // inferred from direct assay//0006910 // phagocytosis, recognition
<b>1.34 Hmgn3</b>	high mobility group nucleosomal binding domain 3	0006357 // regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotype//0016568 // chromatin modification // inferred from electroni
<b>1.34 Dysf</b>	dysferlin	0001778 // plasma membrane repair // inferred from direct assay//0001778 // plasma membrane repair // inferred from mutant phenotype//0006906 // vesicle fusion //
<b>1.34 Cds1</b>	CD5 antigen-like 1	0006898 // receptor-mediated endocytosis // inferred from electronic annotation//0006915 // apoptotic process // inferred from electronic annotation
<b>1.33 Reep2</b>	receptor accessory protein 2	0002230 // positive regulation of defense response to virus by host // not recorded//0032386 // regulation of intracellular transport // inferred from direct assay//003259
<b>1.33 Ftsj3</b>	FtsI homolog 3 (E. coli)	0000453 // enzyme-directed rRNA 2'-O-methylation // inferred from electronic annotation//0000463 // maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRN
<b>1.32 Gpr85</b>	G-protein-coupled receptor 85	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // inferred from electronic annotation//0

Gene Symbol	Gene Title	Gene Ontology Biological Process
<b>1.32 Hmgcs2</b>	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	0001822 // kidney development // inferred from electronic annotation//0001889 // liver development // inferred from electronic annotation//0006629 // lipid metabolic p
<b>1.32 Sypl2</b>	synaptophysin-like 2	0006810 // transport // inferred from electronic annotation//0006874 // cellular calcium ion homeostasis // inferred from mutant phenotype//0021762 // substantia nigra
<b>1.31 Myh2</b>	myosin, heavy polypeptide 2, skeletal muscle, adult	0001778 // plasma membrane repair // inferred from mutant phenotype//0006936 // muscle contraction // not recorded//0008152 // metabolic process // inferred from
<b>1.31 Jsrp1</b>	junctional sarcoplasmic reticulum protein 1	0003009 // skeletal muscle contraction // not recorded//0006941 // striated muscle contraction // inferred from sequence or structural similarity//00060314 // regulation c
<b>1.30 Aas</b>	achalasia, adrenocortical insufficiency, alacrimia	0006810 // transport // inferred from electronic annotation//0006913 // nucleocytoplasmic transport // not recorded//0007612 // learning // inferred from mutant phen
<b>1.30 Hoxd9</b>	homeobox D9	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0006351 // transcription, DNA-templated // inferred from electronic an
<b>1.30 Mmp3</b>	matrix metalloproteinase 3	0006508 // proteolysis // inferred from mutant phenotype//0006508 // proteolysis // not recorded//0010727 // negative regulation of hydrogen peroxide metabolic proc
<b>1.29 Wnt4</b>	wingless-type MMTV integration site family, member 4	0001656 // metanephros development // inferred from mutant phenotype//0001656 // metanephros development // traceable author statement//0001656 // branching
<b>1.28 Adh7</b>	alcohol dehydrogenase 7 (class IV), mu or sigma polypept	0001523 // retinoid metabolic process // not recorded//0006067 // ethanol metabolic process // not recorded//0006068 // ethanol catabolic process // inferred from mut
<b>1.28 Bcl11b</b>	B cell leukemia/lymphoma 11B	0003334 // keratinocyte development // inferred from mutant phenotype//0003382 // epithelial cell morphogenesis // inferred from mutant phenotype//0006351 // tran
<b>1.27 Mlec</b>	malectin	0002250 // adaptive immune response // inferred from electronic annotation//0002376 // immune system process // inferred from electronic annotation//0005975 // car
<b>1.26 AU014973</b>	expressed sequence AU014973	
<b>1.25 Sult2b1</b>	sulfotransferase family, cytosolic, 2B, member 1	0000103 // sulfate assimilation // inferred from direct assay//0006629 // lipid metabolic process // inferred from electronic annotation//0008202 // steroid metabolic pro
<b>1.24 Gpc1</b>	glypican 1	0014037 // Schwann cell differentiation // not recorded//0030200 // heparan sulfate proteoglycan catabolic process // not recorded//0032288 // myelin assembly // not r
<b>1.24 A930009E05Rik</b>	RIKEN cDNA A930009E05 gene//transmembrane protein 1788	
<b>1.23 Cyp13</b>	cytochrome perinuclear theca 3	
<b>1.22 Slc7a3</b>	solute carrier family 7 (cationic amino acid transporter, y+)	0003333 // amino acid transmembrane transport // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006865 // amino a
<b>1.20 Pascin3</b>	protein kinase C and casein kinase substrate in neurons 3	0006897 // endocytosis // inferred from electronic annotation//0007010 // cytoskeleton organization // not recorded//0016310 // phosphorylation // inferred from electr
<b>-1.19 A630052C17Rik</b>	RIKEN cDNA A630052C17 gene	
<b>-1.19 Kpna7</b>	karyopherin alpha 7 (importin alpha 8)	0006606 // protein import into nucleus // inferred from electronic annotation//0006607 // NLS-bearing protein import into nucleus // not recorded//0006810 // transport
<b>-1.20 Cxos</b>	cone-rod homeobox, opposite strand	
<b>-1.20 Nmur1</b>	neuromedin U receptor 1	0006816 // calcium ion transport // not recorded//0006821 // chloride transport // not recorded//0006939 // smooth muscle contraction // inferred from electronic anno
<b>-1.21 Pyroxd2</b>	pyridine nucleotide-disulphide oxidoreductase domain 2	0055114 // oxidation-reduction process // inferred from electronic annotation
<b>-1.21 Dgkq</b>	diacylglycerol kinase, theta	0006357 // regulation of transcription from RNA polymerase II promoter // not recorded//0007165 // signal transduction // inferred from electronic annotation//0007186
<b>-1.21 Trim43a</b>	tripartite motif-containing 43A	
<b>-1.21 Pebp4</b>	phosphatidylethanolamine binding protein 4	
<b>-1.21 Cyb5r2</b>	cytochrome b5 reductase 2	0006629 // lipid metabolic process // inferred from electronic annotation//0006694 // steroid biosynthetic process // inferred from electronic annotation//0008202 // ste
<b>-1.21 Cd83</b>	CD83 antigen	0006952 // defense response // not recorded//0006959 // humoral immune response // not recorded//0007165 // signal transduction // not recorded//0014070 // resp
<b>-1.22 Atp8b3</b>	ATPase, class I, type 8B, member 3	0006810 // transport // inferred from electronic annotation//0006869 // lipid transport // inferred from electronic annotation//0007030 // Golgi organization // not recor
<b>-1.22 Dram2</b>	DNA damage regulated autophagy modulator 2	0006915 // apoptotic process // inferred from electronic annotation//0007601 // visual perception // inferred from sequence or structural similarity//0010506 // regulatic
<b>-1.22 Pou6f1</b>	POU domain, class 6, transcription factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annota
<b>-1.22 Cep112</b>	centrosomal protein 112	0097120 // receptor localization to synapse // not recorded
<b>-1.23 Lckr1</b>	leucine, glutamate and lysine rich 1	
<b>-1.23 4933402C06Rik</b>	RIKEN cDNA 4933402C06 gene	
<b>-1.23 Dcc</b>	deleted in colorectal carcinoma	0001764 // neuron migration // inferred from mutant phenotype//0006915 // apoptotic process // inferred from electronic annotation//0007275 // multicellular organis
<b>-1.23 H2-Eb2</b>	histocompatibility 2, class II antigen E beta2	0002376 // immune system process // inferred from electronic annotation//0002504 // antigen processing and presentation of peptide or polysaccharide antigen via MHC
<b>-1.23 Kcnj14</b>	potassium inwardly-rectifying channel, subfamily J, mem	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006813 // potassium ion transport // infer
<b>-1.24 Impg1</b>	interphotoreceptor matrix proteoglycan 1	
<b>-1.24 Cadps2</b>	Ca2+ dependent activator protein for secretion 2	0006810 // transport // inferred from electronic annotation//0006887 // exocytosis // inferred from electronic annotation//0009267 // cellular response to starvation // ir
<b>-1.24 Clp1</b>	CLP1, cleavage and polyadenylation factor I subunit	0006378 // mRNA polyadenylation // not recorded//0006379 // mRNA cleavage // not recorded//0006388 // tRNA splicing, via endonuclease cleavage and ligation // no
<b>-1.24 Ces2c//Ces2d-ps</b>	carboxylesterase 2C//carboxylesterase 2D, pseudogene	0001101 // response to acid chemical // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation
<b>-1.24 Zfp125</b>	zinc finger protein 125	
<b>-1.25 LOC102638850/R</b>	40S ribosomal protein S21, pseudogene//ribosomal prote	0000447 // endonucleolytic cleavage in ITS1 to separate SSU-rRNA and LSU-rRNA and LSU-rRNA from tritranscript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) // not r
<b>-1.25 Oas1b</b>	2'-5' oligoadenylate synthetase 1B	0002376 // immune system process // inferred from electronic annotation//0006955 // immune response // inferred from electronic annotation//0008152 // metabolic p
<b>-1.25 Krt222</b>	keratin 222	
<b>-1.26 Exd2</b>	exonuclease 3'-5' domain containing 2	0006139 // nucleobase-containing compound metabolic process // inferred from electronic annotation//0090305 // nucleic acid phosphodiester bond hydrolysis // inferre
<b>-1.26 Haoo</b>	3-hydroxyanthranilate 3,4-dioxygenase	0006569 // tryptophan catabolic process // inferred from electronic annotation//0009435 // NAD biosynthetic process // inferred from electronic annotation//0010043 //
<b>-1.26 a</b>	nonagouti	0006091 // generation of precursor metabolites and energy // inferred from genetic interaction//0008343 // adult feeding behavior // inferred from genetic interaction//
<b>-1.26 Gm30054</b>	predicted gene, 30054	
<b>-1.26 Kik7</b>	kallikrein related-peptidase 7 (chymotryptic, stratum corr	0002803 // positive regulation of antibacterial peptide production // not recorded//0006508 // proteolysis // inferred from electronic annotation
<b>-1.26 Fam208a</b>	family with sequence similarity 208, member A	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annota
<b>-1.26 Kcnq1</b>	potassium voltage-gated channel, subfamily Q, member	10002230 // positive regulation of defense response to virus by host // not recorded//0006349 // regulation of gene expression by genetic imprinting // inferred from muta
<b>-1.27 Trh</b>	thyrotropin releasing hormone	0001666 // response to hypoxia // inferred from electronic annotation//0001692 // histamine metabolic process // not recorded//0007628 // adult walking behavior // inf
<b>-1.27 Bcar3</b>	breast cancer anti-estrogen resistance 3	0002089 // lens morphogenesis in camera-type eye // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic annotation//0007264 //
<b>-1.27 Klr1b1f</b>	killer cell lectin-like receptor subfamily B member 1F	
<b>-1.27 Gm9873</b>	predicted gene 9873	
<b>-1.28 Adams3</b>	a disintegrin-like and metalloproteinase (repolysin type)	v0006508 // proteolysis // inferred from electronic annotation//0007229 // integrin-mediated signaling pathway // inferred from electronic annotation//0010573 // vasculi
<b>-1.28 Lrif1</b>	ligand dependent nuclear receptor interacting factor 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inferred from electronic annota
<b>-1.29 Stra8</b>	stimulated by retinoic acid gene 8	0001541 // ovarian follicle development // inferred from mutant phenotype//0006260 // DNA replication // inferred from electronic annotation//0007066 // female meio
<b>-1.29 Gm4951</b>	predicted gene 4951	0035458 // cellular response to interferon-beta // inferred from direct assay
<b>-1.30 Ptk3cd</b>	phosphatidylinositol 3-kinase catalytic delta polypeptide	0001782 // B cell homeostasis // inferred from mutant phenotype//0002250 // adaptive immune response // not recorded//0002376 // immune system process // inferre
<b>-1.31 Gimp4a</b>	GTPase, IMAP family member 4	
<b>-1.31 Ear-ps2//Ear1//E</b>	eosinophil-associated, ribonuclease A family, pseudogene	0006935 // chemotaxis // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation//0090305 // nucleic acid phosphodiester bond
<b>-1.31 Efnb3</b>	efrin B3	0007275 // multicellular organismal development // inferred from electronic annotation//0007399 // nervous system development // inferred from electronic annotation//
<b>-1.31 Gna14</b>	guanine nucleotide binding protein, alpha 14	0007165 // signal transduction // inferred from electronic annotation//0007186 // G-protein coupled receptor signaling pathway // not recorded//0007188 // adenylate c
<b>-1.31 Dusp2</b>	dual specificity phosphatase 2	0000188 // inactivation of MAPK activity // inferred from electronic annotation//0001706 // endoderm formation // not recorded//0006470 // protein dephosphorylation
<b>-1.31 Ear-ps2//Ear1//E</b>	eosinophil-associated, ribonuclease A family, pseudogene	0006935 // chemotaxis // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation//0090305 // nucleic acid phosphodiester bond
<b>-1.31 Gm11783</b>	predicted gene 11783	
<b>-1.32 Irs3</b>	insulin receptor substrate 3	0008286 // insulin receptor signaling pathway // not recorded//0019216 // regulation of lipid metabolic process // not recorded
<b>-1.32 Clk1</b>	CDC-like kinase 1	0006468 // protein phosphorylation // inferred from electronic annotation//0016310 // phosphorylation // inferred from electronic annotation//0018105 // peptidyl-serin
<b>-1.32 Ptprr</b>	protein tyrosine phosphatase, receptor type, R	0001701 // in utero embryonic development // inferred from sequence or structural similarity//0001701 // in utero embryonic development // inferred from electronic an
<b>-1.32 Gm21847//Gm386</b>	predicted gene, 21847//predicted gene, 38698//spermatogone	0000442 // inactivation of GTPase activity // inferred from electronic annotation//0001934 // positive regulation of protein phosphorylation // not recorded//0002082 // regulation of oxidative phosphorylation //
<b>-1.32 Pink1</b>	PTEN induced putative kinase 1	
<b>-1.32 D3Ert162e</b>	DNA segment, Chr 3, ERATO D0162, expressed	
<b>-1.32 Cubn</b>	cubilin (intrinsic factor-cobalamin receptor)	0001701 // in utero embryonic development // not recorded//0006629 // lipid metabolic process // inferred from electronic annotation//0006810 // transport // inferred
<b>-1.33 Gm10804</b>	predicted gene 10804	
<b>-1.33 Yes1</b>	Yamaguchi sarcoma viral (y-yes) oncogene homolog 1	0006468 // protein phosphorylation // inferred from electronic annotation//0007169 // transmembrane receptor protein tyrosine kinase signaling pathway // not recorded
<b>-1.33 Trpa1</b>	transient receptor potential cation channel, subfamily A,	0006810 // transport // inferred from electronic annotation//0006811 // ion transport // inferred from electronic annotation//0006816 // calcium ion transport // inferred
<b>-1.34 Adamdec1</b>	ADAM-like, decysin 1	0006508 // proteolysis // inferred from electronic annotation

Gsr-KO, Air[raw]	Gsr-KO, O2[raw]	RefSeq	Transcript ID	p	FC (Air: O2 at PND5)	Gene Symbol	Gene Title	Gene Ontology Biological Process
1114.1965	838.9059	NM_007894	//NM_001	0.005128	-1.34	<b>Ear1</b>	eosinophil-associated, ribonuclease A family, member 1	0008152 // metabolic process // inferred from electronic annotation//0090305 // nucleic acid phosphodiester bond hydrolysis // ---//0090305 // nucleic acid phosphodies
677.8456	511.4963	NM_009811		0.009966	-1.34	<b>Casp6</b>	caspase 6	0002525 // acute inflammatory response to non-antigenic stimulus // not recorded//0006508 // proteolysis // not recorded//0006508 // proteolysis // inferred from revie
1353.5447	1016.87146	NM_010423	//XM_006	0.003032	-1.34	<b>Hey1</b>	hairly/enhancer-of-split related with YRPW motif 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay//0000122 // negative regulation of transcription from RNA
196.79095	149.0175	XR_406477	//XR_87825	0.004869	-1.35	<b>Gm38561</b>	predicted gene, 38561	
55.505066	40.343925	NR_040646		9.58E-04	-1.35	<b>A330049N07Rik</b>	RIKEN cDNA A330049N07 gene	
101.593994	75.07389	NM_001025564	//NR_	9.19E-04	-1.36	<b>Gm15698</b>	transcription elongation factor B (SIII), polypeptide 2 pseu	0006368 // transcription elongation from RNA polymerase II promoter // not recorded
208.89912	156.01512	NM_148935	//XM_006	0.003946	-1.36	<b>Foxn4</b>	forkhead box N4	0001947 // heart looping // inferred from sequence or structural similarity//0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // r
112.4806	83.24882	NR_045298		0.005816	-1.36	<b>2900009J06Rik</b>	RIKEN cDNA 2900009J06 gene	
289.98132	215.11813	NM_001164563	//NM_	0.007088	-1.37	<b>Amigo2</b>	adhesion molecule with Ig like domain 2	0007155 // cell adhesion // not recorded//0007156 // homophilic cell adhesion via plasma membrane adhesion molecules // not recorded//0007156 // homophilic cell ad
30.81708	21.533033			0.004368	-1.37	<b>C79240</b>	expressed sequence C79240	
2047.1757	1500.6091	NM_001012766	//NM_	0.007611	-1.38	<b>Ear-ps2</b>	eosinophil-associated, ribonuclease A family, pseudogene	0006935 // chemotaxis // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation//0090305 // nucleic acid phosphodiester bond
98.24313	70.459274	NM_001301353	//NM_	0.00669	-1.39	<b>Apod</b>	apolipoprotein D	0000302 // response to reactive oxygen species // inferred from mutant phenotype//0000302 // response to reactive oxygen species // not recorded//0006006 // glucose
244.69336	175.83081	NM_001146328	//NM_	0.003411	-1.41	<b>Rbm46</b>	RNA binding motif protein 46	
60.79609	42.06468	NM_001080809	//XM_	0.002325	-1.42	<b>Cps1</b>	carbamoyl-phosphate synthetase 1	0000050 // urea cycle // not recorded//0000050 // urea cycle // inferred by curator//0001889 // liver development // inferred from electronic annotation//0005980 // gh
864.3497	613.0662	NM_153170	//XM_006	0.002885	-1.43	<b>Slc36a2</b>	solute carrier family 36 (proton/amino acid symporter), n	0010155 // regulation of proton transport // not recorded//0015808 // L-alanine transport // inferred from direct assay//0015816 // glycine transport // inferred from dire
207.42911	146.9297	NM_001045516	//XM_	0.007125	-1.43	<b>Proca1</b>	protein interacting with cyclin A1	
92.5706	63.493557	XR_882338	//XR_88233	0.004557	-1.45	<b>Gm28840</b>	predicted gene 28840	//oppositely-transcribed, rearranged locus on the Y
120.14404	83.24557	NM_177814	//XM_006	0.009396	-1.46	<b>Erc2</b>	ELKS/RAB6-interacting/CAST family member 2	
1060.3413	713.14526	NR_002896	//NR_0044	0.008032	-1.50	<b>Snhg1</b>	small nucleolar RNA host gene 1	//small nucleolar RNA, C/D box 22
120.54032	78.887665	NM_010643	//XM_006	0.006882	-1.53	<b>Klk1b24</b>	kallikrein 1-related peptidase b24	0002526 // acute inflammatory response // ---//0003073 // regulation of systemic arterial blood pressure // ---//0006508 // proteolysis // non-traceable author statement
70.1823	44.966255	NM_001130419	//NM_	0.001959	-1.53	<b>Hpca</b>	hippocalcin	0007420 // brain development // inferred from electronic annotation//0010518 // positive regulation of phospholipase activity // not recorded//0014070 // response to o
125.827644	76.53345	NM_001305549	//NM_	0.009845	-1.64	<b>Apoa2</b>	apolipoprotein A-II	0002526 // acute inflammatory response // inferred from electronic annotation//0002740 // negative regulation of cytokine secretion involved in immune response // not
529.0853	291.58115	NM_001316729	//NM_	0.008948	-1.83	<b>Qpct</b>	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	0017186 // peptidyl-pyroglytamic acid biosynthetic process, using glutaminyl-peptide cyclotransferase // not recorded
147.48763	80.17735	NM_054063		4.28E-04	-1.86	<b>Psg28</b>	pregnancy-specific glycoprotein 28	0007565 // female pregnancy // inferred from electronic annotation
68.43109	27.991377	XR_391854	//XR_39192	3.56E-04	-2.37	<b>Astx</b>	amplified spermatogenic transcripts X encoded 6	//predicted gene 28133//predicted gene 28220//predicted gene 28260//predicted gene 28365//predicted gene 28606//predi
374.6742	144.01358	NM_001164047	//NM_	0.008354	-2.61	<b>Mb</b>	myoglobin	0001666 // response to hypoxia // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0007507 // heart development // inferr
121.2285	220.95337	NM_010859		0.00206	-2.82	<b>Myl3</b>	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
1358.016	126.57135	NM_010861	//XM_006	0.004603	-10.65	<b>Myl2</b>	myosin, light polypeptide 2, regulatory, cardiac, slow	0002026 // regulation of the force of heart contraction // not recorded//0003007 // heart morphogenesis // inferred from genetic interaction//0007507 // heart developn
2265.6091	118.197014	NM_008725		0.002362	-19.06	<b>Nppa</b>	natriuretic peptide type A	0001666 // response to hypoxia // inferred from electronic annotation//0003085 // negative regulation of systemic arterial blood pressure // not recorded//0006182 // cc