Table S7. Lung genes (n=403) significantly changed at 56 days post-hyperoxia (O2) in wild-type (*Gsr* -WT) mice (moderated t-test, $p < 0.01$).

Blue(-): fold lower in neonate-O2. Red : fold higher in neonate-O2.

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	p	RefSeq Tra	FC (neonate-Air vs neonate-O2 at PND56)	Gene Symbol	Gene Title	Gene Ontology Biological Process
160.45352	1108.9347	8.56E-04	NM_00914	6.91	***Cxcl5***	chemokine (C-X-C motif) ligand 5	0001776 // leukocyte homeostasis // inferred from mutant phenotype///0001816 // cytokine production // not reco
15.179602	79.0113	5.98E-04	NM_20332	5.21	***Cxcl3***	chemokine (C-X-C motif) ligand 3	0002690 // positive regulation of leukocyte chemotaxis // not recorded///0006935 // chemotaxis // inferred from e
122.03934	491.43213	4.83E-04	NM_01186	4.03	***Slc26a4***	solute carrier family 26, member 4	0006810 // transport // inferred from electronic annotation///0006821 // chloride transport // not recorded///0006
14.616371	43.786827	4.94E-04	NM_00108	3.00	***Xlr3a///Xlr3b///Xlr3c***	X-linked lymphocyte-regulated 3A///X-linked lymphocyte-regulated 3B///X-linked lymp	0007286 // spermatid development // not recorded///0051965 // positive regulation of synapse assembly // inferre
47.468723	133.17143	0.009997213	NM_00860	2.81	***Mmp12***	matrix metallopeptidase 12	0006508 // proteolysis // inferred from electronic annotation///0014070 // response to organic cyclic compound //
28.481337	75.41425	1.09E-04	NM_00914	2.65	***Cxcl2***	chemokine (C-X-C motif) ligand 2	0001975 // response to amphetamine // inferred from electronic annotation///0002237 // response to molecule of
74.89079	185.64212	0.006322086	NM_01107	2.48	***Phex***	phosphate regulating endopeptidase homolog, X-linked	0006508 // proteolysis // not recorded///0019637 // organophosphate metabolic process // inferred from mutant p
124.5391	285.3428	0.00266994	NM_17729	2.29	***Itgb8***	integrin beta 8	0001573 // ganglioside metabolic process // inferred from mutant phenotype///0007155 // cell adhesion // inferred
337.2531	753.41034	8.66E-04	NM_01131	2.23	***Saa3***	serum amyloid A 3	0006953 // acute-phase response // inferred from electronic annotation///0007252 // I-kappaB phosphorylation //
165.72777	346.01883	7.00E-05	NM_01076	2.09	***Marco***	macrophage receptor with collagenous structure	0002376 // immune system process // inferred from electronic annotation///0006897 // endocytosis // inferred fro
623.4232	1291.712	0.003187251	NM_00940	2.07	***Pglyrp1***	peptidoglycan recognition protein 1	0002221 // pattern recognition receptor signaling pathway // not recorded///0002376 // immune system process //
50.312	102.8253	0.008796419	NM_00126	2.04	***Slco1a5***	solute carrier organic anion transporter family, member 1a5	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic a
216.17557	426.01157	0.001299659	NM_18324	1.97	***Wfdc21***	WAP four-disulfide core domain 21	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0032496 // response t
90.62632	178.31107	0.006205168	NM_01133	1.97	***Ccl17***	chemokine (C-C motif) ligand 17	0002548 // monocyte chemotaxis // ---///0006935 // chemotaxis // traceable author statement///0006954 // inflam
185.67882	361.4865	3.54E-04	NM_00108	1.95	***LOC102642186///Wfdc17***	WAP four-disulfide core domain protein 18-like///WAP four-disulfide core domain 17	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative re
1397.9376	2716.0068	0.001128585	NM_00849	1.94	***Lcn2***	lipocalin 2	0002376 // immune system process // inferred from electronic annotation///0006810 // transport // inferred from
167.47597	314.58688	0.003592327	NM_00832	1.88	***Ifi202b///LOC100044068***	interferon activated gene 202B///interferon-activable protein 202-like	0002376 // immune system process // inferred from electronic annotation///0006954 // inflammatory response // i
73.78068	138.49205	4.44E-04	NM_01981	1.88	***Slc5a1***	solute carrier family 5 (sodium/glucose cotransporter), member 1	0001656 // metanephros development // inferred from mutant phenotype///0006810 // transport // inferred from
53.356308	99.03036	8.50E-04	NM_00966	1.86	***Alox15***	arachidonate 15-lipoxygenase	0001503 // ossification // inferred from mutant phenotype///0002820 // negative regulation of adaptive immune re
92.105484	169.88239	0.002920989	NM_02966	1.84	***Mfsd2a***	major facilitator superfamily domain containing 2A	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic
54.371243	98.499794	4.52E-04	NM_20137	1.81	***Prmt8***	protein arginine N-methyltransferase 8	0006355 // regulation of transcription, DNA-templated // not recorded///0006479 // protein methylation // inferre
273.74545	490.9798	0.002535304	NM_05409	1.79	***Steap4***	STEAP family member 4	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic a
121.52661	213.07585	0.002070303	NM_00970	1.75	***Arg2***	arginase type II	0000050 // urea cycle // inferred from electronic annotation///0001657 // ureteric bud development // inferred fro
802.8379	1405.1028	0.005361897	NM_00984	1.75	***Cd14***	CD14 antigen	0002237 // response to molecule of bacterial origin // inferred from direct assay///0002376 // immune system proc
970.7131	1692.6278	0.001552247	NM_02979	1.74	***Lrg1***	leucine-rich alpha-2-glycoprotein 1	0001938 // positive regulation of endothelial cell proliferation // inferred from mutant phenotype///0030511 // pos
253.69846	429.0834	1.32E-04	NM_00817	1.69	***Cxcl1***	chemokine (C-X-C motif) ligand 1	0002237 // response to molecule of bacterial origin // not recorded///0002526 // acute inflammatory response // n
79.5308	133.85153	0.008657853	NM_02683	1.68	***Ms4a6d***	membrane-spanning 4-domains, subfamily A, member 6D	
147.74992	248.09619	0.009389659	NM_00117	1.68	***Sertad4***	SERTA domain containing 4	
228.96149	382.4917	0.004369808	NM_00839	1.67	***Itgae***	integrin alpha E, epithelial-associated	0007155 // cell adhesion // inferred from electronic annotation///0007229 // integrin-mediated signaling pathway
346.2966	574.3057	0.003533099	NM_00962	1.66	***Adm***	adrenomedullin	0001570 // vasculogenesis // not recorded///0001666 // response to hypoxia // inferred from electronic annotation
429.16483	707.2988	0.007730759	NM_02789	1.65	***Rhpn2***	rhophilin, Rho GTPase binding protein 2	0007165 // signal transduction // inferred from electronic annotation
88.938065	144.16412	2.74E-04	NM_00782	1.62	***Cyp7b1***	cytochrome P450, family 7, subfamily b, polypeptide 1	0006629 // lipid metabolic process // inferred from electronic annotation///0006699 // bile acid biosynthetic proce
489.19864	791.8601	0.003541607	NM_00939	1.62	***Tnfaip2***	tumor necrosis factor, alpha-induced protein 2	0001525 // angiogenesis // inferred from electronic annotation///0006887 // exocytosis // not recorded///0007275
77.8204	124.29989	0.001246387	NM_01040	1.60	***Hal***	histidine ammonia lyase	0006547 // histidine metabolic process // inferred from electronic annotation///0006548 // histidine catabolic proc
27.589792	44.030464	0.005063105	NM_00108	1.60	***Apobec4***	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 4 (putative)	0006397 // mRNA processing // inferred from electronic annotation
37.68251	59.952892	0.004336717	NM_00910	1.59	***Rptn***	repetin	
1393.7108	2206.045	0.006213602	NM_00128	1.58	***Ifi27l2a***	interferon, alpha-inducible protein 27 like 2A	0007568 // aging // inferred from direct assay///0009615 // response to virus // inferred from direct assay
103.747055	164.1735	7.34E-04	NM_17889	1.58	***Hepacam2***	HEPACAM family member 2	0007049 // cell cycle // inferred from electronic annotation///0007067 // mitotic nuclear division // inferred from e
79.49889	125.05292	0.00416294	NM_01188	1.57	***Sept3***	septin 3	0007049 // cell cycle // inferred from electronic annotation///0051301 // cell division // inferred from electronic an
29.550974	45.499527	0.005427833	NM_00111	1.54	***Efcab12***	EF-hand calcium binding domain 12	
43.930847	67.59953	4.09E-04	NM_00798	1.54	***Fap***	fibroblast activation protein	0001525 // angiogenesis // inferred from electronic annotation///0006508 // proteolysis // not recorded///000691
204.86887	314.52658	0.002320256	NM_00131	1.54	***Rgs5***	regulator of G-protein signaling 5	0007165 // signal transduction // not recorded///0007186 // G-protein coupled receptor signaling pathway // trace
183.69272	281.75977	0.005423922	NM_14494	1.53	***Cd207***	CD207 antigen	0051607 // defense response to virus // not recorded
82.25848	125.55188	0.004743074	NM_00788	1.53	***Atn1***	atrophin 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///00
52.794518	80.482445	0.00771485	NM_00103	1.52	***Cd69***	CD69 antigen	0035690 // cellular response to drug // inferred from expression pattern
47.343937	72.09121	0.001875296		1.52	***D3Wsu106e***	DNA segment, Chr 3, Wayne State University 106, expressed	
306.2107	465.40314	0.007771956	NM_18331	1.52	***Ctxn1***	cortexin 1	
40.14017	60.255722	0.004502521	NM_01373	1.50	***Plek2***	pleckstrin 2	0035556 // intracellular signal transduction // inferred from electronic annotation
290.21262	434.23376	0.001688143	NM_00977	1.50	***C1qb***	complement component 1, q subcomponent, beta polypeptide	0002376 // immune system process // inferred from electronic annotation///0006958 // complement activation, cla
185.29271	276.324	0.008864501	NM_00812	1.49	***Gjb2***	gap junction protein, beta 2	0007154 // cell communication // inferred from electronic annotation///0007267 // cell-cell signaling // inferred fro
67.0897	99.49912	0.008166593	NM_13324	1.48	***Ppargc1b***	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	0001503 // ossification // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred f
330.95035	487.78784	0.008430106	NM_01178	1.47	***Adamts5***	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 r	0006508 // proteolysis // inferred from electronic annotation///0042742 // defense response to bacterium // inferr
72.834885	106.539406	0.00986055	NM_00111	1.46	***Dclk1***	doublecortin-like kinase 1	0001764 // neuron migration // inferred from genetic interaction///0006468 // protein phosphorylation // inferred
38.884678	56.83209	0.007502906	NM_00102	1.46	***Cdc6***	cell division cycle 6	0006260 // DNA replication // inferred from electronic annotation///0006270 // DNA replication initiation // inferre
91.46453	133.1988	0.007729532	NM_01938	1.46	***Cd86***	CD86 antigen	0001878 // response to yeast // inferred from electronic annotation///0002224 // toll-like receptor signaling pathw
290.891	421.7043	0.001146297	NM_02640	1.45	***Rab32***	RAB32, member RAS oncogene family	0006886 // intracellular protein transport // not recorded///0007264 // small GTPase mediated signal transduction
15.133514	21.88079	0.001247762		1.45	***AI594671***	expressed sequence AI594671	
33.051933	47.434956	0.007584661	NM_00120	1.44	***AI607873***	expressed sequence AI607873	0000122 // negative regulation of transcription from RNA polymerase II promoter // ---
101.96524	145.0782	0.002542561	NM_00111	1.42	***Zfp385b***	zinc finger protein 385B	0006915 // apoptotic process // inferred from electronic annotation///0072332 // intrinsic apoptotic signaling path
50.433205	71.72307	0.005982272	NM_13922	1.42	***Rhbdl3***	rhomboid, veinlet-like 3 (Drosophila)	0006508 // proteolysis // inferred from electronic annotation///0016485 // protein processing // not recorded
343.12473	487.0162	0.001673632	NM_00131	1.42	***Kdm6a***	lysine (K)-specific demethylase 6A	0001701 // in utero embryonic development // inferred from mutant phenotype///0001843 // neural tube closure
14.488875	20.423174	0.009849513	NR_07722	1.41	***Gm6297***	predicted gene 6297	
16.098097	22.65619	0.005918719		1.41	***C76798***	expressed sequence C76798	
36.69145	51.520348	0.009432683	NM_00102	1.40	***Pla2g4f***	phospholipase A2, group IVF	0001516 // prostaglandin biosynthetic process // inferred from direct assay///0006629 // lipid metabolic process //
32.784462	45.97425	0.005819492	NM_00110	1.40	***Lin9***	lin-9 homolog (C. elegans)	0006351 // transcription, DNA-templated // inferred from electronic annotation///0007049 // cell cycle // inferred
35.842834	49.98524	0.006939644	NM_17862	1.39	***Fbxl2***	F-box and leucine-rich repeat protein 2	0006511 // ubiquitin-dependent protein catabolic process // inferred from mutant phenotype///0006513 // protein
70.999565	98.24687	0.008711631	NM_00102	1.38	***Ms4a7***	membrane-spanning 4-domains, subfamily A, member 7	
130.01857	179.53609	0.009249731	NM_01087	1.38	***Naip5***	NLR family, apoptosis inhibitory protein 5	0002376 // immune system process // inferred from electronic annotation///0006915 // apoptotic process // infer
398.17203	548.8051	0.004148808	NM_00129	1.38	***Preb***	prolactin regulatory element binding	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcri
96.99668	133.31953	0.005958783	NM_17726	1.37	***Tmem154***	transmembrane protein 154	
153.95074	211.4337	0.006135753	NM_02798	1.37	***Noxo1***	NADPH oxidase organizer 1	0006801 // superoxide metabolic process // inferred from direct assay///0022617 // extracellular matrix disassembl
38.381245	52.666073	0.001891153	NM_02847	1.37	***Nwd2***	NACHT and WD repeat domain containing 2	
91.808205	125.38302	0.008303902	NM_00128	1.37	***Lrmp***	lymphoid-restricted membrane protein	0002376 // immune system process // inferred from electronic annotation///0007338 // single fertilization // inferr
52.735573	71.885925	0.004436436	NM_01107	1.36	***Abcb1b***	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	0006810 // transport // not recorded///0006855 // drug transmembrane transport // not recorded///0008152 // m
80.28159	109.415375	0.00610617	NM_01078	1.36	***Cma1***	chymase 1, mast cell	0006508 // proteolysis // not recorded///0006518 // peptide metabolic process // inferred from electronic annotati
26.7142	36.253036	0.003406007	NM_00127	1.36	***Adam5***	a disintegrin and metallopeptidase domain 5	0006508 // proteolysis // inferred from electronic annotation
69.31296	94.01435	0.007565392	NM_05308	1.36	***Tcf23***	transcription factor 23	0007275 // multicellular organismal development // inferred from electronic annotation///0007517 // muscle orgar
207.03404	280.40192	0.002961725	NM_00115	1.35	***Fgd2***	FYVE, RhoGEF and PH domain containing 2	0035023 // regulation of Rho protein signal transduction // inferred from electronic annotation///0043507 // positi
147.02959	198.83836	0.008421873	NM_17386	1.35	***Gpt2***	glutamic pyruvate transaminase (alanine aminotransferase) 2	0006103 // 2-oxoglutarate metabolic process // not recorded///0009058 // biosynthetic process // inferred from ele

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	p	RefSeq Tra	FC (neonate-Air vs neonate-O2 at PND56)	Gene Symbol	Gene Title	Gene Ontology Biological Process
27.880014	37.659985	0.005276762	NM_01951	1.35	***Astn2***	astrotactin 2	2000009 // negative regulation of protein localization to cell surface // inferred from direct assay
36.756874	49.50593	0.003642043	XR_378441	1.35	***Sox6os***	SRY (sex determining region Y)-box 6, opposite strand	
58.820873	78.94708	0.002647361	NM_13425	1.34	***Havcr2***	hepatitis A virus cellular receptor 2	0001819 // positive regulation of cytokine production // inferred from mutant phenotype///0002519 // natural kille
23.426474	31.409649	0.005348173	NM_00790	1.34	***Edn2***	endothelin 2	0001516 // prostaglandin biosynthetic process // inferred from direct assay///0001516 // prostaglandin biosyntheti
115.15525	153.72656	0.008440082	NM_14722	1.33	***Abca9***	ATP-binding cassette, sub-family A (ABC1), member 9	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // not recorded///000815
573.971	766.05975	0.00690024	NM_01577	1.33	***Mfap5***	microfibrillar associated protein 5	0043206 // extracellular fibril organization // inferred from direct assay///0060216 // definitive hemopoiesis // infe
657.6893	875.4245	0.005582593	NM_01670	1.33	***C6***	complement component 6	0001701 // in utero embryonic development // inferred from genetic interaction///0001970 // positive regulation o
446.70416	594.31305	0.006751983	NM_01026	1.33	***Gda***	guanine deaminase	0006147 // guanine catabolic process // inferred from electronic annotation///0031116 // positive regulation of mi
792.27637	1044.4856	0.007959247	NM_02963	1.32	***Plet1***	placenta expressed transcript 1	0001953 // negative regulation of cell-matrix adhesion // inferred from mutant phenotype///0030154 // cell differe
5116.9478	6734.9746	0.0079921	NM_00769	1.32	***Chil1***	chitinase-like 1	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006032 // chitin catabolic pr
470.82602	618.0451	0.007345832	NM_00116	1.31	***Sema4a***	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cy	0001525 // angiogenesis // inferred from electronic annotation///0001755 // neural crest cell migration // not reco
28.032845	36.780437	0.007910694	NM_01996	1.31	***Brinp1***	bone morphogenic protein/retinoic acid inducible neural specific 1	0007049 // cell cycle // inferred from electronic annotation///0007050 // cell cycle arrest // inferred from electroni
733.4679	958.2934	0.009465014	NM_00103	1.31	***Golm1***	golgi membrane protein 1	0006997 // nucleus organization // inferred from mutant phenotype///0019216 // regulation of lipid metabolic pro
115.67084	150.88017	0.007378882	NM_00129	1.30	***Hnf1b***	HNF1 homeobox B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///00
1666.4786	2167.2485	0.008717786	NM_01042	1.30	***Hexb***	hexosaminidase B	0001501 // skeletal system development // inferred from genetic interaction///0005975 // carbohydrate metabolic
757.7507	983.9726	0.004688831	NM_15352	1.30	***Insig1***	insulin induced gene 1	0006629 // lipid metabolic process // inferred from electronic annotation///0006641 // triglyceride metabolic proce
71.324974	91.484276	0.006599128	NM_00977	1.28	***C3ar1***	complement component 3a receptor 1	0002430 // complement receptor mediated signaling pathway // not recorded///0002462 // tolerance induction to
17.56537	22.414295	0.009616536	XR_37651	1.28	***4933424M12Rik***	RIKEN cDNA 4933424M12 gene	
551.6129	702.27747	0.006189729	NM_08041	1.27	***Igsf8***	immunoglobulin superfamily, member 8	2000145 // regulation of cell motility // inferred from genetic interaction
55.406307	70.44439	0.004641838	NM_19902	1.27	***Zbtb26***	zinc finger and BTB domain containing 26	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded
17.210026	21.567137	0.009463575	NM_03060	1.25	***Clca2///Clca3a2///Clca1///Clca3a***	chloride channel accessory 2///chloride channel accessory 3A2///chloride channel acc	0006508 // proteolysis // inferred from electronic annotation///0006810 // transport // inferred from electronic an
51.473385	64.1107	0.00652821	NM_17059	1.25	***Igsf11***	immunoglobulin superfamily, member 11	0007155 // cell adhesion // inferred from electronic annotation///0040008 // regulation of growth // inferred from
36.60131	45.27813	0.009885551	NM_14598	1.24	***Fam83f***	family with sequence similarity 83, member F	
14.085622	17.359968	0.007001574	NM_00103	1.23	***Elavl4***	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	0007399 // nervous system development // inferred from electronic annotation///0007568 // aging // inferred fro
88.03151	76.520424	0.009080005	NM_17695	-1.15	***Fbxl7***	F-box and leucine-rich repeat protein 7	0000086 // G2/M transition of mitotic cell cycle // inferred from direct assay///0007049 // cell cycle // inferred fro
255.51285	217.4706	0.009358007	NM_01153	-1.17	***Tbx5***	T-box 5	0002009 // morphogenesis of an epithelium // inferred from mutant phenotype///0003166 // bundle of His develo
154.75983	131.20175	0.007505782	NM_01995	-1.18	***Chst5***	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006044 // N-acetylglucosami
34.832626	29.465021	0.008163204	NM_01666	-1.18	***Mtag2***	metastasis associated gene 2	
178.32079	150.26088	0.004155105	NM_00128	-1.19	***Dtna***	dystrobrevin alpha	
496.71188	417.74704	0.008160782	NM_17259	-1.19	***Arl15***	ADP-ribosylation factor-like 15	0007264 // small GTPase mediated signal transduction // inferred from electronic annotation
144.8654	121.54545	0.007822624	NM_13868	-1.19	***Wfdc12***	WAP four-disulfide core domain 12	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative r
377.6963	315.73477	0.009568824	NM_00754	-1.20	***Prdm1***	PR domain containing 1, with ZNF domain	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0
71.98826	60.03685	0.008354457	NM_00923	-1.20	***Sox11***	SRY (sex determining region Y)-box 11	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///0
527.78656	437.91776	0.006835324	NM_00858	-1.21	***Mertk***	c-mer proto-oncogene tyrosine kinase	0001779 // natural killer cell differentiation // inferred from genetic interaction///0006468 // protein phosphorylati
327.74048	271.418	0.006430389	NM_01087	-1.21	***Nck2***	non-catalytic region of tyrosine kinase adaptor protein 2	0001771 // immunological synapse formation // not recorded///0006417 // regulation of translation // inferred fro
23.078152	19.085468	0.009757232	NM_17258	-1.21	***Tmem63c***	transmembrane protein 63c	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
5445.8486	4491.2197	0.008105569	NM_00116	-1.21	***Dynlt1a///Dynlt1b///Dynlt1c///D***	dynein light chain Tctex-type 1A///dynein light chain Tctex-type 1B///dynein light cha	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype///0006810 // transport
240.80606	198.52603	0.008427013	NM_00108	-1.21	***Bod1l***	biorientation of chromosomes in cell division 1-like	0006281 // DNA repair // inferred from electronic annotation///0006974 // cellular response to DNA damage stimu
8141.2065	6710.715	0.006518072	NM_00116	-1.21	***Dynlt1a///Dynlt1b///Dynlt1c///D***	dynein light chain Tctex-type 1A///dynein light chain Tctex-type 1B///dynein light cha	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype///0006810 // transport
391.46735	322.5736	0.00832384	NM_01125	-1.21	***Rbm6***	RNA binding motif protein 6	
105.23527	86.58028	0.00997164		-1.22	***AI428301***	expressed sequence AI428301	
35.787224	29.421627	0.008334961	NM_15310	-1.22	***Padi6***	peptidyl arginine deiminase, type VI	0007010 // cytoskeleton organization // inferred from mutant phenotype///0007028 // cytoplasm organization // i
50.67753	41.661213	0.005942517	NM_00103	-1.22	***Rmi2***	RMI2, RecQ mediated genome instability 2, homolog (S. cerevisiae)	0006260 // DNA replication // inferred from electronic annotation
1008.2284	826.8482	0.006630503	NM_00116	-1.22	***Add3***	adducin 3 (gamma)	0042493 // response to drug // not recorded
331.26093	271.58884	0.003984637	NM_00128	-1.22	***Ddx46***	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0000398 // mRNA splicing, via spliceosome // not recorded///0006397 // mRNA processing // inferred from electro
291.13568	238.61769	0.004497157	NM_01970	-1.22	***Cdh13***	cadherin 13	0000278 // mitotic cell cycle // inferred from electronic annotation///0001558 // regulation of cell growth // inferre
190.66716	156.093	0.009322567	NM_00870	-1.22	***Nqo1***	NAD(P)H dehydrogenase, quinone 1	0006801 // superoxide metabolic process // not recorded///0006979 // response to oxidative stress // inferred fro
270.69284	221.52563	0.008234817	NM_01179	-1.22	***Car14***	carbonic anhydrase 14	0006885 // regulation of pH // inferred by curator///0008152 // metabolic process // inferred from electronic anno
156.62955	128.11458	0.008070216	NM_18299	-1.22	***Tmem59l***	transmembrane protein 59-like	
192.96407	157.63745	0.003455828	NM_00108	-1.22	***Rsf1***	remodeling and spacing factor 1	0006334 // nucleosome assembly // not recorded///0006338 // chromatin remodeling // not recorded///0006352 /
2334.7888	1906.2751	0.007780545	NM_02139	-1.22	***Slc43a3***	solute carrier family 43, member 3	0055085 // transmembrane transport // inferred from electronic annotation
330.9814	269.91238	0.00287453	NM_00108	-1.23	***Chd2///1810026B05Rik***	chromodomain helicase DNA binding protein 2///RIKEN cDNA 1810026B05 gene	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcri
351.91345	286.9263	0.005019383	NM_15380	-1.23	***Dnttip2***	deoxynucleotidyltransferase, terminal, interacting protein 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcri
549.52026	447.88007	0.003894585	NM_00103	-1.23	***Cntf///Zfp91///Zfp91Cntf***	ciliary neurotrophic factor///zinc finger protein 91///Zfp91-Cntf readthrough transcrip	0007250 // activation of NF-kappaB-inducing kinase activity // not recorded///0007259 // JAK-STAT cascade // not
1724.6565	1404.5717	0.009684066	NM_01019	-1.23	***Fgf1***	fibroblast growth factor 1	0001525 // angiogenesis // inferred from electronic annotation///0001759 // organ induction // inferred from dire
151.7211	123.1564	0.002375387	NM_01876	-1.23	***Chst2***	carbohydrate sulfotransferase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006044 // N-acetylglucosami
124.54507	100.91543	0.00902426	NM_00100	-1.23	***Armcx6***	armadillo repeat containing, X-linked 6	
307.45016	247.00006	0.006611202	NM_00117	-1.24	***Rapgef3***	Rap guanine nucleotide exchange factor (GEF) 3	0001525 // angiogenesis // inferred from electronic annotation///0001932 // regulation of protein phosphorylation
80.819595	64.91005	0.002225848	NM_00100	-1.25	***Tro***	trophinin	0030308 // negative regulation of cell growth // inferred from direct assay
464.0766	372.63522	0.006544279	NM_17865	-1.25	***Pkn2***	protein kinase N2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcri
513.2304	412.08582	0.005533211	NM_02993	-1.25	***Chst15***	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	0019319 // hexose biosynthetic process // not recorded
2047.4869	1635.7606	0.006902511	NM_03331	-1.25	***Slco2a1***	solute carrier organic anion transporter family, member 2a1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
554.6338	442.89008	0.002821337	NM_00108	-1.25	***Pphln1***	periphilin 1	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcri
569.11163	454.33658	0.008331779	NM_00104	-1.25	***Arrdc4***	arrestin domain containing 4	0051443 // positive regulation of ubiquitin-protein transferase activity // not recorded
790.74384	630.491	0.009492315	NM_00103	-1.25	***Xaf1***	XIAP associated factor 1	0006915 // apoptotic process // inferred from electronic annotation///0031333 // negative regulation of protein co
146.76526	116.8441	0.004715547	NM_00103	-1.26	***4932431P20Rik***	RIKEN cDNA 4932431P20 gene	
559.0871	444.96008	0.0059986	NM_08084	-1.26	***Higd1b***	HIG1 domain family, member 1B	
5264.8296	4175.985	0.004329287	NM_00116	-1.26	***Csde1***	cold shock domain containing E1, RNA binding	0006355 // regulation of transcription, DNA-templated // inferred from electronic annotation///0070966 // nuclear
40.666904	32.248867	0.003652636		-1.26	***D12Ertd673e***	DNA segment, Chr 12, ERATO Doi 673, expressed	
2245.788	1780.178	0.00854816	NM_01141	-1.26	***Smarca2***	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily	0006325 // chromatin organization // traceable author statement///0006334 // nucleosome assembly // traceable
21.243055	16.822937	0.008495412	NM_01378	-1.26	***Mmel1***	membrane metallo-endopeptidase-like 1	0006508 // proteolysis // inferred from electronic annotation
553.0098	437.9377	0.006690188	NM_15317	-1.26	***Gimap6***	GTPase, IMAP family member 6	
1626.4589	1286.786	0.009155978	NM_00103	-1.26	***Myzap***	myocardial zonula adherens protein	0035556 // intracellular signal transduction // inferred from direct assay
1230.0446	972.98663	0.009750093	NM_00128	-1.26	***Angpt1***	angiopoietin 1	0001525 // angiogenesis // inferred from direct assay///0001525 // angiogenesis // inferred from mutant phenotyp
405.00385	319.95724	0.004533111	NM_00103	-1.27	***Gng2***	guanine nucleotide binding protein (G protein), gamma 2	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor sign
2507.4622	1980.404	0.006936397	NM_00130	-1.27	***Cdkn2c***	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	0000079 // regulation of cyclin-dependent protein serine/threonine kinase activity // not recorded///0000082 // G1
2997.1758	2367.149	0.007392416	NM_00102	-1.27	***Npnt***	nephronectin	0001657 // ureteric bud development // inferred from mutant phenotype///0001658 // branching involved in urete
69.42604	54.780785	0.009373836	NM_01347	-1.27	***Apoh***	apolipoprotein H	0001937 // negative regulation of endothelial cell proliferation // not recorded///0006641 // triglyceride metabolic
573.24414	452.25226	0.005162949	NM_01033	-1.27	***Ednra***	endothelin receptor type A	0001569 // patterning of blood vessels // inferred from genetic interaction///0001666 // response to hypoxia // inf
158.23666	124.64604	0.007013865	NM_00116	-1.27	***Endou***	endonuclease, polyU-specific	0006508 // proteolysis // not recorded///0006898 // receptor-mediated endocytosis // inferred from electronic an
294.50735	231.69405	0.004888337	NM_01167	-1.27	***Ugcg***	UDP-glucose ceramide glucosyltransferase	0006629 // lipid metabolic process // inferred from electronic annotation///0006665 // sphingolipid metabolic proc

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	p	RefSeq Tra	FC (neonate-Air vs neonate-O2 at PND56)	Gene Symbol	Gene Title	Gene Ontology Biological Process
1354.9279	1060.6588	0.005993265	NM_18132	-1.28	***Ctcf***	CCCTC-binding factor	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenotyp
133.64636	104.477394	0.006932467	NM_01953	-1.28	***Sh3gl2***	SH3-domain GRB2-like 2	0002090 // regulation of receptor internalization // inferred from direct assay///0006897 // endocytosis // inferred
61.262894	47.789597	0.004389897	NM_02348	-1.28	***Sync***	syncoilin	0045103 // intermediate filament-based process // inferred from direct assay
149.13467	115.98326	0.007513741	NM_00119	-1.29	***Ddx55***	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	0010501 // RNA secondary structure unwinding // not recorded
53.087296	41.207138	0.006724734	NM_01674	-1.29	***Mybph***	myosin binding protein H	0007155 // cell adhesion // inferred from electronic annotation
1363.2074	1057.7847	0.004989315	NM_00116	-1.29	***Cyth3***	cytohesin 3	0016192 // vesicle-mediated transport // ---///0032012 // regulation of ARF protein signal transduction // inferred
962.7201	743.7094	0.003754453	NM_02666	-1.29	***Ubn1***	ubinuclein 1	0006336 // DNA replication-independent nucleosome assembly // not recorded///0006357 // regulation of transcri
525.04517	405.39517	0.002391014	NM_00129	-1.30	***Elf2***	E74-like factor 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcri
256.32123	197.8123	0.006339138	NM_01737	-1.30	***Tuba8***	tubulin, alpha 8	0000226 // microtubule cytoskeleton organization // not recorded///0007017 // microtubule-based process // infer
351.07025	270.8946	0.003168191	NM_17290	-1.30	***Olfml1***	olfactomedin-like 1	
1304.5967	1006.64343	0.002300988	NM_00103	-1.30	***Mef2a***	myocyte enhancer factor 2A	0000002 // mitochondrial genome maintenance // inferred from mutant phenotype///0000122 // negative regulati
379.8684	292.96353	0.007960286	NM_01886	-1.30	***Wisp1***	WNT1 inducible signaling pathway protein 1	0001558 // regulation of cell growth // inferred from electronic annotation///0007155 // cell adhesion // not recor
5782.0254	4450.121	0.006109754	NM_00116	-1.30	***Dynlt1-ps1///Dynlt1a///Dynlt1b//***	dynein light chain Tctex-type 1, pseudogene 1///dynein light chain Tctex-type 1A///d	0000132 // establishment of mitotic spindle orientation // inferred from mutant phenotype///0006810 // transport
107.10526	82.39641	0.001689527	NM_00116	-1.30	***Dcaf17***	DDB1 and CUL4 associated factor 17	0016567 // protein ubiquitination // inferred from electronic annotation
3882.4314	2980.9773	0.00924435	NM_00124	-1.30	***Col6a3***	collagen, type VI, alpha 3	0010951 // negative regulation of endopeptidase activity // inferred from electronic annotation
122.36338	93.879654	0.009531946	NM_02389	-1.30	***Sapcd1***	suppressor APC domain containing 1	
526.7514	403.9221	0.005635986	NM_13377	-1.30	***Stard4***	StAR-related lipid transfer (START) domain containing 4	0006810 // transport // inferred from electronic annotation///0006869 // lipid transport // inferred from electronic
1877.9907	1432.2484	0.002843046	NM_15351	-1.31	***BC028528***	cDNA sequence BC028528	
5889.2046	4482.737	0.003757528	NM_01023	-1.31	***Fmo1***	flavin containing monooxygenase 1	0006082 // organic acid metabolic process // not recorded///0006970 // response to osmotic stress // inferred fro
826.41766	628.5506	0.001562718	NM_00115	-1.31	***Gjc1***	gap junction protein, gamma 1	0001570 // vasculogenesis // inferred from mutant phenotype///0007154 // cell communication // inferred from el
4092.0732	3109.9126	0.009418829	NM_14605	-1.32	***Fermt2***	fermitin family homolog 2 (Drosophila)	0007155 // cell adhesion // inferred from electronic annotation///0007160 // cell-matrix adhesion // inferred from
94.37079	71.71373	0.00626986	NM_00839	-1.32	***Itga2***	integrin alpha 2	0002687 // positive regulation of leukocyte migration // not recorded///0006929 // substrate-dependent cell migra
2324.9429	1764.7217	9.17E-04	NM_00824	-1.32	***Plpp1***	phospholipid phosphatase 1	0006470 // protein dephosphorylation // inferred from direct assay///0006470 // protein dephosphorylation // trac
569.5836	431.7645	0.008394625	NM_00127	-1.32	***Ackr2***	atypical chemokine receptor 2	0006898 // receptor-mediated endocytosis // not recorded///0006935 // chemotaxis // inferred from electronic an
141.8412	107.273445	0.007077453	XM_00650	-1.32	***Adh6b***	alcohol dehydrogenase 6B (class V)	0055114 // oxidation-reduction process // inferred from electronic annotation
599.2929	452.55402	0.008302302	NM_17374	-1.32	***Maoa***	monoamine oxidase A	0006584 // catecholamine metabolic process // inferred from electronic annotation///0042135 // neurotransmitter
1421.4601	1071.5709	0.004672894	NM_00131	-1.33	***Crispld2***	cysteine-rich secretory protein LCCL domain containing 2	0030198 // extracellular matrix organization // inferred from direct assay///0030324 // lung development // inferre
3688.0056	2779.2708	0.003744515	NM_02708	-1.33	***Clic3***	chloride intracellular channel 3	0006749 // glutathione metabolic process // ---///0006810 // transport // inferred from electronic annotation///00
2579.1719	1941.751	0.003241317	NM_17892	-1.33	***Afap1l1***	actin filament associated protein 1-like 1	
739.07855	555.992	0.006605902	NM_00116	-1.33	***Phax***	phosphorylated adaptor for RNA export	0006408 // snRNA export from nucleus // inferred from direct assay///0006810 // transport // inferred from electro
337.1927	253.24078	0.008633235	NM_00111	-1.33	***Synrg***	synergin, gamma	0006810 // transport // inferred from electronic annotation///0006897 // endocytosis // inferred from electronic a
1685.3572	1262.7155	0.001672245	NM_00128	-1.33	***Daam1***	dishevelled associated activator of morphogenesis 1	0016043 // cellular component organization // inferred from electronic annotation///0030036 // actin cytoskeleton
2721.9685	2034.5537	0.005853636	NM_00116	-1.34	***Snrk***	SNF related kinase	0006468 // protein phosphorylation // not recorded///0016310 // phosphorylation // inferred from electronic anno
379.24768	282.72717	0.005726045	NM_01381	-1.34	***Dnah8***	dynein, axonemal, heavy chain 8	0007018 // microtubule-based movement // inferred from electronic annotation///0008152 // metabolic process //
940.12823	700.0069	0.002964669	NM_00128	-1.34	***Elk3***	ELK3, member of ETS oncogene family	0001525 // angiogenesis // inferred from mutant phenotype///0006351 // transcription, DNA-templated // inferred
58.674236	43.522366	0.001734882	NM_01036	-1.35	***Gypa***	glycophorin A	0007016 // cytoskeletal anchoring at plasma membrane // inferred from mutant phenotype///0047484 // regulatio
972.37067	721.0148	5.93E-04	NM_00128	-1.35	***Rcan2***	regulator of calcineurin 2	0006950 // response to stress // inferred from genetic interaction///0006950 // response to stress // inferred from
749.1642	553.1385	0.001537129	NM_02591	-1.35	***Tmem88***	transmembrane protein 88	0007275 // multicellular organismal development // inferred from electronic annotation///0016055 // Wnt signalin
477.73456	352.49316	0.005939077	NM_14479	-1.36	***Lmcd1***	LIM and cysteine-rich domains 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interacti
817.06866	602.78564	0.001245283	NM_00131	-1.36	***Prkch***	protein kinase C, eta	0006468 // protein phosphorylation // not recorded///0010744 // positive regulation of macrophage derived foam
34.840076	25.661274	0.006128062	NM_00891	-1.36	***Ppy***	pancreatic polypeptide	0002230 // positive regulation of defense response to virus by host // not recorded///0007218 // neuropeptide sig
889.69666	655.2427	0.009978712	NM_00116	-1.36	***Cdkn1c***	cyclin-dependent kinase inhibitor 1C (P57)	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from genetic interacti
193.39479	142.3918	6.24E-04	NM_01184	-1.36	***Mid2***	midline 2	0010508 // positive regulation of autophagy // inferred from sequence or structural similarity///0016567 // protein
174.11421	127.99915	4.56E-04	NM_17213	-1.36	***Adap2***	ArfGAP with dual PH domains 2	0007507 // heart development // non-traceable author statement///0043547 // positive regulation of GTPase activi
388.07947	285.08374	8.45E-04	NM_02608	-1.36	***Zc3h13***	zinc finger CCCH type containing 13	
290.53336	213.34914	4.52E-04	NM_17546	-1.36	***Nmnat2***	nicotinamide nucleotide adenylyltransferase 2	0006767 // water-soluble vitamin metabolic process // not recorded///0009058 // biosynthetic process // inferred
3253.2273	2385.698	0.001249235	NM_00127	-1.36	***Dag1***	dystroglycan 1	0002011 // morphogenesis of an epithelial sheet // inferred from mutant phenotype///0006509 // membrane prote
9519.707	6951.3833	0.00549867	NM_13874	-1.37	***Sdpr***	serum deprivation response	0045944 // positive regulation of transcription from RNA polymerase II promoter // not recorded
757.85187	553.33234	0.003289562	NM_00752	-1.37	***Bcl6b***	B cell CLL/lymphoma 6, member B	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay
98.634964	71.937546	0.003878087	NM_00103	-1.37	***Zcchc18***	zinc finger, CCHC domain containing 18	0030509 // BMP signaling pathway // not recorded
558.375	406.41235	0.004839883	NM_08059	-1.37	***Emid1***	EMI domain containing 1	
161.63545	117.38556	0.009112365	NM_00799	-1.38	***Fbp2***	fructose bisphosphatase 2	0005975 // carbohydrate metabolic process // inferred from electronic annotation///0006094 // gluconeogenesis //
51.934258	37.66331	0.004050829	NM_19903	-1.38	***Cep135***	centrosomal protein 135	0007099 // centriole replication // not recorded///0010457 // centriole-centriole cohesion // not recorded
1001.4492	724.69794	0.006075849	NM_03356	-1.38	***Klf7***	Kruppel-like factor 7 (ubiquitous)	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcri
1332.6403	963.85547	0.001487617	NM_01180	-1.38	***Ets2***	E26 avian leukemia oncogene 2, 3' domain	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0001712 // ect
930.3197	672.4694	0.001638608	NM_18154	-1.38	***Nostrin***	nitric oxide synthase trafficker	0006897 // endocytosis // inferred from electronic annotation///0045892 // negative regulation of transcription, D
120.21006	86.03727	0.001692956	NM_00129	-1.40	***LOC102641273///Ttc14***	tetratricopeptide repeat protein 14 pseudogene///tetratricopeptide repeat domain 14	0001947 // heart looping // ---///0003341 // cilium movement // ---///0003356 // regulation of cilium beat frequen
54.444614	38.943493	0.002706605	NM_01160	-1.40	***Tnfrsf17***	tumor necrosis factor receptor superfamily, member 17	0002250 // adaptive immune response // inferred from electronic annotation///0002260 // lymphocyte homeostasi
2082.3865	1488.7704	2.93E-04	NM_00108	-1.40	***Scn3b***	sodium channel, voltage-gated, type III, beta	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
1169.6152	829.3296	0.006166396	NM_00111	-1.41	***Ddx6***	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	0006417 // regulation of translation // not recorded///0010501 // RNA secondary structure unwinding // not recor
333.38388	236.18637	0.004603687	NM_01072	-1.41	***Lipg***	lipase, endothelial	0006629 // lipid metabolic process // inferred from electronic annotation///0007584 // response to nutrient // infe
7442.302	5272.0146	0.002912802	NM_00792	-1.41	***Emp2***	epithelial membrane protein 2	0001765 // membrane raft assembly // inferred from direct assay///0001913 // T cell mediated cytotoxicity // infer
2587.8662	1826.6166	0.001730402	NM_02583	-1.42	***Baiap2l1***	BAI1-associated protein 2-like 1	0007009 // plasma membrane organization // inferred from electronic annotation///0008286 // insulin receptor sig
1083.4781	764.56384	0.006863724	NM_02847	-1.42	***Bmper***	BMP-binding endothelial regulator	0001657 // ureteric bud development // inferred from expression pattern///0002043 // blood vessel endothelial ce
1097.989	774.5618	7.62E-04	NM_18331	-1.42	***Synm***	synemin, intermediate filament protein	0045104 // intermediate filament cytoskeleton organization // inferred from electronic annotation
1396.2255	980.5527	0.002823039	NM_00116	-1.42	***Gucy1b3***	guanylate cyclase 1, soluble, beta 3	0006182 // cGMP biosynthetic process // not recorded///0007165 // signal transduction // not recorded///0007263
394.7551	276.3262	0.002817492	NM_01737	-1.43	***Pcdh12***	protocadherin 12	0005977 // glycogen metabolic process // inferred from mutant phenotype///0007155 // cell adhesion // inferred f
90.344536	63.157875	0.002427835	NM_02347	-1.43	***Upk3a***	uroplakin 3A	0000902 // cell morphogenesis // inferred from mutant phenotype///0001822 // kidney development // inferred fr
1124.4457	784.2161	0.002098427	NM_01158	-1.43	***Nr1d2***	nuclear receptor subfamily 1, group D, member 2	0006351 // transcription, DNA-templated // inferred from electronic annotation///0006355 // regulation of transcri
83.67772	58.288177	1.83E-04	NM_00103	-1.44	***Wfdc6a***	WAP four-disulfide core domain 6A	0010466 // negative regulation of peptidase activity // not recorded///0010951 // negative regulation of endopepti
880.44916	599.7348	0.003583245	NM_14614	-1.47	***Jak1***	Janus kinase 1	0006468 // protein phosphorylation // inferred from electronic annotation///0007167 // enzyme linked receptor pr
738.8207	503.1607	0.006593663	NM_02445	-1.47	***Luzp1***	leucine zipper protein 1	0003281 // ventricular septum development // inferred from mutant phenotype///0021503 // neural fold bending
2401.713	1635.0742	7.67E-04	NM_00119	-1.47	***Lims1***	LIM and senescent cell antigen-like domains 1	0007160 // cell-matrix adhesion // inferred from mutant phenotype///0007163 // establishment or maintenance of
124.23487	84.51717	0.001011481	NM_00750	-1.47	***Atp2a1***	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
53.983192	36.614254	0.003483273	NM_00127	-1.47	***Ahsg***	alpha-2-HS-glycoprotein	0001503 // ossification // inferred from direct assay///0006461 // protein complex assembly // not recorded///000
155.99841	105.64493	0.001898921	NM_00103	-1.48	***Cntf///Zfp91///Zfp91Cntf***	ciliary neurotrophic factor///zinc finger protein 91///Zfp91-Cntf readthrough transcrip	0007250 // activation of NF-kappaB-inducing kinase activity // not recorded///0007259 // JAK-STAT cascade // not
1211.9332	820.30225	4.85E-04	NM_02580	-1.48	***Slc16a9***	solute carrier family 16 (monocarboxylic acid transporters), member 9	0006810 // transport // inferred from electronic annotation///0015718 // monocarboxylic acid transport // ---///00
131.06548	87.92938	0.001745614	NM_00131	-1.49	***Atf7***	activating transcription factor 7	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0006351 // tra
106.741684	71.49692	0.006861682	NM_00112	-1.49	***Trp53***	transformation related protein 53	0000060 // protein import into nucleus, translocation // inferred from direct assay///0000122 // negative regulatio
1236.9542	821.3603	0.001469482	NM_00865	-1.51	***Gadd45b***	growth arrest and DNA-damage-inducible 45 beta	0000185 // activation of MAPKKK activity // not recorded///0000186 // activation of MAPKK activity // inferred fro
245.32516	162.25024	1.01E-04	NM_00112	-1.51	***Igf2***	insulin-like growth factor 2	0001503 // ossification // inferred from electronic annotation///0001649 // osteoblast differentiation // inferred fr

[C3H/HeN, Air](raw)	[C3H/HeN, O2](raw)	p	RefSeq Tra	FC (neonate-Air vs neonate-O2 at PND56)	Gene Symbol	Gene Title	Gene Ontology Biological Process
93.168015	61.005875	9.70E-05	NM_15307	-1.53	***Gprc6a***	G protein-coupled receptor, family C, group 6, member A	0007165 // signal transduction // inferred from electronic annotation///0007186 // G-protein coupled receptor sig
22.566032	14.750648	3.43E-04	NM_01126	-1.53	***Rhag***	Rhesus blood group-associated A glycoprotein	0006810 // transport // inferred from electronic annotation///0006873 // cellular ion homeostasis // not recorded/
822.4235	537.4037	2.35E-04	NM_00764	-1.53	***Cd38***	CD38 antigen	0001666 // response to hypoxia // not recorded///0007204 // positive regulation of cytosolic calcium ion concentra
1286.883	836.3257	0.00551773	NM_00125	-1.54	***Mest***	mesoderm specific transcript	0007498 // mesoderm development // not recorded///0008152 // metabolic process // not recorded///0010883 //
658.00104	422.8983	9.08E-04	NM_15339	-1.56	***Col23a1***	collagen, type XXIII, alpha 1	0070207 // protein homotrimerization // not recorded
1259.2003	804.66504	0.005947487	NM_17835	-1.56	***Klf11***	Kruppel-like factor 11	0000083 // regulation of transcription involved in G1/S transition of mitotic cell cycle // not recorded///0000122 //
3325.123	2088.996	0.002306288	NM_01089	-1.59	***Nedd4***	neural precursor cell expressed, developmentally down-regulated 4	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from mutant phenoty
379.88022	234.83817	0.006076203	NM_02996	-1.62	***9230104L09Rik***	RIKEN cDNA 9230104L09 gene	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative r
236.66086	145.57121	0.006097783	NM_00790	-1.63	***Edn3***	endothelin 3	0001755 // neural crest cell migration // inferred from mutant phenotype///0002690 // positive regulation of leuko
347.34525	212.3035	0.003057372	NM_01140	-1.64	***Slc4a1***	solute carrier family 4 (anion exchanger), member 1	0006810 // transport // inferred from electronic annotation///0006811 // ion transport // inferred from electronic
297.37445	180.14381	1.97E-04	NM_00129	-1.65	***Adcy8***	adenylate cyclase 8	0006171 // cAMP biosynthetic process // not recorded///0007189 // adenylate cyclase-activating G-protein couple
767.60785	453.8218	0.00566817	NM_15345	-1.69	***Dusp7***	dual specificity phosphatase 7	0000188 // inactivation of MAPK activity // not recorded///0006470 // protein dephosphorylation // not recorded/
34.509075	20.343918	0.008078477	NM_18184	-1.70	***Fgb***	fibrinogen beta chain	0002250 // adaptive immune response // inferred from electronic annotation///0002376 // immune system process
525.4309	308.6053	0.002106925	NM_01191	-1.70	***Xrn2***	5'-3' exoribonuclease 2	0000738 // DNA catabolic process, exonucleolytic // not recorded///0006139 // nucleobase-containing compound
293.49832	169.69853	0.007421678	NM_00117	-1.73	***Cyp26b1***	cytochrome P450, family 26, subfamily b, polypeptide 1	0001709 // cell fate determination // inferred from mutant phenotype///0001768 // establishment of T cell polarity
217.13885	125.328575	0.006831768	NM_00119	-1.73	***Bend7***	BEN domain containing 7	
191.05328	106.985535	6.21E-04	NM_15340	-1.79	***Neurl3***	neuralized E3 ubiquitin protein ligase 3	0016567 // protein ubiquitination // inferred from genetic interaction
1026.606	574.3703	2.29E-04	NM_00790	-1.79	***S1pr1***	sphingosine-1-phosphate receptor 1	0001525 // angiogenesis // inferred from direct assay///0001955 // blood vessel maturation // inferred from mutan
3852.278	2151.8381	0.001361943	NR_00284	-1.79	***Malat1***	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from mutant phenotype///0035063
185.40262	97.6724	0.003106583	XR_37852	-1.90	***Gm33248***	predicted gene, 33248	
310.7118	162.58124	1.95E-05	NM_01073	-1.91	***Zbtb7a***	zinc finger and BTB domain containing 7a	0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from direct assay///00
408.60727	199.38464	0.005052957	NM_02728	-2.05	***Nt5dc2***	5'-nucleotidase domain containing 2	0006470 // protein dephosphorylation // ---///0016311 // dephosphorylation // ---
439.93048	192.35175	0.001140304	NM_14543	-2.29	***Nr1d1***	nuclear receptor subfamily 1, group D, member 1	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded///0005978 // gly
377.5021	162.36482	0.002887926	NM_00127	-2.33	***Acta1***	actin, alpha 1, skeletal muscle	0009612 // response to mechanical stimulus // inferred from electronic annotation///0009991 // response to extra
235.96065	101.15667	5.56E-05	NM_01697	-2.33	***Dbp***	D site albumin promoter binding protein	0001889 // liver development // inferred from electronic annotation///0006351 // transcription, DNA-templated //
831.9619	229.24924	6.07E-04	NR_00159	-3.63	***H19***	H19, imprinted maternally expressed transcript	0008285 // negative regulation of cell proliferation // inferred from genetic interaction///0010468 // regulation of
225.87642	36.23993	0.009964186	NM_02528	-6.23	***Stfa3///BC100530///Stfa1***	stefin A3///cDNA sequence BC100530///stefin A1	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative r
371.3008	47.51264	0.009735196	NM_00108	-7.81	***BC100530///Stfa1///Stfa3***	cDNA sequence BC100530///stefin A1///stefin A3	0010466 // negative regulation of peptidase activity // inferred from electronic annotation///0010951 // negative r
261.86676	16.937466	0.004212725	NM_01201	-15.46	***Eif2s3y***	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	0001731 // formation of translation preinitiation complex // ---///0006412 // translation // inferred from electronic
497.55447	17.751776	0.003091645	NM_01200	-28.03	***Ddx3y***	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	0006413 // translational initiation // not recorded///0007059 // chromosome segregation // not recorded///00104