Appendix 1. Genes identified as hyperoxia regulated using ANOVA.

				Fold Change		
Probe ID	***Gene Symbol***	***Gene Title***	***P value***	***3 Days***	***7 Days***	***14 Days***
1443056_at		0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130111E17 product: unclassifiable, full insert sequence	0.031	-2.10	-2.34	-3.16
1419734_at	Actb	actin, beta, cytoplasmic	0.041	NC	NC	***2.79***
1421830_at	Ak3l1	adenylate kinase 3 alpha-like 1	0.031	-3.00	-2.29	-2.31
1418204_s_at	Aif1	allograft inflammatory factor 1	0.027	NC	***2.14***	***5.68***
1434719_at	A2m	alpha-2-macroglobulin	0.007		NC	***4.76***
1430515_s_at	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	0.008	NC	***2.57***	NC
1426708_at	Antxr2	anthrax toxin receptor 2	0.035	NC	NC	***2.77***
1418133_at	Bcl3	B-cell leukemia/lymphoma 3	0.004	NC	***8.25***	***46.57***
1434543_a_at	Bola2	bolA-like 2 (E. coli)	0.044	-2.04	NC	***2.63***
1447940_a_at	Braf	Braf transforming gene	0.045	***2.25***	NC	-2.79
1443814_x_at	Ctsh	cathepsin H	0.043	NC	NC	***2.56***
1449031_at	Cited1	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1	0.029	NC	NC	***3.11***
1418901_at	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	0.014	NC	NC	***3.40***
1423233_at	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	0.001	NC	***2.70***	***9.65***
1460218_at	Cd52	CD52 antigen	0.001	-2.30	NC	***5.85***
1455393_at	Cp	ceruloplasmin	0.001	NC	NC	***6.38***
1417494_a_at	Cp	ceruloplasmin	0.013	NC	NC	***3.53***
1417266_at	Ccl6	chemokine (C-C motif) ligand 6	0.049	NC	NC	***2.89***
1419872_at	Csf1r	colony stimulating factor 1 receptor	0.009	NC	NC	***3.13***
1419873_s_at	Csf1r	colony stimulating factor 1 receptor	0.026	NC	NC	***2.96***
1417063_at	C1qb	complement component 1, q subcomponent, beta polypeptide	0.009	NC	NC	***3.90***
1437726_x_at	C1qb	complement component 1, q subcomponent, beta polypeptide	0.017	NC	NC	***4.56***
1449401_at	C1qg	complement component 1, q subcomponent, gamma polypeptide	0.002	NC	NC	***6.43***
1423954_at	C3	complement component 3	0.004	NC	-6.21	***10.42***
1455269_a_at	Coro1a	coronin, actin binding protein 1A	0.028	NC	NC	***3.77***
1416776_at	Crym	crystallin, mu	0.004	NC	NC	***3.97***
1420699_at	Clec7a	C-type lectin domain family 7, member a	0.009	NC	***2.03***	***6.33***
1446670_at	Cugbp2	CUG triplet repeat, RNA binding protein 2, mRNA (cDNA clone MGC:25225 IMAGE:4503295)	0.036	-2.11	-2.40	-2.58
1448538_a_at	D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	0.041	***2.34***	NC	-2.12
1436659_at	Dcamkl1	Double cortin and calcium/calmodulin-dependent protein kinase-like 1, mRNA (cDNA clone IMAGE:5006471)	0.020	NC	NC	***3.75***
1432181_s_at	Ecgf1	endothelial cell growth factor 1 (platelet-derived)	0.044	NC	NC	***2.75***
1449161_at	Edn2	endothelin 2	0.041	***2.93***	NC	***13.15***
1434976_x_at	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	0.038	NC	NC	***3.47***
1448808_a_at	Nme2	expressed in non-metastatic cells 2, protein	0.013	NC	NC	***3.83***
1426509_s_at	Gfap	glial fibrillary acidic protein	0.005	NC	***2.31***	***16.64***
1449773_s_at	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	0.003	***2.68***	NC	***5.80***

1450971_at	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	0.016	NC	NC	***4.54***
1460180_at	Hexb	hexosaminidase B	0.015	NC	NC	***2.98***
1437874_s_at	Hexb	hexosaminidase B	0.016	NC	NC	***2.93***
1451931_x_at	H2-D1	histocompatibility 2, D region locus 1	0.014	NC	NC	***3.57***
1451683_x_at	H2-D1	Histocompatibility 2, D region, mRNA (cDNA clone IMAGE:5008280)	0.049	NC	NC	***3.39***
1454803_a_at	Hdac11	histone deacetylase 11	0.016	NC	NC	***3.39***
1426278_at	Ifi27	interferon, alpha-inducible protein 27	0.013	NC	***4.91***	***18.99***
1415899_at	Junb	Jun-B oncogene	0.041	NC	NC	***3.18***
1449172_a_at	Lin7b	lin 7 homolog b (C. elegans)	0.003	NC	NC	***5.38***
1418683_at	Lin7b	lin 7 homolog b (C. elegans)	0.017	NC	NC	***4.39***
1439240_x_at	Lin7b	lin 7 homolog b (C. elegans)	0.020	NC	NC	***3.79***
1427747_a_at	Lcn2	lipocalin 2	0.004	***8.78***	NC	***6.78***
1422903_at	Ly86	lymphocyte antigen 86	0.001	NC	NC	***6.25***
1426025_s_at	Laptm5	lysosomal-associated protein transmembrane 5	0.001	NC	NC	***5.02***
1436905_x_at	Laptm5	lysosomal-associated protein transmembrane 5	0.002	NC	NC	***6.48***
1456586_x_at	Mvp	major vault protein	0.039	NC	NC	***3.36***
1422557_s_at	Mt1	metallothionein 1	0.025	NC	NC	***3.62***
1428942_at	Mt2	metallothionein 2	0.007	***23.32***	NC	***4.12***
1452298_a_at	Myo5b	myosin Vb	0.037	NC	NC	***2.54***
1419665_a_at	Nupr1	nuclear protein 1	0.010	***2.12***	NC	***4.47***
1419666_x_at	Nupr1	nuclear protein 1	0.038	NC	NC	***4.32***
1424510_at	Nudt6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	0.041	NC	NC	***2.72***
1418674_at	Osmr	oncostatin M receptor	0.015	NC	NC	***2.98***
1448817_at	Otub1	OTU domain, ubiquitin aldehyde binding 1	0.042	NC	NC	***2.18***
1417356_at	Peg3	paternally expressed 3	0.035	***2.63***	NC	-5.75
1417928_at	Pdlim4	PDZ and LIM domain 4	0.025	NC	NC	***2.75***
1416166_a_at	Prdx4	peroxiredoxin 4	0.031	NC	NC	***3.61***
1427893_a_at	Pmvk	phosphomevalonate kinase	0.046	NC	NC	***2.48***
1419309_at	Pdpn	podoplanin	0.017	NC	NC	***2.98***
1434820_s_at	Pkig	protein kinase inhibitor, gamma	0.032	NC	NC	***2.66***
1439440_x_at	Ptk9l	protein tyrosine kinase 9-like (A6-related protein)	0.031	NC	NC	***3.08***
1422962_a_at	Psmb8	proteosome (prosome, macropain) subunit, beta type 8 (large multifunctional peptidase 7)	0.022	NC	NC	***3.04***
1442326_at	Pcdh15	protocadherin 15	0.029	-2.20	-2.26	-3.88
1417346_at	Pycard	PYD and CARD domain containing	0.010	NC	NC	***4.24***
1436058_at	Rsad2	radical S-adenosyl methionine domain containing 2	0.039	NC	NC	***2.66***
1418395_at	1300013J15Rik	RIKEN cDNA 1300013J15 gene	0.020	NC	***3.43***	***11.04***
1439387_x_at	2310061F22Rik	RIKEN cDNA 2310061F22 gene	0.046	NC	NC	***2.41***
1429906_at	A930035E12Rik	RIKEN cDNA A930035E12 gene	0.046	-2.15	-2.22	-4.46
1436014_a_at	Rusc1	RUN and SH3 domain containing 1	0.039	NC	NC	***3.31***
1437991_x_at	Rusc1	RUN and SH3 domain containing 1, mRNA (cDNA clone MGC:67218 IMAGE:5687517)	0.037	NC	NC	***3.10***
1418704_at	S100a13	S100 calcium binding protein A13	0.030	NC	NC	***2.84***
1425560_a_at	S100a16	S100 calcium binding protein A16	0.034	NC	NC	***2.53***
1447676_x_at	S100a16	S100 calcium binding protein A16 (S100a16), mRNA	0.025	NC	NC	***2.61***
1421375_a_at	S100a6	S100 calcium binding protein A6 (calcyclin)	0.002	NC	NC	***4.94***
1437503_a_at	MGI:1915044	scotin gene	0.014	NC	NC	***3.11***
1455385_at	Sec15l1	SEC15-like 1 (S. cerevisiae)	0.037	-2.07	NC	***2.41***

1419100_at	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	0.007	NC	***25.45***	***85.33***
1416625_at	Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1	0.002	NC	NC	***5.26***
1460700_at	Stat3	signal transducer and activator of transcription 3	0.020	NC	NC	***2.86***
1426587_a_at	Stat3	signal transducer and activator of transcription 3	0.026	NC	NC	***2.72***
1445676_at	Kcnn2	Small conductance calcium-activated potassium channel SK2 (Kcnn2)	0.041	NC	-2.72	-4.42
1449005_at	Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	0.036	-4.08	-3.83	-4.08
1422756_at	Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	0.046	NC	NC	***2.45***
1416576_at	Socs3	suppressor of cytokine signaling 3	0.006	-2.12	NC	***3.87***
1460227_at	Timp1	tissue inhibitor of metalloproteinase 1	0.005	NC	***7.93***	***75.56***
1419606_a_at	Tnnt1	troponin T1, skeletal, slow	0.005	NC	NC	***3.74***
1448412_a_at	Tsc22d4	TSC22 domain family 4	0.049	NC	NC	***2.60***
1450792_at	Tyrobp	TYRO protein tyrosine kinase binding protein	0.029	NC	NC	***5.90***
1423726_at	Vat1	vesicle amine transport protein 1 homolog (T californica)	0.023	NC	NC	***3.03***
1443471_at	Zbtb20	zinc finger and BTB domain containing 20	0.049	NC	-3.04	-6.25

The genes listed were identified using ANOVA as hyperoxia-regulated by two criteria - a greater than 2-fold change and a P value < 0.05. The genes highlighted in red were examined by qPCR to validate the GeneChip® results. These include BCL-3, C3, GFAP, Edn2, Lin7b, Gadd45b. Highlighted in black bold are the increases, while decrease are in normal text. NC= No change.