Supplemental materials:

Figure S1. Distribution of β-catenin protein in O2/air recovered mouse lung.

Representative β-catenin immunohistochemical staining of WT and HO-1KO lungs exposed to 3 days of hyperoxia and recovered in air for 11 days are shown at 10 x magnification. Arrows indicate clusters of cells expressing β-catenin in the HO-1KO lung.

Figure S2. Detection of protein-protein interaction of β-catenin and HO-1.

A. A representative Western blot demonstrating FLAG tagged-full length and truncated HO-1 protein in cytoplasmic and nuclear fractions. **B**. Representative Western blot after immunoprecipitation with FLAG and immunoblotting with anti-β-catenin and HO-1 antibodies. The schematic representation of HO-1 constructs is shown in Figure 6B. V: empty vector, FL: full length HO-1, TR: truncated HO-1 lacking 53 amino acids from the c-terminus. Calnexin was used as a loading control for cytoplasm and Lamin B was used as a loading control for nucleus. Input lanes represent 10% of the cell lysates before immunoprecipitation.

Table. 1. Identification of potential HO-1 binding partner proteins.

HEK293 cells stably transfected with full-length FLAG-HO-1 cDNA were exposed to hypoxia (3% O2 for 24 hours) (19). Nuclear fractions were passed through a FLAG affinity column. Eluates were run on a SDS-PAGE gel and stained with colloidal blue to separate protein bands (Inset). Band numbers were referred to as orders of the appearance

on the colloidal blue stained gel (Inset). These were excised, trpsin digested and subjected to liquid chromoatography/MS/MS analysis to identify potential HO-1 binding candidates. The resulting peptide masses and MS/MS spectra were searched against the nonredundant NCBI data base using the TurboSEQUEST brower. Identified proteins with top scores and amino acid sequence coverage of over 20% are listed.

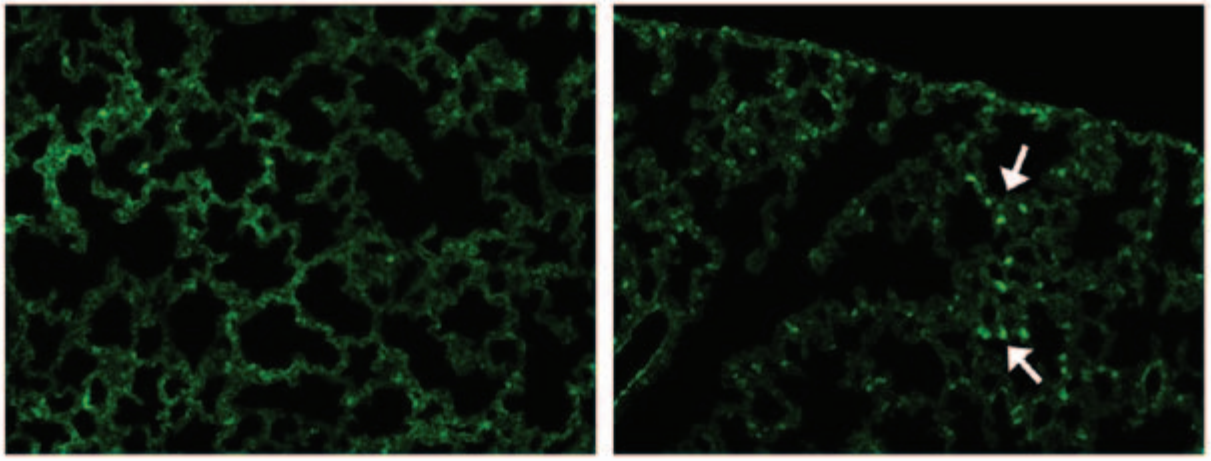
Table. 2. Lung cell cycle mRNA levels in the lungs of WT and HO-1KO neonatal mice exposed to 3 days of hyperoxia.

Total RNA was extracted and three lung RNAs were pooled in each group before the reverse transcription.

Table. 3. Lung cell cycle mRNA levels in the lungs of WT vs HO-1KO mice exposed to hyperoxia and recovered in air (O2) or air controls (Air).

Total RNA was extracted and three lung RNAs were pooled in each group before the reverse transcription.

β-catenin



WT

HO-1KO

Figure S1.

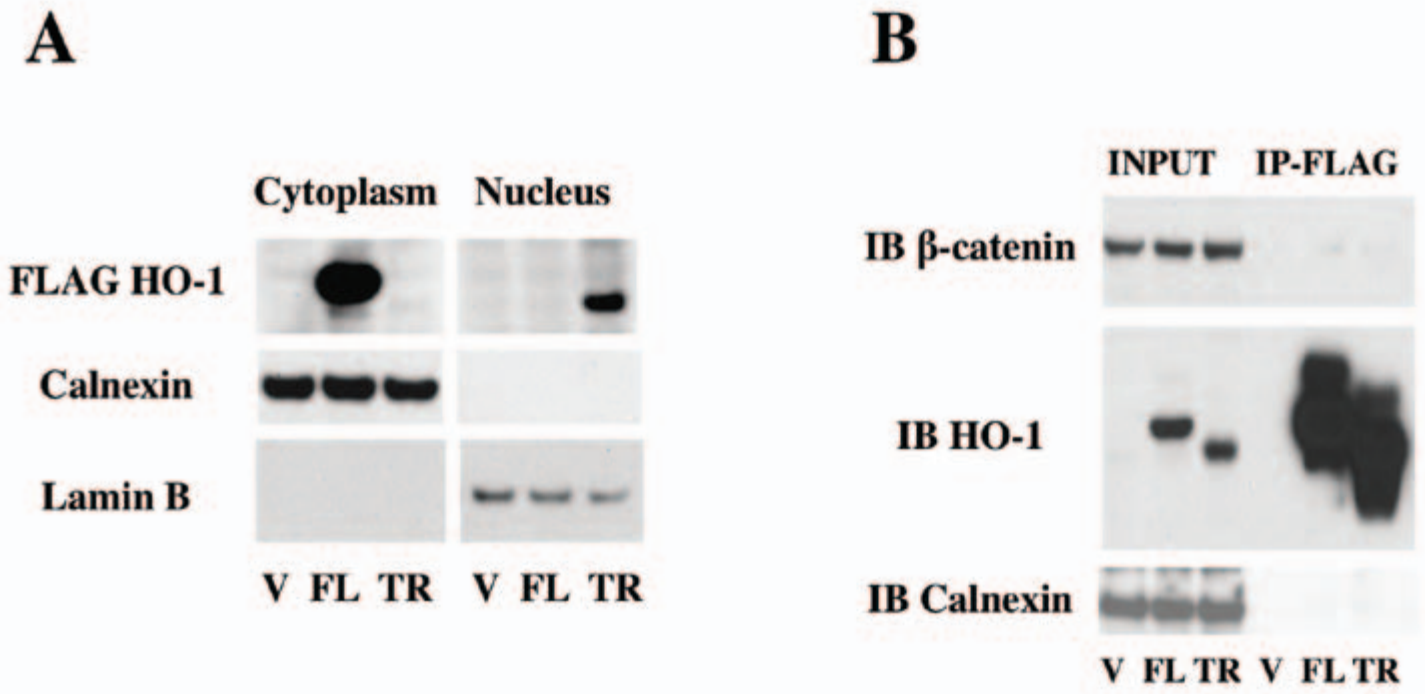

A
Cytoplasm
Nucleus
FLAG HO-1
Calnexin
Lamin B
V FL TR V FL TR
B
INPUT
IP-FLAG
IB β-catenin
IB HO-1
IB Calnexin
V FL TR V FL TR

Figure S2.

Table 1. Proteins identified as potential nuclear HO-1 binding candidates after hypoxic stress.

Protein Name	Symbol	Selected Functions	Reference	Band#
Myb-binding protein 1A	MYBBP1A	Activates or represses transcription via interaction with sequence specific DNA-binding proteins.	gi/71153825	1
DEAH (Asp-Glu-Ala-His) box polypeptide 9	DHX9	Unwinds double-stranded DNA and RNA in a 3' to 5' direction.	gi/100913206	1
Poly (ADP-ribose) polymerase-1	PARP1	Involved in the base excision repair pathway.	gi/130781	2
Nucleolin	NCL	Involved in the synthesis and maturation of ribosomes.	gi/109101818	3
14-3-3 protein major isoform	Bmh1p	Binds proteins and DNA, involved in regulation of exocytosis, vesicle transport, Ras/MAPK signaling, and rapamycin-sensitive signaling.	gi/6321025	3
DNA topoisomerase I	TOP1	Controls and alters the topologic states of DNA during transcription.	gi/11225260	3
SFPQ splicing factor proline/glutamine-rich	SFPQ	Pre-mRNA splicing factor that also acts as a transcriptional co-repressor, and is a constituent of the PERIOD (PER) complex involved in the generation of circadian rhythms.	gi/38014635	4
Heat shock 70 kDa protein-1	HSPA1A	Stabilizes existing proteins against aggregation and mediates the folding of newly translated proteins in the cytosol and in organelles.	gi/462325	5
ATP-dependent DNA helicase II, 70 kDa subunit	XRCC6	Functions as a single stranded DNA-dependent ATP-dependent helicase. Involved in the repair of non-homologous DNA ends such as that required for double-strand break repair, transposition, and V(D)J recombination.	gi/4503841	5

Ribophorin II precursor	**RPN2**	**Catalyzes the transfer of a high mannose oligosaccharide from a lipid linked oligosaccharide chain donor to an asparagine residue within an Asn-X-Ser/Thr consensus motif in nascent polypeptide chains.**	**gi/35493916**	**6**
Heterogeneous nuclear ribonucioprotein L	**hnRNPL**	**Provides the substrate for the processing events that pre-mRNAs undergo before becoming functional, translatable mRNAs in the cytoplasm. Is associated with most nascent transcripts including those of the landmark giant loops of amphibian lampbrush chromosomes. Associates, together with APEX1, to the negative calcium responsive element (nCaRE) B2 of the APEX2 promoter.**	**gi/109124618**	**6**
Non-POU domain, octamer-binding	**NONO**	**Contains highly abundant domains of ribonucleoprotein (RNP) in eukaryotes found in proteins involved in post-transcriptional gene expression processes.**	**gi/114053303**	**7**
Heterogeneous nuclear ribonucioprotein K	**hnRNPK**	**Associates with pre-mRNAs in the nucleus and appears to influence pre-mRNA processing and other aspects of mRNA metabolism and transport. Located in the nucleoplasm and has three repeats of KH domains that binds to RNAs. Thought to have a role during cell cycle progression.**	**gi/109111925**	**8**
Guanine nucleotide-binding protein, beta-2-like 1	**GNB2L1**	**Provides a functional link between PKC signaling and ribosome activation. Is an essential component of an oxygen-independent mechanism for regulating HIF1A stability.**	**gi/109080187**	**9**

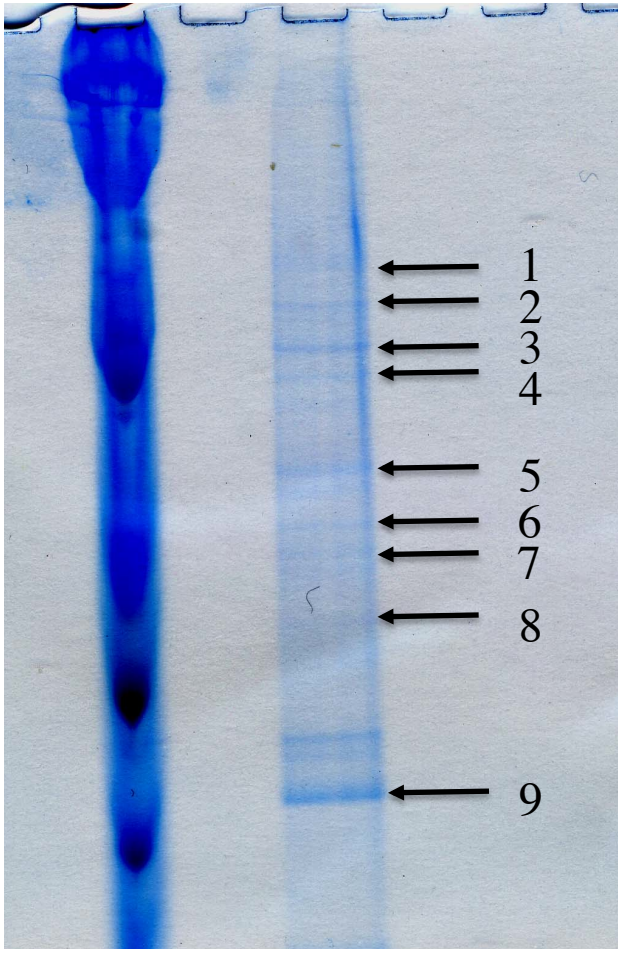


Table 1 inset

Table 2. Comparison of changes in cell cycle genes between hyperoxia and room air exposure in WT or HO-1KO mouse lungs.

		O3WT vs. P3WT						O3HO-1KO vs. P3HO-1KO					
Symbol	Well	AVG ΔC_t (Ct(GOI) - Ave Ct (HKG))		$2^{-\Delta C_t}$		Fold Difference	Fold Up- or Down-Regulation	AVG ΔC_t (Ct(GOI) - Ave Ct (HKG))		$2^{-\Delta C_t}$		Fold Difference	Fold Up- or Down-Regulation
		Test Sample	Control Sample	Test Sample	Control Sample	Test Sample /Control Sample	Test Sample /Control Sample	Test Sample	Control Sample	Test Sample	Control Sample	Test Sample /Control Sample	Test Sample /Control Sample
Abl1	A01	3.75	3.86	7.4E-02	6.9E-02	1.08	1.08	3.00	2.45	1.2E-01	1.8E-01	0.68	-1.46
Ak1	A02	0.65	1.44	6.4E-01	3.7E-01	1.72	1.72	0.83	1.15	5.6E-01	4.5E-01	1.25	1.25
Apbb1	A03	2.26	3.12	2.1E-01	1.2E-01	1.81	1.81	1.70	2.78	3.1E-01	1.5E-01	2.11	**2.11**
Atm	A04	2.20	2.51	2.2E-01	1.8E-01	1.23	1.23	1.67	1.69	3.1E-01	3.1E-01	1.01	1.01
Brca1	A05	3.01	3.03	1.2E-01	1.2E-01	1.02	1.02	2.31	1.79	2.0E-01	2.9E-01	0.70	-1.43
Brca2	A06	3.38	3.31	9.6E-02	1.0E-01	0.95	-1.05	2.69	2.32	1.6E-01	2.0E-01	0.77	-1.30
Camk2a	A07	3.53	4.67	8.6E-02	3.9E-02	2.20	**2.20**	2.78	2.62	1.5E-01	1.6E-01	0.90	-1.12
Camk2b	A08	4.15	6.13	5.6E-02	1.4E-02	3.95	**3.95**	3.48	2.79	9.0E-02	1.4E-01	0.62	-1.61
Casp3	A09	1.36	0.67	3.9E-01	6.3E-01	0.62	-1.62	0.77	0.80	5.9E-01	5.7E-01	1.02	1.02
Ccna1	A10	4.37	4.81	4.8E-02	3.6E-02	1.35	1.35	3.57	2.84	8.4E-02	1.4E-01	0.60	-1.66
Ccna2	A11	1.26	-0.21	4.2E-01	1.2E+00	0.36	**-2.77**	1.29	0.14	4.1E-01	9.1E-01	0.45	**-2.22**
Ccnb1	A12	2.72	1.30	1.5E-01	4.1E-01	0.37	**-2.67**	2.38	1.32	1.9E-01	4.0E-01	0.48	**-2.07**
Ccnb2	B01	2.98	0.90	1.3E-01	5.3E-01	0.24	**-4.21**	3.14	1.88	1.1E-01	2.7E-01	0.42	**-2.39**
Ccnc	B02	3.60	3.18	8.2E-02	1.1E-01	0.75	-1.34	3.20	2.89	1.1E-01	1.3E-01	0.80	-1.24
Ccnd1	B03	-0.29	-0.15	1.2E+00	1.1E+00	1.10	1.10	-0.50	0.43	1.4E+00	7.4E-01	1.91	1.91
Ccne1	B04	4.52	4.51	4.4E-02	4.4E-02	0.99	-1.01	3.81	3.09	7.1E-02	1.2E-01	0.61	-1.65
Ccnf	B05	4.63	5.55	4.0E-02	2.1E-02	1.89	1.89	3.85	3.46	7.0E-02	9.1E-02	0.77	-1.30
Cdc25a	B06	2.17	2.00	2.2E-01	2.5E-01	0.88	-1.13	1.91	1.84	2.7E-01	2.8E-01	0.95	-1.05
Cdk2	B07	-0.17	-0.44	1.1E+00	1.4E+00	0.83	-1.21	-0.27	-0.10	1.2E+00	1.1E+00	1.13	1.13
Cdk4	B08	3.75	3.53	7.5E-02	8.7E-02	0.86	-1.16	2.79	2.61	1.4E-01	1.6E-01	0.88	-1.13
Cdk5rap1	B09	2.82	3.84	1.4E-01	7.0E-02	2.04	**2.04**	2.61	2.50	1.6E-01	1.8E-01	0.92	-1.08
Cdkn1a	B10	-2.35	0.54	5.1E+00	6.9E-01	7.40	**7.40**	-2.68	-0.27	6.4E+00	1.2E+00	5.33	**5.33**
Cdkn1b	B11	2.95	3.05	1.3E-01	1.2E-01	1.07	1.07	1.97	1.98	2.5E-01	2.5E-01	1.01	1.01
Cdkn2a	B12	4.91	6.99	3.3E-02	7.9E-03	4.24	**4.24**	4.62	3.89	4.1E-02	6.8E-02	0.60	-1.66
Chek1	C01	3.68	3.22	7.8E-02	1.1E-01	0.73	-1.37	2.77	2.28	1.5E-01	2.1E-01	0.71	-1.41
Cks1b	C02	0.99	0.23	5.0E-01	8.6E-01	0.59	-1.69	1.04	0.63	4.9E-01	6.4E-01	0.76	-1.32
Ddit3	C03	0.50	2.04	7.1E-01	2.4E-01	2.90	**2.90**	-0.13	1.49	1.1E+00	3.6E-01	3.08	**3.08**
Dnaic2	C04	0.69	0.71	6.2E-01	6.1E-01	1.01	1.01	0.43	0.68	7.4E-01	6.2E-01	1.19	1.19
Dst	C05	0.86	0.55	5.5E-01	6.8E-01	0.81	-1.24	0.24	0.51	8.4E-01	7.0E-01	1.20	1.20
E2f1	C06	2.96	2.48	1.3E-01	1.8E-01	0.71	-1.40	2.60	2.28	1.7E-01	2.1E-01	0.80	-1.24
E2f2	C07	4.22	6.16	5.4E-02	1.4E-02	3.82	**3.82**	3.28	3.14	1.0E-01	1.1E-01	0.91	-1.10
E2f3	C08	3.16	2.71	1.1E-01	1.5E-01	0.73	-1.36	2.69	2.59	1.5E-01	1.7E-01	0.93	-1.07
E2f4	C09	0.49	0.61	7.1E-01	6.6E-01	1.08	1.08	-0.08	0.53	1.1E+00	6.9E-01	1.53	1.53
Gadd45a	C10	0.70	1.38	6.2E-01	3.9E-01	1.60	1.60	-0.02	0.82	1.0E+00	5.7E-01	1.79	1.79
Gpr132	C11	4.48	4.80	4.5E-02	3.6E-02	1.25	1.25	3.30	2.63	1.0E-01	1.6E-01	0.63	-1.60
Hus1	C12	2.94	2.92	1.3E-01	1.3E-01	0.99	-1.01	4.07	2.76	5.9E-02	1.5E-01	0.40	**-2.49**
Inha	D01	3.35	3.82	9.8E-02	7.1E-02	1.39	1.39	2.58	2.30	1.7E-01	2.0E-01	0.83	-1.21
Itgb1	D02	-2.95	-2.78	7.7E+00	6.9E+00	1.12	1.12	-3.45	-2.45	1.1E+01	5.5E+00	1.99	1.99
Macf1	D03	-2.25	-2.43	4.8E+00	5.4E+00	0.88	-1.13	-2.90	-2.29	7.5E+00	4.9E+00	1.53	1.53
Mad2l1	D04	2.79	2.24	1.4E-01	2.1E-01	0.69	-1.46	2.12	1.67	2.3E-01	3.1E-01	0.73	-1.36
Mcm2	D05	1.12	0.36	4.6E-01	7.8E-01	0.59	-1.70	0.96	0.60	5.1E-01	6.6E-01	0.78	-1.29
Mcm3	D06	0.77	-0.09	5.9E-01	1.1E+00	0.55	-1.81	0.72	0.23	6.1E-01	8.6E-01	0.71	-1.41
Mcm4	D07	0.82	-0.06	5.6E-01	1.0E+00	0.54	-1.85	0.74	0.30	6.0E-01	8.1E-01	0.74	-1.36
Mdm2	D08	-1.30	0.14	2.5E+00	9.1E-01	2.70	**2.70**	-1.37	0.14	2.6E+00	9.1E-01	2.85	**2.85**
Mki67	D09	0.37	-1.16	7.7E-01	2.2E+00	0.35	**-2.89**	0.44	-0.75	7.4E-01	1.7E+00	0.44	**-2.28**
Mre11a	D10	3.13	3.48	1.1E-01	8.9E-02	1.28	1.28	2.37	2.14	1.9E-01	2.3E-01	0.86	-1.17
Msh2	D11	1.55	1.22	3.4E-01	4.3E-01	0.79	-1.26	1.46	1.61	3.6E-01	3.3E-01	1.11	1.11
Mtbp	D12	2.75	2.88	1.5E-01	1.4E-01	1.10	1.10	2.12	1.87	2.3E-01	2.7E-01	0.84	-1.19
Myb	E01	3.13	3.29	1.1E-01	1.0E-01	1.12	1.12	2.55	2.60	1.7E-01	1.6E-01	1.04	1.04
Nek2	E02	5.19	4.00	2.7E-02	6.3E-02	0.44	**-2.28**	4.54	3.57	4.3E-02	8.4E-02	0.51	-1.96
Nfatc1	E03	1.64	1.55	3.2E-01	3.4E-01	0.94	-1.06	1.01	1.13	5.0E-01	4.6E-01	1.08	1.08
Notch2	E04	2.17	2.39	2.2E-01	1.9E-01	1.17	1.17	1.21	1.55	4.3E-01	3.4E-01	1.27	1.27
Npm2	E05	4.58	6.27	4.2E-02	1.3E-02	3.24	**3.24**	3.54	3.18	8.6E-02	1.1E-01	0.78	-1.28
Pcna	E06	-1.01	-1.58	2.0E+00	3.0E+00	0.68	-1.48	-1.07	-1.13	2.1E+00	2.2E+00	0.96	-1.05
Pes1	E07	0.00	0.34	1.0E+00	7.9E-01	1.26	1.26	-0.32	0.26	1.2E+00	8.3E-01	1.49	1.49
Pkd1	E08	0.41	0.40	7.5E-01	7.6E-01	0.99	-1.01	-0.35	0.42	1.3E+00	7.4E-01	1.72	1.72
Pmp22	E09	-2.65	-2.72	6.3E+00	6.6E+00	0.95	-1.05	-2.67	-2.22	6.4E+00	4.6E+00	1.37	1.37
Ppm1d	E10	1.46	1.47	3.6E-01	3.6E-01	1.00	1.00	1.00	1.24	5.0E-01	4.2E-01	1.17	1.17
Ppp2r3a	E11	3.99	3.99	6.3E-02	6.3E-02	1.00	-1.00	3.46	3.56	9.1E-02	8.5E-02	1.07	1.07
Ppp3ca	E12	-1.28	-0.71	2.4E+00	1.6E+00	1.49	1.49	-1.49	-0.44	2.8E+00	1.4E+00	2.07	**2.07**
Prm1	F01	4.65	6.61	4.0E-02	1.0E-02	3.90	**3.90**	3.67	3.29	7.9E-02	1.0E-01	0.77	-1.30
Rad17	F02	1.79	1.69	2.9E-01	3.1E-01	0.93	-1.07	1.56	2.10	3.4E-01	2.3E-01	1.45	1.45
Rad21	F03	-0.44	-1.22	1.4E+00	2.3E+00	0.58	-1.72	-0.75	-0.63	1.7E+00	1.5E+00	1.09	1.09
Rad51	F04	4.77	4.06	3.7E-02	6.0E-02	0.61	-1.63	4.57	4.45	4.2E-02	4.6E-02	0.92	-1.09
Rad9	F05	2.71	3.00	1.5E-01	1.2E-01	1.23	1.23	2.41	2.55	1.9E-01	1.7E-01	1.10	1.10
Ran	F06	-3.63	-3.60	1.2E+01	1.2E+01	1.02	1.02	-3.49	-3.16	1.1E+01	8.9E+00	1.26	1.26
Rbl1	F07	2.53	2.35	1.7E-01	2.0E-01	0.88	-1.14	1.86	1.65	2.8E-01	3.2E-01	0.87	-1.16
Rbl2	F08	1.70	1.24	3.1E-01	4.2E-01	0.73	-1.38	1.01	1.45	5.0E-01	3.7E-01	1.35	1.35
Sesn2	F09	3.09	4.37	1.2E-01	4.8E-02	2.43	**2.43**	2.53	3.28	1.7E-01	1.0E-01	1.69	1.69
Sfn	F10	1.11	3.36	4.6E-01	9.8E-02	4.75	**4.75**	0.09	1.60	9.4E-01	3.3E-01	2.83	**2.83**
Shc1	F11	0.05	0.28	9.7E-01	8.3E-01	1.17	1.17	-0.48	0.03	1.4E+00	9.8E-01	1.43	1.43
Skp2	F12	4.44	4.07	4.6E-02	6.0E-02	0.77	-1.30	4.06	3.63	6.0E-02	8.1E-02	0.74	-1.35
Sfn1	G01	3.68	4.59	7.8E-02	4.1E-02	1.88	1.88	2.28	2.25	2.1E-01	2.1E-01	0.98	-1.02
Smc1a	G02	1.15	0.69	4.5E-01	6.2E-01	0.73	-1.37	0.77	0.86	5.9E-01	5.5E-01	1.07	1.07
Stag1	G03	0.90	0.87	5.4E-01	5.5E-01	0.98	-1.02	0.47	0.97	7.2E-01	5.1E-01	1.42	1.42
Sumo1	G04	-0.96	-0.83	1.9E+00	1.8E+00	1.09	1.09	-1.07	-0.68	2.1E+00	1.6E+00	1.31	1.31
Taf10	G05	-0.67	-0.39	1.6E+00	1.3E+00	1.22	1.22	-0.86	-0.23	1.8E+00	1.2E+00	1.55	1.55
Terf1	G06	3.06	2.86	1.2E-01	1.4E-01	0.87	-1.15	2.34	2.42	2.0E-01	1.9E-01	1.06	1.06
Tfdp1	G07	-0.21	-0.25	1.2E+00	1.2E+00	0.98	-1.03	-0.36	-0.05	1.3E+00	1.0E+00	1.24	1.24
Psmg2	G08	0.92	1.18	5.3E-01	4.4E-01	1.20	1.20	0.87	1.34	5.5E-01	4.0E-01	1.38	1.38
Trp53	G09	1.37	0.10	3.9E-01	9.3E-01	0.41	**-2.41**	-0.18	0.25	1.1E+00	8.4E-01	1.35	1.35
Trp63	G10	4.90	8.34	3.4E-02	3.1E-03	10.85	**10.85**	4.03	3.45	6.1E-02	9.1E-02	0.67	-1.49
Tsg101	G11	-0.80	-0.61	1.7E+00	1.5E+00	1.14	1.14	-1.02	-0.43	2.0E+00	1.3E+00	1.50	1.50
Wee1	G12	3.80	3.89	7.2E-02	6.8E-02	1.06	1.06	3.05	3.40	1.2E-01	9.5E-02	1.27	1.27
Gusb	H01	0.00	0.00	1.0E+00	1.0E+00	1.00	-1.00	0.00	0.00	1.0E+00	1.0E+00	1.00	-1.00
Hprt1	H02	-1.01	-0.75	2.0E+00	1.7E+00	1.20	1.20	-1.10	-0.53	2.1E+00	1.4E+00	1.48	1.48
Hsp90ab1	H03	-3.65	-3.64	1.3E+01	1.2E+01	1.01	1.01	-3.62	-3.13	1.2E+01	8.8E+00	1.40	1.40
Gapdh	H04	-3.06	-2.24	8.3E+00	4.7E+00	1.76	1.76	-3.92	-4.00	1.5E+01	1.6E+01	0.94	-1.06
Actb	H05	-5.64	-5.44	5.0E+01	4.4E+01	1.14	1.14	-6.21	-5.47	7.4E+01	4.4E+01	1.67	1.67

O3WT: WT neonatal mice exposed to hyperoxia for 3 days; P3WT: WT neonatal mice kept in room air for 3 days; O3HO-1KO: HO-1KO neonatal mice exposed to hyperoxia for 3 days; P3HO-1KO: HO-1KO neonatal mice kept in room air for 3 days. Genes over two fold increases are indicated in red, genes over two fold decreases are indicated in blue.

Table 3. Lung cell cycle mRNA levels in the lungs of WT and HO-1KO mice exposed to hyperoxia and recovered in air (O2) vs air controls (Air).

		O2 WT vs. Air WT						O2 HO-1KO vs. Air HO-1KO					
Symbol	Well	AVG ΔC_t (Ct(GOI) - Ave Ct (HKG))		$2^{-\Delta C_t}$		Fold Difference	Fold Up- or Down-Regulation	AVG ΔC_t (Ct(GOI) - Ave Ct (HKG))		$2^{-\Delta C_t}$		Fold Difference	Fold Up- or Down-Regulation
		Test Sample	Control Sample	Test Sample	Control Sample	Test Sample /Control Sample	Test Sample /Control Sample	Test Sample	Control Sample	Test Sample	Control Sample	Test Sample /Control Sample	Test Sample /Control Sample
Abl1	A01	3.13	0.87	1.1E-01	5.5E-01	0.21	-4.79	-5.56	2.10	4.7E+01	2.3E-01	201.69	201.69
Ak1	A02	1.68	0.55	3.1E-01	6.8E-01	0.46	-2.19	-6.26	1.07	7.6E+01	4.8E-01	160.01	160.01
Apbb1	A03	2.61	1.35	1.6E-01	3.9E-01	0.42	-2.40	-5.42	2.00	4.3E+01	2.5E-01	170.54	170.54
Atm	A04	2.29	1.06	2.1E-01	4.8E-01	0.43	-2.33	-3.11	1.91	8.7E+00	2.7E-01	32.54	32.54
Brca1	A05	3.09	1.30	1.2E-01	4.1E-01	0.29	-3.45	-3.26	1.96	9.5E+00	2.6E-01	37.17	37.17
Brca2	A06	3.50	1.90	8.9E-02	2.7E-01	0.33	-3.02	-3.26	2.35	9.6E+00	2.0E-01	49.04	49.04
Camk2a	A07	3.62	1.71	8.1E-02	3.1E-01	0.27	-3.76	2.97	1.98	1.3E-01	2.5E-01	0.50	-1.98
Camk2b	A08	3.68	1.47	7.8E-02	3.6E-01	0.22	-4.65	-5.56	2.02	4.7E+01	2.5E-01	191.08	191.08
Casp3	A09	0.95	1.06	5.2E-01	4.8E-01	1.08	1.08	-3.64	1.09	1.3E+01	4.7E-01	26.54	26.54
Ccna1	A10	3.51	1.33	8.8E-02	4.0E-01	0.22	-4.53	-5.44	1.61	4.4E+01	3.3E-01	132.79	132.79
Ccna2	A11	1.32	0.92	4.0E-01	5.3E-01	0.76	-1.31	-2.75	0.80	6.7E+00	5.8E-01	11.66	11.66
Ccnb1	A12	2.65	0.96	1.6E-01	5.1E-01	0.31	-3.23	-1.33	1.54	2.5E+00	3.4E-01	7.35	7.35
Ccnb2	B01	3.31	2.17	1.0E-01	2.2E-01	0.46	-2.20	1.13	3.34	4.6E-01	9.9E-02	4.64	4.64
Ccnc	B02	3.39	1.82	9.5E-02	2.8E-01	0.34	-2.98	-1.99	2.71	4.0E+00	1.5E-01	26.01	26.01
Ccnd1	B03	1.13	0.91	4.6E-01	5.3E-01	0.86	-1.16	3.90	1.36	6.7E-02	3.9E-01	0.17	-5.82
Ccne1	B04	4.60	2.13	4.1E-02	2.3E-01	0.18	-5.55	-0.36	2.76	1.3E+00	1.5E-01	8.70	8.70
Ccnf	B05	4.29	2.09	5.1E-02	2.3E-01	0.22	-4.59	0.77	2.71	5.9E-01	1.5E-01	3.82	3.82
Cdc25a	B06	1.95	1.62	2.6E-01	3.3E-01	0.79	-1.26	-1.22	1.71	2.3E+00	3.1E-01	7.62	7.62
Cdk2	B07	0.93	0.82	5.2E-01	5.7E-01	0.93	-1.08	2.17	0.65	2.2E-01	6.4E-01	0.35	-2.87
Cdk4	B08	3.41	1.24	9.4E-02	4.2E-01	0.22	-4.51	-2.14	1.84	4.4E+00	2.8E-01	15.71	15.71
Cdk5rap1	B09	3.71	1.82	7.6E-02	2.8E-01	0.27	-3.70	-2.75	2.01	6.7E+00	2.5E-01	27.17	27.17
Cdkn1a	B10	0.49	0.38	7.1E-01	7.7E-01	0.93	-1.08	-1.19	0.47	2.3E+00	7.2E-01	3.17	3.17
Cdkn1b	B11	3.63	1.43	8.1E-02	3.7E-01	0.22	-4.58	0.53	2.08	6.9E-01	2.4E-01	2.93	2.93
Cdkn2a	B12	3.98	1.78	6.3E-02	2.9E-01	0.22	-4.59	1.83	2.44	2.8E-01	1.8E-01	1.53	1.53
Chek1	C01	3.64	1.33	8.0E-02	4.0E-01	0.20	-4.95	3.35	2.35	9.8E-02	2.0E-01	0.50	-1.99
Cks1b	C02	2.66	1.22	1.6E-01	4.3E-01	0.37	-2.72	-0.22	1.93	1.2E+00	2.6E-01	4.44	4.44
Ddit3	C03	2.39	0.84	1.9E-01	5.6E-01	0.34	-2.93	1.96	1.56	2.6E-01	3.4E-01	0.76	-1.31
Dnajc2	C04	0.32	0.00	8.0E-01	1.0E+00	0.80	-1.24	2.79	0.31	1.4E-01	8.1E-01	0.18	-5.59
Dst	C05	1.55	0.82	3.4E-01	5.7E-01	0.60	-1.66	-0.22	1.09	1.2E+00	4.7E-01	2.47	2.47
E2f1	C06	3.25	2.20	1.0E-01	2.2E-01	0.48	-2.07	1.22	2.39	4.3E-01	1.9E-01	2.25	2.25
E2f2	C07	4.73	3.22	3.8E-02	1.1E-01	0.35	-2.85	-4.75	3.58	2.7E+01	8.4E-02	320.02	320.02
E2f3	C08	3.85	2.30	6.9E-02	2.0E-01	0.34	-2.92	1.59	2.84	3.3E-01	1.4E-01	2.38	2.38
E2f4	C09	1.78	1.06	2.9E-01	4.8E-01	0.61	-1.65	2.87	1.08	1.4E-01	4.7E-01	0.29	-3.46
Gadd45a	C10	0.75	0.46	6.0E-01	7.3E-01	0.82	-1.22	-3.26	0.27	9.6E+00	8.3E-01	11.54	11.54
Gpr132	C11	3.40	1.97	9.5E-02	2.6E-01	0.37	-2.70	-0.12	2.13	1.1E+00	2.3E-01	4.76	4.76
Hus1	C12	1.90	1.08	2.7E-01	4.7E-01	0.57	-1.76	3.89	1.33	6.7E-02	4.0E-01	0.17	-5.92
Inha	D01	3.51	1.33	8.8E-02	4.0E-01	0.22	-4.55	-2.05	2.00	4.1E+00	2.5E-01	16.54	16.54
Itgb1	D02	-1.97	-1.61	3.9E+00	3.0E+00	1.29	1.29	3.21	-1.70	1.1E-01	3.2E+00	0.03	-30.00
Macf1	D03	-1.21	-0.55	2.3E+00	1.5E+00	1.58	1.58	-0.05	-0.58	1.0E+00	1.5E+00	0.69	-1.44
Mad2l1	D04	2.26	0.76	2.1E-01	5.9E-01	0.35	-2.82	-4.90	1.29	3.0E+01	4.1E-01	73.06	73.06
Mcm2	D05	2.00	1.29	2.5E-01	4.1E-01	0.61	-1.63	-0.31	1.42	1.2E+00	3.7E-01	3.31	3.31
Mcm3	D06	1.03	1.14	4.9E-01	4.6E-01	1.08	1.08	-1.46	1.03	2.8E+00	4.9E-01	5.64	5.64
Mcm4	D07	0.59	0.89	6.6E-01	5.4E-01	1.23	1.23	-1.66	0.68	3.2E+00	6.2E-01	5.07	5.07
Mdm2	D08	1.06	0.85	4.8E-01	5.5E-01	0.87	-1.15	3.68	1.01	7.8E-02	5.0E-01	0.16	-6.36
Mki67	D09	0.04	-0.30	9.7E-01	1.2E+00	0.79	-1.26	1.73	-0.45	3.0E-01	1.4E+00	0.22	-4.55
Mre11a	D10	3.61	1.58	8.2E-02	3.4E-01	0.24	-4.10	0.41	1.93	7.5E-01	2.6E-01	2.85	2.85
Msh2	D11	0.64	0.56	6.4E-01	6.8E-01	0.95	-1.05	2.78	0.61	1.5E-01	6.5E-01	0.22	-4.48
Mtbp	D12	2.97	1.03	1.3E-01	4.9E-01	0.26	-3.84	1.65	1.61	3.2E-01	3.3E-01	0.97	-1.03
Myb	E01	3.36	1.36	9.8E-02	3.9E-01	0.25	-4.00	1.91	2.10	2.7E-01	2.3E-01	1.14	1.14
Nek2	E02	4.66	2.63	4.0E-02	1.6E-01	0.25	-4.07	-0.51	3.50	1.4E+00	8.8E-02	16.20	16.20
Nfatc1	E03	1.82	0.86	2.8E-01	5.5E-01	0.51	-1.94	2.10	1.15	2.3E-01	4.5E-01	0.52	-1.93
Notch2	E04	3.46	1.78	9.1E-02	2.9E-01	0.31	-3.20	-2.67	2.16	6.3E+00	2.2E-01	28.38	28.38
Npm2	E05	3.88	2.21	6.8E-02	2.2E-01	0.31	-3.18	-0.91	2.46	1.9E+00	1.8E-01	10.35	10.35
Pcna	E06	0.65	0.71	6.4E-01	6.1E-01	1.05	1.05	-1.23	0.39	2.3E+00	7.7E-01	3.07	3.07
Pes1	E07	0.25	-0.32	8.4E-01	1.2E+00	0.67	-1.49	-0.59	-0.23	1.5E+00	1.2E+00	1.28	1.28
Pkd1	E08	0.93	1.04	5.3E-01	4.9E-01	1.08	1.08	-0.14	0.84	1.1E+00	5.6E-01	1.96	1.96
Pmp22	E09	-3.40	-3.09	1.1E+01	8.5E+00	1.23	1.23	0.61	-3.16	6.6E-01	8.9E+00	0.07	-13.62
Ppm1d	E10	1.72	1.23	3.0E-01	4.3E-01	0.71	-1.40	-2.82	1.37	7.1E+00	3.9E-01	18.30	18.30
Ppp2r3a	E11	4.63	2.82	4.0E-02	1.4E-01	0.28	-3.51	-4.05	3.08	1.7E+01	1.2E-01	140.36	140.36
Ppp3ca	E12	-0.43	-0.52	1.4E+00	1.4E+00	0.94	-1.06	2.66	-0.50	1.6E-01	1.4E+00	0.11	-8.95
Prm1	F01	3.99	1.53	6.3E-02	3.5E-01	0.18	-5.50	0.97	2.22	5.1E-01	2.2E-01	2.37	2.37
Rad17	F02	1.31	0.74	4.0E-01	6.0E-01	0.67	-1.48	1.86	1.28	2.8E-01	4.1E-01	0.67	-1.49
Rad21	F03	-0.93	-0.38	1.9E+00	1.3E+00	1.46	1.46	-0.82	-0.57	1.8E+00	1.5E+00	1.18	1.18
Rad51	F04	6.06	4.37	1.5E-02	4.8E-02	0.31	-3.22	0.11	4.85	9.2E-01	3.5E-02	26.69	26.69
Rad9	F05	3.05	2.14	1.2E-01	2.3E-01	0.53	-1.89	2.12	2.30	2.3E-01	2.0E-01	1.13	1.13
Ran	F06	-2.53	-2.28	5.8E+00	4.9E+00	1.18	1.18	3.84	-2.79	7.0E-02	6.9E+00	0.01	-99.18
Rbl1	F07	2.90	1.47	1.3E-01	3.6E-01	0.37	-2.70	1.67	1.72	3.1E-01	3.0E-01	1.04	1.04
Rbl2	F08	1.67	1.62	3.1E-01	3.3E-01	0.96	-1.04	0.31	1.52	8.1E-01	3.5E-01	2.33	2.33
Sesn2	F09	4.47	2.91	4.5E-02	1.3E-01	0.34	-2.95	-1.24	2.89	2.4E+00	1.3E-01	17.48	17.48
Sfn	F10	2.78	0.98	1.5E-01	5.1E-01	0.29	-3.48	1.31	1.15	4.0E-01	4.5E-01	0.89	-1.12
Shc1	F11	1.37	0.43	3.9E-01	7.4E-01	0.52	-1.91	0.88	0.80	5.4E-01	5.7E-01	0.95	-1.05
Skp2	F12	4.48	2.79	4.5E-02	1.4E-01	0.31	-3.22	2.33	-12.41	2.0E-01	5.5E+03	0.00	-27345.20
Slfn1	G01	3.58	1.27	8.3E-02	4.1E-01	0.20	-4.97	3.74	1.87	7.5E-02	2.7E-01	0.27	-3.66
Smc1a	G02	2.47	1.61	1.8E-01	3.3E-01	0.55	-1.82	2.38	1.88	1.9E-01	2.7E-01	0.71	-1.41
Stag1	G03	0.88	0.85	5.4E-01	5.6E-01	0.98	-1.02	-1.30	0.95	2.5E+00	5.2E-01	4.77	4.77
Sumo1	G04	-0.29	-0.19	1.2E+00	1.1E+00	1.07	1.07	2.96	-0.56	1.3E-01	1.5E+00	0.09	-11.46
Taf10	G05	-0.09	0.31	1.1E+00	8.0E-01	1.33	1.33	2.28	-0.16	2.1E-01	1.1E+00	0.18	-5.41
Terf1	G06	3.29	2.64	1.0E-01	1.6E-01	0.64	-1.56	-0.40	2.33	1.3E+00	2.0E-01	6.60	6.60
Tfdp1	G07	0.90	0.88	5.3E-01	5.4E-01	0.98	-1.02	0.92	0.16	5.3E-01	8.9E-01	0.59	-1.69
Psmg2	G08	2.16	1.65	2.2E-01	3.2E-01	0.70	-1.42	3.65	1.29	8.0E-02	4.1E-01	0.19	-5.13
Trp53	G09	1.68	1.28	3.1E-01	4.1E-01	0.76	-1.32	3.77	0.98	7.3E-02	5.1E-01	0.14	-6.94
Trp63	G10	4.23	2.17	5.3E-02	2.2E-01	0.24	-4.17	-0.34	2.16	1.3E+00	2.2E-01	5.64	5.64
Tsg101	G11	-0.40	-0.07	1.3E+00	1.0E+00	1.26	1.26	0.92	-0.58	5.3E-01	1.5E+00	0.35	-2.84
Wee1	G12	4.79	2.88	3.6E-02	1.4E-01	0.27	-3.76	1.39	3.32	3.8E-01	1.0E-01	3.82	3.82
Gusb	H01	0.00	0.00	1.0E+00	1.0E+00	1.00	-1.00	0.00	0.00	1.0E+00	1.0E+00	1.00	-1.00
Hprt1	H02	-1.04	-0.51	2.1E+00	1.4E+00	1.44	1.44	-1.09	-0.61	2.1E+00	1.5E+00	1.39	1.39
Hsp90ab1	H03	-4.00	-3.09	1.6E+01	8.5E+00	1.88	1.88	2.74	-3.50	1.5E-01	1.1E+01	0.01	-75.27
Gapdh	H04	-2.94	-4.65	7.7E+00	2.5E+01	0.31	-3.26	-0.40	-4.42	1.3E+00	2.1E+01	0.06	-16.30
Actb	H05	-3.10	-2.23	8.6E+00	4.7E+00	1.83	1.83	3.44	-3.34	9.2E-02	1.0E+01	0.01	-109.74

O2WT: Wild type neonatal mice exposed to hyperoxia for 3 days and recovered in room air for 11 days; Air WT: Wild type neonatal mice kept in room air for 14 days; O2 HO-1KO: HO-1KO neonatal mice exposed to hyperoxia for 3 days and recovered in room air for 11 days; Air HO-1KO: HO-1KO neonatal mice kept in room air for up to 14 days. Genes with greater than a two fold increase are indicated in red; genes with greater than a two fold decrease are indicated in blue. The Skp2 PCR cycle number in the air HO-1KO sample was an outlier in the initial data quality analysis therefore it was not included in subsequent analysis.