

p (Genotype)	p (Exposure)	[CH/HeN, Air][raw]	[CH/HeN, O2][raw]	[Gr-KO, Air][raw]	[Gr-KO, O2][raw]	RefSeq Transcript ID	p (Genotype-Exposure)	FC in WT (Air-O2)	FC in KO (Air-O2)	FD (WT O2 vs KO O2)	Gene Symbol	Gene Title	Gene Ontology Biological Process
0.2903104	0.025988186	318.0659	331.1289	335.27103	298.3071	NM_001100591//NM_0007281573	1.04	-1.12	-1.11		<i>Rch2</i>	ring finger and CCHC-type zinc finger domains 2	0000209 // protein polyubiquitination // not recorded//0001782 // B cell homeostasis // inferred from genetic interaction//0009791 // post-er
0.07800728	0.8453955	16.340852	17.858604	17.322233	16.055773	NM_023135	1.07	-1.08	-1.11		<i>Sulf1zf</i>	sulfotransferase family 1E, member 1	0007565 // female pregnancy // inferred from mutant phenotype//0006210 // estrogen metabolic process // inferred from direct assay//00086
0.47712605	0.08072522	798.17804	827.0046	824.5663	742.5771	NM_027098//NM_00548005864975	1.04	-1.11	-1.11		<i>Mpi130</i>	mitochondrial ribosomal protein L30	
0.33910736	0.8743928	23.702065	26.93612	26.731722	24.161081	NM_183030//NR_02808.0001805932	1.14	-1.11	-1.11		<i>Smi102a</i>	small integral membrane protein 10 like 2A	
0.037662134	0.3203201	218.51404	234.4993	226.06665	210.28682	NM_025578	1.07	-1.07	-1.12		<i>Mps25</i>	mitochondrial ribosomal protein S25	0032543 // mitochondrial translation // inferred by curator
0.07695606	0.97664875	5885.496	6235.394	6097.597	5551.951	NM_011653	1.06	-1.10	-1.12		<i>Tuba1a</i>	tubulin, alpha 1A	0007017 // microtubule-based process // inferred from electronic annotation//0008152 // metabolic process // inferred from electronic annotation
0.11579136	0.37080194	13.883798	14.869218	14.763236	13.233142	NM_170597//NM_00645.0001202977	1.11	-1.12	-1.12		<i>Cret2</i>	cellular repressor of E1A-stimulated genes 2	005114 // oxidation-reduction process // inferred from electronic annotation
0.001559537	7.75E-04	33.41498	39.426548	51.94689	35.05513	NM_009162	1.18	-1.48	-1.12		<i>Scg5</i>	secretogranin V	0006810 // transport // inferred from electronic annotation//0006886 // intracellular protein transport // inferred from direct assay//0007218
0.0675284	0.02617646	259.37936	280.8956	406.44058	248.93655	NM_001099774	1.08	-1.63	-1.13		<i>Krtap17-1</i>	keratin associated protein 17-1	
0.7924486	0.6431704	120.54288	143.55479	147.13474	127.162674	NM_016866//NM_00648.0002123031	1.19	-1.16	-1.13		<i>Skp39</i>	serine/threonine kinase 39	0001933 // negative regulation of protein phosphorylation // inferred from direct assay//0006468 // protein phosphorylation // not recorded//
0.5230976	0.005739873	309.65298	326.20502	338.36047	288.9452	NM_026844//NM_00551.00070E-04	1.05	-1.17	-1.13		<i>Cm2</i>	CD4 assembly mitochondrial protein 2	
0.46572787	0.43188995	2822.9985	2983.1397	2988.9175	2642.2893	NM_011327//NM_01124.000789655	1.06	-1.13	-1.13		<i>Scp2</i>	sterol carrier protein 2, liver	0006637 // acyl-CoA metabolic process // traceable author statement//0006694 // steroid biosynthetic process // not recorded//0006701 // p
0.9860367	0.44730213	53.07649	62.51307	65.57573	55.15674	NM_016662//NR_87349.000125412	1.18	-1.19	-1.13		<i>Mod3</i>	Max dimerization protein 3	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inf
0.005637219	0.08278733	57.3333	66.9638	60.187172	59.00381	NM_001113478//NM_0003351502	1.17	-1.02	-1.13		<i>Frr1</i>	ferric-chelate reductase 1	0006810 // transport // inferred from electronic annotation//0055114 // oxidation-reduction process // inferred from electronic annotation
0.003472009	0.90408813	102.89054	120.43201	107.66417	106.05429	NM_001301407//NM_30.0007864923	1.17	-1.02	-1.14		<i>Tspan33</i>	tetraspanin 33	0045747 // positive regulation of Notch signaling pathway // not recorded//0051604 // protein maturation // inferred from mutant phenotype,
0.1061421	0.4775329	11.898493	13.12598	12.987037	11.551271	NM_175488//NM_00651.0002101363	1.10	-1.12	-1.14		<i>Ccd38</i>	coiled-coil domain containing 38	
0.9901541	0.19400911	45.44407	51.24861	56.275387	44.9879	NM_007662	1.13	-1.25	-1.14		<i>Cdh15</i>	cadherin 15	0007155 // cell adhesion // inferred from electronic annotation//0007156 // homophilic cell adhesion via plasma membrane adhesion molecule
7.41E-04	0.08986641	1001.4492	724.69794	580.5746	635.4509	NM_033563//NM_00645.0009038049	-1.18	1.09	-1.14		<i>Klf7</i>	Kruppel-like factor 7 (ubiquitous)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inf
0.038364775	0.5657878	7.312391	8.018694	7.751234	6.9740005	NM_177162	1.10	-1.11	-1.15		<i>Tmprss11g</i>	transmembrane protease, serine 11g	0006508 // proteolysis // inferred from electronic annotation
0.5911136	0.47230577	67.01783	81.80634	89.667046	70.985016	NR_015249	1.22	-1.26	-1.15		<i>Eloha2</i>	ethanol decreased 2	
0.5868689	0.63585263	8.800447	10.484583	10.233674	9.079129	NM_177744//NM_00551.000237379	1.19	-1.13	-1.15		<i>Scp12</i>	serine/arginine-rich splicing factor 12	0000381 // regulation of alternative mRNA splicing, via spliceosome // inferred from electronic annotation//0000395 // mRNA 5'-splice-site rec
0.9555525	0.048695326	39.95345	44.094017	45.47682	38.13308	NM_016982//NM_01698.494E-04	1.10	-1.19	-1.16		<i>Vpreb1//Vpreb2</i>	pre-B lymphocyte gene 1//pre-B lymphocyte gene 2	0000902 // cell morphogenesis // inferred from genetic interaction//0002377 // immunoglobulin production // inferred from genetic interactio
0.5459284	0.20049705	28.868834	38.72149	36.402557	33.1805	NM_001290397//NM_0007991966	1.34	-1.10	-1.17		<i>Mylb1</i>	myoblastin oncogene 1	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // inf
0.5671585	0.00856795	398.17203	548.8051	482.23813	467.35214	NM_001294302//NM_01.0003081897	1.38	-1.03	-1.17		<i>Preb</i>	prolactin regulatory element binding	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not
0.47870213	0.2193896	300.20813	347.8457	348.97882	281.4759	NM_009293//NM_00101818157	1.16	-1.24	-1.24		<i>Sts</i>	steroid sulfatase	0006629 // lipid metabolic process // inferred from electronic annotation//0007565 // female pregnancy // inferred from electronic annotation
1.76E-04	0.49507868	7399.8096	7760.3833	6742.2266	6219.299	NM_011125//NM_00648.0008738595	1.05	-1.08	-1.25		<i>Ptp</i>	phosphotyrosyl transfer protein	0006629 // lipid metabolic process // inferred from electronic annotation//0006810 // transport // inferred from electronic annotation//0006
0.522295	0.22264111	32.784462	45.97425	41.877045	36.10311	NM_001103182//NM_31.000214569	1.40	-1.16	-1.27		<i>Lin9</i>	lin-9 homolog (C. elegans)	0006351 // transcription, DNA-templated // inferred from electronic annotation//0007049 // cell cycle // inferred from electronic annotation//,
0.32234672	2.97E-04	28.481337	75.41425	47.716915	59.164722	NM_009140	2.65	1.24	-1.27		<i>Cxcl2</i>	chemokine (C-X-C motif) ligand 2	0001975 // response to amphetamine // inferred from electronic annotation//0002237 // response to molecule of bacterial origin // inferred fr
0.24736327	0.50651183	24.590448	32.157936	29.573622	25.206678	NM_001290779//NM_31.001707604	1.31	-1.17	-1.28		<i>Zfp879</i>	zinc finger protein 879	0006351 // transcription, DNA-templated // inferred from electronic annotation//0006355 // regulation of transcription, DNA-templated // not
0.043703277	0.7279481	55.93547	72.03841	61.92084	56.35559	NM_026637//NM_02663.0006108716	1.29	-1.10	-1.28		<i>Rwd4d</i>	RWD domain containing 3	003208 // negative regulation of NF-kappaB transcription factor activity // not recorded//003235 // positive regulation of protein sumoylatio
2.15E-04	0.05562703	322.78778	394.3657	308.6342	293.3602	NM_001033272//NM_0002134426	1.22	-1.05	-1.34		<i>Spot13</i>	spermatogenesis associated 13	0016477 // cell migration // not recorded//0030032 // lamellipodium assembly // not recorded//0030334 // regulation of cell migration // not
0.10320588	0.028439551	40.14017	60.255722	47.371956	44.777042	NM_013738//NM_00651.0003471293	1.50	-1.06	-1.35		<i>Plek2</i>	plekstrin 2	0035556 // intracellular signal transduction // inferred from electronic annotation
0.45284718	0.0739012	37.68251	59.952892	48.501804	44.39286	NM_009100	1.59	-1.09	-1.35		<i>Rpn</i>	ribonucleoprotein	
0.1615148	0.5074813	685.0561	814.30096	764.7367	601.46423	NM_001081322//NM_0003057414	1.19	-1.27	-1.35		<i>Myp5c</i>	myosin VC	0008152 // metabolic process // inferred from electronic annotation//0032254 // establishment of secretory granule localization // not recorde
0.0399295	9.96E-05	73.79068	138.40205	83.03101	101.89759	NM_019810	1.88	-1.23	-1.36		<i>Slc5a1</i>	solute carrier family 5 (sodium/glucose cotransporter), member 1	0001656 // melanogenesis development // inferred from mutant phenotype//0006810 // transport // inferred from electronic annotation//0006
0.5889784	0.049493894	94.72826	112.03129	113.71745	80.16662	NM_201638	1.88	-1.41	-1.40		<i>Mett14</i>	methyltransferase like 14	0000398 // mRNA splicing, via spliceosome // not recorded//0006139 // nucleobase-containing compound metabolic process // inferred from e
0.004151421	0.21870469	27.880014	37.659985	30.800669	26.246265	NM_019514//NM_20711.6.26E-04	1.35	-1.16	-1.43		<i>Astin2</i>	astrotactin 2	2000009 // negative regulation of protein localization to cell surface // inferred from direct assay
0.14543886	0.75992215	94.96745	135.1971	116.40971	92.20429	NM_006504243//NM_0003929869	1.42	-1.26	-1.47		<i>Tmem156</i>	transmembrane protein 156	
7.40E-04	0.21091159	80.28159	109.415375	85.37532	74.47691	NM_010780	1.36	-1.15	-1.47		<i>Cm1</i>	chymase 1, mast cell	0006508 // proteolysis // not recorded//0006518 // peptide metabolic process // inferred from electronic annotation//0016485 // protein pro
0.86537766	0.00902173	65.09017	70.67845	40.061073	NM_010861//NM_00651.0005792308	1.09	-1.09	-3.33	-1.76		<i>Myz</i>	myosin, light polypeptide 2, regulatory, cardiac, slow	0002026 // regulation of the force of heart contraction // not recorded//0003007 // heart morphogenesis // inferred from genetic interaction//
0.7703997	0.001061831	15.179602	79.0113	33.033127	43.647808	NM_203320	5.21	1.32	-1.81		<i>Cxcl3</i>	chemokine (C-X-C motif) ligand 3	0002690 // positive regulation of leukocyte chemotaxis // not recorded//0006935 // chemotaxis // inferred from electronic annotation//0006