

[CBH/HeN, Air][raw]	[CBH/HeN, O2][raw]	[Gsr-KO, Air][raw]	[Gsr-KO, O2][raw]	RefSeq Transcript ID	p (Genotype-Exposure)	FC [WT, Air vs O2]	FC [KO, Air vs O2]	FD [WT O2 vs KO O2]	Gene Symbol	Gene Title	Gene Ontology Biological Process
78.50476	83.57728	81.85938	74.15306	NM_153061//NR_10	0.009946417	1.065	-1.104	-1.127	Tsp2	TGF-beta1-induced anti-apoptotic factor 2	
548.4758	680.0645	770.6171	601.928	NM_001039181//NM	0.005818703	1.240	-1.280	-1.130	Npr3	natriuretic peptide receptor 3	0001501 // skeletal system development // inferred from direct assay//0001501 // skeletal system development // inferred from mutant phenotype//0002158 // osteob
498.83173	577.6723	542.535	504.32684	NM_001039215//NM	0.001658322	1.156	-1.076	-1.145	Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 4	0006000 // fructose metabolic process // inferred from electronic annotation//0006003 // fructose 2,6-bisphosphate metabolic process // inferred from electronic annota
760.32666	871.6596	893.9743	759.65546	NM_001081150	0.001133994	1.167	-1.177	-1.147	Lonf1	LON peptidase N-terminal domain and ring finger 1	0006508 // proteolysis // inferred from electronic annotation
385.27368	449.71663	483.1919	387.40793	NM_013867//NM_OC	1.30E-04	1.146	-1.247	-1.161	Bca3	breast cancer anti-estrogen resistance 3	0002089 // lens morphogenesis in camera-type eye // inferred from mutant phenotype//0007165 // signal transduction // inferred from electronic annotation//0007264
554.0281	765.62036	619.1688	656.87244	NM_001114098//NM	0.00805221	1.382	1.061	-1.166	Mtn1	microtubule crosslinking factor 1	0001578 // microtubule bundle formation // inferred from direct assay//0010506 // regulation of autophagy // inferred from electronic annotation//0045197 // establis
110.14734	123.800865	115.75199	105.61847		0.000804004	1.124	-1.096	-1.172	C77097	expressed sequence C77097	
67.583115	38.96788	36.072266	33.06806	NM_145146	0.005742774	-1.734	-1.091	-1.178	Afm	afamin	0006810 // transport // inferred from electronic annotation//0051180 // vitamin transport // not recorded
2915.611	3436.7405	3575.5144	2819.8708	NM_133725//NM_1	0.00999848	1.179	-1.268	-1.219	Secibp2l	SECS binding protein 2-like	
1710.4757	2207.7852	1961.248	1809.4072	NM_001025250//NM	0.003167039	1.291	-1.084	-1.220	Vegfa	vascular endothelial growth factor A	0000122 // negative regulation of transcription from RNA polymerase II promoter // not recorded//0001525 // angiogenesis // inferred from direct assay//0001525 // ar
355.8095	425.62427	379.70976	347.82846	NM_175187//NR_O2	0.004542776	1.196	-1.092	-1.224	Tmm151b	transmembrane protein 151B	
37.44921	44.33614	38.355804	36.149307		0.009915507	1.184	-1.061	-1.226	D11rat644e	DNA segment, Chr 1, ERATO Dsl 646, expressed	
66.743034	73.25703	68.7475	59.705116	NM_177052//NM_OC	0.004596748	1.098	-1.151	-1.227	Kif6	kinesin family member 6	0007018 // microtubule-based movement // not recorded//0008152 // metabolic process // inferred from electronic annotation
605.0476	679.1741	614.92474	544.8614	NM_026368//NM_OC	0.001098655	1.123	-1.129	-1.247	Coap1	casepase activity and apoptosis inhibitor 1	0006915 // apoptotic process // inferred from electronic annotation
32.1485	32.640057	30.868538	25.986841		0.008977985	1.015	-1.188	-1.256	943008723Rik	RIKEN cDNA 943008723 gene	
28.196205	36.272247	32.59862	28.606833		0.005570435	1.266	-1.140	-1.268	D71rat558e	DNA segment, Chr 7, ERATO Dsl 558, expressed	
166.81755	211.61995	168.47212	166.18628	NM_030110//NM_OC	0.006348874	1.269	-1.014	-1.273	Micu3	mitochondrial calcium uptake family, member 3	
143.05722	28.310953	20.604244	21.480125	NM_001150749//NM	0.007889654	-5.053	1.043	-1.318	Rdh7	retinol dehydrogenase 7	0008152 // metabolic process // inferred from electronic annotation//0042572 // retinol metabolic process // inferred from electronic annotation//0055114 // oxidator
511.498	723.33057	550.2367	547.33636	NM_007707//NM_O1	0.006182605	1.414	-1.005	-1.322	Soc3	suppressor of cytokine signaling 3	0001666 // response to hypoxia // inferred from electronic annotation//0001932 // regulation of protein phosphorylation // inferred from direct assay//0006469 // negi
1531.4441	1833.0116	1756.8998	1347.1793	NM_001012766//NM	0.003918618	1.197	-1.304	-1.361	Eorps2//Eor1//Eor2//Eor2l	eosinophili-associated, ribonuclease A family, pseudogene 2//eosinophili	0006935 // chemotaxis // inferred from direct assay//0008152 // metabolic process // inferred from electronic annotation//0050305 // nucleic acid phosphodiester bon
128.37373	20.784555	15.921132	15.100804	NM_029562//NM_OC	0.005814837	-6.176	-1.053	-1.375	Cyp2d6	cytochrome P450, family 2, subfamily 6, polypeptide 2c	0006865 // xenobiotic metabolic process // not recorded//0007565 // female pregnancy // inferred from electronic annotation//0003969 // arachidonic acid metabolic p
125.92949	179.2413	2265.6091	118.197014	NM_008725	0.008516206	1.423	-19.168	-1.516	Napa	natriuretic peptide type A	0001666 // response to hypoxia // inferred from electronic annotation//0003085 // negative regulation of systemic arterial blood pressure // not recorded//0006182 //
481.74808	49.186993	36.431168	30.955608	NM_007376	0.004647014	-9.794	-1.177	-1.589	Pzp	pregnancy zone protein	0007566 // embryo implantation // inferred from genetic interaction//0010466 // negative regulation of peptidase activity // inferred from electronic annotation//0010