

Table E1. Nrf2+/+ Mice: Air PBS vs SFN transcripts with \geq +/- 1.45 fold change

Moderated T-Test (p-value cut-off:0.01)/Fold Change 1.5

*Fold change (FC) in red-increased by SFN, in blue-decreased by SFN.

RefSeq Transcript ID	p	*FC (SFN vs	Gene Symbol	Gene Title
NM_008725	0.001336	31.747	<i>Nppa</i>	natriuretic peptide type A
NM_008522	0.006068	13.076	<i>Ltf</i>	lactotransferrin
NM_001141927///NM_023129	0.001845	10.130	<i>Pln</i>	phospholamban
NM_009605	0.001909	8.728	<i>Adipoq</i>	adiponectin, C1Q and collagen domain containing
NM_001122756///NM_016869	0.000607	7.761	<i>Corin</i>	corin
NM_027416	0.004907	7.612	<i>Calml3</i>	calmodulin-like 3
NM_009406	0.003266	6.943	<i>Tnni3</i>	troponin I, cardiac 3
NM_007702	0.001799	6.877	<i>Cidea</i>	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A
	0.007252	6.574	<i>BB144871</i>	expressed sequence BB144871
NM_013459	0.001343	6.098	<i>Cfd</i>	complement factor D (adipsin)
NM_010859	0.003246	5.904	<i>MyI3</i>	myosin, light polypeptide 3
NM_001195006///NM_145602	0.001537	5.767	<i>NdrG4</i>	N-myc downstream regulated gene 4
NM_028801	0.005436	5.742	<i>Muc5b</i>	mucin 5, subtype B, tracheobronchial
NR_045305	0.007929	5.680	<i>AU040972</i>	expressed sequence AU040972
NM_009363	0.006365	5.612	<i>Tff2</i>	trefoil factor 2 (spasmolytic protein 1)
NM_023868	0.004956	5.157	<i>Ryr2</i>	ryanodine receptor 2, cardiac
NM_029803	0.007178	5.069	<i>Ifi2712a</i>	interferon, alpha-inducible protein 27 like 2A
NM_009814	0.000465	5.030	<i>Casq2</i>	calsequestrin 2
NM_013505	0.001478	4.909	<i>Dsc2</i>	desmocollin 2
NM_008653	0.002806	4.904	<i>Mybpc3</i>	myosin binding protein C, cardiac
NM_024406	0.000658	4.898	<i>Fabp4</i>	fatty acid binding protein 4, adipocyte
NM_009393	0.000432	4.846	<i>Tnnc1</i>	troponin C, cardiac/slow skeletal
NM_016771	0.008286	4.766	<i>Sult1d1</i>	sulfotransferase family 1D, member 1
NM_001130174///NM_00113010	0.004729	4.664	<i>Tnnt2</i>	troponin T2, cardiac
NM_001198841///NM_013808	0.002152	4.636	<i>Csrp3</i>	cysteine and glycine-rich protein 3
NM_008469	0.003916	4.404	<i>Krt15</i>	keratin 15
NM_001271402///NM_00127140	0.000002	4.361	<i>Ephx2</i>	epoxide hydrolase 2, cytoplasmic
NM_008664	0.000697	4.325	<i>Myom2</i>	myomesin 2
NM_175441	0.000836	4.245	<i>Mylk3</i>	myosin light chain kinase 3
NM_009381	0.009208	4.107	<i>Thrsp</i>	thyroid hormone responsive
NM_007606	0.003685	4.087	<i>Car3</i>	carbonic anhydrase 3
NM_009944	0.000907	4.060	<i>Cox7a1</i>	cytochrome c oxidase subunit VIIa 1
NM_007692///NM_009948///NM_000271	0.000271	3.977	<i>Chkb///Cpt1b</i>	choline kinase beta///carnitine palmitoyltransferase 1b, muscle
NM_021503	0.000372	3.967	<i>Myoz2</i>	myozenin 2

RefSeq Transcript ID	p	*FC (SFN vs Gene Symbol)	Gene Title
NM_007664	0.000663	3.796	Cdh2 cadherin 2
NM_001003914///NM_0011715	0.000714	3.792	Obscn obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
NM_010473	0.001059	3.752	Hrc histidine rich calcium binding protein
NM_175276	0.002259	3.732	Fhod3 formin homology 2 domain containing 3
NM_144936	0.000614	3.712	Tmem45b transmembrane protein 45b
NM_007751	0.002047	3.698	Cox8b cytochrome c oxidase subunit VIIIb
NM_001164171///NM_010856/	0.008996	3.629	Myh6///Myh7 myosin, heavy polypeptide 6, cardiac muscle, alpha///beta
NM_001204959///NM_022984	0.003423	3.608	Retn resistin
NM_021282	0.003714	3.518	Cyp2e1 cytochrome P450, family 2, subfamily e, polypeptide 1
NM_001013013	0.000914	3.508	Dhrs7c dehydrogenase/reductase (SDR family) member 7C
NM_011978	0.007727	3.503	Slc27a2 solute carrier family 27 (fatty acid transporter), member 2
NM_145635	0.004460	3.425	Adig adipogenin
NM_022020	0.000080	3.418	Rbp7 retinol binding protein 7, cellular
NM_175347	0.006336	3.324	Srl sarcalumenin
NM_029844	0.004513	3.300	Mrap melanocortin 2 receptor accessory protein
NM_001252591///NM_025357/	0.005819	3.278	Smpx small muscle protein, X-linked
NM_011082	0.007537	3.220	Pigr polymeric immunoglobulin receptor
NM_027402	0.000379	3.124	Fndc5 fibronectin type III domain containing 5
NM_010174	0.004529	3.101	Fabp3 fatty acid binding protein 3, muscle and heart
NM_007403	0.007147	3.040	Adam8 a disintegrin and metallopeptidase domain 8
NM_008768	0.001750	3.026	Orm1 orosomucoid 1
NM_153576	0.009283	2.956	Cxcl17 chemokine (C-X-C motif) ligand 17
NM_011196	0.006267	2.954	Ptger3 prostaglandin E receptor 3 (subtype EP3)
NM_001205219///NM_172752	0.006490	2.942	Sorbs2 sorbin and SH3 domain containing 2
NM_013868	0.001282	2.851	Hspb7 heat shock protein family, member 7 (cardiovascular)
NM_001077348///NM_025874	0.000596	2.801	Plin5 perilipin 5
NM_001037740///NM_177204	0.000944	2.785	Strip2 striatin interacting protein 2
NM_009943	0.004628	2.781	Cox6a2 cytochrome c oxidase subunit VIa polypeptide 2
NM_029095///NR_027967	0.003734	2.738	Hhat1 hedgehog acyltransferase-like
NM_020568	0.001259	2.737	Plin4 perilipin 4
NM_019697	0.003016	2.725	Kcnd2 potassium voltage-gated channel, Shal-related family, member 2
NM_023784	0.009142	2.687	Yipf7 Yip1 domain family, member 7
NM_001039071///NM_0010390	0.003697	2.677	Ldb3 LIM domain binding 3
NM_008243	0.007580	2.650	Mst1 macrophage stimulating 1 (hepatocyte growth factor-like)
NM_009608	0.003936	2.637	Actc1 actin, alpha, cardiac muscle 1
NM_145838	0.005199	2.623	St8sia6 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6
NM_019662	0.000465	2.617	Rrad Ras-related associated with diabetes

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NM_001254761///NM_023270	0.001811	2.610	Rnf128 ring finger protein 128
NM_001253860///NM_021544	0.003531	2.586	Scn5a sodium channel, voltage-gated, type V, alpha
NM_138628	0.009483	2.555	Txlnb taxilin beta
NM_001136080///NM_009161	0.005900	2.480	Sgca sarcoglycan, alpha (dystrophin-associated glycoprotein)
NM_026384	0.002076	2.474	Dgat2 diacylglycerol O-acyltransferase 2
NM_009903	0.005395	2.453	Cldn4 claudin 4
NM_145831	0.008535	2.439	Dmrt2 doublesex and mab-3 related transcription factor 2
NM_009700	0.005835	2.434	Aqp4 aquaporin 4
NM_001083934///NM_010867	0.009525	2.431	Myom1 myomesin 1
NM_011652///NM_028004	0.003352	2.418	Ttn titin
NM_080639	0.003399	2.407	Timp4 tissue inhibitor of metalloproteinase 4
NM_080728///NM_001164171/	0.000419	2.394	Myh7///Myh6 myosin, heavy polypeptide 7, cardiac muscle, beta/// alpha
NM_001008973	0.007646	2.340	Tmem232 transmembrane protein 232
NM_023049	0.002372	2.327	Asb2 ankyrin repeat and SOCS box-containing 2
NM_026633	0.000385	2.325	Fam195a family with sequence similarity 195, member A
NM_027395	0.003440	2.324	Basp1 brain abundant, membrane attached signal protein 1
NM_001276387///NM_010095	0.000310	2.321	Ebf2 early B cell factor 2
NM_001033170	0.000261	2.300	Fam83e family with sequence similarity 83, member E
NM_153801	0.001195	2.282	Tecrl trans-2,3-enoyl-CoA reductase-like
NM_001122635///NM_177090/	0.002613	2.247	Cdhr4 cadherin-related family member 4
NM_001039543///NM_010801	0.004318	2.244	Mlf1 myeloid leukemia factor 1
NM_001034168///NM_178655	0.004238	2.238	Ank2 ankyrin 2, brain
NM_001170847	0.001080	2.228	Rbm20 RNA binding motif protein 20
NM_010362	0.007650	2.216	Gsto1 glutathione S-transferase omega 1
NM_001081425	0.008401	2.193	Rbm24 RNA binding motif protein 24
NM_001081984///NM_022318	0.003675	2.186	Popdc2 popeye domain containing 2
NM_009204	0.003733	2.185	Slc2a4 solute carrier family 2 (facilitated glucose transporter), member 4
NM_001177373///NM_019974	0.003130	2.176	Klk11 kallikrein related-peptidase 11
NM_001160127///NM_009762	0.004209	2.155	Smyd1 SET and MYND domain containing 1
NM_009129	0.000526	2.118	Scg2 secretogranin II
NM_025529	0.003592	2.115	Nudt8 nudix (nucleoside diphosphate linked moiety X)-type motif 8
NM_029920	0.004363	2.105	Mtus2 microtubule associated tumor suppressor candidate 2
NM_026443	0.004267	2.073	Mtfp1 mitochondrial fission process 1
NM_001110140///NM_009722/	0.003410	2.070	Atp2a2 ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
NM_181728	0.003706	2.055	Art3 ADP-ribosyltransferase 3
NM_001162878///NM_029283	0.007160	2.049	Fam183b family with sequence similarity 183, member B
NM_001081369	0.007703	2.038	Ccdc153 coiled-coil domain containing 153

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NM_008963	0.008434	2.007	<i>Ptgds</i> prostaglandin D2 synthase (brain)
NM_207531	0.008918	1.994	<i>Agr3</i> anterior gradient 3
NM_016966///NR_076393	0.001802	1.982	<i>Phgdh</i> 3-phosphoglycerate dehydrogenase
NM_001162998	0.000639	1.967	<i>Smim6</i> small integral membrane protein 6
NM_013473	0.009288	1.963	<i>Anxa8</i> annexin A8
NM_054098	0.006300	1.956	<i>Steap4</i> STEAP family member 4
NM_001168318///NM_028903	0.005314	1.955	<i>Scara5</i> scavenger receptor class A, member 5 (putative)
NM_172469	0.009787	1.954	<i>Clic6</i> chloride intracellular channel 6
NM_001146217///NM_022316	0.003897	1.953	<i>Smoc1</i> SPARC related modular calcium binding 1
NM_001122683///NM_175177	0.005542	1.949	<i>Bdh1</i> 3-hydroxybutyrate dehydrogenase, type 1
NM_007906	0.004963	1.945	<i>Eef1a2</i> eukaryotic translation elongation factor 1 alpha 2
NM_008509	0.000706	1.911	<i>Lpl</i> lipoprotein lipase
NM_133681	0.006145	1.902	<i>Tspan1</i> tetraspanin 1
NM_010444	0.000053	1.901	<i>Nr4a1</i> nuclear receptor subfamily 4, group A, member 1
NM_133689	0.008347	1.896	<i>Ppp1r32</i> protein phosphatase 1, regulatory subunit 32
NM_145562	0.005681	1.891	<i>Parm1</i> prostate androgen-regulated mucin-like protein 1
NM_001166173///NM_00116610	0.007545	1.889	<i>Dmkn</i> dermokine
NM_009063	0.005394	1.887	<i>Rgs5</i> regulator of G-protein signaling 5
NM_009026	0.002284	1.881	<i>Rasd1</i> RAS, dexamethasone-induced 1
NM_177629	0.007964	1.872	<i>Fam216b</i> family with sequence similarity 216, member B
NM_026438	0.003181	1.852	<i>Ppa1</i> pyrophosphatase (inorganic) 1
NM_001197028///NM_028813	0.000133	1.850	<i>Vit</i> vitrin
NM_001145948///NM_153392	0.007162	1.840	<i>Ttc39a</i> tetratricopeptide repeat domain 39A
NM_001161419///NM_007506	0.008970	1.836	<i>Atp5g1</i> ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c1 (subunit 9)
NM_027951	0.007729	1.827	<i>Tekt4</i> tektin 4
NM_001204252///NM_010796	0.000713	1.824	<i>Clec10a</i> C-type lectin domain family 10, member A
NM_001162973///NM_00116290	0.007996	1.821	<i>Lrrc51</i> leucine rich repeat containing 51
NM_008630	0.009726	1.820	<i>Mt2</i> metallothionein 2
NM_080637	0.005412	1.813	<i>Nme5</i> NME/NM23 family member 5
NM_009922	0.001738	1.813	<i>Cnn1</i> calponin 1
NM_001163103	0.002251	1.799	<i>Ppp1r36</i> protein phosphatase 1, regulatory subunit 36
NM_010726	0.001562	1.790	<i>Phyh</i> phytanoyl-CoA hydroxylase
NM_009879	0.000534	1.784	<i>Ift81</i> intraflagellar transport 81
NM_030677	0.004519	1.780	<i>Gpx2</i> glutathione peroxidase 2
NM_008904///NR_027710	0.005380	1.765	<i>Ppargc1a</i> peroxisome proliferative activated receptor, gamma, coactivator 1 alpha
NM_007995	0.009159	1.763	<i>Fcna</i> ficolin A
NM_029556	0.007158	1.757	<i>Clybl</i> citrate lyase beta like

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NM_007381	0.000591	1.753	Acadl acyl-Coenzyme A dehydrogenase, long-chain
NM_181816	0.006992	1.752	Ccdc67 coiled-coil domain containing 67
NM_172604	0.002839	1.751	Scara3 scavenger receptor class A, member 3
NM_178378	0.001773	1.740	Iqcg IQ motif containing G
NM_010924	0.001189	1.739	Nnmt nicotinamide N-methyltransferase
NM_080633	0.002091	1.735	Aco2 aconitase 2, mitochondrial
NM_009208	0.003513	1.734	Slc4a3 solute carrier family 4 (anion exchanger), member 3
NM_177068	0.002176	1.733	Olfml2b olfactomedin-like 2B
NM_001002927	0.003844	1.731	Penk preproenkephalin
NM_001033443	0.009668	1.706	Cdkl4 cyclin-dependent kinase-like 4
NM_001195431///NM_012043	0.008170	1.702	Islr immunoglobulin superfamily containing leucine-rich repeat
NM_146052	0.008670	1.702	Lrrc3b leucine rich repeat containing 3B
NM_008035	0.001255	1.700	Folr2 folate receptor 2 (fetal)
NM_001159731///NM_009107	0.006011	1.700	Rxrg retinoid X receptor gamma
NM_001164640///NM_029419/	0.000338	1.699	Apol7a///Apol7c apolipoprotein L 7a///apolipoprotein L 7c///apolipoprotein L 7c pseudogene
NM_029784	0.000661	1.697	Fam81a family with sequence similarity 81, member A
NM_007808	0.002115	1.697	Cyts cytochrome c, somatic
NM_023557	0.006981	1.694	Slc44a4 solute carrier family 44, member 4
NM_001164248///NM_0011642	0.007401	1.691	Tpm1 tropomyosin 1, alpha
NM_013569	0.004710	1.691	Kcnh2 potassium voltage-gated channel, subfamily H (eag-related), member 2
NM_025567	0.004231	1.682	Cyc1 cytochrome c-1
NM_198414	0.006936	1.680	Paqr9 progesterone and adiponectin receptor family member IX
NM_011309	0.007218	1.677	S100a1 S100 calcium binding protein A1
NM_008013	0.009346	1.673	Fgl2 fibrinogen-like protein 2
NM_013603	0.000673	1.667	Mt3 metallothionein 3
NM_001205076///NM_021566/	0.005270	1.667	Jph2 junctophilin 2
NM_007981	0.000617	1.662	Acsl1 acyl-CoA synthetase long-chain family member 1
NM_001159577///NM_0011595	0.004290	1.660	Lnx1 ligand of numb-protein X 1
NM_007382	0.001168	1.655	Acadm acyl-Coenzyme A dehydrogenase, medium chain
NM_001013386	0.003063	1.655	Rasl10b RAS-like, family 10, member B
NM_153527	0.003896	1.654	Dnajb13 DnaJ (Hsp40) related, subfamily B, member 13
NM_027728	0.009273	1.653	Enkur enkurin, TRPC channel interacting protein
NM_010844	0.006683	1.650	Muc5ac mucin 5, subtypes A and C, tracheobronchial/gastric
NM_025794	0.000643	1.643	Etfdh electron transferring flavoprotein, dehydrogenase
NM_001190373	0.004985	1.641	Kcng2 potassium voltage-gated channel, subfamily G, member 2
NM_001033784///NM_028384	0.001304	1.640	Ccdc13 coiled-coil domain containing 13
NM_026439	0.001603	1.634	Ccdc80 coiled-coil domain containing 80

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NM_001160038///NM_001160038	0.005983	1.634	Ndufs1 NADH dehydrogenase (ubiquinone) Fe-S protein 1
NM_001146196///NM_009132	0.000584	1.632	Scin scinderin
NM_011838	0.007814	1.629	Lynx1 Ly6/neurotoxin 1
NM_026452	0.007411	1.624	Coq9 coenzyme Q9 homolog (yeast)
NM_010043	0.007743	1.619	Des desmin
NM_017366	0.000897	1.616	Acadvl acyl-Coenzyme A dehydrogenase, very long chain
NM_139269	0.000140	1.615	Pla2g16 phospholipase A2, group XVI
NM_009849	0.004704	1.611	Entpd2 ectonucleoside triphosphate diphosphohydrolase 2
NM_026865	0.004553	1.611	Ptges3l prostaglandin E synthase 3 (cytosolic)-like
NM_001199337///NM_001199337	0.002441	1.609	Apoa apolipoprotein O
NM_020047	0.001244	1.607	Tacstd2 tumor-associated calcium signal transducer 2
NM_153781	0.002975	1.606	Pygb brain glycogen phosphorylase
NM_028177	0.000642	1.605	Ndufab1 NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1
NM_172864	0.005757	1.596	Wdr63 WD repeat domain 63
NM_025557	0.009637	1.591	Pcp4l1 Purkinje cell protein 4-like 1
NM_026614	0.003124	1.587	Ndufa5 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5
NM_001163621///NM_028010	0.005540	1.585	Apol6 apolipoprotein L 6
NM_011347	0.009181	1.584	Selp selectin, platelet
NM_023374///XM_003946338	0.003531	1.584	Sdhb succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial-like
NM_177564	0.005461	1.582	Dhrs11 dehydrogenase/reductase (SDR family) member 11
NM_025384	0.003746	1.581	Dnajc15 DnaJ (Hsp40) homolog, subfamily C, member 15
NM_025710	0.001482	1.578	Uqcrcs1 ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
NM_009028	0.000950	1.576	Rasl2-9 RAS-like, family 2, locus 9
NM_134147	0.006444	1.576	Macrocl1 MACRO domain containing 1
NM_026172	0.000780	1.575	Decr1 2,4-dienoyl CoA reductase 1, mitochondrial
NM_013834	0.002670	1.574	Sfrp1 secreted frizzled-related protein 1
NM_011977	0.000166	1.572	Slc27a1 solute carrier family 27 (fatty acid transporter), member 1
NM_027244///XM_358948///XM_358948	0.008258	1.572	Ndufa11 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11
NM_001170395///NM_053094	0.000472	1.566	Cd163 CD163 antigen
NM_001024945///NM_023268	0.004285	1.565	Qsox1 quiescin Q6 sulfhydryl oxidase 1
NM_001276358///NM_030716/0	0.004356	1.565	Kcni2 Kv channel-interacting protein 2
NM_016772	0.006273	1.560	Ech1 enoyl coenzyme A hydratase 1, peroxisomal
NM_027941	0.007094	1.559	Lrrc34 leucine rich repeat containing 34
NM_029573	0.001189	1.558	Idh3a isocitrate dehydrogenase 3 (NAD+) alpha
NM_007883	0.004848	1.555	Dsg2 desmoglein 2
NM_009738	0.001014	1.552	Bche butyrylcholinesterase
NM_025407	0.003858	1.551	Uqcrc1 ubiquinol-cytochrome c reductase core protein 1

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NM_008824	0.001905	1.545	Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1
NM_001164763	0.006924	1.536	Rarres1	retinoic acid receptor responder (tazarotene induced) 1
NM_021329	0.006906	1.533	Rangrf	RAN guanine nucleotide release factor
NM_010045	0.000234	1.527	Darc	Duffy blood group, chemokine receptor
NM_013754	0.009620	1.525	Insl6	insulin-like 6
NM_145615	0.002016	1.523	Etfa	electron transferring flavoprotein, alpha polypeptide
NM_001164567///NM_011700	0.004181	1.522	Vill	villin-like
NM_025838///NM_028336	0.007657	1.521	Tmem107	transmembrane protein 107
NM_009949	0.000229	1.520	Cpt2	carnitine palmitoyltransferase 2
NM_012013	0.006327	1.520	Figla	folliculogenesis specific basic helix-loop-helix
NM_009942///XM_001475417	0.006443	1.516	Cox5b	cytochrome c oxidase subunit 5B, mitochondrial-like
NM_026928	0.009844	1.513	Fuom	fucoase mutarotase
NM_001122758///NM_018764	0.003654	1.509	Pcdh7	protocadherin 7
NM_175191	0.004150	1.508	Gpr22	G protein-coupled receptor 22
NM_009610	0.001446	1.507	Actg2	actin, gamma 2, smooth muscle, enteric
NM_029422	0.009666	1.505	Dcstamp	dendrocyte expressed seven transmembrane protein
NM_172693	0.005744	1.504	Galnt12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12
NM_001083891///NM_030087	0.004090	1.502	Ndufv3	NADH dehydrogenase (ubiquinone) flavoprotein 3
NM_026061	0.004816	1.502	Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8
NM_001185164///NM_011697	0.006755	1.501	Vegfb	vascular endothelial growth factor B
NM_025352	0.001316	1.499	Uqcrcq	ubiquinol-cytochrome c reductase, complex III subunit VII
	0.004029	1.499	Gm11633	predicted gene 11633
NM_025650	0.009713	1.498	Uqcr11	ubiquinol-cytochrome c reductase, complex III subunit XI
NM_016925	0.006177	1.497	Fanca	Fanconi anemia, complementation group A
NM_008993	0.003030	1.497	Pxmp2	peroxisomal membrane protein 2
NM_133249	0.001691	1.496	Ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator 1 beta
NM_145558	0.001431	1.495	Hadhb	hydroxyacyl-Coenzyme A dehydrogenase, beta subunit
	0.008984	1.495	D1ErtD705e	DNA segment, Chr 1, ERATO Doi 705, expressed
NM_007507	0.004475	1.495	Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e
NM_001026214///NM_007647	0.008745	1.493	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5
NM_001042615///NM_030127	0.006916	1.493	Htra3	HtrA serine peptidase 3
NM_177235	0.009028	1.487	Bend6	BEN domain containing 6
NM_145614	0.002263	1.487	Dlat	dihydrolipoamide S-acetyltransferase
NM_008618	0.004165	1.486	Mdh1	malate dehydrogenase 1, NAD (soluble)
NM_009264	0.005077	1.486	Sprr1a	small proline-rich protein 1A
NM_007633	0.003390	1.485	Ccne1	cyclin E1
NM_026818	0.004610	1.485	Cilp2	cartilage intermediate layer protein 2

RefSeq Transcript ID	p	*FC (SFN vs Gene Symbol)	Gene Symbol	Gene Title
NM_025358	0.003184	1.484	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9
NM_007747	0.001660	1.481	Cox5a	cytochrome c oxidase subunit Va
NM_172793	0.002396	1.479	Btn19	butyrophilin-like 9
NM_001102404//NM_001102404	0.000757	1.479	Acp5	acid phosphatase 5, tartrate resistant
NM_177470	0.005908	1.478	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)
NM_026695//NR_075104	0.002112	1.477	Etfb	electron transferring flavoprotein, beta polypeptide
NM_024197	0.003016	1.474	Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10
NM_027733//NM_029485	0.003720	1.472	Spata24	spermatogenesis associated 24
NM_001163510//NM_008433	0.004904	1.469	Kcnn4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
NM_001033458	0.008727	1.468	Gm1673	predicted gene 1673
NM_023842	0.005994	1.468	Dsp	desmoplakin
NM_153107	0.005334	1.466	Cpz	carboxypeptidase Z
NM_019737	0.001601	1.465	B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6
NM_001004138//NM_010609	0.005772	1.462	Kcnk7	potassium channel, subfamily K, member 7
NM_001252459//NM_001252459	0.002077	1.461	Cyfp2	cytoplasmic FMR1 interacting protein 2
NM_023172	0.009839	1.457	Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9
XM_134476//XM_910911	0.005551	1.457	Ces1h	carboxylesterase 1H
NM_001083904//NM_001083904	0.006885	1.456	Fetub	fetuin beta
NM_001112722//NM_001112722	0.000151	1.455	Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like
NM_001034876//NM_001253301	0.006979	1.452	B4galt2//Ccgc24	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2
NM_146108	0.004232	1.449	Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase
NM_020567	0.000820	1.449	Gmnn	geminin
NM_020519	0.009054	1.447	Slurp1	secreted Ly6/Plaur domain containing 1
NM_145924	0.003666	1.446	Cenpi	centromere protein I
NM_001198914//NM_010848/	0.003252	1.446	Myb	myeloblastosis oncogene
NM_001190451//NM_007833	0.000613	1.445	Dcn	decorin
NM_001271019//NM_145581	0.000197	-3.092	Siglec5	sialic acid binding Ig-like lectin 5
NM_175692	0.005718	-2.994	Snhg11	small nucleolar RNA host gene 11
NM_001039181//NM_008728	0.002168	-2.932	Npr3	natriuretic peptide receptor 3
NM_001123394	0.009199	-2.485	Ang3	angiogenin, ribonuclease A family, member 3
NR_045048	0.000024	-2.374	Gm19990	predicted gene, 19990
NM_007746	0.005517	-2.354	Map3k8	mitogen-activated protein kinase kinase kinase 8
NM_134110	0.000190	-2.186	Kcne2	potassium voltage-gated channel, Isk-related subfamily, gene 2
NM_007894//XM_003946320/	0.001116	-2.068	Ear1	eosinophil-associated, ribonuclease A family, member 1
NM_001081088	0.000215	-2.055	Lrp2	low density lipoprotein receptor-related protein 2
NM_008604	0.000035	-2.050	Mme	membrane metallo endopeptidase
NM_001163136	0.001726	-2.031	Macc1	metastasis associated in colon cancer 1

RefSeq Transcript ID	p	*FC (SFN vs Gene Symbol)	Gene Symbol	Gene Title
NM_138648	0.001730	-2.000	<i>Olr1</i>	oxidized low density lipoprotein (lectin-like) receptor 1
NM_019683	0.002782	-1.997	<i>Ankrd49</i>	ankyrin repeat domain 49
NM_139306	0.000007	-1.966	<i>Acer2</i>	alkaline ceramidase 2
NM_009892///NM_145126	0.003663	-1.959	<i>Chi3l3///Chi3l4</i>	chitinase 3-like 3///chitinase 3-like 4
NM_010406	0.002831	-1.954	<i>Hc</i>	hemolytic complement
NM_027468	0.008751	-1.952	<i>Cpm</i>	carboxypeptidase M
NM_023794	0.003856	-1.910	<i>Etv5</i>	ets variant gene 5
NM_009036	0.000697	-1.910	<i>Rbpjl</i>	recombination signal binding protein for immunoglobulin kappa J region-like
NM_010172	0.007265	-1.909	<i>F7</i>	coagulation factor VII
NM_007548	0.006406	-1.903	<i>Prdm1</i>	PR domain containing 1, with ZNF domain
NM_001004173	0.000188	-1.877	<i>Sgpp2</i>	sphingosine-1-phosphate phosphatase 2
NM_019397	0.000031	-1.865	<i>Egfl6</i>	EGF-like-domain, multiple 6
NM_001167997///NM_031384	0.000784	-1.864	<i>Tex11</i>	testis expressed gene 11
NM_175522	0.000291	-1.840	<i>Elfn1</i>	leucine rich repeat and fibronectin type III, extracellular 1
NM_001081212	0.008374	-1.839	<i>Irs2</i>	insulin receptor substrate 2
NM_001163314///NM_175508	0.003477	-1.798	<i>Pgap1</i>	post-GPI attachment to proteins 1
NM_031198	0.002433	-1.789	<i>Tfec</i>	transcription factor EC
NM_021050	0.004268	-1.775	<i>Cftr</i>	cystic fibrosis transmembrane conductance regulator
NM_001113323	0.000458	-1.772	<i>Glb1l3</i>	galactosidase, beta 1 like 3
NM_001136496///NM_178875	0.006909	-1.771	<i>Zfp935</i>	zinc finger protein 935
NM_133241	0.002674	-1.764	<i>Mlc1</i>	megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human)
NM_001161731///NM_007447	0.000038	-1.763	<i>Ang</i>	angiogenin, ribonuclease, RNase A family, 5
NM_015760	0.001601	-1.760	<i>Nox4</i>	NADPH oxidase 4
NM_001159986///NM_033354/	0.001035	-1.759	<i>Sec16b</i>	SEC16 homolog B (S. cerevisiae)
NM_175406	0.007123	-1.753	<i>Atp6v0d2</i>	ATPase, H+ transporting, lysosomal V0 subunit D2
NM_011066	0.002544	-1.751	<i>Per2</i>	period circadian clock 2
NM_001002900///NM_0010246	0.001061	-1.748	<i>Higd1c</i>	HIG1 domain family, member 1C
NM_023396	0.001272	-1.748	<i>Rprm</i>	reprimin, TP53 dependent G2 arrest mediator candidate
NM_009421	0.009479	-1.744	<i>Traf1</i>	TNF receptor-associated factor 1
NM_053190	0.002658	-1.733	<i>S1pr5</i>	sphingosine-1-phosphate receptor 5
NM_198170	0.004669	-1.731	<i>Szt2</i>	seizure threshold 2
NM_145219	0.008043	-1.730	<i>Lgi3</i>	leucine-rich repeat LGI family, member 3
NM_001276719///NM_021609	0.000402	-1.723	<i>Ccbp2</i>	chemokine binding protein 2
NM_001163660///NM_027280	0.001873	-1.723	<i>Nkd1</i>	naked cuticle 1 homolog (Drosophila)
NM_009789	0.007760	-1.721	<i>S100g</i>	S100 calcium binding protein G
NM_029415	0.000441	-1.717	<i>Slc10a6</i>	solute carrier family 10 (sodium/bile acid cotransporter family), member 6
NM_001164724///NM_133775	0.008283	-1.701	<i>Il33</i>	interleukin 33

RefSeq Transcript ID	p	*FC (SFN vs Gene Symbol)	Gene Title
NM_001001883///NM_172655	0.001656	-1.700	Hecw2 HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2
NM_030697	0.008440	-1.697	Kank3 KN motif and ankyrin repeat domains 3
NM_013838	0.001124	-1.690	Trpc6 transient receptor potential cation channel, subfamily C, member 6
NM_027052	0.002678	-1.690	Slc38a4 solute carrier family 38, member 4
NM_009511///XM_003946399	0.005856	-1.687	Vipr2 vasoactive intestinal peptide receptor 2
NM_012033	0.003874	-1.678	Tinag tubulointerstitial nephritis antigen
NM_001033258	0.000818	-1.668	D10Bwg1379e DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed
NM_025730	0.002555	-1.667	Lrrk2 leucine-rich repeat kinase 2
NM_001024846///NM_009562	0.000481	-1.659	Zfp62 zinc finger protein 62
NM_026352///NM_177356	0.001217	-1.650	Lamp3///Ppid lysosomal-associated membrane protein 3///peptidylprolyl isomerase D
NM_001037723///NM_0010377	0.001754	-1.647	Adcy7 adenylate cyclase 7
NM_001040654///NM_009877	0.004841	-1.636	Cdkn2a cyclin-dependent kinase inhibitor 2A
NM_172839	0.001023	-1.632	Ccnj cyclin J
NM_007901	0.000789	-1.630	S1pr1 sphingosine-1-phosphate receptor 1
NM_009616	0.001370	-1.630	Adam19 a disintegrin and metallopeptidase domain 19 (meltrin beta)
NM_008730	0.000375	-1.628	Nptx1 neuronal pentraxin 1
NR_002870	0.006014	-1.627	Dnm3os dynamin 3, opposite strand
NM_010728	0.001849	-1.621	Lox lysyl oxidase
NM_212457	0.006216	-1.619	Bex4 brain expressed gene 4
NM_008317///NM_019750	0.002391	-1.616	Hyal1///Nat6 hyaluronoglucosaminidase 1///N-acetyltransferase 6
NM_001172481///NM_025711	0.003787	-1.611	Aspn asporin
NM_013930	0.009647	-1.607	Aass aminoadipate-semialdehyde synthase
NM_177239	0.006622	-1.605	Mysm1 myb-like, SWIRM and MPN domains 1
NM_181595	0.005654	-1.604	Ppp1r9a protein phosphatase 1, regulatory (inhibitor) subunit 9A
NM_008720	0.007785	-1.603	Npc1 Niemann Pick type C1
NM_001163493///NM_146258	0.002365	-1.599	Stard13 StAR-related lipid transfer (START) domain containing 13
NM_178702	0.002633	-1.598	Radil Ras association and DIL domains
NM_178935	0.001568	-1.596	Txlng taxilin gamma
NM_007419	0.004080	-1.593	Adrb1 adrenergic receptor, beta 1
NM_019790	0.002189	-1.593	Tmeff2 transmembrane protein with EGF-like and two follistatin-like domains 2
NM_145442	0.003055	-1.591	Mbip MAP3K12 binding inhibitory protein 1
NM_198702	0.002951	-1.590	Lphn3 latrophilin 3
NM_026433	0.000464	-1.589	Tmem100 transmembrane protein 100
NM_027594	0.006785	-1.587	Ttll7 tubulin tyrosine ligase-like family, member 7
XR_141471///XR_142117	0.002980	-1.586	Gm17739 predicted gene, 17739
NM_001038696///NM_026043/	0.006678	-1.585	Rnpc3///Amy1 RNA-binding region (RNP1, RRM) containing 3///amylase 1, salivary
NM_033079	0.000362	-1.579	M1ap meiosis 1 associated protein

RefSeq Transcript ID	p	*FC (SFN vs Gene Symbol)	Gene Symbol	Gene Title
NM_029620	0.002243	-1.575	Pcolce2	procollagen C-endopeptidase enhancer 2
NM_008437	0.001484	-1.569	Napsa	napsin A aspartic peptidase
NM_009623	0.006958	-1.567	Adcy8	adenylate cyclase 8
NM_022319	0.006438	-1.566	Clstn2	calyntenin 2
NM_001243132///NM_027533	0.001888	-1.561	Tspan2	tetraspanin 2
NM_134160	0.001418	-1.561	Mcoln3	mucoilin 3
NM_172991	0.005479	-1.557	Rbm48	RNA binding motif protein 48
NM_009016///NM_009017///N	0.001152	-1.555	Raet1a	retinoic acid early transcript 1, alpha
NM_133710	0.008281	-1.553	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like
NR_027799	0.008929	-1.552	Tbrg3	transforming growth factor beta regulated gene 3
NM_139142	0.000853	-1.551	Slc6a20a	solute carrier family 6 (neurotransmitter transporter), member 20A
NM_007934	0.003239	-1.550	Enpep	glutamyl aminopeptidase
NM_001164885///NM_022882	0.006686	-1.546	Lpin2	lipin 2
NM_001076676///NM_0012524	0.002149	-1.545	Usp33	ubiquitin specific peptidase 33
NM_001099319///NM_177462	0.001566	-1.541	Zmym6	zinc finger, MYM-type 6
NM_008587///XM_003689343	0.003233	-1.541	Mertk	c-mer proto-oncogene tyrosine kinase
NM_001163332///NM_0011633	0.002572	-1.540	Cttnbp2nl	CTTNBP2 N-terminal like
NM_175930	0.001041	-1.540	Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5
NM_026929	0.006020	-1.535	Chac1	ChaC, cation transport regulator 1
NM_010638	0.004873	-1.532	Klf9	Kruppel-like factor 9
NM_144862	0.000600	-1.531	Lims2	LIM and senescent cell antigen like domains 2
NM_020259	0.007899	-1.530	Hhip	Hedgehog-interacting protein
NM_146249	0.003839	-1.530	Zfp119b	zinc finger protein 119b
NM_001170669///NM_172263	0.007129	-1.525	Pde8b	phosphodiesterase 8B
NM_001177806///NM_013719	0.000412	-1.520	Eif2ak4	eukaryotic translation initiation factor 2 alpha kinase 4
NM_001204165///NM_00120410	0.000734	-1.518	Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4
NM_001001130///NM_198322	0.001656	-1.517	Zfp273///Zfp85-rs1	zinc finger protein 273///zinc finger protein 85, related sequence 1
NM_010680	0.007166	-1.514	Lama3	laminin, alpha 3
NM_001013580///NM_0010135	0.008025	-1.512	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)
NM_026825///NM_177807	0.009713	-1.512	Lrrc16a	leucine rich repeat containing 16A
NM_183312///NM_201639///N	0.000577	-1.511	Synm	synemin, intermediate filament protein
NM_172591	0.004616	-1.510	Fcho2	FCH domain only 2
NM_008760	0.003158	-1.509	Ogn	osteoglycin
NM_016693	0.005024	-1.509	Map3k6	mitogen-activated protein kinase kinase kinase 6
NM_178899	0.001307	-1.507	Hepacam2	HEPACAM family member 2
NM_026856///XM_986833	0.001828	-1.505	Zfp644	zinc finger protein 644
NM_172771	0.001995	-1.504	Dmxl2	Dmx-like 2

RefSeq Transcript ID	p	*FC (SFN vs	Gene Symbol	Gene Title
NR_028300	0.006963	-1.504	5330426P16Rik	RIKEN cDNA 5330426P16 gene
NM_145953	0.006739	-1.504	Cth	cystathionase (cystathionine gamma-lyase)
NM_133753	0.006808	-1.504	Errfi1	ERBB receptor feedback inhibitor 1
NM_009128	0.008295	-1.500	Scd2	stearoyl-Coenzyme A desaturase 2
NM_029128	0.001949	-1.498	Qtrtd1	queuine tRNA-ribosyltransferase domain containing 1
NM_009517	0.005902	-1.496	Zmat3	zinc finger matrin type 3
NM_175480	0.004184	-1.496	Zfp612	zinc finger protein 612
NM_001164572///NM_133741/	0.005455	-1.493	Snrk	SNF related kinase
NM_011545	0.007500	-1.491	Tcf21	transcription factor 21
NM_178633	0.005603	-1.490	Klhl2	kelch-like 2, Mayven
NM_001110327///NM_011806	0.004647	-1.490	Dmtf1	cyclin D binding myb-like transcription factor 1
NM_199317	0.003245	-1.487	Phf16	PHD finger protein 16
NM_011107	0.005905	-1.487	Pla2g1b	phospholipase A2, group IB, pancreas
NM_025811	0.001981	-1.485	Nhlrc2	NHL repeat containing 2
NM_054077	0.001630	-1.481	Prelp	proline arginine-rich end leucine-rich repeat
NM_016886	0.008683	-1.479	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)
NM_001122733///NM_021099	0.006665	-1.479	Kit	kit oncogene
NM_010423	0.003290	-1.479	Hey1	hairy/enhancer-of-split related with YRPW motif 1
NM_001114098///NM_172963	0.003211	-1.478	Soga2	SOGA family member 2
NM_201372	0.001593	-1.478	Ccdc84	coiled-coil domain containing 84
NM_009180	0.001331	-1.477	St6galnac2	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
NM_001110100///NM_016812	0.006055	-1.476	Banp	BTG3 associated nuclear protein
NM_001168525///NM_0011685	0.002552	-1.475	Sgms1	sphingomyelin synthase 1
NM_001190371	0.006082	-1.473	Ankrd29	ankyrin repeat domain 29
NM_020260	0.007640	-1.473	Arhgap31	Rho GTPase activating protein 31
NM_029949	0.001670	-1.473	Snopc3	small nuclear RNA activating complex, polypeptide 3
NM_021398	0.001425	-1.471	Slc43a3	solute carrier family 43, member 3
NM_026917	0.007471	-1.470	Zdhhc3	zinc finger, DHHC domain containing 3
NM_053072	0.004910	-1.470	Fgd6	FYVE, RhoGEF and PH domain containing 6
NM_001002846///NM_013911	0.003377	-1.469	Fbx12	F-box and leucine-rich repeat protein 12
NM_207213	0.001515	-1.469	Snx25	sorting nexin 25
NM_001163073///NM_172153/	0.001528	-1.469	Lcorl	ligand dependent nuclear receptor corepressor-like
NM_053132	0.001701	-1.469	Pcdhb7	protocadherin beta 7
NM_026382	0.004359	-1.466	Snrnp48	small nuclear ribonucleoprotein 48 (U11/U12)
NM_001164493	0.001139	-1.462	Klhl29	kelch-like 29
NM_022886	0.002178	-1.460	Scel	sciellin

RefSeq Transcript ID	p	*FC (SFN vs Gene Symbol)	Gene Symbol	Gene Title
NM_001077364///NM_010286	0.004604	-1.460	Tsc22d3	TSC22 domain family, member 3
NM_010216	0.001544	-1.459	Figf	c-fos induced growth factor
NM_023363	0.007214	-1.459	Zfp788	zinc finger protein 788
NM_001081034	0.003166	-1.454	Fbxo11	F-box protein 11
NM_133725///NM_177608	0.002938	-1.454	Secisbp2l	SECIS binding protein 2-like
NM_001045483///NM_027115	0.004468	-1.454	Mapk1ip1	mitogen-activated protein kinase 1 interacting protein 1
NM_172530	0.002694	-1.454	She	src homology 2 domain-containing transforming protein E
NM_145589	0.005671	-1.452	Prr14	proline rich 14
NM_001161817///NM_010863	0.004967	-1.451	Myo1b	myosin IB
NM_144551	0.008711	-1.449	Trib2	tribbles homolog 2 (Drosophila)
NM_001081295	0.009547	-1.449	Arhgef26	Rho guanine nucleotide exchange factor (GEF) 26
NM_001082414///NM_012059	0.008511	-1.448	Sh3d19	SH3 domain protein D19
NM_010929	0.002278	-1.447	Notch4	notch 4
NM_020518	0.003985	-1.447	Vsig2	V-set and immunoglobulin domain containing 2
NM_001122899///NM_010704/	0.009831	-1.446	Lepr	leptin receptor

Table E2. Nrf2^{-/-} mice: Air PBS vs SFN:

Moderated T-Test (p-value cut-off:0.01)/Fold Change 1.45

*Fold change (FC) in red incates increased and in blue decreased by SFN.

RefSeq Transcript ID	p	*FC (SFN vs PBS)	Gene Symbol	Gene Title
NM_027150	0.007016	2.97	2310046A06Rik	RIKEN cDNA 2310046A06 gene
NM_021503	0.002281	2.66	Myoz2	myozenin 2
	0.000275	2.33	9030411K21Rik	RIKEN cDNA 9030411K21 gene
	0.002366	2.13	AI451250	expressed sequence AI451250
NM_009626	0.002661	2.09	Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide
NM_001177713///NM_	0.003699	2.08	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1
NM_008185	0.000468	1.87	Gstt1	glutathione S-transferase, theta 1
NM_053254	0.000104	1.77	Tle6	transducin-like enhancer of split 6, homolog of Drosophila E(spl)
NM_018808	0.004650	1.76	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1
NM_016808///NM_198	0.006660	1.66	Usp2	ubiquitin specific peptidase 2
NM_181407	0.005373	1.64	Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial
	0.006271	1.63	AI120166	expressed sequence AI120166
NM_175441	0.003228	1.62	Mylk3	myosin light chain kinase 3
NM_001143776///NM_	0.000613	1.60	Fam13c	family with sequence similarity 13, member C
NM_027829	0.002368	1.58	Izumo4	IZUMO family member 4
NM_001113478///NM_	0.000510	1.53	Frrs1	ferric-chelate reductase 1///Ferric-chelate reductase 1
NM_011330	0.004814	1.52	Ccl11	chemokine (C-C motif) ligand 11
NM_207677	0.003661	1.48	Dedd2	death effector domain-containing DNA binding protein 2
NM_001159738///NM_	0.004642	1.46	Ccl20	chemokine (C-C motif) ligand 20
NM_013794	0.001797	-2.63	Klra16	killer cell lectin-like receptor, subfamily A, member 16
NM_001080971	0.001696	-2.42	Tubb1	tubulin, beta 1
NM_008981	0.000514	-2.01	Ptprg	protein tyrosine phosphatase, receptor type, G
NM_201371	0.002041	-1.98	Prmt8	protein arginine N-methyltransferase 8
NM_009704	0.009709	-1.78	Areg	amphiregulin
NM_011198	0.003664	-1.78	Ptgs2	prostaglandin-endoperoxide synthase 2
NM_025633	0.005264	-1.76	Metap1d	methionyl aminopeptidase type 1D (mitochondrial)
NM_001099774	0.000677	-1.75	Krtap17-1	keratin associated protein 17-1
NM_023900	0.000638	-1.73	Plekhl1	pleckstrin homology domain containing, family J member 1
XM_001476669	0.001763	-1.68	Gm3426	Predicted gene 3426
NM_001081128	0.004736	-1.63	Mtr	5-methyltetrahydrofolate-homocysteine methyltransferase
XR_105482///XR_1067C	0.004751	-1.62	LOC100503961	hypothetical LOC100503961

RefSeq Transcript ID	<i>p</i>	*FC (SFN vs PBS)	Gene Symbol	Gene Title
NM_029816	0.001113	-1.60	2610028H24Rik	RIKEN cDNA 2610028H24 gene
NM_009789	0.003389	-1.58	S100g	S100 calcium binding protein G
NM_001042725///NM_	0.007480	-1.55	Calcr	calcitonin receptor
NM_001159986///NM_	0.000165	-1.52	Sec16b	SEC16 homolog B (<i>S. cerevisiae</i>)
NM_009616	0.000355	-1.52	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)
NM_012033	0.000080	-1.51	Tinag	tubulointerstitial nephritis antigen
NM_001004150///NM_	0.008967	-1.51	A4galt	alpha 1,4-galactosyltransferase
NM_001024139	0.001064	-1.50	Adamts15	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 15
NM_023186	0.001372	-1.48	Chia	chitinase, acidic
NR_015549///NR_0279:	0.003098	-1.45	Trmt61b	tRNA methyltransferase 61 homolog B (<i>S. cerevisiae</i>)

Table E3. Potential AREs in selected (n=193) sulforaphane-responsive lung genes
Fold increase (F) by SFN over PBS-pretreatment in Nrf2+/- mice

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
<i>Acaa2</i>	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) NM_177470 chr18 74938865 74965861 + chr18 E2 18 45.0 cM	NM_177470	74933855	74933875	ACTATAGCTGGTATATAGAAA	RC	7	0.778	-5010	upstream	1.48				
			74934402	74934422	GGGTCTGCTATGTCCacctggcc	RC	10.8	0.89	-4463	upstream					
			74935801	74935821	CATATGGCTACGTGACAGTGT	RC	7.5	0.777	-3064	upstream					
			74937267	74937287	TGAGACTGAAACTGCAGATAT	FW	10.4	0.805	-1598	upstream					
			74937571	74937591	TAGATGTGAACACAGCAACAG	FW	10.1	0.837	-1294	upstream					
			74941636	74941656	agtagtcagagtaattcttt	RC	12.1	0.815	2771	intron1					
			66908259	66908279	TATCATTACTTGGCAGTTAA	FW	7	0.77	1624	¹ intron1					
<i>Acaal</i>	acyl-Coenzyme A dehydrogenase, long-chain NM_007381 chr1 66877412 66909883 - chr1 C3 1 27.3 cM 1-Ch12 Mafk chr1:66908009-66909511 2-Ch12 Mafk chr1:66908009-66909511 3-Ch12 Mafk chr1:66908009-66909511 Ese14 Mafk chr1:66908411-66908772 4-Ch12 Mafk chr1:66908009-66909511	NM_007381	66908377	66908397	agggtctcaactaagcagctcc	FW	6.5	0.8	1506	² intron1	1.75				
			66908594	66908614	ATAAATGCTGACTCAGACTGC	RC	14.2	0.889	1289	³ intron1					
			66908858	66908878	CAGCAATGAGTCAGTGGCCT	FW	8.9	0.834	1025	⁴ intron1					
			66904942	66904962	CGTGCCTGACACTGCATCGCG	FW	8.9	0.85	4941	intron1					
			66905609	66905629	CTAGCTGAGTATAGCAATCTG	FW	9.7	0.849	4274	intron1					
			66906572	66906592	ctgactggcttggcagcgcct	RC	7.5	0.839	3311	intron1					
			66907399	66907419	gctacattaccaagccattgt	FW	7.3	0.763	2484	intron1					
			66911413	66911433	ccacgatgacgaaggaaaggcc	FW	9.1	0.79	-1530	upstream					
			66912001	66912021	gagatggctcagtgattaaaga	RC	6.8	0.788	-2118	upstream					
			66913162	66913182	TCGGAATACGAAGCCAATAA	FW	7.8	0.765	-3279	upstream					
			66913395	66913415	GTGGCTGCTGTGTACAAAGTG	RC	11.6	0.902	-3512	upstream					
			66913521	66913541	CAACCCTGAGACAGCCACCAC	FW	9.6	0.818	-3638	upstream					
			66914038	66914058	cacctgtcttagtcagagttt	RC	8.5	0.784	-4155	upstream					
			66914074	66914094	acaccattgaccaaggaagtc	FW	9.2	0.768	-4191	upstream					
			<i>Acadm</i>	acyl-Coenzyme A dehydrogenase, medium chain NM_007382 chr3 153585316 153607607 - chr3 H3 3 73.6 cM	NM_007382	153602802	153602822	gccaggtgaggcagcacaacac	FW	7.4		0.828	4805	intron2	1.66
						153605473	153605493	TAAATGTCTCAGTCACTTCTCA	RC	17.4		0.946	2134	intron1	
						153607655	153607675	GTCCTTTCAGGCTCAAGGGGT	RC	6.5		0.787	-48	upstream	
153608556	153608576	CCTGTAGCATTTGTCAGGCACA				RC	6.9	0.805	-949	upstream					
153608849	153608869	ctaacagctttgtgaccatta				RC	8	0.773	-1242	upstream					
153609051	153609071	gatattgctacttcattggaa				RC	7.9	0.813	-1444	upstream					
153610842	153610862	CTTTATGCTCAGTACTGAAA				RC	7.4	0.812	-3235	upstream					
153611754	153611774	GATCGAGCTGAGTGAGGAGC				RC	7.1	0.805	-4147	upstream					
153612478	153612498	GCAAGATGACTCTGACACAT				FW	8.1	0.765	-4871	upstream					
<i>Acads</i>	acyl-Coenzyme A dehydrogenase, short chain NM_007383 chr5 115560307 115569355 - chr5 F 5 65.0 cM	NM_007383				115564724	115564744	TGTTTGTGAACAGCCAAAAG	FW	9	0.809	4631	intron2	1.41	
						115565297	115565317	tcagctgactttgaacttgg	FW	9.9	0.779	4058	intron2		
			115567550	115567570	TCACAGTGAGGCTGTGCACCT	FW	6.7	0.777	1805	intron2					
			115567632	115567652	TTCTCGGCAAGTCAAGCGCAT	RC	8.7	0.844	1723	exon2					
			115568532	115568552	TTAATGTGACTCTGGATTAGC	FW	8.6	0.789	823	intron1					
			115571613	115571633	agggactgagcaagcagaggt	FW	6.9	0.798	-2258	upstream					
			115572042	115572062	CTGCAATGACAATGCAAAAGCC	FW	9.1	0.844	-2687	upstream					
			115573415	115573435	CCAGGATGACTGAGCACCCGG	FW	14.6	0.936	-4060	upstream					
			<i>Acadv1</i>	acyl-Coenzyme A dehydrogenase, very long chain NM_017366 chr11 69823684 69828930 - chr11 B2-B5 11 38.0 cM	NM_017366	69824037	69824057	CAGCTATCACAGAGCAATTTTC	FW	8.2	0.792	4893	exon19		1.62
						69824335	69824355	TGCAGAGCTCACTCACTGACA	RC	6.4	0.812	4595	intron17		
69824492	69824512	TTTAAAGCTCACTCAACAGTT				RC	6.8	0.809	4438	intron16					
69826885	69826905	CCGTGAGCAGTGTCACTCC				RC	9.1	0.841	2045	intron7					
69827859	69827879	TTCTTGGCAGGGTCAATCACT				RC	7	0.818	1071	exon6					
69828108	69828128	AGTGACTGACTAAGCCTTTAC				FW	10.3	0.88	822	intron4					
69829266	69829286	GAGGTGGCAGACTCAAGCTGG				RC	8.1	0.805	-336	upstream					
69830415	69830435	cagtgagccatgtcactgccc				RC	7.6	0.815	-1485	upstream					
69831448	69831468	TAGTACTGACTGAGGAGTTGG				FW	8.8	0.796	-2518	upstream					
69833083	69833103	GAGGCCTGATACAGCCTTACC				FW	7.5	0.801	-4153	upstream					
<i>Acat1</i>	acetyl-Coenzyme A acetyltransferase 1 NM_144784 chr9 53388626 53418455 - chr9 C-D 9 30.0 cM	NM_144784	53413605	53413625	tctccatgacacagggcaaca	FW	10.3	0.785	4850	intron1	1.35				
			53413979	53413999	TGAAAAGCAGAGTCAGCCTTA	RC	11.3	0.872	4476	intron1					
			53416146	53416166	TCATGATGAAGAGGCAAAAAG	FW	8.1	0.787	2309	intron1					
			53418110	53418130	GATCGCCCTGTGTCAGGCCCA	RC	7.3	0.804	345	intron1					
			53420794	53420814	ATTTTGGCTAATTCAGCTGGA	RC	8.8	0.816	-2339	upstream					
			53420976	53420996	tagctttgacctgagtgat	FW	7.3	0.83	-2521	upstream					
			<i>Aco2</i>	aconitase 2, mitochondrial NM_080633 chr15 81702892 81745567 + chr15 E1 15	NM_080633	81699053	81699073	GAGGGATGAGAAAGCGATTAC	FW	6.9		0.784	-3839	upstream	1.74
81703523	81703543	AAGAGTGTCTTCTCACTTTTG				RC	11.6	0.838	631	intron1					
81703695	81703715	GAGCAGTGACCCCTGCAGACCC				FW	9.8	0.859	803	intron1					
81703750	81703770	GAACCTTCTGAATCAGGGTGT				RC	10.8	0.778	858	intron1					
81704162	81704182	CAAACTGCAAAATCAAACTCA				RC	8.3	0.809	1270	intron1					
81705284	81705304	ttaaccactgagtcacggctc				RC	11.7	0.812	2392	intron1					
81705601	81705621	tttagtctaagtaactgtga				RC	15.5	0.86	2709	intron1					
81706642	81706662	ggagactgaaactgcatacagg				FW	7.5	0.792	3750	intron1					
81707698	81707718	TAGATTCTTATGCTATTTTC				RC	8.9	0.811	4806	intron1					
<i>Acsf2</i>	acyl-CoA synthetase family member 2 NM_153807 chr11 94418415 94463100 - chr11 D 11	NM_153807				94458756	94458776	acgtcaatgactcagcgggatg	FW	15.3	0.925	4344	intron1	1.30	
			94458920	94458940	taaagctcaactgagcagataca	FW	8.4	0.816	4180	intron1					
			94461682	94461702	TAGAGTGCTAATTCacataca	RC	8.8	0.842	1418	intron1					
			94462413	94462433	cagaagcagagtcagagcaaa	RC	11.7	0.872	687	intron1					
			94464335	94464355	TGGCCTTGAACCGGATGATG	FW	7	0.786	-1235	upstream					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
			94464657	94464677	TTTCTGACTCAGAAATGGA	FW	8.7	0.815	-1557	upstream	
			94464832	94464852	TCAACATGAAGTAGCTTTTT	FW	8	0.802	-1732	upstream	
			94465527	94465547	aaagatgctgctcaaaaataa	RC	8	0.834	-2427	upstream	
			94466586	94466606	GACTGTTGACTCGGAGTTTC	FW	7.1	0.777	-3486	upstream	
			47551763	47551783	agacctgatatagctgctc	FW	7.6	0.796	-4627	upstream	
			47553488	47553508	tgcaatgactgccccctta	FW	6.9	0.832	-2902	upstream	
			47553828	47553848	TTCCAGTGACATGGCTAAATG	FW	8.2	0.818	-2562	upstream	
			47554389	47554409	ttcattgctgctcaacta	RC	14.5	0.916	-2001	upstream	
			47554534	47554554	cagcgtgATATGGCAGCTGT	FW	6.6	0.768	-1856	upstream	
			47554643	47554663	CCTTGATGAGTCAGCTTGA	FW	9	0.837	-1747	upstream	
47554947	47554967	tatacctgactcggccttca	FW	9.7	0.857	-1443	upstream				
47556072	47556092	GGAGAGCGGAGTCAGCAGGA	RC	7.6	0.851	-318	upstream				
47556808	47556828	TGCACCCGGAGTCAAGAGGT	RC	7.1	0.853	418	intron1				
47560238	47560258	CACCGTTGATTAGCAGAATG	FW	10.2	0.846	3848	intron1				
47560834	47560854	CTTGATTGATTACGATAGGT	FW	7.1	0.844	4444	intron1				
47561174	47561194	GGTATTGCCCAAGTACTCTGA	RC	9.5	0.795	4784	intron1				
Acs1l	acyl-CoA synthetase long-chain family member 1 NM_007981 chr8 47556390 47621405 + chr8 8 B2	NM_007981	113874774	113874794	GACTGACTGAGTAAGATGCC	RC	7	0.798	3837	intron5	1.66
			113875188	113875208	GCATATGCTGTGTCAGATAac	RC	8.9	0.887	3423	intron4	
			113875251	113875271	CAGTGGTGACAAAGGAGTACC	FW	8.7	0.778	3360	exon4	
			113875807	113875827	AGAAGAGCTAACTCAACGGGT	RC	7.3	0.817	2804	intron3	
			113875960	113875980	TTCCACGCAAGTCAAGTGGT	RC	7.8	0.84	2651	intron3	
			113876265	113876285	GGTACTTCAGAGTCAGGATAC	RC	7	0.778	2346	exon3	
			113876487	113876507	aggcatgcttgttcatgacctc	RC	7.2	0.807	2124	intron2	
			113879088	113879108	AGAGGAGCAGAGTCATAGGCA	RC	10.3	0.865	-477	upstream	
			113880436	113880456	GAACCTGCTGTGCACCATTC	RC	12.7	0.9	-1825	upstream	
			113882909	113882929	GGCACCTGACTGAGCTGCTGT	FW	7.6	0.867	-4298	upstream	
113883005	113883025	GAGAAGTAACTGCACTTAA	FW	8.3	0.813	-4394	upstream				
Adhfe1	alcohol dehydrogenase, iron containing, 1 NR_027664 chr1 9538126 9568049 + chr1 A2 1	NM_175236 NR_027664	9533788	9533808	CAAAGATGAATTTGCCATCAT	FW	7	0.78	-4338	upstream	1.34
			9534314	9534334	AAATAATTACTTTGGATTCTA	FW	8.3	0.783	-3812	upstream	
			9536579	9536599	CGGCCCGCGGTCAGGGAGA	RC	7.3	0.827	-1547	upstream	
			9540791	9540811	GAGAAGCCAGAGTCAGAGGT	RC	9	0.861	2665	intron2	
			158325695	158325715	AGCTTCTGACCCAGCCTGTG	FW	10	0.886	-2652	upstream	
Adig	adipogenin NM_145635 chr2 158328347 158333934 + chr2 H1 2	NM_145635	158325850	158325870	TTCTCTGCTTATTCAAGCCTGG	RC	12	0.862	-2497	upstream	3.43
			158326462	158326482	Tgataaatgataaagctttaa	FW	7.8	0.798	-1885	upstream	
			158326935	158326955	atcttagcttgcctgatgttcc	RC	6.4	0.787	-1412	upstream	
			158326981	158327001	tcagggtgaaeggaaattct	FW	10.1	0.763	-1366	upstream	
			158328218	158328238	GTGACTCTGGGTCAAGCCAG	RC	6.8	0.776	-129	upstream	
			158328589	158328609	TTTCTTACTTAGTCAAGGTGA	RC	11.8	0.828	242	exon1	
			158329521	158329541	TAGGGCTGACTGGGCAACAGT	FW	11.2	0.869	1174	intron1	
			158330453	158330473	CTGTAGGCTCAATCAGTGTG	RC	7	0.815	2106	intron1	
			158330625	158330645	TTGTCTGTAACCTCAGCCTGC	RC	11.2	0.858	2278	intron1	
			158332525	158332545	cttccctcaacagctgttgg	FW	8.4	0.786	4178	intron2	
158332622	158332642	CCCCCTGACTCTGCCTACT	FW	14.1	0.909	4275	intron2				
158332977	158332997	CTCTGAGCTCTGCATCTCC	RC	7.1	0.843	4630	intron2				
158333299	158333319	AACCTTCTGGGTCATAGCT	RC	8.3	0.788	4952	intron2				
Adipoq	adiponectin, C1Q and collagen domain containing NM_009605 chr16 23146608 23158041 + chr16 B3-B4 16 16.0 cM 1-Ch12 Mafk chr16:23144184-23145174 2-Ch12 Mafk chr16:23144184-23145174	NM_009605	23144752	23144772	AGCCTATAACTAGAGCAGAGGT	FW	8.4	0.813	-1856	¹ upstream	8.73
			23145147	23145167	AGAGAGTGATACAGCTTTGAG	FW	8.7	0.817	-1461	² upstream	
			23143248	23143268	cattttaccagctcagaattgt	RC	6.9	0.765	-3360	upstream	
			23143764	23143784	TGTGGATAACACAGCTTTTCT	FW	7	0.776	-2844	upstream	
			23144159	23144179	TCTGTGGCTGCTCTCACTCTGG	RC	8.9	0.819	-2449	upstream	
			23146397	23146417	AAACATGCTGAATTATTGFC	RC	9.6	0.783	-211	upstream	
			23147724	23147744	ATTTGATCAGAGTCATTTCTGT	RC	9	0.777	1116	intron1	
			23148783	23148803	CCAAAGGCTGAGTGACACCTT	RC	9	0.809	2175	intron1	
			23150428	23150448	AGTCTTTCAAAGTCAGAGTGC	RC	7.4	0.777	3820	intron1	
			23151227	23151247	gcaagatgactcagtgagtaa	FW	10.6	0.813	4619	intron1	
Aldh1l2	aldehyde dehydrogenase 1 family, member L2 NM_153543 chr10 82950191 82996885 - chr10 C1 10	NM_153543	82992296	82992316	GTGTGGTGACATAGCATGAAA	FW	9.4	0.878	4589	intron1	1.66
			82992739	82992759	TATCAGTGACTTAGTGTAA	FW	8.8	0.782	4146	intron1	
			82992993	82993013	gctgactgattcagctgtgct	FW	7.7	0.829	3892	intron1	
			82993575	82993595	GCCAAAGCTGAGTCACTGTGG	RC	16	0.941	3310	intron1	
			82994136	82994156	attactctctgctcacaacaaac	RC	7.2	0.787	2749	intron1	
			82994306	82994326	cactggctgagttacttctgtt	RC	7.5	0.799	2579	intron1	
			82995339	82995359	TAACGTTTACAGAGCACTGTG	FW	9.4	0.801	1546	intron1	
			82995784	82995804	TGAGGGTTACACAGCAGAATG	FW	14.8	0.839	1101	intron1	
			82995930	82995950	CATATGGCAATGTCAGAGAAA	RC	6.7	0.809	955	intron1	
			82996221	82996241	TGCACGCTGGGTGATCCTGT	RC	8.1	0.789	664	intron1	
83001191	83001211	agatctgctcagtaaaacttcc	RC	7.7	0.813	-4306	upstream				
83001852	83001872	acacatgacccaaggcagctc	FW	8.1	0.764	-4967	upstream				
Alox15	arachidonate 15-lipoxygenase NM_009660 chr11 70157648 70165533 -	NM_009660	70161221	70161241	TAACACTGACTCTGGAGAGGA	FW	10.4	0.792	4312	intron7	2.33
			70162546	70162566	ttaaatcaccacgcaaac	FW	7.6	0.803	2987	intron6	
			70165083	70165103	GGCAGCTGACACTGCTGATAC	FW	6.7	0.817	450	intron1	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
	chr11 B3 11 40.0 cM		70165183	70165203	CAACTGTTACTGAGCGCTCAC	FW	9.2	0.805	350	intron1					
			70168346	70168366	CAGGGCTGAAGAGGCAAGACCG	FW	6.5	0.801	-2813	upstream					
			70168369	70168389	TGACCCCTGAGACCGCCATTGA	FW	8.7	0.781	-2836	upstream					
			70169423	70169443	agatcagcttagtgacagagca	RC	7.5	0.79	-3890	upstream					
			70170214	70170234	AAGTCATCATTCAGCAGAGTG	FW	7.7	0.764	-4681	upstream					
			70170296	70170316	TCACTCTGCACAAATGCTCATGT	FW	10.7	0.838	-4763	upstream					
Aoc3	amine oxidase, copper containing 3 NM_009675 chr11 101191919 101200744 + chr11 11 B2-B5	NM_009675	101187189	101187209	TGGGCATTACTATGACAGACTT	FW	10.8	0.787	-4730	upstream	2.35				
			101189327	101189347	Tggccttgactttgcagctcat	FW	11.7	0.878	-2592	upstream					
			101192021	101192041	CAACCCCTGACCCAGAGAGCAC	FW	6.8	0.763	102	UTR5					
			101192249	101192269	AAGCAATGACCCAGAGAGCCA	FW	7.3	0.784	330	UTR5					
			101192471	101192491	GCTTCTGACCAAGCACCTGG	FW	9.9	0.877	552	exon1					
			101192660	101192680	CCAACCTGAGTGAAGCTGGTGG	FW	8.9	0.831	741	exon1					
			101193068	101193088	AGAGTCTCACTCAGCTGGAGG	FW	7	0.8	1149	exon1					
			101194576	101194596	Tggaatttactctgcagatca	FW	6.8	0.781	2657	intron1					
Apol6	apolipoprotein L 6 NM_001163621 chr15 76875504 76882781 + chr15 15 E1	NM_001163621 NM_028010	76870626	76870646	ATGTATGCATCTACACAGGGG	RC	9.2	0.816	-4878	upstream	1.58				
			76870991	76871011	AGAAGTGCAGGGTCAAGATGC	RC	10.8	0.87	-4513	upstream					
			76871646	76871666	tcaacttgacacagctggagt	FW	12	0.892	-3858	upstream					
			76871968	76871988	cttgccttctggctcatgatgc	RC	8.4	0.784	-3536	upstream					
			76872003	76872023	aaacctgactaaagacaatt	FW	10.9	0.795	-3501	upstream					
			76873239	76873259	agatttgagctgagcctgat	FW	8.7	0.849	-2265	upstream					
			76873507	76873527	tcaacttgacacagctggagt	FW	12	0.892	-1997	upstream					
			76873812	76873832	cttgccttctggctcatgatgc	RC	8.5	0.784	-1692	upstream					
			76873847	76873867	aaacctgactaaagacacag	FW	8.9	0.785	-1657	upstream					
			76874867	76874887	gaatcattactctgacagctg	FW	10.4	0.806	-637	upstream					
			76875024	76875044	GCTGGGTAAACATAGCACATAC	FW	8.6	0.794	-480	upstream					
			76879760	76879780	TCAGAGTGACTTAGGTTCTGC	FW	9.1	0.792	4055	intron3					
			76879782	76879802	GCATcctgactagcatgtca	FW	6.4	0.811	4077	intron3					
			Apol7a	apolipoprotein L 7a//apolipoprotein L 7c//apolipoprotein L, 3-like NM_001164640 chr15 77218646 77229540 - chr15 E1 15	NM_001164640 NM_029419 NM_175391 NR_033577	77226334	77226354	CCACTGTGACCTAGGACTGGG	FW	9.6		0.793	3206	intron2	1.70
						77226769	77226789	CCCACAGCTTAGTGATTAGGG	RC	6.7		0.786	2771	intron1	
						77226917	77226937	agaattgccatgtaattggggc	RC	9.8		0.768	2623	intron1	
77226989	77227009	agaagaactctgctcactgttg				RC	11.9	0.879	2551	intron1					
77227116	77227136	AAGGACTGACTCTGCACACAA				FW	11.7	0.886	2424	intron1					
77227678	77227698	ccctaatgaccaagcatcaaa				FW	10.5	0.883	1862	intron1					
77228521	77228541	CAGTGGTGAAGTCAAGTCTAGA				FW	7.7	0.787	1019	intron1					
77232289	77232309	CCAGATGCAAAATTCATCTTA				RC	7	0.795	-2749	upstream					
77232758	77232778	AGACCTTGACTCAGAGTTTCA				FW	8.6	0.802	-3218	upstream					
77233263	77233283	AATGCCCTGGGTCAAGGGTT				RC	8.9	0.772	-3723	upstream					
Apol7c	apolipoprotein L 7a//apolipoprotein L 7c//apolipoprotein L, 3-like NM_001164640 chr15 77218646 77229540 - chr15 E1 15	NM_001164640 NM_029419 NM_175391 NR_033577				77358872	77358892	acacttgctgagctcaagctg	RC	10.9	0.84	4873	intron4	1.70	
						77361047	77361067	CACTGGGCTCTGCTCACTGCTA	RC	11.2	0.867	2698	intron1		
			77362551	77362571	TGTTAGGCTCTGTCACATTGT	RC	9	0.869	1194	intron1					
			77362846	77362866	AGGAATTGACTTTGCACTCAG	FW	7.5	0.855	899	intron1					
			77366014	77366034	gTtttctgcttagtataat	RC	8.8	0.821	-2269	upstream					
			77366232	77366252	aggctgsgacaagctggaaa	FW	9.6	0.86	-2487	upstream					
			77367701	77367721	gtgtgtctctgctcatggtgt	RC	7.8	0.762	-3956	upstream					
			77368065	77368085	tatgtatgaatcagctttagt	FW	9.6	0.837	-4320	upstream					
			77368337	77368357	tcatgggctcagtcagaccoca	RC	10.2	0.878	-4592	upstream					
			Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 NM_009722 chr5 122903521 122952234 - chr5 F 5 65.0 cM 1-Ch12 Mafk chr5:122948123-122948641 2-Ch12 Mafk chr5:122950857-122951357	NM_001110140 NM_009722 NR_027838	122948256	122948276	aaactagctgaaatcagcagc	RC	10.3	0.843	3978	¹ intron3		2.07
122951205	122951225	ATTTACAGCTGGGTCATCATT				RC	10.5	0.869	1029	² intron1					
122947886	122947906	taaaaggctaaagtaaggcaag				RC	6.5	0.779	4348	intron3					
122949084	122949104	AGAAAATAACTTGGCACAATAT				FW	7.9	0.779	3150	intron3					
122949121	122949141	ACATGTTCACTTGGCACAATTT				FW	7.6	0.782	3113	intron3					
122949472	122949492	AGTAAATAACTCAGCAGTATG				FW	10.6	0.836	2762	intron3					
122949773	122949793	AGAACCCTGGGTCAAGACTTA				RC	7.8	0.766	2461	intron3					
122950536	122950556	GACCCCTGCAGTCAGGGGTC				RC	8	0.859	1698	intron3					
122950787	122950807	CAAAGTCTCAATCAACAGTT				RC	9.4	0.844	1447	exon3					
122951868	122951888	CGGGCCGCTGAATCACCCGAG				RC	6.7	0.824	366	UTR3					
122953434	122953454	TTGCATTGAATTTGCAATAT				FW	6.8	0.796	-1200	upstream					
Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 NM_001112738 chr2 9977658 10002137 - chr2 A1 2 1-Ch12 Mafk chr2:10004398-10004767 2-Ch12 Mafk chr2:10004398-10004767	NM_001112738 NM_020615				10004579	10004599	cagaccTGACCTGCAGTTTA	FW	10.1	0.855	-2442	¹ upstream	1.44	
			10004711	10004731	AATATTGCTTTGTAACCTTTA	RC	13.6	0.821	-2574	² upstream					
			9997363	9997383	GACATGTGACACAGGAGCCAC	FW	6.5	0.781	4774	intron1					
			9999063	9999083	GTGAGATGACAGGGCCACAGTG	FW	6.7	0.83	3074	intron1					
			9999985	10000005	TGGAGTACTGAGTCAAAGGCC	RC	6.9	0.809	2152	intron1					
			10003587	10003607	gaacttgcctgagtaaccagga	RC	7	0.808	-1450	upstream					
			10005100	10005120	CCACCATGAGGGTGCAGTTCA	FW	7.8	0.791	-2963	upstream					
			10005944	10005964	gagttgccttggctcatggtgt	RC	9	0.768	-3807	upstream					
			10006941	10006961	tttctactgggtcaccagag	RC	6.4	0.776	-4804	upstream					
			Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c1 (subunit 9) NM_001161419 NM_007506	NM_001161419 NM_007506	95932445	95932465	AGAAATGCAGAGTCAATGTCA	RC	14.1	0.912	4500	¹ downstream		1.83
95932515	95932535	TCTTGATGAGTCAGCAGCTG				FW	13.3	0.879	4430	² downstream					
95932806	95932826	tcgtaactcactgagctatctc				FW	7.2	0.79	4139	downstream					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
	NM_001161419 chr11:95934106-95936945 - chr11 D 11 1-Ch12 Mafk chr11:95932309-95932696 Mel Mafk chr11:95932010-95932712 2-Ch12 Mafk chr11:95932309-95932696 Mel Mafk chr11:95932010-95932712		95933743	95933763	GCAATGGCTGTGTGACACCTT	RC	8.4	0.782	3202	downstream	
			95934129	95934149	TGAAAGTGACAAGACCAAC	FW	13.7	0.905	2816	UTR3	
			95934202	95934222	CACCTGCCTTATCACCAAGG	RC	7	0.778	2743	UTR3	
			95938247	95938267	cctctttgaccagcaatct	FW	7.2	0.788	-1239	upstream	
			95940075	95940095	latgltgtaagLaaccoccg	RC	11.4	0.807	-3067	upstream	
			95940686	95940706	tctaactgattcagcctccta	FW	7.8	0.83	-3678	upstream	
Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e NM_007507 chr5:108862271-108863397 - chr5 F 5 56.0 cM 1-Ch12 Nrf2 chr5:108863169-108863660	NM_007507	108863261	108863281	GGCAATGCTAAGTCAAGGGAG	RC	12.5	0.922	136	¹ intron1	1.49
			108858418	108858438	AAATGTCTtactcaacctga	RC	11.2	0.766	4979	downstream	
			108859529	108859549	GATCAGTGAACAGCATGGTG	FW	9.4	0.837	3868	downstream	
			108859762	108859782	TTAACCCCTAAGTCAATGCTG	RC	7.1	0.771	3635	downstream	
			108860323	108860343	ACAGCTTCTGGGTCAATAGGAG	RC	6.7	0.781	3074	downstream	
			108862889	108862909	GCTTCGTGAAAAGCCGACTC	FW	7	0.793	508	intron2	
			108862990	108863010	GCAGTGTACACACAGCTTTCA	FW	8.8	0.798	407	intron2	
			108864835	108864855	CCTCTGCCAACTCACTGCTC	RC	8.5	0.805	-1438	upstream	
			108865568	108865588	TAGGAGTTACCCAGCTATCAG	FW	7.9	0.775	-2171	upstream	
			108865731	108865751	CAGCCTGCAGGCTCACTCCCA	RC	7.2	0.785	-2334	upstream	
			108865861	108865881	CTGAGGGCCGTGTCAAGACTG	RC	7.3	0.823	-2464	upstream	
			108865938	108865958	TGCCCATGACCCAGCTACAGA	FW	11.8	0.879	-2541	upstream	
			108866202	108866222	aaaaCTGCACAAGCATACAT	FW	12.3	0.895	-2805	upstream	
			108866439	108866459	CTGAGCTCACTTCGAGTTGT	FW	6.9	0.781	-3042	upstream	
			108867050	108867070	AGGAGGTGAGTCTGCCTTTC	FW	7.4	0.792	-3653	upstream	
108867544	108867564	AGTGGATGACACAGCCAGCCC	FW	9.5	0.87	-4147	upstream				
B4gal6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 NM_019737 chr18:20843099-20904905 - chr18 A2 18 1-Ch12 Mafk chr18:20902921-20903933 2-Ch12 Mafk chr18:20902921-20903933	NM_019737	20903064	20903084	ACCAAGTCACTCAGCATTAAA	FW	11.2	0.845	1841	¹ intron1	1.47
			20903535	20903555	TAAAGGTGACTAGTAAAACCT	FW	9.3	0.776	1370	² intron1	
			20900041	20900061	AGGAAGTTACTCGGCCTCTC	FW	9.4	0.796	4864	intron1	
			20900387	20900407	AATAGAGCTTCCTCATGGGGC	RC	6.6	0.791	4518	intron1	
			20906334	20906354	ATGTATGCTAAGTGAGAATGA	RC	9.1	0.823	-1429	upstream	
			20906369	20906389	TTATGAGCTTAGTAAAATTA	RC	6.6	0.786	-1464	upstream	
			20906825	20906845	agactagctgaatcagggagc	RC	9.4	0.84	-1920	upstream	
			20907242	20907262	AATCTGCTGAGTAAAAGGA	RC	11.7	0.843	-2337	upstream	
			20907675	20907695	TTATCAGCCCAAGTCAACTCA	RC	8.7	0.845	-2770	upstream	
			20907736	20907756	GCTCCTTCACTCGGCGGGTA	FW	6.7	0.79	-2831	upstream	
			20907843	20907863	ATAGGGTCTGTGTCAAGGATTC	RC	7.5	0.766	-2938	upstream	
			20908028	20908048	CTACGTTCAATTCAGCAGATTG	FW	7.1	0.77	-3123	upstream	
			73508166	73508186	ctagggccttactcaactagcc	RC	7.4	0.776	4171	intron1	
			73508745	73508765	TATTGATGAATCTCGAGTGT	FW	10.4	0.826	3592	intron1	
			73511558	73511578	AGTGTGCTTGGTAAAAGTGC	RC	7.4	0.794	779	intron1	
73513326	73513346	AATCTTCTATGTTACTAGCC	RC	7.5	0.783	-989	upstream				
Bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide NM_007533 chr7:26414870-26443780 - chr7 A3 7	NM_007533	26440729	26440749	GGAGACTGAGCCAGCAGGAAA	FW	8.9	0.83	3051	intron1	1.26
			26441758	26441778	aaccttgaaccagatgtgt	FW	6.9	0.779	2022	intron1	
			26442626	26442646	gctcagtgactaagagcactg	FW	8.4	0.786	1154	intron1	
			26446521	26446541	ttcatggcttgttcaagcctgc	RC	7	0.791	-2741	upstream	
			26446937	26446957	tagatagcatggtcagggcca	RC	7.8	0.81	-3157	upstream	
			26447403	26447423	ACGTTAGCAAGTCAACAGAG	RC	6.6	0.831	-3623	upstream	
Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide NM_199195 chr9:83842387-84017847 + chr9 E2 9	NM_199195	83837499	83837519	cagtcgcagactcattcatt	RC	7.2	0.789	-4888	upstream	1.38
			83838892	83838912	aggaatgatctcgcatttt	FW	7.5	0.79	-3495	upstream	
			83840185	83840205	ccttccgctgagtttaagccct	RC	8.5	0.805	-2202	upstream	
			83841057	83841077	gggaaatgatttgcagataa	FW	7	0.794	-1330	upstream	
			83842269	83842289	gacaaataactcagcagggat	FW	8.7	0.825	-118	upstream	
			83843577	83843597	GTGTGCTGACACAGAACATA	FW	6.7	0.778	1190	intron1	
			83844120	83844140	tcaacttgacacagccttaggg	FW	11.6	0.891	1733	intron1	
			83845241	83845261	AAAGCTTCAAAGTCATGCATA	RC	8.2	0.762	2854	intron1	
			83846894	83846914	tcctatgaaggtcaggattg	RC	7.2	0.836	4507	intron2	
			31418125	31418145	ccaccatgatcctgctccac	FW	6.4	0.774	-4257	upstream	
			31418207	31418227	TGTGAAGCTGTGTACCAAGG	RC	9.6	0.877	-4175	upstream	
31418502	31418522	gaggcagctcagtcagtgagc	RC	8.5	0.879	-3880	upstream				
31422314	31422334	AAACAGTAAACAAGCTGAAC	FW	7.5	0.773	-68	upstream				
31423716	31423736	tagtgatcgcctcagcatgc	RC	7	0.812	1334	intron1				
31424311	31424331	ACTTTCTGAACAGCAGTAA	FW	8.3	0.829	1929	intron1				
31425116	31425136	agcctggctggttcaattgagc	RC	6.4	0.801	2734	intron1				
31427075	31427095	TAGACTTAACTCAGCACTGCC	FW	8.3	0.826	-1763	upstream				
31427726	31427746	ACTGGTGACACAGTATACTG	FW	9.3	0.8	-1112	upstream				
31430003	31430023	TCTACTGCGAGCTCAGGCAGC	RC	6.4	0.822	1165	intron1				
31430222	31430242	GCAGGTGCAGAGTCACTGTCT	RC	15.3	0.917	1384	intron1				
31430295	31430315	ATTTTGTGACGACGAGATGC	FW	8.9	0.889	1457	intron1				
31431911	31431931	GGGTGACCTAAGTCATCGAGG	RC	6.5	0.774	3073	intron1				
31432868	31432888	TACTCCTGACACTGCAGATGT	FW	12.5	0.866	4030	intron1				
Calml3	calmodulin-like 3 NM_027416 chr13:3802138-3803564 -	NM_027416	3801317	3801337	gtagcttgcgtgataaactcctga	RC	9.8	0.762	2247	downstream	7.61
			3803107	3803127	CCCCAGCTTGTGTCACAGT	RC	7.5	0.847	457	exon1	
			3803140	3803160	CTGCACAGCAAGCCATTGC	FW	7.9	0.846	424	exon1	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
	chr13 A1 13		3803335	3803355	ACCGCATGACAGTGGCCCAATT	FW	9.8	0.827	229	exon1	
			3803422	3803442	TTTGTCTCCTCAGTCAAGTGGT	RC	6.8	0.79	142	exon1	
			3805799	3805819	ACATATGCATTTTCACATTTA	RC	8	0.787	-2235	upstream	
			3807107	3807127	tttgttctgcttcaataaactt	RC	7	0.819	-3543	upstream	
			14636938	14636958	CATCTCTGTATCACTGCACAGAT	FW	6.6	0.783	-4788	upstream	
<i>Car13</i>	carbonic anhydrase 13 NM_024495 chr3 14641726 14663002 + chr3 3 A2	NM_024495	14637151	14637171	gcaggctgaaacaagccatgga	FW	7	0.791	-4575	upstream	1.55
			14637433	14637453	TATATAGCTAGTAACCTAGT	RC	10.8	0.822	-4293	upstream	
			14639731	14639751	gagacagctatatacagggtcc	RC	7.5	0.795	-1995	upstream	
			14641210	14641230	CTTCTGCACAGTCAAGATGG	RC	10.6	0.879	-516	upstream	
			14642073	14642093	CAGATCACTAAGTCACGGGAC	RC	7.5	0.779	347	intron1	
			14643357	14643377	GGGAAGTACCAAGCATTTTT	FW	10.6	0.877	1631	intron1	
			14645410	14645430	AAGTATGCTGGGTGATATTTT	RC	7.7	0.803	3684	intron2	
			14859285	14859305	ACAAGATGACTTTGCAGAGAT	FW	13.1	0.893	-4252	upstream	
			14859401	14859421	caacagttacatagcaacacagc	FW	9.9	0.8	-4136	upstream	
			14860880	14860900	TCAAGTGCATTTGCAAGGG	FW	10.2	0.854	-2657	upstream	
14861874	14861894	ACTACAGCTTACTACTCAACA	RC	8.8	0.817	-1663	upstream				
14862740	14862760	ACTGCTGTGACTGAGGCTAG	RC	7.6	0.767	-797	upstream				
14863110	14863130	TTAGTTGCTAAGTAACACCAG	RC	8.9	0.814	-427	upstream				
14863810	14863830	GAGAAGTCACTCAGCCAGAG	FW	7.8	0.801	273	intron1				
14864459	14864479	CCTTCGGCAGGGTCACTGAG	RC	6.7	0.819	922	intron2				
14864858	14864878	GAAAAGCCAGGCTCACTGTGT	RC	12.4	0.862	1321	intron2				
14865615	14865635	AACACATGAATAGCATTTTT	FW	9.7	0.822	2078	intron2				
14866575	14866595	TTAAGATGACAGGCGATGCCA	FW	8.1	0.845	3038	intron2				
14867047	14867067	AAATATGCTAGGTCAGAGAGA	RC	11.9	0.89	3510	intron3				
14868197	14868217	AGTATTGCTTATTAATATTTA	RC	8.9	0.764	4660	intron3				
14868252	14868272	CAACCGTGAGACTGCACACCT	FW	11.2	0.818	4715	intron3				
<i>Car5b</i>	carbonic anhydrase 5b, mitochondrial NM_181315 chrX 160414753 160465942 - chrX F5 X	NM_181315	160463868	160463888	GAGCCATTACAAGCTAGACA	FW	7	0.763	2074	intron1	1.46
			160464310	160464330	CAGAGAGCTGTATCAATGTGC	RC	8.6	0.822	1632	intron1	
			160465704	160465724	GACCAAGCCTAGTCAGGCCCG	RC	7.3	0.831	238	intron1	
			160467057	160467077	TGGTTGTGACTCAGTGCCTCG	FW	9.1	0.797	-1115	upstream	
			160469436	160469456	ctgattgcaaaatccaataga	RC	7.4	0.805	-3494	upstream	
160469789	160469809	taagaaagagcctgcaattga	FW	10.8	0.808	-3847	upstream				
<i>Car6</i>	carbonic anhydrase 6 NM_009802 chr4 149561124 149575244 - chr4 E2 4	NM_009802	149570751	149570771	ACGCAATGACACAGATTCACT	FW	7.1	0.77	4493	intron3	1.37
			149571244	149571264	agatgtgacagaggaagaca	FW	6.4	0.774	4000	intron3	
			149571372	149571392	AGAAAGTGACTCTGGAGCGTG	FW	8.7	0.786	3872	intron3	
			149573992	149574012	TAGCTTTGAATGAGCACACAG	FW	7.2	0.833	1252	intron1	
			149574703	149574723	GGAGTCTGACTGAGCATCTGA	FW	11.4	0.914	541	intron1	
			149575100	149575120	AGGGCTGCTTTGTCACTCTGT	RC	13.9	0.912	144	intron1	
			149576837	149576857	ggagttgagacAGcacacac	FW	8.4	0.834	-1593	upstream	
			149577014	149577034	CAGAGGTCACAAGCACTTCC	FW	8	0.789	-1770	upstream	
			149578630	149578650	AGTAAAGCAAGTCAATTTTG	RC	7	0.83	-3386	upstream	
			149579931	149579951	atgcatgctgggtcagatctc	RC	8.4	0.88	-4687	upstream	
			149580008	149580028	ATGCTGCTCTGTCACTCGCT	RC	11.3	0.886	-4764	upstream	
			101885838	101885858	ACCTGTGCTGGGTAAAGCCATG	RC	8	0.791	-4539	upstream	
			101886561	101886581	AGGACTGCTTATGTCACACACA	RC	13.5	0.923	-3816	upstream	
			101888185	101888205	AAATATGCATGTCACTACACA	RC	9.5	0.844	-2192	upstream	
101889518	101889538	ggtcctccagagtcagccagc	RC	6.9	0.772	-859	upstream				
101889821	101889841	CTGTATGCTGGGTCAAGTAGGA	RC	11.3	0.897	-556	upstream				
101890823	101890843	CCTGTATGAGAGAGCATTAGT	FW	9	0.824	446	intron1				
101893703	101893723	TCAGTTGCTAGGTGATGGTCT	RC	8.9	0.796	3326	intron1				
101895098	101895118	tctctttctgctgctatggttg	RC	10.4	0.806	4721	intron1				
<i>Cfd</i>	complement factor D (adipsin) NM_013459 chr10 79353597 79355405 + chr10 C1 10 43.0 cM	NM_013459	79350241	79350261	AACTGTGCTCTGTGACTTCTT	RC	6.6	0.78	-3356	upstream	6.10
			79350766	79350786	TGTGCTGAGTGTTCAGATTG	FW	8.2	0.797	-2831	upstream	
			79350974	79350994	ATGCTGCTGCTCAGGATGT	RC	9.6	0.84	-2623	upstream	
			79353641	79353661	GAGCCTCTGGGTCACTGCTCT	RC	11.4	0.895	44	UTR5	
			79353746	79353766	CCAGTTTGACACACAGCCGCC	FW	11.6	0.913	149	intron1	
			79354007	79354027	CCTACTGCAGGTTCACTGTGG	RC	11.3	0.819	410	intron1	
			79354688	79354708	TTTTCTTGACTCTGCCCTAC	FW	6.5	0.843	1091	intron3	
			79357129	79357149	CCCAGAGCTGGGTCACTGTGG	RC	13.6	0.9	3532	downstream	
			79358094	79358114	GTTCCCACTGTGTCAACAGCG	RC	8.7	0.778	4497	downstream	
			79358136	79358156	GCATGGTGACACAGCCACACC	FW	13.2	0.9	4539	downstream	
			79358498	79358518	CACAGTGCCTGTCAAGCAGG	RC	9.7	0.847	4901	downstream	
			89259360	89259380	TCTTACTGACTGAGAAATCTT	FW	7.6	0.797	998	intron2	
			89260468	89260488	ACAGCTCTGTGTGAGACACT	RC	7	0.792	-110	upstream	
			89262033	89262053	TGGCTTGTATCTGTCTATCTG	FW	7.4	0.793	-1675	upstream	
			89263156	89263176	caaatctctgtgtcagagagta	RC	8.9	0.767	-2798	upstream	
89264077	89264097	TGAGAGTGAAGTATAGCTGCC	FW	7.5	0.82	-3719	upstream				
<i>Chrne</i>	cholinergic receptor, nicotinic, epsilon polypeptide NM_009603 chr11 70428384 70432696 -	NM_009603	70428463	70428483	GCCAGTGCAGGCTCATGGTGT	RC	10.2	0.809	4233	UTR3	1.43
			70428831	70428851	GCAAGCGCTAGGTCATTAATA	RC	7.3	0.843	3865	intron10	
			70430858	70430878	CATAGGCACAGTCAGCCCGC	RC	9.8	0.847	1838	intron6	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
	chr11 B3 11 42.0 cM		70431112	70431132	AAAGCTGCCGTGCAATGTCA	RC	13.2	0.882	1584	exon6	
			70431658	70431678	GAAAAATGAGAGGAGGTTCT	FW	9.1	0.826	1038	exon5	
			70435076	70435096	aaacctgacttggaaaaaaa	FW	9.0	0.772	-2380	upstream	
<i>Cidea</i>	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A NM_007702 chr18 67503217 67527448 + chr18 E1 18 1-Ch12 Mafk chr18:67506370-67506589	NM_007702	67506489	67506509	tcagctgctgagtcactctctg	RC	15.2	0.94	3272	¹ intron1	6.88
			67506523	67506543	AGATCCTGAACAGCCTGTGTG	FW	8.2	0.809	3306	intron1	
			67500156	67500176	tcttaactcaactgacccatctc	FW	6.8	0.788	-3061	upstream	
			67501257	67501277	ATGACTTCTGAGTCAAGGGGCG	RC	11	0.832	-1960	upstream	
			67504424	67504444	TGGCTTTCAGAGTCAAGGCCA	RC	6.4	0.771	1207	intron1	
			67504460	67504480	GCGACTTACAAGCAGGTTA	FW	7.8	0.789	1243	intron1	
			67505285	67505305	CGGAAGTGACTCAGTAAATCA	FW	10.6	0.824	2068	intron1	
<i>Clybl</i>	citrate lyase beta like NM_029556 chr14 122580915 122801456 + chr14 E5 14 1-Ch12 Mafk chr14:122583173-122583506 Mel Mafk chr14:122582649-122583625 Mel Mafk chr14:122583053-12 2-Ch12 Mafk chr18:67506370-67506589	NM_029556	122583206	122583226	ttttgttgactgtgcagaagt	FW	6.8	0.851	2291	¹ intron1	1.76
			122583356	122583376	TACTCTGCTGACTCATCGTCT	RC	15	0.892	2441	² intron1	
			122576038	122576058	TACAAATGACCCGTCAAGG	FW	6.4	0.816	-4877	upstream	
			122577658	122577678	TCATTTTACTAGGCACCTCA	FW	6.5	0.779	-3257	upstream	
			122577682	122577702	tcacctgattcttcccaatcca	FW	9.7	0.831	-3233	upstream	
			122577986	122578006	cccatgtgaccagaaataatc	FW	7.8	0.79	-2929	upstream	
			122578030	122578050	acatatgctgagtGACACAAAT	RC	8.9	0.83	-2885	upstream	
<i>Coq3</i>	coenzyme Q3 homolog, methyltransferase (yeast) NM_172687 chr4 21806821 21839273 + chr4 A3 4 16.6 cM 1-Ch12 Mafk chr4:21806070-21807519	NM_172687	21807349	21807369	CCTAGCGCTGCTCACTACTT	RC	7.1	0.799	528	¹ intron1	1.37
			21804813	21804833	acttttgtaatgagcagccag	FW	6.7	0.836	-2008	upstream	
			21805132	21805152	ggatctcactgagccatttc	FW	6.5	0.778	-1689	upstream	
			21805489	21805509	TATTTCTGACACAGCTCAACT	FW	8.9	0.864	-1332	upstream	
			21805807	21805827	TGACAGTGATAGAGCAGCTGG	FW	10.6	0.835	-1014	upstream	
			21805868	21805888	ATGAGAGCTTAGTAAATTTCC	RC	7.1	0.787	-953	upstream	
			21810055	21810075	aagtggtcagtcagttacag	RC	7.5	0.866	3234	intron1	
<i>Coq7</i>	demethyl-Q 7 NM_009940 chr7 125668575 125676870 - chr7 F2 7 53.5 cM	NM_009940	125673072	125673092	CCTGAATGACAGGCCAACAC	FW	6.9	0.813	3798	exon2	1.32
			125673252	125673272	CTGCAATGAAAAGCAAGTGT	FW	9.5	0.822	3618	intron1	
			125673370	125673390	ttaccacctgagtcataatcgc	RC	7.9	0.794	3500	intron1	
			125674104	125674124	TCTTTGGCTCTTTCATCAAGA	RC	6.8	0.789	2766	intron1	
			125674371	125674391	FTGCTCCTCACTCAGCTCAGTG	FW	8.7	0.807	2499	intron1	
			125675116	125675136	ccagctgaggttggcagagct	FW	10.9	0.826	1754	intron1	
			125675154	125675174	tcctggtgacaacaagatc	FW	8.4	0.816	1716	intron1	
			125676202	125676222	ctagtgcagattcaaacctcc	RC	6.6	0.807	668	intron1	
			125677927	125677947	tcacaagtgcacccagcctctc	FW	13.9	0.916	-1057	upstream	
			125678386	125678406	caacttgcctgtctcatccaag	RC	16.1	0.927	-1516	upstream	
			125678633	125678653	tcacagtcacacagcaaaGAG	FW	13.9	0.843	-1763	upstream	
			125679211	125679231	GTGACTGCATAGTTACTGGAA	RC	6.6	0.773	-2341	upstream	
			125680058	125680078	AAAATGTTACAAAGCACATGT	FW	10.5	0.805	-3188	upstream	
			125680277	125680297	cacatCTGACAAAGCACCCCT	FW	9.5	0.874	-3407	upstream	
			125680860	125680880	FTGAAATCACTCTGCACTCTT	FW	10	0.803	-3990	upstream	
			125681131	125681151	TGATACTGACTGGGCTAGGGT	FW	9.3	0.867	-4261	upstream	
			125681807	125681827	CTGCTCTGACTCAGGTAAGG	FW	7.2	0.785	-4937	upstream	
<i>Coq9</i>	coenzyme Q9 homolog (yeast) NM_026452 chr8 97362316 97378795 + chr8 C5-D1 8 1-Ch12 Mafk chr8:97357816-97358529 Ese14 Mafk chr8:97357726-97358544 Mel Mafk chr8:97357683-97358394 2-Ch12 Nrf2 chr8:97362100-97362908	NM_026452	97358099	97358119	CTACCTGACTCAGCAAAAG	FW	17.4	0.959	-4217	¹ upstream	1.62
			97362779	97362799	ACCACGTCACTAAGCTGGTGA	FW	6.6	0.788	463	² intron1	
			97358821	97358841	TAAGACTGACTAAGaatcccca	FW	7.6	0.8	-3495	upstream	
			97358972	97358992	AAAGACTGACTAAGAACCCCT	FW	8.4	0.802	-3344	upstream	
			97359768	97359788	TAACCTGCTTCGTCAAATGGC	RC	7	0.868	-2548	upstream	
			97360502	97360522	GAGCTGTGACTCAGGGCTGTT	FW	11	0.808	-1814	upstream	
			97360641	97360661	Accgggtgaaatgcatattgc	FW	9.8	0.817	-1675	upstream	
			97360717	97360737	gggtctgctaagtaccagca	RC	7.6	0.807	-1599	upstream	
			97360856	97360876	TGGGGTGACTCAGTGTAGC	FW	11.3	0.806	-1460	upstream	
			97365639	97365659	agacctgaccacaaggaagga	FW	7.2	0.774	3323	intron1	
<i>Corin</i>	corin NM_016869 chr5 72891263 72895447 - chr5 C3.2 5 1-Ch12 Mafk chr5:72891894-72892206 Ese14 Mafk chr5:72891924-72892206	NM_01122756 NM_016869	72892055	72892075	tcgagatgactcagcaagaaa	FW	17.2	0.955	3392	¹ intron1	7.76
			72890480	72890500	CCCACCTCTGAGTCAAGCCAGG	RC	11.2	0.827	4967	intron1	
			72891485	72891505	CAGTTTGCCCAAGTATGATGT	RC	8.6	0.79	3962	intron1	
			72893610	72893630	AATATGGCAGACTCAGGGGCGC	RC	10	0.802	1837	intron1	
			72894251	72894271	GAACCTGAAACAGCAAGCAG	FW	11.3	0.849	1196	intron1	
			72895534	72895554	AAAGTTGACTCTGAAGTCAAC	FW	7.4	0.779	-87	upstream	
			72897229	72897249	TAAACCTGAAATAGCTAAGTA	FW	6.8	0.789	-1450	upstream	
			72898628	72898648	ggggctgcatagtaagactgt	RC	6.6	0.777	-2849	upstream	
			72898730	72898750	AATATTTCTGAGTCAACCTCC	RC	14.5	0.849	-2951	upstream	
			72899107	72899127	tctatatgaccagcagaag	FW	9	0.832	-3328	upstream	
			72899428	72899448	acagttttacaagaaccaggtt	FW	6.5	0.768	-3649	upstream	
			72900001	72900021	tactggcagtgctattggca	RC	10.8	0.842	-4222	upstream	
<i>Cox4i1</i>	cytochrome c oxidase subunit IV isoform 1 NM_009941 chr8 123192124 123198109 + chr8 E1 8 64.0 cM	NM_009941	123191848	123191868	AGGCTCGCTAGTCAGCTTCA	RC	8.8	0.867	-276	¹ upstream	1.30
			123190573	123190593	AAATGTGCCCAAGTAAACGTGC	RC	9.5	0.794	-1551	upstream	
			123191170	123191190	CAAACCCAGAGTATGAATTC	RC	6.8	0.766	-954	upstream	
			123194804	123194824	GAAGGGTGACTGAGGCGCTGGC	FW	8	0.783	2680	intron2	
			123196127	123196147	CTGCCGTGACTCTGCTTGTTC	FW	7.3	0.796	4003	intron2	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
Cox5a	1-Ch12 Nrf2 chr8:123191829-123192308 cytochrome c oxidase, subunit Va NM_007747 chr9 57369038 57380233 + chr9 B 9 1-Ch12 Mafk chr9:57369628-57369793	NM_007747	57369667	57369687	TAGCCCTGATCAGGCAATTCT	FW	7.7	0.774	629	¹ intron1	1.49				
			57365016	57365036	caagcagccttgctcatggaag	RC	7	0.813	-4022	upstream					
			57366579	57366599	gagagatgacttagtgcctct	FW	9.4	0.878	-2459	upstream					
			57367656	57367676	agctggtgagcagcctctctt	FW	6.4	0.793	-1382	upstream					
			57368031	57368051	ctctgatgaccaaagcattcaa	FW	8.4	0.87	-1007	upstream					
			57369947	57369967	TTCACTGCTGACTTATGAAGT	RC	7.8	0.77	909	intron1					
			57370473	57370493	TAAAAAATACTTAGCCAGGTA	FW	7.4	0.791	1435	intron1					
			57371811	57371831	TCTTTAGCTGTGTGACCTTGT	RC	9.2	0.797	2773	intron1					
			57372558	57372578	ttcattgctactcatagctg	RC	7.2	0.809	3520	intron1					
			57373574	57373594	tatagattcggatcattatgc	RC	11	0.816	4536	intron1					
			57373819	57373839	aaaagttcagggtcattctga	RC	10.7	0.775	4781	intron1					
			Cox5b	cytochrome c oxidase, subunit Vb NM_009942 chr1 36748331 36750233 + chr1 B 1	NM_009942	36744557	36744577	GCAATTACTctgctcatctgca	RC	7.7		0.772	-3774	upstream	1.52
						36744936	36744956	gagttgctctggtcatggtgt	RC	8.4		0.766	-3395	upstream	
36745787	36745807	taactgtgattttgctgctgt				FW	7.4	0.786	-2544	upstream					
36745991	36746011	TGCTCTGACTGAGTCTATGA				FW	9.7	0.875	-2340	upstream					
36746189	36746209	GCAACTCCTCAGTCATTATA				RC	8.6	0.799	-2142	upstream					
36746501	36746521	GCACAttgactaaagatgacc				FW	7.1	0.808	-1830	upstream					
36746539	36746559	ttgaaggctctgctcattaggg				RC	7.6	0.85	-1792	upstream					
36748735	36748755	GAAAGTCCCGGTGACCTTGG				RC	7.8	0.774	404	intron1					
36750701	36750721	TAACCTCAGCAGGACTTAG				FW	11.5	0.808	2370	downstream					
36751109	36751129	GGAAATGCCTTCTCATTCTGT				RC	9.1	0.798	2778	downstream					
36752251	36752271	ttatatacttaagtcactgcat				RC	9	0.805	3920	downstream					
Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2 NM_009943 chr7 135348948 135349880 - chr7 F3 7 61.0 cM	NM_009943				135346112	135346132	ACAAGCCCTTTCTCACCACTG	RC	9.2	0.797	3768	downstream	2.78	
						135346982	135347002	TGACTCTGACTTGTGTAGTCTAG	FW	6.5	0.762	2898	downstream		
			135347205	135347225	GCTTCGGCTGGATCAGTCAAG	RC	6.4	0.794	2675	downstream					
			135348626	135348646	AGATCCTGACCCAGCCGCCA	FW	8.1	0.864	1254	downstream					
			Cox6b1	cytochrome c oxidase, subunit Vlb polypeptide 1 NM_025628 chr7 31401992 31411170 - chr7 B1 7 10.0 cM	NM_025628	31408296	31408316	GGCCCTCACTGAGCAGGGAT	FW	7.6	0.806	2874	intron3		1.34
31408507	31408527	GTCAATGCCTTCTCACAGCGG				RC	9.1	0.793	2663	exon3					
31409987	31410007	ccaaggtcacacagacCCCGAG				FW	10.2	0.823	1183	intron1					
31412904	31412924	AGGGACTGAGTGAAGCAGAAAT				FW	10.1	0.841	-1734	upstream					
31415129	31415149	ATAGTCTCTCAGTCAAGATTG				RC	6.7	0.771	-3959	upstream					
31415624	31415644	caaggtgagagagcccattg				FW	9	0.802	-4454	upstream					
31415852	31415872	cttgctcttggtcatgatgt				RC	8.5	0.784	-4682	upstream					
31415883	31415903	aaacctgactaaagCTgggtg				FW	12.3	0.899	-4713	upstream					
31415928	31415948	tggggagcagagtcaggggga				RC	10	0.866	-4758	upstream					
31416081	31416101	AAACCTGACTTAAGCAAACC				FW	8.9	0.786	-4911	upstream					
31416136	31416156	ATTTTCACTAAAGTCACTCCT				RC	7.8	0.773	-4966	upstream					
Cox7a1	cytochrome c oxidase, subunit VIIa 1 NM_009944 chr7 30964635 30971049 + chr7 B1 7 8.0 cM	NM_009944				30964465	30964485	GAGTAAGTACTGTGGCTTTGG	FW	7.9	0.837	-4724	upstream	4.06	
						30964540	30964560	TTGAAGTTACTGTGCAATTTT	FW	8.2	0.778	-4649	upstream		
			30965068	30965088	aaggctcagagtgagaccct	RC	6.4	0.777	-4121	upstream					
			30966089	30966109	tttctgtttacacagcggcttac	FW	7.2	0.78	-3100	upstream					
			30967724	30967744	TGGCTGCCATGTCACTCTGT	RC	7.2	0.832	-1465	upstream					
			30968438	30968458	taaaagttctgggtcaccacgg	RC	8.3	0.77	-751	upstream					
			30968885	30968905	AGATCCTGACTTGGCCCTGAG	FW	9.1	0.845	-304	upstream					
			30972440	30972460	TGACCATGAAATGCGGCTGC	FW	8	0.766	3251	downstream					
			30973581	30973601	ACCAAGGCTGAGTCAACCA	RC	14.2	0.916	4392	downstream					
			30973743	30973763	atgagtgcttggtcacaacc	RC	6.9	0.829	4554	downstream					
			30973999	30974019	CATGGCTGACTCTGCCCTTT	FW	10.4	0.857	4810	downstream					
			Cox7c	cytochrome c oxidase, subunit VIIc NM_007749 chr13 86184402 86186400 - chr13 C3 13	NM_007749	86184055	86184075	GCATATGCATTTCTCATTGGG	RC	6.9	0.777	2345	downstream		1.30
						86188684	86188704	ctactgtgaaatgcaagtgcc	FW	8.6	0.816	-2284	upstream		
86190185	86190205	tcattgtagctctgctcttta				FW	10.7	0.781	-3785	upstream					
86190993	86191013	ttttagtgacatagcacaac				FW	9.6	0.879	-4593	upstream					
86191176	86191196	tgtgctctggtcagctttt				RC	7.5	0.789	-4776	upstream					
Cox8b	cytochrome c oxidase, subunit VIIIb NM_007751 chr7 148084840 148086345 - chr7 F5 7 68.8 cM	NM_007751				148084875	148084895	GGATGTCAACTTCAGTCTGTC	RC	6.7	0.782	1470	UTR3	3.70	
			148085318	148085338	AGAGGTTCACTCAGCTCCTGT	FW	7.3	0.803	1027	intron1					
			148086808	148086828	GTTAGTGTGCTGTATCTCTGC	RC	13.2	0.837	-463	upstream					
			148087771	148087791	ATAAAGCTGGGTATCTTCA	RC	7.4	0.78	-1426	upstream					
			148090407	148090427	TGACATTGAAGCAGCACTGA	FW	8.8	0.836	-4062	upstream					
Cpt1b	cDNA sequence BC090627///carnitine palmitoyltransferase 1b, muscle NM_009948 chr15 89246835 89256293 - chr15 E3 15///chr15 E3 15 52.6 cM	NM_009948 NR_004843	89252833	89252853	GATGGAGCAGAGTCAGTAGGC	RC	8.9	0.856	3460	intron7	3.98				
Cpt2	carnitine palmitoyltransferase 2 NM_009949 chr4 107594592-107594759 Mel Mafk chr4:107593721-107595009 2-Ch12 Mafk chr4:107594592-107594759 Mel Mafk chr4:107593721-107595009	NM_009949	107594150	107594170	AATTGCTGACACGAAAGTCT	FW	6.8	0.778	2044	¹ intron1	1.52				
			107594640	107594660	CCCATCTGACTCAGCAATGA	FW	15	0.941	1554	² intron1					
			107591589	107591609	tgccactgactctgaaactaa	FW	9.4	0.781	4605	intron1					
			107591785	107591805	cggagctgactcagagagctct	FW	7.1	0.781	4409	intron1					
			107592719	107592739	TAAGCTACTGAGTCACTGCT	RC	10.1	0.821	3475	intron1					
			107593557	107593577	AGTCACTGACAGACCATCA	FW	9.7	0.878	2637	intron1					
			107598252	107598272	CAAAAGTACTGAGCCACAAA	FW	11.3	0.894	-2058	upstream					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
<i>Crat</i>	carnitine acetyltransferase NM_007760 chr2:30255995-30271268 - chr2 B 2 18.0 cM	NM_007760	107601105	107601125	agataatgacccccgctatgt	FW	7.7	0.829	-4911	upstream	1.29				
			107601142	107601162	gagtttgcctccatagaga	RC	7.5	0.826	-4948	upstream					
			30266662	30266682	CCACCTGCTGACTCATAGCCA	RC	13.3	0.877	4606	intron2					
			30268778	30268798	AGAAGCAGCCTACTACTTCTCT	RC	7.6	0.785	2490	intron1					
			30270971	30270991	AAGGTCCGCGAGTCACTGCCG	RC	12.7	0.876	297	UTR5					
			30273244	30273264	CCCgggctcagtaagagtcgc	RC	6.9	0.793	-1976	upstream					
			30274916	30274936	CCAATTGCAGACTCAGGCTGA	RC	14.6	0.856	-3648	upstream					
<i>Cs</i>	citrate synthase NM_026444 chr10:127774887-127799535 + chr10 D3 10 1-Ch12 Mafk chr10:127777377-127777949 2-Ch12 Mafk chr10:127777377-127777949 Ese14 Mafk chr10:127777460-127777973	NM_026444	127777406	127777426	CCGTTCCTTATGTCATTGGTG	RC	8.6	0.779	2519	¹ intron1	1.43				
			127777614	127777634	gagagatgactcagcaggttaa	FW	16.2	0.947	2727	² intron1					
			127775480	127775500	TGTAAGTGACCCCGCGTTTT	FW	7.7	0.825	593	intron1					
			127776320	127776340	TGAACCTGAAAAGGCTTTGG	FW	6.7	0.792	1433	intron1					
			127776402	127776422	GGAGGGTGCAGTGGCCACATT	FW	11	0.858	1515	intron1					
			127776999	127777019	gtgattgctggtgaagcataa	RC	10.1	0.815	2112	intron1					
			127778325	127778345	CAACATGCTTATCAGCCTTA	RC	10.3	0.827	3438	intron1					
			127778463	127778483	GGGAATCTGTGTCAAGTGA	RC	8.5	0.797	3576	intron1					
			127778774	127778794	AACAAGCAGAGTCAATTTTC	RC	11.2	0.874	3887	intron1					
			127778943	127778963	TCATGGGCTCAGTCAAGTCA	RC	10	0.882	4056	intron1					
			127779466	127779486	cgcattgctcaacacagcattac	FW	8.9	0.806	4579	intron1					
			<i>Csrp3</i>	cysteine and glycine-rich protein 3 NM_013808 chr7:56085767-56099041 - chr7 B4 7	NM_001198841 NM_013808	56094506	56094526	TCTCTCTTAAGTACAGAGA	RC	9.8		0.827	4535	intron2	4.64
						56095911	56095931	CCTCGGTGACTGGGCTTTCCC	FW	7.5		0.846	3130	intron1	
56096371	56096391	GGAAAGGCTGAATCAAGTCTG				RC	7	0.824	2670	intron1					
56097098	56097118	AACAGCCCTGGGTCACTTTC				RC	7.4	0.768	1943	intron1					
56097460	56097480	GGGAACGTATACAGCAATTAG				FW	9.8	0.832	1581	intron1					
56097957	56097977	TGACTGTCACTCAGCAGTGT				FW	11.4	0.793	1084	intron1					
56099592	56099612	TCCAGTGACCAAGCATCTCA				FW	9.4	0.88	-551	upstream					
56102215	56102235	GGAAACTGATGATGAGCAGTA				FW	7.2	0.8	1206	intron1					
56102305	56102325	CATACTGCTTATTAACTGGCC				RC	9.5	0.762	1116	intron1					
<i>Cyc1</i>	cytochrome c-1 NM_025567 chr15:76173952-76176364 + chr15 D3 15	NM_025567				76169003	76169023	ccccggcttgcctcagcctga	RC	7.1	0.79	-4949	upstream	1.68	
						76169166	76169186	actccagctgctcgaagtga	RC	12	0.892	-4786	upstream		
			76173414	76173434	acagctacagctgctcagtgca	RC	9	0.762	-538	upstream					
			76175328	76175348	TAACCTGAGGCTGCAAGAGC	FW	8.7	0.799	1376	exon4					
			76176122	76176142	ATGCCATGACGGCGCATAAGT	FW	6.5	0.786	2170	exon7					
			76177963	76177983	CCCCAATGACTGAGGAAACAA	FW	10.4	0.815	4011	downstream					
			76178196	76178216	GCCCAATGACCCAGCGCTCCA	FW	11.2	0.883	4244	downstream					
			76178600	76178620	GCCGCTGCTTCTCATCCCCA	RC	9.3	0.818	4648	downstream					
			<i>Cycs</i>	cytochrome c, somatic NM_007808 chr6:50512561-50516473 - chr6 B2.3 6 23.0 cM 1-Ch12 Nrf2 chr6:50516052-50517407 2-Ch12 Nrf2 chr6:50516052-50517407	NM_007808	50516198	50516218	CCAGATGCTTAATCAGGAAA	RC	7	0.829	275	¹ intron1		1.70
50516894	50516914	ACCCAGGCTTGGTCAAGGCTT				RC	6.7	0.84	-421	² upstream					
50512787	50512807	ACTAGTCTTAGGTCATGCCA				RC	6.4	0.763	3686	UTR3					
50514771	50514791	AAAACCTGCAGTCAAGAAATA				RC	8.7	0.838	1702	UTR3					
50515755	50515775	CAGGGTGTCAACTCAGTCCAC				RC	6.8	0.826	718	intron1					
50519362	50519382	TCTTTCGACCGTCACTTCTC				RC	7.9	0.839	-2889	upstream					
50520045	50520065	cttgcctctctggctcagatgt				RC	8.5	0.784	-3572	upstream					
50521466	50521486	TCCCAATGACTTTGTAAGGT				FW	9.3	0.774	-4993	upstream					
<i>Cyp2e1</i>	cytochrome P450, family 2, subfamily e, polypeptide 1 NM_021282 chr7:147949730-147960876 + chr7 F5 7 68.4 cM	NM_021282				147946657	147946677	GTTAATGCTGAGTTAATACTG	RC	8.4	0.824	-3073	upstream	3.52	
			147947066	147947086	AGCTGTGCAGATTCAGGCATT	RC	7.7	0.81	-2664	upstream					
			147947157	147947177	TAAGATTGACTCAGCCTGAGC	FW	12.3	0.911	-2573	upstream					
			147947582	147947602	tgatgatgactgggctaggca	FW	7.3	0.84	-2148	upstream					
			147948894	147948914	CCTGGATGACCAAGCAGTGG	FW	9.1	0.818	-836	upstream					
			147950411	147950431	TGTACTGTAGGTAAAGTAGA	RC	6.8	0.78	681	intron1					
<i>D10hu81e</i>	DNA segment, Chr 10, Johns Hopkins University 81 expressed NM_138601 chr10:77624811-77632513 - chr10 C1 10 41.7 cM	NM_138601	77628609	77628629	GCTAAACCTCAGTCAACCTTC	RC	7.7	0.782	3904	intron4	1.48				
			77630170	77630190	AAAATGGCAGCATCATGGTTA	RC	10	0.788	2343	exon4					
			77630235	77630255	CCTTGTGACTCTGCCAAAAC	FW	10.6	0.863	2278	exon4					
			77631897	77631917	GGTTGTGACTCCGCGAGTGT	FW	8	0.871	616	intron2					
			77632044	77632064	CACTGCGCTTGGTCACTCTCT	RC	11.2	0.868	469	intron2					
			77634016	77634036	TCAGCATGAGTGGCACCTGT	FW	12.5	0.833	-1503	upstream					
			77634560	77634580	TGGCTTGTGCTCCTAGGCGAG	RC	9.5	0.838	-2047	upstream					
			77635602	77635622	GCAACTGCTCAGTGACAGATA	RC	9.4	0.821	-3089	upstream					
			77636261	77636281	CAATGGCTGGGTCACTTGAT	RC	9.7	0.87	-3748	upstream					
			77637222	77637242	CGTGCCTGACACAGGATAACA	FW	8.1	0.785	-4709	upstream					
<i>Decr1</i>	2,4-dienoyl CoA reductase 1, mitochondrial NM_026172 chr4:15844386-15872654 - chr4 A2 4 1-Ch12 Mafk chr4:15871913-15872113	NM_026172	15871937	15871957	TAGCTTTGACTAAGGCTTGC	FW	7.5	0.775	717	¹ intron1	1.58				
			15869397	15869417	gaacagtgactaaagacagatg	FW	9	0.79	3257	intron1					
			15870227	15870247	AAACAGTTACTGAGCTATTTC	FW	10.8	0.812	2427	intron1					
			15874304	15874324	aaaacggctaggttatattgg	RC	6.8	0.768	-1650	upstream					
			15875143	15875163	ttecttacagagctactgctc	RC	8.4	0.781	-2489	upstream					
			15875868	15875888	taaaatgctttatcagaaaga	RC	8.6	0.819	-3214	upstream					
			15877021	15877041	GGAGCTGCTGAATCAGGTCTT	RC	9.5	0.854	-4367	upstream					
			15877387	15877407	caagcttcacatagcccttgt	FW	6.8	0.764	-4733	upstream					
			<i>Dgat2</i>	diacylglycerol O-acyltransferase 2 NM_026384	NM_026384	106326548	106326568	GCTGAGGCCAAGTCAAGGATG	RC	6.9		0.828	4675	intron1	2.47
106326604	106326624	CAGACTGCAAACTCAGACCCA				RC	7.5	0.796	4619	intron1					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
	NM_026384 chr7 106302172 106331223 - chr7 7 F1		106327126	106327146	ACTTATGCACAGTGTGGAGG	RC	8.2	0.783	4097	intron1	
			106327882	106327902	CTTGCACCTGAGTCACTTCCC	RC	6.5	0.782	3341	intron1	
			106330918	106330938	CTCGCGTGACAGGGCAGATCC	FW	8.1	0.839	305	exon1	
			106331473	106331493	GCGACCGCCTGTCTATTCTCC	RC	9.4	0.828	-250	upstream	
			106332342	106332362	Tctagtgctgagtgaaaggca	RC	9.9	0.834	-1119	upstream	
			106332566	106332586	GCAGCATCAGTCAGCATGTCT	FW	9.8	0.788	-1343	upstream	
			106335194	106335214	GAACACTGACTGGGATTTCG	FW	7.5	0.767	-3971	upstream	
			106335354	106335374	TCTAGACCTGTGTCACTCTC	RC	7.3	0.763	-4131	upstream	
<i>Dhrs11</i>	dehydrogenase/reductase (SDR family) member 11 NM_177564 chr11 84634229 84642505 - chr11 C 11	NM_177564	84639750	84639770	GAGCCCTGAGAAAGCAGAGCC	FW	8.5	0.815	2755	intron1	1.58
			84639829	84639849	AGTGAGTCACTGAGCCTTGTG	FW	9.9	0.883	2676	intron1	
			84641718	84641738	CCTCACCTCAGTCAATGGTC	RC	6.8	0.771	787	intron1	
			84642819	84642839	TCCTTTGCTCAATCAGCCCTA	RC	9.3	0.837	-314	upstream	
			84643816	84643836	Tgcctttgatccagcaactca	FW	10.1	0.861	-1311	upstream	
			84644361	84644381	TTTCACTCACTAAGCACCCAT	FW	6.5	0.802	-1856	upstream	
			84644539	84644559	GATGTTGCTCAGTGATCTACA	RC	7.7	0.808	-2034	upstream	
			84644885	84644905	AAGCCCTAATATGCAATTCG	FW	7.9	0.775	-2380	upstream	
84646877	84646897	AAAACCTAATCACTGAGTTGTT	FW	7.1	0.802	-4372	upstream				
<i>Dhrs7c</i>	dehydrogenase/reductase (SDR family) member 7C NM_001013013 chr11 67611772 67629504 + chr11 B3 11	NM_001013013	67607568	67607588	tcaaatgacactgacacaagg	FW	7.4	0.839	-4204	upstream	3.51
			67609297	67609317	ctaaagaacacagctactcttc	RC	7	0.835	-2475	upstream	
			67609458	67609478	gaactataaactcaagcaattcc	FW	10.8	0.838	-2314	upstream	
			67611498	67611518	CAGATGGCTCAGTCAACCACT	RC	6.4	0.781	-274	upstream	
			67612091	67612111	GCCAATCCTTTGTCATCCCGC	RC	9.4	0.786	319	intron1	
			67612437	67612457	GGGTTGCCAATCAACAGTTT	RC	7.7	0.811	665	intron2	
			67612814	67612834	CATCACACTCAGTCACTGCTT	RC	6.7	0.773	1042	intron2	
			67613178	67613198	TCTCCCTGAGACTGCTGCTTC	FW	7	0.77	1406	intron2	
			67615270	67615290	TCAAGTGTGTGTACCTTGT	RC	12.4	0.835	3498	intron2	
			67616559	67616579	ATCATGGCTGCTCAACCCCT	RC	7.9	0.802	4787	intron2	
<i>Dlat</i>	dihydroipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex) NM_145614 chr9 50442737 50467885 - chr9 A5.3 9 1-Ch12 Mafk chr9:50466382-50467000 2-Ch12 Mafk chr9:50466382-50467000	NM_145614	50466372	50466392	ACAGTGGCTTTATCAGTTTCA	RC	7.3	0.79	1513	1 st exon3	1.49
			50466973	50466993	GTATTTACTGAGTCACATTTT	RC	11.8	0.837	912	2 nd intron1	
			50463779	50463799	gatataggctaaagtgattca	RC	9.6	0.8	4106	intron4	
			50464585	50464605	TTTGTGCACAATCACCACTA	RC	6.9	0.795	3300	intron4	
			50465606	50465626	GGACTTTCAATCAGCAATAG	FW	7.2	0.77	2279	intron4	
			50467081	50467101	TGGATCTGAGAAAGCAGTGA	FW	7	0.804	804	intron1	
			50469528	50469548	CTAGTGTCACTGAGCAGCATC	FW	7.9	0.819	-1643	upstream	
			<i>Dnajc15</i>	DnaJ (Hsp40) homolog, subfamily C, member 15 NM_025384 chr14 78226023 78274724 - chr14 D3 14	NM_025384	78273146	78273166	gaattggctcttgcaaccaagg	RC	8.9	
78274589	78274609	CGCGCGCAGACTCACCGCTG				RC	6.9	0.791	135	intron1	
78274889	78274909	AGACCCCTTACAGAGCCTTGT				FW	7.9	0.771	-165	upstream	
78276257	78276277	CAGGAGTGAAGCCAGCTCTTT				FW	9.3	0.809	-1533	upstream	
78277951	78277971	ttaacttgacacagctggaat				FW	7.6	0.86	-3227	upstream	
78278277	78278297	cttgcttcttggtcaatgatgt				RC	8.5	0.784	-3553	upstream	
78278312	78278332	aaactctgactaaagcaCTTC				FW	8	0.782	-3588	upstream	
78278716	78278736	acgggtgctgcatcactgtca				RC	10.6	0.846	-3992	upstream	
<i>Dsc2</i>	desmocollin 2 NM_013505 chr18 20189133 20218055 - chr18 A2 18 7.0 cM	NM_013505	20213365	20213385	ACAATTGCTGTTTCATGTAC	RC	11	0.843	4690	intron1	4.91
			20216323	20216343	GGCAGTGTATATCAGGAAGA	RC	7.6	0.813	1732	intron1	
			20216895	20216915	TCGATGGCCTAGTCACTCCCA	RC	10.9	0.852	1160	intron1	
			20217375	20217395	TGACCGTGACCCAGGCTGGG	FW	10.2	0.783	680	intron1	
			20218230	20218250	GCCCTGGCTGAGTTACAGCTG	RC	8.4	0.807	-175	upstream	
			20219177	20219197	ATGTTTGCCAGTGATGATTT	RC	7.5	0.779	-1122	upstream	
			20222458	20222478	catgaagccaagtcaaggTct	RC	8.2	0.846	-4403	upstream	
			125068447	125068467	AAACAGTGACACAGGCCAGAG	FW	9.7	0.783	-4536	upstream	
<i>Dut</i>	deoxyuridine triphosphatase NM_001159646 chr2 125072983 125084785 + chr2 F1 2 70.0 cM	NM_001159646 NM_023595	125069717	125069737	AATAATGCCCTGTCAATGTGA	RC	10.8	0.85	-3266	upstream	1.30
			125070403	125070423	ACAGCTTGAGACTGCAATTTT	FW	11	0.819	-2580	upstream	
			125072054	125072074	acaccatgaccaaggaactc	FW	9	0.768	-929	upstream	
			125073770	125073790	AAAGCGTTACTGTGCAGCGTG	FW	8.7	0.786	520	intron1	
			125075201	125075221	TCACATTGACCCAGTGTGTG	FW	7.4	0.774	1951	intron2	
			125075789	125075809	AGCTATTGACACAGCGCTTC	FW	8.7	0.864	2539	intron2	
			125076808	125076828	TAAGTCTGAAATGCAATAGC	FW	9.9	0.815	3558	intron3	
			<i>Ech1</i>	enoyl coenzyme A hydratase 1, peroxisomal NM_016772 chr7 29610356 29617258 + chr7 A3 7	NM_016772	29605582	29605602	CATTATGCCCTGGTCAGTCATA	RC	8.1	
29605737	29605757	TCGAGGTGACTGAGGAGAAT				FW	10.3	0.813	-4619	upstream	
29606096	29606116	TCTTGTGCTGCTCATGGAGG				RC	11.2	0.847	-4260	upstream	
29607071	29607091	TTAAATGCTAGGTCACTAGAG				RC	7.5	0.862	-3285	upstream	
29608046	29608066	GGTCTCGTAATCACTGATC				RC	7.4	0.815	-2310	upstream	
29608654	29608674	aaagtggctgagttagatggg				RC	8	0.802	-1702	upstream	
29611618	29611638	cctggatgacagagccagatc				FW	10.5	0.865	1262	intron3	
29614939	29614959	AGAGGTGACTCAGAGCTGGC				FW	9.5	0.805	4583	exon4	
<i>Echs1</i>	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial NM_053119 chr7 147291621 147302322 - chr7 F4 7	NM_053119	147298588	147298608	TTGAGGACTGTGCAGGCACT	RC	6.7	0.762	3734	intron2	1.43
			147299386	147299406	cctaagctctggctcaactctg	RC	7.1	0.766	2936	intron1	
			147303174	147303194	caaccctgacacagcaggaca	FW	15.2	0.925	-852	upstream	
			147304315	147304335	cgagggtgacagcaggcaaaa	FW	8	0.781	-1993	upstream	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
			147305083	147305103	AGGGACTGAGCAAGCAGAGTT	FW	7.5	0.802	-2761	upstream	
			147305532	147305552	gtggggtagccagcaagatt	FW	9.6	0.832	-3210	upstream	
			147306000	147306020	ACACTggcttagttagggttt	RC	9.6	0.801	-3678	upstream	
			147306036	147306056	acaccatgaccaaggcaactc	FW	9	0.768	-3714	upstream	
			147306780	147306800	ACATGATGAAAAGGGCGAAGTA	FW	7.1	0.763	-4458	upstream	
<i>Eci1</i>	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase) NM_010023 chr17 24563627 24576261 + chr17 A3.3 17	NM_010023	24559705	24559725	TGCCTATAAGTCAGACTCTTA	FW	7.9	0.768	-3922	upstream	1.34
			24562408	24562428	CACAGATGACCCAGAACCCAGA	FW	6.5	0.775	-1219	upstream	
			24562661	24562681	TCATGGTGATGTTGCAGGTTA	FW	7	0.783	-966	upstream	
			24562984	24563004	AGAAGCTGACTCTGCCTGAGA	FW	9.2	0.859	-643	upstream	
			24564465	24564485	GGACAGTGACAAATGCACCTTAT	FW	14.2	0.876	838	intron2	
			24564743	24564763	ACCATGGCAAAGTCAGTGGAT	RC	7.5	0.833	1116	intron2	
			24564914	24564934	CTCTAGTGAAAAGCAAGGT	FW	7.5	0.81	1287	intron2	
<i>Endog</i>	endonuclease G NM_007931 chr2 30027043 30029589 + chr2 B 2	NM_007931	30024166	30024186	tgagcttgatccctgagcttgt	FW	7.4	0.768	-2877	upstream	1.23
			30024746	30024766	acagctggaagcagccccata	FW	6.7	0.805	-2297	upstream	
			30028518	30028538	GGGCTTTCTGTGTCACGTGAG	RC	8.6	0.803	1475	intron2	
			30029523	30029543	AGATGGGCTGACTCACATTA	RC	9.6	0.846	2480	UTR3	
			30029867	30029887	CCGTCTGCATAGTCACTGCC	RC	12.2	0.882	2824	downstream	
			30031008	30031028	tagtctgagactgcaACAGG	FW	7.8	0.786	3965	downstream	
			30031445	30031465	GCTGCTGCTGGTTCAAGTCGA	RC	7.8	0.817	4402	downstream	
			30031709	30031729	ctttaaactgagtcacctctc	RC	7.3	0.786	4666	downstream	
<i>Ephx2</i>	epoxide hydrolase 2, cytoplasmic NM_007940 chr14 66703208 66743359 - chr14 D 14 32.5 cM	NM_007940	66738523	66738543	gatggctgactagggccattt	FW	9.1	0.839	4836	intron1	4.36
			66740683	66740703	agcaactgactcagctacaga	FW	10.3	0.891	2676	intron1	
			66741571	66741591	GAAGTACAAGTCAACACGA	RC	6.9	0.763	1788	intron1	
			66742998	66743018	TTTTAATTAAGTTCAGATTAG	FW	8.5	0.813	361	intron1	
			66743143	66743163	GGACACTGACCCAGCGCGCT	FW	9.8	0.874	216	intron1	
			66743280	66743300	CGGGCTGCAGCGTCAAGCTGA	RC	8.9	0.864	79	UTR5	
			66743423	66743443	cAGTACTGACACTGCCTGCC	FW	7	0.82	-64	upstream	
			66745548	66745568	TGGGTTGAAAAGCAAACGT	FW	7.4	0.808	-2189	upstream	
			66745635	66745655	TAAAGTTCAAAAGCAAAGAA	FW	12.6	0.818	-2276	upstream	
			66745956	66745976	gTcaactgcttcttatcttag	RC	7.3	0.791	-2597	upstream	
<i>Etfa</i>	electron transferring flavoprotein, alpha polypeptide NM_145615 chr9 55302242 55360050 - chr9 B 9	NM_145615	55355629	55355649	TAATTTGCTAAGTCACTGACA	RC	15.4	0.932	4421	intron1	1.52
			55356838	55356858	ATACAATAACTCAGCAAGAA	FW	12.3	0.853	3212	intron1	
			55357156	55357176	GACATGCTCAGTACACACAGA	RC	9.8	0.826	2894	intron1	
			55359659	55359679	GCAGCGTGACCCGGAAGAGGT	FW	9	0.767	391	intron1	
			55360632	55360652	CTCTGCCCTTAGTCAAGCTCA	RC	7.9	0.777	-582	upstream	
			55361118	55361138	cctccatgataaagcaaaaaca	FW	8.8	0.799	-1068	upstream	
			55361976	55361996	TGGCCTGCAGACTCACTGGGT	RC	8.5	0.824	-1926	upstream	
			55362595	55362615	ACTCTTGTGAGTCACTGGT	RC	16.4	0.951	-2545	upstream	
			55362755	55362775	AAGCTGGCTGAGTGAAGTACC	RC	6.7	0.797	-2705	upstream	
			55364754	55364774	TAAAGTGCATAGTAAGTCTG	RC	8.8	0.776	-4704	upstream	
<i>Etfb</i>	electron transferring flavoprotein, beta polypeptide NM_026695 chr7 50699441 50713170 + chr7 B2 7 23.0 cM	NM_026695	50696181	50696201	ATATCTCTGCTTCAACAGATA	RC	11.3	0.849	-3260	upstream	1.48
			50697622	50697642	CGAGAGGCGAGTCAAGCAGT	RC	10.8	0.872	-1819	upstream	
			50697672	50697692	CAGCGGTGAGAAAGCAGTCA	FW	8.4	0.784	-1769	upstream	
			50699484	50699504	GCAACCTGACCCGGCCAGTGA	FW	8.8	0.837	43	UTR5	
			50699604	50699624	GCAACCTGAGACCCGAGCTAT	FW	10	0.813	163	intron1	
			50703248	50703268	acctatgctctgctcagcatat	RC	8.2	0.873	3807	intron1	
			50703403	50703423	ACTGCTGCTTCTCAGACAGG	RC	6.7	0.804	3962	intron1	
<i>Etfdh</i>	electron transferring flavoprotein, dehydrogenase NM_025794 chr3 79407709 79432689 - chr3 E3 3 31.8 cM	NM_025794	79427860	79427880	TATGAGTGTACAGCTAACT	FW	8.9	0.81	4829	intron1	1.64
			79428679	79428699	tatcaagctTAATCACAAITTT	RC	7.3	0.82	4010	intron1	
			79431515	79431535	TAGAAAGCAAAGTCAAGTCA	RC	9.1	0.85	1174	intron1	
			79432050	79432070	ATGGCTGCAAAGTCAAGTCA	RC	7.7	0.854	639	intron1	
<i>Fabp3</i>	fatty acid binding protein 3, muscle and heart NM_010174 chr4 129986021 129992707 + chr4 D2.2 4 61.0 cM 1-Ese14 Mafk chr4:129984619-129985343 2-Ese14 Mafk chr4:129984619-129985343	NM_010174	129984792	129984812	agatgctgactTGGTAATAAT	FW	7.9	0.763	-1229	¹ upstream	3.10
			129984906	129984926	TGAGTGTGACCATGCCCTGAA	FW	8.1	0.82	-1115	² upstream	
			129981501	129981521	TCCTTCTGACTCAGAGTCGTA	FW	6.4	0.784	-4520	upstream	
			129981664	129981684	acaaatgctctgctcagtgagc	RC	12.2	0.896	-4357	upstream	
			129982084	129982104	TCCCCTGGAAGCAGCTGGAGA	FW	6.7	0.8	-3937	upstream	
			129983416	129983436	aaactggctcaggtagtggtgc	RC	8.8	0.779	-2605	upstream	
			129987160	129987180	CCTACTGCTGAGTTAATCTCC	RC	12.7	0.853	1139	intron1	
			129987425	129987445	TCCCCTGGCTATATCATCTCC	RC	8.4	0.803	1404	intron1	
			129987468	129987488	AACAGGACTGTGTCTGCCCTG	RC	9.7	0.774	1447	intron1	
			129989010	129989030	TGAAACTGACCGTCCATACA	FW	7.5	0.827	2989	intron1	
			129989041	129989061	AGCACTGCTGTCTCAGTTTTC	RC	9.7	0.839	3020	intron1	
			129989562	129989582	CTAGCATGACCAAGCCTACTA	FW	9.3	0.86	3541	exon2	
			129990060	129990080	TCTACAGCGAGTCACTCTGG	RC	7.7	0.821	4039	intron2	
<i>Fabp4</i>	fatty acid binding protein 4, adipocyte NM_024406 chr3 10204342 10208576 - chr3 A1 3 13.9 cM	NM_024406	10204746	10204766	TATATTGCTCATTCACTCCA	RC	11.3	0.852	3830	intron3	4.90
			10205795	10205815	GCCGACTGACGGAGCTGGTT	FW	6.4	0.843	2781	intron2	
			10205915	10205935	CCCCCTCACTCTGCATCAGC	FW	8.8	0.797	2661	intron2	
			10206647	10206667	GAACATGCTGTTTCAACATTC	RC	10.1	0.846	1929	intron1	
			10206855	10206875	TTAGAACCTTAGTCAACCTGT	RC	9.1	0.793	1721	intron1	
			10207421	10207441	CTCAGTGCATAGTACTACCA	RC	8.7	0.778	1155	intron1	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
			10207460	10207480	CGATGGGCTAAGTCATGCTGA	RC	15.6	0.92	1116	intron1	
			10208684	10208704	TTTTCTCTGAGTCATGTTTT	RC	10.5	0.808	-108	upstream	
			10212003	10212023	TTCCGATGACTAAGCACTGAC	FW	14.3	0.927	-3427	upstream	
			10212054	10212074	AAAGAATGAGTAAGCCACAGA	FW	10	0.829	-3478	upstream	
Fh1	fumarate hydratase 1	NM_010209	177551426	177551446	CTTTAATGACTGAGCCATCTC	FW	8.5	0.875	4340	intron1	1.35
			177553238	177553258	caetCCACTGTGTCACTTGTA	RC	7.2	0.762	2528	intron1	
			177553466	177553486	aaegtgccttgagtcagtggt	RC	9.7	0.771	2300	intron1	
			177556025	177556045	GGTCCGTGAGACAGCCTAGAA	FW	8.3	0.81	-259	upstream	
			177557735	177557755	agagaatgatgtgacccaaat	FW	6.8	0.787	-1969	upstream	
			177559963	177559983	GCAGTCTGACACAGTAAACAT	FW	10.5	0.808	-4197	upstream	
			177560049	177560069	acaccatgaccaaggcaagtc	FW	9.2	0.768	-4283	upstream	
			47099818	47099838	catcactgactctgacttgg	FW	13.4	0.898	-5006	upstream	1.50
			47102836	47102856	gagagatgactcagtgatcca	FW	7.1	0.786	-1988	upstream	
			47104119	47104139	CGACTATGATACAGCAACACA	FW	11.6	0.854	-705	upstream	
			47104686	47104706	CTCTCTGCTCTCATGTGGG	RC	8.4	0.819	-138	upstream	
			47105116	47105136	AGAGCGTGAAGCAGCACCAGA	FW	10.3	0.843	292	exon1	
			47105481	47105501	TGGTGTGACTCCGGAGAGCT	FW	8.2	0.781	657	intron1	
			47106617	47106637	CCATGGTATGCAGCTGCCTT	FW	7.4	0.812	1793	intron1	
			47106716	47106736	TGCCCTTGACTCAGGCTGCC	FW	7.6	0.787	1892	intron1	
			47106969	47106989	gcactgtgataccgcactgtg	FW	10	0.82	2145	intron1	
			47107015	47107035	atggctctaaagtgcgacgag	RC	9.8	0.823	2191	intron1	
			47107357	47107377	GTCGGTAAATCAGCAGAGAG	FW	7.4	0.766	2533	intron1	
			47108762	47108782	TCAGATAACTCTGCATATTT	FW	13.2	0.826	3938	intron1	
			75048984	75049004	GGAAATGACAAGGCAAGATC	FW	10.5	0.854	-3141	upstream	1.29
			75049923	75049943	CCTCATGCTGTGCAAGGTC	RC	13.8	0.921	-2202	upstream	
			75053568	75053588	TCAGTCTCTTGTAAACCCAA	RC	7.6	0.784	1443	intron1	
			75054546	75054566	GAGAGTCTGTGTACCATAG	RC	6.6	0.786	2421	intron1	
			75054954	75054974	TCTCTGCTGCTCATGTCCA	RC	8.5	0.826	2829	intron1	
			75055440	75055460	CACACGGTGAAGTGAAGCTGT	RC	10.9	0.824	3315	intron1	
			75056371	75056391	ctcttgcttagctatccccca	RC	13.3	0.896	4246	intron1	
			75056846	75056866	cttattctgactcaccagttc	RC	9.2	0.77	4721	intron1	
			29192441	29192461	ggaccgtgatagctgtctc	FW	8.9	0.807	2884	downstream	1.29
			29192656	29192676	aaagtggcctagtcaagccatc	RC	9.1	0.839	2669	downstream	
			29195469	29195489	CTCCGGTGAAGTGGCCATGTT	FW	9.3	0.847	-144	upstream	
			29198150	29198170	atatgtgcacactcacacaca	RC	7.8	0.801	-2825	upstream	
			29198674	29198694	ltaacttgacacagaaaaaga	FW	8.2	0.795	-3349	upstream	
			29198980	29199000	caacatccttagtccaccagag	RC	7.9	0.797	-3655	upstream	
			77444760	77444780	tgggctgactgagcccatga	FW	10.2	0.878	-4637	upstream	1.70
			77445394	77445414	acaccatgaccaagacaacac	FW	7.8	0.762	-4003	upstream	
			77445970	77445990	ccatgccctggtcgaagattc	RC	7.5	0.771	-3427	upstream	
			77447078	77447098	atattataactaaagcaaaaac	FW	8.8	0.821	-2319	upstream	
			77449938	77449958	CCAACCTGACTctgaaacccct	FW	7.9	0.785	541	UTR5	
			77450274	77450294	CTGATTGCAAAAGTCAATTCCT	RC	8	0.857	877	UTR5	
			77450571	77450591	ACAATGTGACAGAGCTTAACA	FW	9	0.869	1174	UTR5	
			77450960	77450980	GATCTAATGGGTCAAGCTGA	RC	7	0.769	1563	UTR5	
			77451526	77451546	AGAGGATGACTGGGAGTCTC	FW	6.8	0.764	2129	UTR5	
			77452049	77452069	TAGCAGTGACAGAGCCAGTG	FW	11.2	0.867	2652	UTR5	
			126597854	126597874	TGTGGCTGCAATGCCATCTC	FW	7.8	0.81	4932	exon3	4.75
			126598295	126598315	CACCAAGCTTTGCTCACTCAGG	RC	9.2	0.861	4491	intron2	
			126600774	126600794	TGCAGGTTACTTGCAGCCCTG	FW	8.8	0.792	2012	UTR5	
			126601364	126601384	ggagcctgatagctgtctc	FW	6.8	0.789	1422	intron1	
			126601627	126601647	aggatggcctagtcaagtcac	RC	7.3	0.832	1159	intron1	
			126602618	126602638	TAAGTCCAGAGTCACTCTG	RC	8.8	0.779	168	intron1	
			126602981	126603001	GAAGTGTCTTTCACACCGGA	RC	12.1	0.853	-195	upstream	
			126603035	126603055	AGGTGGCTGTATCAGGCGCA	RC	8	0.801	-249	upstream	
			126604049	126604069	accattgcagattcaaacTTT	RC	9	0.826	-1263	upstream	
			126604847	126604867	TCTTACTGAGAAAGCATTTGT	FW	9.6	0.822	-2061	upstream	
			126605698	126605718	GGAACAGCTGGGTCAAGAAA	RC	7.2	0.858	-2912	upstream	
			126606221	126606241	cattagtgacttggcaaatgt	FW	11.8	0.876	-3435	upstream	
			126606897	126606917	CATCTCTGACTAGGCAATTAG	FW	11.7	0.876	-4111	upstream	
			99543423	99543443	TAACCTGCTGCTCAAGTGTCC	RC	12	0.851	-4600	upstream	2.19
			99544046	99544066	CAGAATGCAAAAGCCCTGCG	FW	8.2	0.845	-3977	upstream	
			99544199	99544219	CCACAGTGCACTGGACAGCC	FW	10	0.777	-3824	upstream	
			99545835	99545855	AGCGGTGACTGAGTGGCAT	FW	9	0.876	-2188	upstream	
			99546627	99546647	CCAGAGTGAAGTGGAAACCCG	FW	7.5	0.773	-1396	upstream	
			99551593	99551613	aaaggtaccaggtgagtggtg	RC	8.6	0.765	3570	intron5	
			99551784	99551804	caacagtggagaagcagaggg	FW	9.4	0.827	3761	intron5	
			77896482	77896502	CCGGATGACTTAGCAAAAAA	FW	16.6	0.937	59	UTR5	1.78
			77895394	77895414	ttatgagctaaagtcacactct	RC	9.2	0.882	1147	intron1	
			77895517	77895537	aggactcccaagtcACCGACA	RC	7.8	0.764	1024	intron1	

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	chr12 C3 12 36.0 cM 1-Ese14 Mafk chr12:77896350-77896694		77897755	77897775	CAAGCTACAGAGTCAGAGGGA	RC	9.2	0.786	-1214	upstream	
			77897987	77898007	CTTACTGCTGAGTAAACCAT	RC	8.8	0.827	-1446	upstream	
			77898127	77898147	GCTTGTCTTAGTCATAGTAG	RC	10.7	0.82	-1586	upstream	
			77898422	77898442	TTCTTGTCTGTTTCACTGCTT	RC	10.1	0.837	-1881	upstream	
			77898531	77898551	CCATGGCTATCTCATGGGAT	RC	6.9	0.788	-1990	upstream	
			77899147	77899167	GGCCAATGACACAGCCCAAGC	FW	12.7	0.886	-2606	upstream	
			77899271	77899291	CACGGTACAGAGTCACAGCCC	RC	7.9	0.78	-2730	upstream	
			77899598	77899618	TTGTTTGTAAAGTCAGGGAGA	RC	15.1	0.931	-3057	upstream	
			77899722	77899742	TTGAATGCTCGGTCAAGTGCCT	RC	8.7	0.87	-3181	upstream	
			77900737	77900757	CCTTAGGCAGAAACAGGAAGG	RC	6.5	0.787	-4196	upstream	
Gstm4	glutathione S-transferase, mu 4 NM_001160411 chr3:107843325-107847777 - chr3:F2.3 3 1-Ch12 Mafk chr3:107847634-107848831 Ese14 Mafk chr3:107847700-107848385 Mel Mafk chr3:107847629-107848448 2-Ch12 Mafk chr3:107849799-107850908 Ese14 Mafk chr3:107850198-107850495 Mel Mafk chr3:107850032-107851211 3-Ch12 Mafk chr3:107849799-107850908 Ese14 Mafk chr3:107850198-107850495 Mel Mafk chr3:107850032-107851211	NM_001160411 NM_026764	107847966	107847986	AAGTGCTGATTAGCACTTCA	FW	9.2	0.839	-189	¹ upstream	1.30
			107850337	107850357	TACCTGTGACTCAGCATCTTC	FW	16.5	0.952	-2560	² upstream	
			107850404	107850424	gcaagatgactcaagcaataa	FW	19	0.972	-2627	³ upstream	
			107843705	107843725	CCCGGTCACAGGCGCCAC	FW	6.9	0.775	4069	UTR3	
			107844134	107844154	CTTCTGCCAGTCAAGGCTC	RC	9.1	0.865	3640	UTR3	
			107844448	107844468	GCACACTGACTATGAATCTGT	FW	8.5	0.776	3326	intron7	
			107844512	107844532	ATCCAGTGACTCTGCAAAACC	FW	12.4	0.898	3262	intron7	
			107845211	107845231	GAAGAAATGACAAATGCTCAACT	FW	8.9	0.825	2563	intron6	
			107846067	107846087	GATAGTTCAGTGCATGGGGA	RC	11.7	0.779	1707	intron5	
			107849526	107849546	TATCCTTGAATAAGCGTGATT	FW	7.8	0.815	-1749	upstream	
107852749	107852769	ACAATAACTAAGTCACTTAGC	RC	7.1	0.777	-4972	upstream				
Gsto1	glutathione S-transferase omega 1 NM_010362 chr19:47929462-47939278 + chr19:D1 19 1-Ch12 Mafk chr19:47932488-47932937	NM_010362	47932619	47932639	CTAGGCTGACTCAGCGTCC	FW	12.2	0.911	3157	¹ intron3	2.22
			47926086	47926106	CTTCATCCTGTGTCACAGCAG	RC	8.3	0.793	-3376	upstream	
			47926736	47926756	lggatagctgagtcactgccc	RC	13.1	0.916	-2726	upstream	
			47926818	47926838	lagatagctgagttacacca	RC	9.3	0.811	-2644	upstream	
			47927743	47927763	GCTATGGCTTGGTCAAGCTGT	RC	11	0.871	-1719	upstream	
			47928490	47928510	ATGTTTGTAGTTCATCCACA	RC	7.8	0.806	-972	upstream	
			47929382	47929402	TTAAGCTCACACAGCATCAGG	FW	9.2	0.816	-80	upstream	
			47930171	47930191	CCGTGTGCACAGTCATTAGG	RC	9.3	0.869	709	intron2	
			47931890	47931910	AATGAGCTTTGTCAAGCTGA	RC	13.7	0.885	2428	intron2	
			30477803	30477823	TGGCACTGAATCAGCTCCTGT	FW	9.8	0.834	-3989	upstream	
Hadhb	hydroxyacyl-Coenzyme A dehydrogenase 3-ketoacyl-Coenzyme A thiolase enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit NM_145558 chr5:30481792-30511133 + chr5:B1 5	NM_145558	30478290	30478310	CTCAGGCGAGGTTATTATCT	RC	6.7	0.767	-3502	upstream	1.50
			30479935	30479955	gaaagggcaaaagcaacagct	RC	6.9	0.83	-1857	upstream	
			30480394	30480414	TAAAGGTGAATTAGCACCCAG	FW	10.3	0.853	-1398	upstream	
			30481093	30481113	AACTTAGCGGTGTCAAGGCCA	RC	9.8	0.836	-699	upstream	
			30481216	30481236	AGAGCCTGACACTGCCGAGGC	FW	10	0.84	-576	upstream	
			30482143	30482163	CGCTGGCTTGTGTCAAGCGG	RC	11.1	0.882	351	intron1	
			30482272	30482292	CAGTCTGCTTGGTATCCAGG	RC	7.3	0.784	480	intron1	
			30483878	30483898	gaactgctaatcaagctgag	RC	10.8	0.835	2086	intron1	
			30486312	30486332	ttccaagctcaagtcacatgag	RC	6.9	0.874	4052	intron1	
			52586955	52586975	GCACATTTAATAAGCAAATTT	FW	9.9	0.773	3339	intron1	
Hibadh	3-hydroxyisobutyrate dehydrogenase NM_145567 chr6:52496223-52590294 - chr6:B3 6 chr6:B3	NM_145567	52589633	52589653	CCACTTTAGGACGACCAACT	FW	9.2	0.844	661	intron1	1.27
			52590600	52590620	GCAACTGCCTCTCACTGSGC	RC	6.8	0.779	-306	upstream	
			52592619	52592639	CAAAGGGCTAAGTCATAGTTT	RC	14.7	0.914	-2325	upstream	
			52592854	52592874	gaactgctatgtaaaactagg	RC	6.6	0.782	-2560	upstream	
			52594273	52594293	GCCTTCTGATTCAAGCTGTATG	FW	8.6	0.833	-3979	upstream	
			52899711	52899731	ccacaatgacacagtctctct	FW	9.4	0.787	-2170	upstream	
			52900819	52900839	gatgctgacaaagccatcat	FW	7.5	0.809	-1062	upstream	
			52901056	52901076	aggctctgacagagctctct	FW	6.9	0.844	-825	upstream	
			52901078	52901098	gagatagctgatacaggcgcc	RC	7.6	0.8	-803	upstream	
			52902139	52902159	GTCCTCTGACTTTGCTCTTTT	FW	7.3	0.834	258	intron1	
Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase NM_146108 chr1:52901881-52977830 + chr1:C1.1 1	NM_146108	52904805	52904825	lgtgaaatgatgacagcagaaa	FW	7.8	0.822	2924	intron1	1.45
			52905746	52905766	TGAGGCTTACTATGCATCTTT	FW	10.1	0.789	3865	intron1	
			52905856	52905876	GGGACTGCTGGGTGAAGGAGA	RC	7	0.801	3975	intron1	
			52906540	52906560	AATACAGCTGTGTGATTTGT	RC	10	0.8	4659	intron1	
			82722158	82722178	CGTGGTCCCACTCAGTCACC	RC	6.9	0.85	2290	intron1	
			82722187	82722207	GGATGGCACAGTCACCTGCA	RC	7.6	0.836	2261	intron1	
			82723935	82723955	GCTCCGTGAATAAGCAGGCGA	FW	10.9	0.859	513	exon1	
			82724713	82724733	GCCACCOCGCGTCAAGGCTCA	RC	9.3	0.836	-265	upstream	
			82725894	82725914	TTAGTCTAATCTAGCAAATCA	FW	8	0.815	-1446	upstream	
			82727009	82727029	AGTAGATGATTAGCAATGAC	FW	8.7	0.838	-2561	upstream	
82728416	82728436	GAAAAATCAATCAGCACATGT	FW	8.7	0.775	-3968	upstream				
Hk2	hexokinase 2 NM_013820 chr6:82675020-82724448 - chr6:C3 6 34.5 cM	NM_013820	52586498	52586518	CTCAGGCTCTGTCACTGATA	RC	10.1	0.862	-4140	upstream	3.75
			52588307	52588327	lgcagagctatgtaagctgag	RC	7.3	0.777	-2331	upstream	
			52588355	52588375	CCGGATGACACAGAAAGCCG	FW	9.5	0.8	-2283	upstream	
			52589579	52589599	ACAAAGTGATAGAGCAACAGA	FW	9.3	0.831	-1059	upstream	
			52590867	52590887	CAGTGGTGACCCAGGAGTTGA	FW	9.7	0.792	229	exon1	
			52591600	52591620	AGACGGTGAATCTGGTGAATA	FW	9.5	0.771	962	exon1	
			52591912	52591932	TGAGGATGACTCAGAGAAAGA	FW	14	0.845	1274	exon1	
			52592272	52592292	GCCAGGCGAGGTCACAGAGA	RC	6.4	0.828	1634	exon1	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
			52593479	52593499	TGTCCTGACTCAGTCCCTTG	FW	9.2	0.794	2841	intron3					
			52594516	52594536	ctcagtcgagagtcagagagca	RC	12.7	0.895	3878	downstream					
			52595533	52595553	CCAAATCACTAGCAGAGTA	FW	7.6	0.792	4895	downstream					
			140976001	140976021	CGGCAGTGACTCAGGCCCTCA	FW	9.3	0.798	-692	upstream					
			140976201	140976221	GGGGTTGACAGAGCCCTTA	FW	7.1	0.844	-492	upstream					
Hspb7	heat shock protein family, member 7 (cardiovascular) NM_013868 chr4 140976693 140981225 + chr4 E1 4	NM_013868	140976420	140976440	AAACTGTCACCTGCGCAGGTG	FW	7.5	0.776	-273	upstream	2.85				
			140977160	140977180	CCCTGGGCTTTCTCAGCCTTC	RC	7.1	0.789	467	UTR5					
			140979090	140979110	CCTGAAGCTGAGTCACAACCA	RC	11.6	0.904	2397	intron2					
			140979358	140979378	CAAGAGTGACTCAGCCAGCCA	FW	13.6	0.92	2665	intron2					
			140979465	140979485	GGCACAGCTGTGTACTCTCC	RC	9.6	0.871	2772	intron2					
			140979801	140979821	CTGATGGCACAGTCATGAACA	RC	8.4	0.839	3108	exon3					
			140981061	140981081	GGGCTCTGACTCAGTCTCTGC	FW	6.5	0.781	4368	UTR3					
			140981482	140981502	TGTTCTGCACCTGTCCACAGCC	RC	6.7	0.831	4789	downstream					
			ldh3a	isocitrate dehydrogenase 3 (NAD+) alpha NM_029573 chr9 54434317 54452469 + chr9 A5.3 9 1-Mel Mafk chr9:54430927-54432386 2-Mel Mafk chr9:54430927-54432386 3-Ch12 Mafk chr9:54432007-54432195 Mel Mafk chr9:54430927-54432386	NM_029573	54431088	54431108	AAGGGTGCTTAATCAACAGGAG	RC	9		0.845	-3229	¹ upstream	1.56
						54431868	54431888	gctaactgactcagtagtggct	FW	6.5		0.806	-2449	² upstream	
						54432154	54432174	ttttctctgactcagcagctttg	FW	14.9		0.942	-2163	³ upstream	
						54429695	54429715	gcactgtgagcagcagcagcagc	FW	10.1		0.851	-4622	upstream	
54430525	54430545	TTGCTATGACAAGAATTTAA				FW	8	0.779	-3792	upstream					
54430596	54430616	gcaccatgaccaaggcaagctc				FW	9.1	0.768	-3721	upstream					
54435142	54435162	CCAAGGTCACCTAGCTAATTA				FW	9.6	0.808	825	intron1					
54435340	54435360	aaatcctgacaaaagcattgg				FW	12.3	0.873	1023	intron1					
54435514	54435534	TGGCAGTGATCAAGCAGACAG				FW	8.9	0.816	1197	intron1					
54437791	54437811	CATTATTACTTAGCATTCCT				FW	7.4	0.808	3474	intron2					
54437926	54437946	CATCTGGCTATGTAAGCTTGT				RC	7.5	0.769	3609	intron2					
54439163	54439183	AAGGGCTGATTCAGCCATATA				FW	11	0.838	4846	intron2					
Ifi272a	interferon, alpha-inducible protein 27 like 2A NM_029803 chr12 104680375 104681890 - chr12 E 12	NM_029803	104677582	104677602	GCCCACTGCATAGTCCCTCT	FW	8.8	0.856	4308	downstream	5.07				
			104681358	104681378	AGGATGTGACAGAGCCGTGGT	FW	8.2	0.851	532	intron2					
			104683618	104683638	AAGCCCTGAATGTGCAGCATT	FW	7.9	0.799	-1728	upstream					
			104684317	104684337	TTTCTgtctcagtcaggtctc	RC	7.2	0.777	-2427	upstream					
			104684959	104684979	gtatgtgcatcttcacagaga	RC	8.5	0.79	-3069	upstream					
			104685779	104685799	TATTTTCTGTGTCATCCATA	RC	11.4	0.803	-3889	upstream					
			104686267	104686287	ATATTAACCTAGTCATCTGGC	RC	7.8	0.778	-4377	upstream					
			Kcnd2	potassium voltage-gated channel, Shal-related family, member 2 NM_019697 chr6 21166108 21679805 + chr6 A2-A3.1 6 7.2 cM	NM_019697	21161781	21161801	ccacaatgaggtagcaatagg	FW	11.6		0.841	-4327	upstream	2.55
21162334	21162354	AGACATACTGGGTCACTGTGT				RC	10.2	0.811	-3774	upstream					
21163441	21163461	CACGGTAACTAAGCAGAGAG				FW	9.6	0.816	-2667	upstream					
21165528	21165548	TAACGTGCACACTGCACTGA				FW	9.3	0.782	-580	upstream					
21166882	21166902	TTGCCCTCAAGTCATCGGA				RC	7.2	0.778	774	exon1					
21166996	21167016	ATACCCGCTGTGTCATGATCT				RC	9.4	0.777	888	exon1					
21167068	21167088	TCGTGCGCAGTGTGATGAGTA				RC	9.8	0.836	960	exon1					
21169150	21169170	AATGGGGCTGTGTTACTATTA				RC	9.6	0.793	3042	intron1					
21170045	21170065	ATATTAGCTTTTTCATAGATT				RC	7	0.789	3937	intron1					
Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3 NM_001190869 chr7 107325179 107333379 + chr7 7 F1	190870///NM_001190871///NM				107320228	107320248	GAGTGCACTGAGTCATAGATC	RC	8	0.793	-4951	upstream	2.86	
						107321445	107321465	GGAAACCTGAGTCAGGACCA	RC	7.9	0.786	-3734	upstream		
						107322512	107322532	acatgagctatctcatacaca	RC	6.4	0.782	-2667	upstream		
			107324009	107324029	GAAAGTGTGTGTTAAAAGGG	RC	8.1	0.805	-1170	upstream					
			107324309	107324329	AGCCAGTGAGACAGCTCAGCA	FW	7.1	0.804	-870	upstream					
			107325429	107325449	ACCACCTGACAGGGCTAGTTT	FW	7.8	0.814	250	intron1					
			107330561	107330581	TCTTCATGACAAAGCCATGCT	FW	11.9	0.873	3369	intron1					
			107330827	107330847	TTTCTATGAGACTGCAAACTA	FW	7.4	0.794	3635	intron1					
Krt15	keratin 15 NM_008469 chr11 99993072 99997263 - chr11 D 11 58.5 cM	NM_008469	99994997	99995017	CATACTGCTCCCTCATCTCTG	RC	6.9	0.805	2266	exon4	4.40				
			99996157	99996177	ATGCCTTGACAGAGCCCTTGG	FW	7.7	0.851	1106	intron1					
			99996860	99996880	GGTTCGATGGTCACTTCTCT	RC	9	0.845	403	exon1					
			99998143	99998163	CCATTGGCTTTGCACTGCTC	RC	7.6	0.831	-880	upstream					
			99998726	99998746	CATGATTGACAAGTATTTTT	FW	6.6	0.767	-1463	upstream					
			99998767	99998787	ATCCAATGACACAGAGCTTAA	FW	7.3	0.766	-1504	upstream					
			100000261	100000281	CTGATGGCCAGTCACTGCC	RC	7.2	0.834	-2998	upstream					
			100001695	100001715	catctgcaactctcaacacga	RC	6.5	0.773	-4432	upstream					
			Ldhd	lactate dehydrogenase B NM_008492 chr6 142438768 142456477 - chr6 G2 6 62.0 cM 1-Ese14 Mafk chr6:142456198-142456583	NM_008492	142456412	142456432	GCCACTGCAAGTCAAGCAGCC	RC	10.1		0.869	65	¹ UTR5	1.43
						142451619	142451639	GCTGCAGCTGTGTCACCTGA	RC	9.9		0.8	4858	intron2	
142452910	142452930	AGACAGTTAGACAGCAGAAGG				FW	10.3	0.762	3567	intron2					
142452986	142453006	CCACAATGACTGTGGAACAA				FW	9.5	0.782	3491	intron2					
142454105	142454125	GGAATCTGACTGAGAAGTAGC				FW	7.1	0.797	2372	intron1					
142457462	142457482	GGAGTTGCTGTGAGAAATTT				RC	7.5	0.802	-985	upstream					
142457966	142457986	GTAACCTGAAATAGCAAAAGA				FW	6.8	0.81	-1489	upstream					
142460244	142460264	tctctgtgatgcagctatttg				FW	8.3	0.815	-3767	upstream					
114150104	114150124	AGACCTGACTTTGAAAGTAA				FW	8.1	0.768	4118	downstream					
114155721	114155741	TTACAATGACTCAGACTGGAA				FW	8.1	0.8	-1499	upstream					
114156609	114156629	tcaacttgacacagctggaat				FW	12	0.892	-2387	upstream					
114156933	114156953	cttgctcttgatcatgatgt				RC	8.5	0.784	-2711	upstream					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
Lpl	lipoprotein lipase NM_008509 chr8 71404453 71430831 + chr8 B3.3 8 33.0 cM 1-Ch12 Mafk chr8:71409034-71409265 Mel Mafk chr8:71408974-71409225	NM_008509	114156968	114156988	aaacctgactaagacaCTCA	FW	8.1	0.782	-2746	upstream	1.91
			71409087	71409107	AGAATAGCTGAGTCATGAAAT	RC	11.7	0.906	4634	¹ intron1	
			71400178	71400198	CTAGCAGCAGGTCCACCACTG	RC	8.7	0.83	-4275	upstream	
			71400220	71400240	TTATGAGCTGTCTCATGGGAG	RC	8.5	0.81	-4233	upstream	
			71401301	71401321	CACAATGCTCTTCAACCTTA	RC	7.9	0.819	-3152	upstream	
			71405728	71405748	GAACCTTGATTGAGCTAACAG	FW	6.4	0.815	1275	intron1	
			71407134	71407154	TGATGGTGACTGAGTCTTCT	FW	7.7	0.782	2681	intron1	
			71407276	71407296	GTGATCTGACTAAGCCTGATT	FW	7.6	0.868	2823	intron1	
			71407382	71407402	TAAAGATTACACAGCAAAAGG	FW	13.4	0.831	2929	intron1	
			71407689	71407709	ATGAATGCAGAGTCACAGATA	RC	13.6	0.905	3236	intron1	
			71408252	71408272	AAACATACAAAGTCAGCCTGA	RC	9.2	0.775	3799	intron1	
			71408388	71408408	ATCTTATGACGACGCAATGca	FW	8.3	0.886	3935	intron1	
			Ltf	lactotransferrin NM_008522 chr9 110921795 110945270 + chr9 F 9 70.2 cM	NM_008522	110918087	110918107	CAGCAGGCTGTGTACATGTG	RC	9	
110918459	110918479	gagcaactgactgagctaaagag				FW	9.5	0.877	-3336	upstream	
110921311	110921331	CTAGGCTGACTCGGCTCTCC				FW	7	0.853	-484	upstream	
110921548	110921568	TGACTCTGATCCTGCAGAAAGC				FW	8.1	0.794	-247	upstream	
110923383	110923403	TGGTGTGCTGTGTCAAAATCT				RC	9.9	0.9	1588	exon2	
110924359	110924379	CGAAGGGCTAATCATTCTGA				RC	11.8	0.844	2564	intron2	
110925979	110925999	ACATTTGCCCACTCAGCATGG				RC	9.7	0.816	4184	intron5	
7129930	7129950	ttaactgtctgagctcactctctc				RC	16.2	0.947	-1327	¹ upstream	
Macrod1	MACRO domain containing 1 NM_134147 chr19 7131257 7272552 + chr19 A 19 1-Ch12 Mafk chr19:7129780-7130082 Ese14 Mafk chr19:7129638-7130202	NM_134147	7126796	7126816	ataaaggcagggttcactgtga	RC	9.6	0.791	-4461	upstream	1.58
			7128056	7128076	ectggttgactgagctgagcat	FW	7.2	0.871	-3201	upstream	
			7128106	7128126	cctgcatgactctgagccaga	FW	12.2	0.876	-3151	upstream	
			7130943	7130963	AGCAGAGCTGGGTGATGCGGA	RC	7.1	0.777	-314	upstream	
			7132408	7132428	ATGGGGGCTGGGTCAAGCGGG	RC	8.8	0.866	1151	intron1	
			7135778	7135798	GCAAGTTGAGGCTCAGTGTG	RC	9.1	0.765	4521	intron1	
			7136067	7136087	AGCTGCTGAGCCAGCATACTG	FW	6.7	0.812	4810	intron1	
			21472276	21472296	GAACGGCAGCTTCACCGTIG	RC	6.6	0.771	-339	¹ upstream	
			21467482	21467502	ttaaccaactgagctcaGCCTTA	RC	11.3	0.809	4455	intron1	
			21467548	21467568	ggcatgtgacacagcttgtca	FW	7.5	0.863	4389	intron1	
21467942	21467962	ATGAGCAGCTGAGTAATGGAAA	RC	10.8	0.819	3995	intron1				
21470827	21470847	TCAAAATAACTAGGCCAACAAAT	FW	9.8	0.794	1110	intron1				
21472851	21472871	GACCAATGAATATGCTCTTGG	FW	6.4	0.774	-914	upstream				
21472961	21472981	ATGATgctttagtcaaggctt	RC	9.1	0.779	-1024	upstream				
21473556	21473576	GTTACCTCTGTGTGAGGGACT	RC	7.7	0.769	-1619	upstream				
21474394	21474414	TGAAATGCTGACTGACCCAGGA	RC	8.6	0.776	-2457	upstream				
21475996	21476016	caaaactctctgtcaaaagtgg	RC	8.6	0.791	-4059	upstream				
Mdh2	malate dehydrogenase 2, NAD (mitochondrial) NM_008617 chr5 136254518 136266256 + chr5 G2 5 78.0 cM	NM_008617	136253000	136253020	TTGCTTTCTCTGTCACTGTCC	RC	7.6	0.782	-1518	upstream	1.37
			136253822	136253842	GTGCCATGACAAACCCGAGTAC	FW	6.9	0.814	-696	upstream	
			136255057	136255077	AAATTAGCACAAGTCAGTGGCC	RC	8.5	0.838	539	intron1	
			136255523	136255543	tGAGAGTGAGAAGGCCCTTTGA	FW	7.5	0.763	1005	intron1	
			136255778	136255798	AAGAGGGCAGGGTCAATATT	RC	8.3	0.829	1260	intron1	
			136256217	136256237	ccccggtagcttagagagact	FW	11.1	0.818	1699	intron1	
			136257352	136257372	GGCTGTGCTGTCTCAATGGAA	RC	6.8	0.823	2834	intron1	
			136257588	136257608	TGACAGTGACTCTGGGCTCTC	FW	10.5	0.777	3070	intron1	
			136257672	136257692	TGACAGTGACTCAGGGTAAAG	FW	12.7	0.821	3154	intron1	
			136258293	136258313	ttacttgcatagtgaaactgt	RC	6.4	0.777	3775	intron1	
			136258528	136258548	ctacttctaggttataactgc	RC	7.9	0.794	4010	intron1	
			136259303	136259323	AGCAGATCTGAGTCACATTGA	RC	9.5	0.811	4785	exon2	
			136259448	136259468	TTAGATGACATTCGACAAAT	FW	11.9	0.861	4930	intron2	
			Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial NM_181407 chr7 96781327 97002869 + chr7 E1 7	NM_181407	96776483	96776503	ACTATTGCAAAAGTCAACTAGG	RC	10.4	
96779133	96779153	AGCCACTGACTCTGAAAGATG				FW	8.2	0.774	-2194	upstream	
96782583	96782603	GAAATGCTATGTAAAGGGT				RC	6.7	0.788	1256	intron1	
96782884	96782904	ACTCCCTGACGGTGCAGTCTT				FW	8.2	0.84	1557	intron1	
96785203	96785223	GTAGAATTACATAGCCGATAA				FW	6.8	0.765	3876	intron1	
96785225	96785245	CAAGTCTGAGTGGCATTGGT				FW	7	0.801	3898	intron1	
96785953	96785973	AAAGTTAATCTCAGCAGCACT				FW	8.6	0.833	4626	intron1	
147277546	147277566	CTCTGTGCTGATTCAAGTCCA				RC	11.2	0.861	1472	UTRS	
Mfn2	mitofusin 2 NM_133201 chr4 147247694 147279018 - chr4 E2 4	NM_133201	147277701	147277721	AGGGAAGCTTACTCATTGCGG	RC	7.8	0.822	1317	intron1	1.42
			147277876	147277896	AAGGAGCTGAATCAGGCCAA	RC	7.8	0.825	1142	intron1	
			147282154	147282174	aataatgcagagtaagccagt	RC	10.7	0.804	-3136	upstream	
			8478522	84785242	ttacctgctgagctatTGAGT	RC	16.5	0.955	1845	¹ intron1	
			8472628	8472648	ATTATGGCTTCTCCACAGAGG	RC	7.5	0.796	-4049	upstream	
Mpc1	brain protein 44-like//brain protein 44-like protein-like NM_018819 chr17 8476677 8490526 + chr17 A1 17 7.8 cM 1-Ese14 Mafk chr17:8478371-8478634	NM_018819 XM_003086034 XM_003086035 XM_003086036 XM_003086037	8473372	8473392	tgtagtgctgattaatgatta	RC	11.1	0.788	-3305	upstream	1.41
			8473534	8473554	tcactggcttgctcaagcatgg	RC	6.6	0.788	-3143	upstream	
			8474295	8474315	gtatcatgactcaagacataag	FW	9.8	0.806	-2382	upstream	
			8474810	8474830	CTATAATTACTTAGCACTAGA	FW	10.6	0.828	-1867	upstream	
			8475032	8475052	tcacctgactaagtacacact	RC	7.2	0.806	-1645	upstream	
			8475638	8475658	acatatattactatgcatagaaa	FW	6.4	0.777	-1039	upstream	
			8477259	8477279	CACCCGTGACTGAGAGGACGA	FW	7.1	0.774	582	intron1	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
<i>Mrap</i>	melanocortin 2 receptor accessory protein NM_029844 chr16 90738568 90750021 + chr16 C3.3 16	NM_029844	8477748	8477768	AGAGGTTGAAGAAGCACTTTG	FW	7.5	0.814	1071	intron1	2.77				
			8479667	8479687	TGGGGTTAACCTAGCAGCTTTG	FW	9	0.788	2990	intron1					
			90734958	90734978	aaactctgagccagcccccac	FW	8.2	0.813	-3610	upstream					
			90734998	90735018	gaagtgccttggctcatggtg	RC	9	0.768	-3570	upstream					
			90735790	90735810	CAACTTTCACCTTAGCACAAT	FW	9.3	0.822	-2778	upstream					
			90736140	90736160	lctgcccactgagccacatccT	RC	6.9	0.785	-2428	upstream					
			90736398	90736418	GGAGTTCCTGAGTCAACCACT	RC	9.6	0.818	-2170	upstream					
			90738930	90738950	GGAAGGTGACCAGCGCAGAGGC	FW	8.8	0.843	362	intron1					
			90739300	90739320	tctctcgctaaactcAGAGTGA	RC	10.5	0.837	732	intron1					
			90740448	90740468	ACATCTGCTTGTCTCATCTGCC	RC	7.7	0.806	1880	intron1					
			90741467	90741487	lgtcgtccttggccaccacct	RC	9.7	0.876	2899	intron1					
			90741748	90741768	atcccctgagtcgcgattaaa	FW	7.3	0.813	3180	intron1					
			90742136	90742156	GTGGCTGCCATGTCAGCATCT	RC	7.8	0.836	3568	intron1					
			90743436	90743456	CCGGCTTAACAAGACCAAGA	FW	7.3	0.786	4868	intron1					
			<i>Mrp12</i>	mitochondrial ribosomal protein L12 NM_027204 chr11 120345982 120350068 + chr11 E2 11	NM_027204	120341044	120341064	GGCAGCTGACCCAGCATGTGG	FW	9.4		0.883	-4938	upstream	1.40
120344830	120344850	CACCATGCAGAGTAACACTAC				RC	7.9	0.798	-1152	upstream					
120345423	120345443	GATTCTGCAGACTCACTGTGT				RC	10.9	0.833	-559	upstream					
120348920	120348940	gtcagtcggttccacagga				RC	13.5	0.911	2938	intron3					
149020677	149020697	atactcttactcagcctcaaa				FW	7.6	0.807	-4299	upstream					
<i>Muc5b</i>	mucin 5, subtype B, tracheobronchial NM_028801 chr7 149024976 149058990 + chr7 F5 7 69.01 cM	NM_028801	149021586	149021606	CCAGTGTCACTAAGCAGCACA	FW	10.5	0.836	-3390	upstream	5.74				
			149023238	149023258	CTCAAGGCCCACTCATGTGT	RC	6.4	0.785	-1738	upstream					
			149023668	149023688	gcgcgttgactgagcggggtll	FW	10.2	0.888	-1308	upstream					
			149023895	149023915	ACTCCCTGACATGGCCAACCC	FW	6.9	0.813	-1081	upstream					
			149024280	149024300	TCATTTCTTGTCAAGGCCCC	RC	8.5	0.777	-696	upstream					
			149025599	149025619	CTAATGGCTGAGTCAGGTGGG	RC	14.6	0.919	623	intron1					
			149026405	149026425	GGCCCTTGAGGAAGCATTAAT	FW	6.5	0.806	1429	intron1					
			149027535	149027555	CAGGATGACCAAGATAAAT	FW	7.7	0.767	2559	intron2					
			90954054	90954074	TTCACTGCCCAATTCATTTGGT	RC	7	0.798	-4246	upstream					
			90954087	90954107	ATTAGGCTCACTCACTTCCG	RC	7.6	0.813	-4213	upstream					
<i>Mybpc3</i>	myosin binding protein C, cardiac NM_008653 chr2 90958300 90976673 + chr2 E1 2	NM_008653	90957401	90957421	TGCACATGACTTAGGAGCAGG	FW	9.3	0.801	-899	upstream	4.90				
			90958569	90958589	GACTTCACTAAGTCAGGAAGA	RC	7.2	0.773	269	intron1					
			90959485	90959505	ACACACTGACAGTGGGGATG	FW	9	0.833	1185	exon2					
			90959569	90959589	TCAAGTTCACAGAGCCAGTA	FW	6.5	0.771	1269	exon2					
			90959797	90959817	CCCAGAGCTGTCACCCAGA	RC	7.3	0.814	1497	intron2					
			90959872	90959892	GTTGTGCTGGGTCAAGGCCA	RC	11.4	0.899	1572	intron2					
			90960636	90960656	CAGCTATGACAGAGCCAGCA	FW	8.5	0.854	2336	exon5					
			90961853	90961873	CAAGCTGCCAGTCACTGAGA	RC	10.5	0.852	3553	intron7					
			55580702	55580722	GAGAGTGGAGTAGCAAAAAG	FW	10.7	0.848	4742	intron9					
			55582201	55582221	GTTAGTGTCTGCTCACGTGAT	RC	6.7	0.806	3243	intron6					
			55582465	55582485	TGACGGTACAGCAGAGAGGC	FW	10.1	0.805	2979	exon5					
			55582837	55582857	GTTTCTGCTGATCACTGGT	RC	8	0.833	2607	exon4					
<i>Myh6</i>	myosin, heavy polypeptide 6, cardiac muscle, alpha NM_010856 chr14 55560757 55585444 - chr14 C3 14 20.0 cM	NM_001164171 NM_010856 NM_080728	55584114	55584134	CCGAGTGAATTTGCCCTT	FW	11	0.859	1330	exon3	3.63				
			55584861	55584881	GCACCTGACACaggaaggaa	FW	10.4	0.809	583	intron1					
			55608828	55608848	AGCTCTTCAGAGTCATCAATG	RC	6.7	0.769	4558	exon12					
			55610801	55610821	TGACCGTGCACAGAGAGGC	FW	10.1	0.805	2585	exon6					
			55610909	55610929	CGAAGCGCAGAACTCAGTGG	RC	9.4	0.81	2477	intron5					
			55611181	55611201	GTTTCTGCTGATCACTGGT	RC	8	0.833	2205	exon5					
			55611202	55611222	CCTCCTCAGCTCACCGTCT	RC	7.7	0.777	2184	exon5					
			55611527	55611547	CAGCAGTGAATTTGCCACCT	FW	9	0.844	1859	exon4					
			55611574	55611594	AACTCTTCTTTGTCATCGGC	RC	10.3	0.792	1812	exon4					
			55612846	55612866	TGAACTGCTATTTCAGAGACT	RC	6.7	0.807	540	intron1					
			55615931	55615951	GTCTGGCTCTGTCAACACAC	RC	6.7	0.843	-2545	upstream					
			55617383	55617403	gagaatgccaggtcagtcagg	RC	7.4	0.831	-3997	upstream					
			55617536	55617556	TCAAGTGAATTTGACAAATC	FW	9.4	0.789	-4150	upstream					
55618196	55618216	aaacatgattctgctcaagg	FW	7	0.788	-4810	upstream								
<i>Myh7</i>	myosin, heavy polypeptide 7, cardiac muscle, beta NM_001164171 NM_010856 NM_080728	NM_001164171 NM_010856 NM_080728	110664088	110664108	GAGTCTGCTGTGTCAGGGGGT	RC	14.1	0.92	-2096	upstream	5.90				
			110667168	110667188	CTGAGTCTGAGTCACTTCTT	RC	13	0.841	984	intron1					
			110667813	110667833	CTGTCTCTTTGTCACCTCAA	RC	6.8	0.769	1629	intron1					
			110668237	110668257	TGACCTTGACTTTGGAGACAG	FW	7.6	0.767	2053	intron1					
			110668552	110668572	TGGTGTGACACAGCCTCTGG	FW	10.4	0.869	2368	intron1					
			110669281	110669301	CACCCTGCCAATTCATGTCGG	RC	7.2	0.802	3097	intron3					
			110669605	110669625	TTGCTTTGACTAAGGAAGAGT	FW	7.6	0.796	3421	intron3					
			110669783	110669803	tcgctatgacttggaaagccag	FW	7.1	0.765	3599	intron3					
			110670214	110670234	TCAGGGTGACAAAGGTCTATG	FW	10.9	0.779	4030	intron3					
			110670535	110670555	GCAACGGCAGCGTCACTGGTG	RC	7.5	0.811	4351	exon4					
			<i>Mylk3</i>	myosin light chain kinase 3 NM_175441 chr8 87848827 87889223 - chr8 C3 8	NM_175441	87886765	87886785	TCAGTGTGACCCAGCCTGTG	FW	9.1		0.782	2458	intron1	4.25
						87889213	87889233	CCCTCTGACTGAGCTGTTT	FW	11.4		0.89	10	UTR5	
87891227	87891247	acaCAGTAACCCAGCAGATTA				FW	12.5	0.834	-2004	upstream					
87891259	87891279	CTGTAGTGAATCAGCTGACA				FW	6.5	0.823	-2036	upstream					
87891424	87891444	aaggctgcagcttcaggccta				RC	6.8	0.783	-2201	upstream					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
			87891586	87891606	GAGACTGCCATCTCAGGGCTG	RC	7.6	0.775	-2363	upstream					
			87892017	87892037	aggaatgctatgtcaccacaact	RC	9.6	0.879	-2794	upstream					
			87892290	87892310	TAAAGCTGAGCAGCCTAAGC	FW	7.1	0.8	-3067	upstream					
			87892393	87892413	GGCCCTGACTAGGCTATT	FW	9.6	0.847	-3170	upstream					
			32869982	32870002	TGGAGATGACCCAGAGTGG	FW	8.1	0.784	3666	intron1					
			32872504	32872524	GTTTTTCCTATGTCCACACACC	RC	7.4	0.77	1144	intron1					
			32873245	32873265	GAAAATGCATTTCCAGAGTCT	RC	6.5	0.779	403	intron1					
			32874701	32874721	TCTTGGCGCAGTGCACCATAG	RC	9.7	0.843	-1053	upstream					
			32875676	32875696	ACCCTCACTCCCGCAAGTAG	FW	7.5	0.79	-2028	upstream					
			32875898	32875918	TTCCCTCCTTAGTCAGATGGG	RC	7.1	0.793	-2250	upstream					
32876152	32876172	TCTTGATGACTTTGAAGTGAT	FW	7.6	0.764	-2504	upstream								
32876340	32876360	TGTGAGTAACACTGCACTCT	FW	7.1	0.762	-2692	upstream								
32877306	32877326	TTTGCTACTTAGTCATCAGAG	RC	6.8	0.79	-3658	upstream								
32877381	32877401	CATCAGTGACACAGTCTGTT	FW	8	0.77	-3733	upstream								
Myom2	myomesin 2 NM_008664 chr8 15057652 15133419 + chr8 A1.1 8	NM_008664	15053664	15053684	CAGATTGCTATGTCCACACTGA	RC	16.3	0.924	-3988	upstream	4.29				
			15054711	15054731	TGTGAATGAGAAGCTGTTC	FW	6.6	0.785	-2941	upstream					
			15055838	15055858	caaatagctcagtaagctctt	RC	6.6	0.778	-1814	upstream					
			15056211	15056231	gcgttgcccttggcctatgggtgt	RC	8.5	0.765	-1441	upstream					
			15057008	15057028	GCAGCGTGACCCTGCCAGGTG	FW	8.1	0.824	-644	upstream					
			15057322	15057342	CTAACAGCTGATTCAGATGTT	RC	6.9	0.82	-330	upstream					
			15059345	15059365	TCATTTCCCTGTGCAAAATCA	RC	9	0.797	1693	intron1					
			15060989	15061009	GTGGGTGCATATTCACAGTGA	RC	10.2	0.828	3337	intron1					
			15061647	15061667	CACAGTTCAGTGCACAGTGA	RC	11.3	0.786	3995	intron1					
			15061788	15061808	CAAGCATCACAGAGCAGGAGT	FW	9.4	0.799	4136	intron1					
			122735011	122735031	GAAGGCTCACTCAGCATTCCC	FW	9.9	0.838	2894	intron2					
			122736775	122736795	GATAGGGCTGTGTGACCATTTG	RC	10	0.796	1130	intron2					
			122737408	122737428	TGTACATGACCCAGTACATTG	FW	8.8	0.788	497	intron1					
			122739119	122739139	CCCCACTGAACAGCCAAACCG	FW	7.9	0.808	-1214	upstream					
			122739211	122739231	CTACCTGACTTTGCCTTCT	FW	7.5	0.838	-1306	upstream					
			122740018	122740038	aggaatgacatggcatgaga	FW	8	0.834	-2113	upstream					
			122741927	122741947	GAGGGATGACTCAGACAGCAA	FW	7.9	0.787	-4022	upstream					
			Ndr4	N-myc downstream regulated gene 4 NM_001195006 chr8 98226936 98239019 + chr8 D1 8 1-Ch12 Mafk chr8:98224212-98224509 2-Ch12 Mafk chr8:98224212-98224509 3-Ch12 Mafk chr8:98224212-98224509	NM_001195006 NM_145602	98224291	98224311	CGGCAATGAGTGTGCAGAAAG	FW	8.7		0.805	-2645	¹ upstream	5.77
						98224326	98224346	GTCATCTGAATCAGATTTTC	FW	8.2		0.85	-2610	² upstream	
98224481	98224501	ACATGATGATTTTGTCTCACT				FW	7.1	0.785	-2455	³ upstream					
98222062	98222082	CTTTGTCTGACTCAAGTCC				RC	10.2	0.773	-4874	upstream					
98222183	98222203	TGTGTTGCAGTCTCACAGGGA				RC	9.5	0.805	-4753	upstream					
98222210	98222230	AGTCCTTGAGTCAGCAAGG				FW	11.1	0.865	-4726	upstream					
98223252	98223272	TGAAGGGCTCCGTCATCAGTG				RC	6.4	0.839	-3684	upstream					
98224911	98224931	CGGCGGCATTTGCTACTGTG				RC	7.6	0.824	-2025	upstream					
98225106	98225126	TGACCATGACAAGGCACAGCC				FW	12.8	0.869	-1830	upstream					
98225347	98225367	CCTGAGTGAGAAGCAGCCTG				FW	9.2	0.824	-1589	upstream					
98226996	98227016	ACCGAGTGACTCAGGCTTTTG				FW	11.3	0.811	60	UTR5					
98227574	98227594	TGGGATGACAAGGCTGGAGC				FW	8	0.813	638	intron1					
98228852	98228872	AACTTTTCTTGGTCAAGCGGG				RC	6.9	0.768	1916	intron1					
98229284	98229304	CAACTCTGACCAGGCTGTTGG				FW	9.9	0.861	2348	intron1					
98229646	98229666	GGAATGTGAGAGAGCAGCAGT				FW	7.9	0.82	2710	intron1					
98230293	98230313	CCTCTGTGACCTAGCCTCTGG				FW	8.3	0.855	3357	intron2					
98231654	98231674	GATCCAGCATAGTCAATTTGT				RC	10.2	0.86	4718	intron5					
Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1 NM_019443 chrX 34727583 34731233 - chrX X A2 1-Ch12 Mafk chrX:34733735-34734146 2-Ch12 Mafk chrX:34733735-34734146	NM_019443	34733815	34733835	casagattgactcagaggtgtgt	FW	7.6	0.785	-2582	¹ upstream	1.31				
			34734043	34734063	gtgagatgactcagcgggtaa	FW	11.1	0.901	-2810	² upstream					
			34727671	34727691	ACCATAGCTGAGTAATTTCCT	RC	9.4	0.808	3562	UTR3					
			34727708	34727728	ATGCTTCCCTAGTCAATGTTT	RC	9.2	0.809	3525	UTR3					
			34728903	34728923	GGATTCTCACACAGCAGCGAA	FW	6.6	0.797	2330	intron2					
			34729989	34730009	FATAAGTGACCCAGTAAAGAG	FW	8	0.784	1244	intron1					
			34731028	34731048	CGGGATGACCAGCAGCACC	FW	10.5	0.879	205	exon1					
			34731127	34731147	CAGAGGTGACCCGGCTTTACC	FW	6.5	0.82	106	UTR5					
			34734437	34734457	ltaactgtcgaatcatctcaa	RC	11.8	0.869	-3204	upstream					
			34734930	34734950	cacccctgagcaagcaggttt	FW	9	0.813	-3697	upstream					
34736143	34736163	ggaagagctcagtcagaaagg	RC	7.9	0.875	-4910	upstream								
Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10 NM_024197 chr1 94336295 94370335 - chr1 D 1 1-Ch12 Nrf2 chr1:94370157-94370692	NM_024197	94370308	94370328	AGGCCATGACTTCGGCTCTG	FW	9.6	0.848	27	¹ exon1	1.47				
			94365490	94365510	tcagaatcactcagcacaactt	FW	10.2	0.809	4845	intron3					
			94368774	94368794	aaatcagctttttcaaatg	RC	8.3	0.8	1561	intron1					
			94369651	94369671	GACAGTCTAATTCATAGTGG	RC	13.6	0.878	684	intron1					
			94372727	94372747	cacaaatgactcagcacaat	FW	12.1	0.867	-2392	upstream					
			94373440	94373460	TGGGTGTAAGTCAGCACACC	FW	7.3	0.764	-3105	upstream					
			94374640	94374660	cctgtttcttggctatgatgt	RC	9	0.786	-4305	upstream					
Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 NM_010886 chr6 11850372 11857446 -	NM_010886	11856549	11856569	caecttgatccagaactgg	FW	6.8	0.818	897	intron1	1.35				
			11858200	11858220	TACCATCTAAGTCAATGTTC	RC	7.6	0.802	-754	upstream					
			11859361	11859381	CCATGTTGACTAAGAGAGCA	FW	7.8	0.806	-1915	upstream					

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Ndufa5	chr6 A2 6 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 NM_026614 chr6:24468665-24477687 - chr6 6 A3 1-Ch12 Nrf2 chr6:24477327-24477965 Ese14 Mafk chr6:24477419-24477919	NM_026614	11861815	11861835	AAGCTGTGACAAAGTATCATA	FW	7.9	0.778	-4369	upstream	1.59				
			24477490	24477510	CCATTCCGACGATCCAGGGTGA	RC	10	0.793	197	¹ intron1					
			24473216	24473236	Lgagatcacagagcctaaagg	FW	6.8	0.765	4471	intron2					
			24481280	24481300	GCTTCTGCTTAGTAATCGTGT	RC	14.8	0.855	-3593	upstream					
			24482257	24482277	TACCTTGCCATTTCATTCGCT	RC	6.5	0.772	-4570	upstream					
			24482287	24482307	AAAAGGTGACACTGCAGCCCT	FW	10.9	0.872	-4600	upstream					
			24482593	24482613	TTAATCTCTTAGTCAATGAGG	RC	7.5	0.78	-4906	upstream					
Ndufa8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 NM_026703 chr2:35891853-35904812 - chr2 B 2	NM_026703	35900448	35900468	GAGCATCACAGAGCAGTGT	FW	10.5	0.806	4364	intron1	1.34				
			35902060	35902080	ACACAATCACTGAGCAATTC	FW	10.6	0.814	2752	intron1					
			35902253	35902273	TCAAATTTACCCAGATCCTC	FW	7.4	0.805	2559	intron1					
			35902357	35902377	AGTGTGTGACTGAGCCAGACA	FW	8.3	0.875	2455	intron1					
			35903367	35903387	TCAAAATGACCAAGCCAAAGA	FW	12	0.875	1445	intron1					
			35906276	35906296	TCAGGCTGATCTTGCAAATTA	FW	8	0.781	-1464	upstream					
			35908257	35908277	tcttaactcactgagccatctc	FW	6.8	0.788	-3445	upstream					
			126798983	126799003	CCGAGTGCAGTTTCACAGATG	RC	7.1	0.789	179	¹ intron1					
			126794455	126794475	AATATGGCTATGTCACACAAC	RC	9.6	0.859	4707	intron2					
			126796463	126796483	gctagatgactcaatggttaa	FW	9.2	0.8	2699	intron1					
126797568	126797588	GGCTGTGAGAAATGCAATGA	FW	7.1	0.773	1594	intron1								
126801379	126801399	AGTTTGGCCGAGTCAATCTCA	RC	12.5	0.879	-2217	upstream								
126801846	126801866	cccagctGACCCAGTATTGAT	FW	6.9	0.78	-2684	upstream								
126801913	126801933	TCTGAGCTCAGTAATGCCCA	RC	7.2	0.784	-2751	upstream								
126802626	126802646	TGCCAGTGACAAAGCCAGCAG	FW	10.8	0.865	-3464	upstream								
126802704	126802724	CCAGTGTGAATCAGGATCCTC	FW	8.7	0.77	-3542	upstream								
126803962	126803982	AAATTAGCTTTTCATGAGTT	RC	7.9	0.79	-4800	upstream								
Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 NM_028177 chr7:129231557-129245362 - chr7 F3 7 chr7 F3 1-Ch12 Mafk chr7:129242738-129243034	NM_028177	129242983	129243003	TTAAACTGACACAGAGTGGT	FW	9.2	0.796	2379	¹ intron1	1.61				
			129241531	129241551	agaaaaatgactcgtcgtggtg	FW	6.8	0.794	3831	intron1					
			129242037	129242057	ACTCATTAAATCAGCAACTA	FW	7.4	0.769	3325	intron1					
			129245143	129245163	GCCTCCGCAAGTCAACCGCA	RC	8.1	0.841	219	intron1					
			129246109	129246129	ataccatcaactctgcagccag	FW	8.5	0.802	-747	upstream					
			129247244	129247264	TGGAATCACTCAGCACACAG	FW	7.7	0.82	-1882	upstream					
			129248624	129248644	gatggctcactgagccatctt	FW	9.1	0.839	-3262	upstream					
			129249137	129249157	CATTCTGCCTTGCTATGGTCA	RC	15.3	0.88	-3775	upstream					
			Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 NM_025316 chr3:32635984-32650481 + chr3 A3 3 1-Ch12 Nrf2 chr3:32635257-32636144 2-Ch12 Nrf2 chr3:32635257-32636144	NM_025316	32635453	32635473	GCGACTGCAAGTCAAGCTCT	RC	10.4		0.852	-531	¹ upstream	1.37
32636041	32636061	CCGCGCTGACAGCGCTGCTT				FW	6.7	0.813	57	² exon1					
32630972	32630992	GTAAGGCTATGTTATTCTTT				RC	7	0.767	-5012	upstream					
32632221	32632241	GGGAGGGCAGTGTAACTGTGA				RC	9.3	0.767	-3763	upstream					
32632459	32632479	TAGTGTGACCTCGTGTGAG				FW	7.6	0.818	-3525	upstream					
32633659	32633679	AGATGCCCCAGTCACTGCGC				RC	10.8	0.859	-2325	upstream					
32634350	32634370	GTGTGATGACAAAGGAAAAA				FW	7.4	0.77	-1634	upstream					
32635095	32635115	TAATTTGCAAAAGTATGTGFA				RC	8.2	0.82	-889	upstream					
32636475	32636495	CTCAGGGCAGAATCAGGGTGC				RC	10	0.815	491	intron1					
32637486	32637506	GGCTTATGAGTCTGCAATTGC				FW	7.1	0.789	1502	intron1					
32639745	32639765	AGAGACTGACCCAGCTTCATA				FW	6.5	0.841	3761	intron1					
Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7 NM_025843 chr8:86090656-86095522 + chr8 8 C3 1-Ch12 Nrf2 chr8:86090388-86090880	NM_025843				86090725	86090745	GCGACCTGACCCCGCTATC	FW	8	0.821	69	¹ exon1	1.43	
						86086055	86086075	atatagtgacacagagacaag	FW	6.7	0.768	-4601	upstream		
						86086244	86086264	TGTGTGTGACACAGAGGAGTA	FW	7	0.763	-4412	upstream		
			86088839	86088859	aaacccttaactaagccaactca	FW	8.1	0.795	-1817	upstream					
			86089880	86089900	agggagggctcagtcattactg	RC	9.9	0.881	-776	upstream					
			86091494	86091514	CAGTACTGAATCTGCAGAAACA	FW	7.6	0.809	838	intron1					
			86091640	86091660	CAAGTTGCTTCTCACTCCAG	RC	7	0.807	984	intron1					
			86091818	86091838	CTCTTGTGAGAAGCAAGAGT	FW	7.2	0.81	1162	intron1					
			86092766	86092786	tcaccttcccagtcactgtea	RC	8.3	0.773	2110	intron1					
			86094762	86094782	CCCAGCTGACACTGCAGCAAC	FW	10.3	0.86	4106	exon2					
			86095214	86095234	ACAGGGGCCAAGTCAGAAATC	RC	7.8	0.838	4558	intron2					
			Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 NM_026061 chr19:44624743-44629905 - chr19 19 D1	NM_026061	44625280	44625300	TCTAAGTCACTCAGCTCTTAA	FW	7.9	0.807	4625	intron4		1.50
						44626407	44626427	CTCTCATGACTCAGATACTTT	FW	7.7	0.788	3498	intron4		
						44627402	44627422	gctagtcctttgtcaacttga	RC	9.4	0.791	2503	intron3		
44629524	44629544	ACATGTCCTTGGTCATATGGA				RC	8	0.774	381	exon2					
44629904	44629924	CGCGGTTCACTCTGCACATGC				FW	6.7	0.779	1	UTR5					
44630370	44630390	CTCGCTGACCCAGCCCAAA				FW	7.9	0.855	-465	upstream					
44630532	44630552	ACATTTTGAATGACAGCTAT				FW	7.2	0.807	-627	upstream					
44631697	44631717	gagttgctcttgatcatggtgt				RC	9	0.768	-1792	upstream					
44634900	44634920	ttgggtgctctcactcctg				RC	7.2	0.809	-4995	upstream					
Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 NM_023172 chr15:58765364-58771044 + chr15 15 D2 1-Ch12 Mafk chr15:58769046-58769132	NM_023172				58769047	58769067	CGTTTTCCTGTCAGCATGT	RC	12.2	0.895	3683	¹ intron3	1.46	
			58760701	58760721	TTGGTAGCTGACTCAGAGGGG	RC	6.6	0.822	-4663	upstream					
			58762090	58762110	CCACAATAACTCAGCACTCCG	FW	13.7	0.866	-3274	upstream					
			58762551	58762571	GTTTGGGCTTAGTAATCTTG	RC	6.7	0.786	-2813	upstream					
			58762868	58762888	TCAGTGTGACACAGGGCTCA	FW	10.5	0.794	-2496	upstream					
			58763917	58763937	CTTCAGGCTTTCTCACAGAGT	RC	6.6	0.794	-1447	upstream					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
			58765786	58765806	TAGTTTGCAGAGTAAGTCTCAGA	RC	11.6	0.811	422	intron1	
			58766944	58766964	GGTGGTTGAATTAGTGTATT	FW	6.4	0.805	1580	intron1	
			58767489	58767509	CACGGGTGATCTAGCAGAAGA	FW	7.9	0.807	2125	intron1	
			58767931	58767951	ATTCTGGCAGAATCAGCATCC	RC	7.3	0.791	2567	exon2	
			58768936	58768956	TCCTCTGAGAAGCAATGTA	FW	10.9	0.832	3572	exon3	
			58769854	58769874	GCTTCTGCTTCTCAGTATCC	RC	9.1	0.82	4490	intron3	
			58769925	58769945	AGGCTTGCCAAGTGACAGTGA	RC	8.8	0.795	4561	intron3	
<i>Ndufs1</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 1 NM_145518 chr1:63190165-63223396 - chr1 C2 1 1-Ch12 Nrf2 chr1:63223124-63224147 2-Ch12 Nrf2 chr1:63223124-63224147	NM_001160038 NM_001160039 NM_001160040 NM_145518	63223225	63223245	CTGGCCCTTAAGTCAATATGG	RC	9.7	0.889	171	¹ UTR5	1.63
			63223946	63223966	GGGACCGCGAGTCAGTGCTC	RC	7.9	0.851	-550	² upstream	
			63218740	63218760	tgccatgaaagcagcagcagc	FW	6.4	0.797	4656	intron1	
			63218936	63218956	CAAGTGTGAGACAGCCCTAGG	FW	11	0.827	4460	intron1	
			63219248	63219268	aaagtgccctagtcagccatc	RC	9.1	0.839	4148	intron1	
			63220828	63220848	CAATACTGAATTTGCAGATAC	FW	7.8	0.801	2568	intron1	
			63222875	63222895	TCCTGATGACAGGGCCATCTC	FW	8.5	0.821	521	intron1	
			63224247	63224267	ATATGGCTATGTCATTTACC	RC	9	0.851	-851	upstream	
			63225405	63225425	GGAAAGTGAGGAAGCAAGAA	FW	7.4	0.815	-2009	upstream	
			63227820	63227840	GAAAGGCCCTGTCAGGACCA	RC	7.9	0.81	-4424	upstream	
			63228237	63228257	TGATGTGACTCAGTGGCAGA	FW	7.8	0.789	-4841	upstream	
<i>Ndufs2</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 2 NM_153064 chr1:173164983-173177253 - chr1 H3 1 1-Ch12 Nrf2 chr1:173177015-173177775 2-Ch12 Nrf2 chr1:173177015-173177775	NM_153064	173177014	173177034	TACAGGGCTGGGTCACTTCT	RC	8	0.769	239	¹ intron1	1.44
			173177128	173177148	CTGGCTGACTGGCAAGCGG	FW	8.2	0.855	125	² exon1	
			173172257	173172277	attccccgcaaatcaattttg	RC	7.4	0.781	4996	intron2	
			173174303	173174323	GAACAGGCAAAAGTatata	RC	6.8	0.832	2950	intron2	
			173174871	173174891	ATTGTCTCTGTGTCATTACCG	RC	7.6	0.762	2382	intron2	
			173175538	173175558	AAAAGAGCTAAGTatcgtga	RC	12.6	0.824	1715	intron2	
			173176191	173176211	ACAACCTTGAACAGCAGCTCT	FW	9.8	0.847	1062	intron2	
			173176481	173176501	lctccttcaaaagtcattgctt	RC	7.6	0.762	772	intron1	
			173176623	173176643	TTCAATGCCAAGTCATGACA	RC	11.6	0.88	630	intron1	
			173178702	173178722	TTCACTGCTTAGTCACACTCT	RC	15.3	0.937	-1449	upstream	
			173180300	173180320	TCATCAGCTGGCTCAGTGCCCT	RC	6.4	0.792	-3047	upstream	
			173180454	173180474	TCCCAGTGACCAAGCTTCTGG	FW	9.9	0.863	-3201	upstream	
			173181008	173181028	GGGGCTTGACTGGGCACTGGC	FW	8.6	0.861	-3755	upstream	
			173181045	173181065	CTGCTTGCCGCTTCACACTGG	RC	6.9	0.798	-3792	upstream	
<i>Ndufs3</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 3 NM_026688 chr2:90734792-90744878 - chr2 E1 2 90746748	NM_026688	90741265	90741285	ggacactgactgagagagaag	FW	9	0.806	3613	intron4	1.44
			90742831	90742851	tttatgtactactcatgatta	RC	10	0.827	2047	intron3	
			90743779	90743799	TCATGGTAAACAATGCAACAGT	FW	9.1	0.769	1099	intron2	
			90746650	90746670	TAAAAGCTGCATCACTTTTC	RC	6.7	0.806	-1772	upstream	
			90746748	90746768	TGAAGATGAATCAGTATATCT	FW	8.5	0.763	-1870	upstream	
			90747107	90747127	gtagtatgactcagtgatgta	FW	9.1	0.804	-2229	upstream	
			90747776	90747796	gcttttgccgagtcactaaag	RC	14.2	0.907	-2898	upstream	
<i>Ndufs6</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 6 NM_010888 chr13:73457323-73465930 - chr13 D2 13 1-Ch12 Nrf2 chr13:73468214-73468625	NM_010888 NR_033306	73468618	73468638	CCGGCTGAGTGAGCTCCCGG	FW	7.7	0.819	-2688	¹ upstream	1.43
			73461670	73461690	TCAGGATGAAGATGCACTTAA	FW	7.6	0.785	4260	intron2	
			73462562	73462582	AGACAGTGACACTGGAGACCA	FW	8.4	0.765	3368	intron2	
			73466336	73466356	GGAAGTTTACCAGCATTGGA	FW	6.5	0.796	-406	upstream	
			73466813	73466833	ccaggctaacctagcactcaac	FW	7.5	0.789	-883	upstream	
			73468724	73468744	TCTGATGCCAAGTAACTTTGA	RC	9.5	0.794	-2794	upstream	
			73469363	73469383	agctcggctcggtaaacctggg	RC	7.1	0.769	-3433	upstream	
<i>Ndufv1</i>	NADH dehydrogenase (ubiquinone) flavoprotein 1 NM_133666 chr19:4007498-4012755 - chr19 A 19 1-Ch12 Nrf2 chr19:4012525-4013089	NM_133666	4012535	4012555	ATCAGGGCCGGCTCACCTGTGC	RC	7.2	0.779	220	¹ intron1	1.41
			4007741	4007761	TTAGTGTGACACAGCAGG3CA	FW	12.5	0.916	5014	intron9	
			4011037	4011057	ACCCAGTGTCCAGCAGCCCC	FW	8.3	0.834	1718	intron3	
			4011109	4011129	CTGAGGGCTTATTTCATGAAGC	RC	8.3	0.821	1646	exon3	
			4011763	4011783	CACGGAGCCATGTCACACTTC	RC	6.9	0.817	992	intron1	
			4011872	4011892	TCTCCCTAACTCTGCTGAAGA	FW	7.3	0.767	883	intron1	
			4013601	4013621	ccttcTGCCTTGTGAGCAGGA	RC	12.7	0.894	-846	upstream	
			4014075	4014095	acagctcTgaagcagctctata	FW	7.4	0.81	-1320	upstream	
			4014188	4014208	aATGTCTGACTTAGAAGTGTAT	FW	6.7	0.788	-1433	upstream	
			4014328	4014348	gacctttgactaaaggattat	FW	7.2	0.773	-1573	upstream	
			4015900	4015920	tgaggctgaaacagctttgtt	FW	9.6	0.816	-3145	upstream	
<i>Ndufv2</i>	NADH dehydrogenase (ubiquinone) flavoprotein 2 NM_028388 chr17:66428134-66450899 - chr17 17 E1.2	NM_028388	66446613	66446633	tatgctcctggctcagctctcc	RC	10.2	0.8	4286	intron1	1.44
			66448375	66448395	atggcttgactagcccaagga	FW	8.2	0.872	2524	intron1	
			66450520	66450540	TGACCTTGACTAAGTTAGGGG	FW	6.7	0.777	379	intron1	
			66453906	66453926	gaattgacttgatcagatgat	RC	8.4	0.766	-3007	upstream	
			66454281	66454301	ttgcaactgacaagaagctct	FW	7.4	0.77	-3382	upstream	
			66455422	66455442	gcttcggctgctgaagagca	RC	10	0.793	-4523	upstream	
<i>Ndufv3</i>	NADH dehydrogenase (ubiquinone) flavoprotein 3 NM_030087 chr17:31657059-31668270 + chr17 B1 17	NM_001083891 NM_030087	31653341	31653361	cgatggtgagactgctctaaa	FW	8.5	0.786	-3718	upstream	1.50
			31656146	31656166	AARTACTTACTGTGCACTGGG	FW	6.4	0.769	-913	upstream	
			31661516	31661536	TATGTGctctatgctcttggat	RC	8.8	0.769	4457	intron2	
<i>Nnmt</i>	nicotinamide N-methyltransferase	NM_010924	48408725	48408745	gccccctgaaacagcagcaag	FW	11.2	0.845	4503	intron2	1.74
			48408927	48408947	TAAATGTCTGAGTCACACTCC	RC	11.5	0.815	4301	intron2	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
	NM_010924 chr9 48399981 48413228 - chr9 A5.3 9 29.0 cM		48411000	48411020	aagccatgaatctgcagccaag	FW	9.9	0.826	2228	intron2					
			48414522	48414542	GGGTATGATTAAAGCAAGAGC	FW	10.6	0.847	-1294	upstream					
			48415129	48415149	gagaggtgactcagctcagct	FW	7.2	0.785	-1901	upstream					
			48416004	48416024	cattttctggaatgatcatgc	RC	10.8	0.79	-2776	upstream					
			48416992	48417012	tagccctgagatagctgagta	FW	7.3	0.786	-3764	upstream					
<i>Nppa</i>	natriuretic peptide type A NM_008725 chr4 147374830 147376183 + chr4 E2 4 76.5 cM	NM_008725	147371202	147371222	cgccatgacggagctcaacc	FW	7.6	0.847	-3628	upstream	31.75				
			147371562	147371582	aaacctgcttctcagaggatg	RC	9	0.813	-3268	upstream					
			147372531	147372551	atatttgcaagtgactcgta	RC	9.5	0.772	-2299	upstream					
			147372575	147372595	gtagctgcaaaagtattttaa	RC	7	0.776	-2255	upstream					
			147373549	147373569	ACAGTGTGAACTTGCAAGAT	FW	6.7	0.78	-1281	upstream					
			147373869	147373889	TGGACTGCCTGCTCATGCTCC	RC	6.4	0.776	-961	upstream					
			147375225	147375245	AGGCCCTGAGTGAGCAGACTG	FW	10	0.844	395	exon2					
			147375967	147375987	CAAGCAGCTTGGTCACATTGC	RC	8.2	0.86	1137	UTR3					
			147376671	147376691	CCCAGCTGCGCTCACCACCT	RC	11.8	0.901	1841	downstream					
			147377687	147377707	CCAGCGTGAATGGCGGGAAA	FW	8	0.792	2857	downstream					
			147377852	147377872	ACATGGTGACAGGGCAGGGGC	FW	9.7	0.856	3022	downstream					
			147377885	147377905	GACTGGTGACAGGGCAGCAC	FW	8.2	0.837	3055	downstream					
			147378673	147378693	TGGTAGCTGAGTCAAGCTAA	RC	9.9	0.903	3843	downstream					
			147378956	147378976	TCCACGGCTTAGTTATAGTTC	RC	8.5	0.801	4126	downstream					
<i>Nudt8</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 8 NM_025529 chr19 4000579 4002102 + chr19 A 19	NM_025529	3999701	3999721	TCACAGTCACACAGCAAGTA	FW	14.4	0.846	-878	upstream	2.12				
			4002817	4002837	GGTGAAGCCGAGTCAAGTAGA	RC	6.6	0.85	2238	downstream					
			4003178	4003198	GCCTCCTTACCAGCAGCAGG	FW	8.3	0.798	2599	downstream					
			4003299	4003319	CTCCTGTCTGACTCACACT	RC	10.3	0.905	2720	downstream					
			4003335	4003355	CCTCAGGCTCTGTACCCCTAC	RC	8.4	0.859	2756	downstream					
			4003378	4003398	GCAGTGTGACACAGCTCTCAA	FW	13.1	0.902	2799	downstream					
			4005218	4005238	TTCAAGCCTTACTCAACCCCA	RC	7.5	0.811	4639	downstream					
			58945202	58945222	CCTTACGCCAAGTACACAGCAG	RC	7.9	0.84	4675	exon6					
<i>Obscn</i>	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF NM_001171512 chr11 58807758 58949877 - chr11 B1.3 11 1-Ch12 Mafk chr11:58945062-58945977	NM_001171512 NM_199152	58946226	58946246	GGGACTGCAGAGTAAGCAGCG	RC	6.9	0.78	3651	exon5	3.79				
			58946715	58946735	CAATAGTGACAGGGCGTCC	FW	7	0.818	3162	exon4					
			58949829	58949849	CCTTTGGCCGCTCAGGAAGC	RC	7	0.822	48	exon1					
			58950531	58950551	CTGATGGCCTTGTCACTATTTC	RC	9	0.827	-654	upstream					
			58950692	58950712	TGCCACTGATCCAGCGAGTGG	FW	7.2	0.795	-815	upstream					
			58950844	58950864	CTGCTTTGACACAGCTCCCG	FW	6.4	0.858	-967	upstream					
			58951015	58951035	CGGTTTGTGACTCACTGTCC	RC	13.8	0.888	-1138	upstream					
			58951485	58951505	TGTATTACCAAGTCACTGGCC	RC	7.3	0.762	-1608	upstream					
			58952003	58952023	CTGATGGCCTTGTCACTATTTC	RC	9	0.827	-2126	upstream					
			58953567	58953587	GGGACTGCACACTGCTGTGTG	FW	7.5	0.825	-3690	upstream					
			<i>Oit1</i>	oncoprotein induced transcript 1 NM_146050 chr14 9181461 9211277 - chr14 A1 14	NM_146050	9206565	9206585	CAGACATCTGAGTCAAGGCAA	RC	6.6		0.781	4712	intron1	4.01
						9206796	9206816	AACCTGGCTGAGTGAGCAGGG	RC	8.6		0.804	4481	intron1	
						9206943	9206963	TTCACTTCTTAGTCAACAGTc	RC	10.8		0.814	4334	intron1	
9207778	9207798	gtccggccttgcctatggact				RC	7.7	0.814	3499	intron1					
9207979	9207999	ggataagcacagtcagactcc				RC	7.4	0.839	3298	intron1					
9209107	9209127	ACTTCTGAGATAGTAAATG				FW	6.4	0.784	2170	intron1					
9209246	9209266	CATTATTGACTTGGCTAATTT				FW	6.5	0.827	2031	intron1					
9209437	9209457	ccaaggtgacacggctgacca				FW	9.5	0.848	1840	intron1					
9209695	9209715	GGAATGGTCTTCAAGCTTAA				RC	6.4	0.801	1582	intron1					
9209952	9209972	CAACTGGCAAAGTCAAAACCTT				RC	6.5	0.828	1325	intron1					
9210346	9210366	TCAGGAGCCGGAGTAATAATGA				RC	6.9	0.774	931	intron1					
9210974	9210994	CTTGCTGCTTCTTCATCTTCC				RC	6.8	0.811	303	intron1					
9211879	9211899	TCTAGGCTCTGTCAACCAACA				RC	7.6	0.847	-602	upstream					
9212577	9212597	tctgtccctcagtcaccctcc				RC	8.3	0.783	-1300	upstream					
9212943	9212963	gaatttcagggctcagaagtgt				RC	11.7	0.872	-1666	upstream					
9213884	9213904	TGAAATGCTCAGTCAGGCTCC				RC	13.5	0.926	-2607	upstream					
9214337	9214357	GGAACATAACCCAGCAATGCC				FW	6.4	0.794	-3060	upstream					
9214632	9214652	tgtgtgtgagatagcagagtgt				FW	6.6	0.774	-3355	upstream					
9215925	9215945	AATCGGTGACTAGGCATGAATA				FW	11.2	0.878	-4648	upstream					
<i>Oxct1</i>	3-oxoacid CoA transferase 1 NM_024188 chr15 3976427 4105344 + chr15 A1 15	NM_024188				3972430	3972450	gtggctctggaatcaccacaaa	RC	8.7	0.854	-3997	upstream	1.31	
			3976148	3976168	TGAGGGTCAGTCAGCAGCGTG	FW	9.5	0.78	-279	upstream					
			3977377	3977397	ACCCTGCTGGCTCAAGTTCA	RC	8	0.828	950	intron1					
			3978092	3978112	TTCAAGACTGAGTCATTGCGT	RC	9.8	0.806	1665	intron1					
			3979127	3979147	TCTGGTGTCTGTGACCCCTAA	RC	15.2	0.927	2700	intron1					
			3979617	3979637	AACCTTCTGTGTCATGATTT	RC	11.3	0.811	3190	intron1					
			173122448	173122468	FTTCCCTCAGTCAGGATCA	RC	8	0.777	3951	intron1	1.59				
173122671	173122691	GAAAGTCTTAGTCAAGCAGC	RC	6.5	0.774	3728	intron1								
173123229	173123249	ATTTGAGCAGTGAATGCTG	RC	7.9	0.768	3170	intron1								
173128098	173128118	gaattgtcttgctcagtgatgt	RC	8.4	0.766	-1699	upstream								
173128185	173128205	taggctgacctgctttttgt	FW	7.5	0.806	-1786	upstream								
173130208	173130228	gaattgccttgctcagtgatgt	RC	9	0.768	-3809	upstream								
<i>Pdha1</i>	pyruvate dehydrogenase E1 alpha 1 NM_008810	NM_008810	156572203	156572223	CTACTGCTCTTTCACACTGC	RC	9.9	0.835	4159	intron1	1.34				
			156572757	156572777	AACATAGCTATCTCAAAATGA	RC	6.8	0.796	3605	intron1					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
	NM_008810 chrX 156560150 156576362 - chrX F3-F4 X 66.5 cM		156576247	156576267	AGCGCAGCAGACTCACCGGGC	RC	6.9	0.795	115	UTR5					
			156577638	156577658	gaagagtgactgaaggaagact	FW	10	0.814	-1276	upstream					
			156577963	156577983	AAAAAATTACAAGCCAAAGGC	FW	7.2	0.766	-1601	upstream					
			156578607	156578627	ACTTTGTGACTCTGTAGCAAA	FW	6.9	0.777	-2245	upstream					
<i>Pdhb</i>	pyruvate dehydrogenase (lipoamide) beta NM_024221 chr14 8998504 9005506 - chr14 A1 14 1-Ch12 Nrf2 chr14:9005203-9005957 2-Ch12 Nrf2 chr14:9005203-9005957 3-Ch12 Nrf2 chr14:9005203-9005957 4-Ch12 Mafk chr14:9007100-9007520 Ese14 Mafk chr14:9007154-9007633	NM_024221	9005500	9005520	CCCGCTGCAGCAGCAATAG	FW	10	0.87	6	¹ UTR5	1.44				
			9005610	9005630	CAAGCGCTATTTCATAGCCG	RC	6.4	0.785	-104	² upstream					
			9005870	9005890	GCTGGGACTGAGTCAGTCAG	RC	6.4	0.78	-364	³ upstream					
			9007328	9007348	CTGATTGCTGAGTCATTAAG	RC	13.3	0.934	-1822	⁴ upstream					
			9001050	9001070	ccacagtgactgagcactagc	FW	9.3	0.769	4456	intron8					
			9001994	9002014	TACCAGTGACTCTGTAGGCG	FW	8.5	0.781	3512	intron7					
			9002109	9002129	TAACAAGCTCACTCATTTCTA	RC	8.6	0.824	3397	intron7					
			9003938	9003958	TTGTATGCACCGCTACTAGG	RC	7.6	0.844	1568	exon3					
			9009275	9009295	TCTGAATTACAAGCCAAAGG	FW	9.1	0.773	-3769	upstream					
			<i>Pfkfb1</i>	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 NM_008824 chrX 147024463 147078421 + chrX X F2	NM_008824	147020255	147020275	CCAAGTCACTCAGCCGAGCC	FW	9.3		0.819	-4208	upstream	1.55
147020412	147020432	TCTTGTGCTGTGAAGGAGGG				RC	11.2	0.815	-4051	upstream					
147023792	147023812	AATGGATGAATAAGCAGGGCA				FW	7.9	0.835	-671	upstream					
147023887	147023907	AACTATAACTTTGGATCCTA				FW	6.4	0.778	-576	upstream					
147024480	147024500	AAGGGTGTCTCTCAGCCTTC				RC	7.2	0.81	17	UTR5					
147025829	147025849	TCTGATGCTGAGTGAACCTTG				RC	7	0.817	1366	intron1					
147027404	147027424	GTTAATCCTGTGTACAGCAA				RC	10.1	0.8	2941	intron1					
147027594	147027614	ACTAAATGAAAAAGCAGAAACA				FW	7.8	0.817	3131	intron1					
147028314	147028334	TTTAGTGTGGCTCATCTCAG				RC	8.3	0.825	3851	intron1					
147028370	147028390	CTCTCTGCCAAGTAATGACTG				RC	7.9	0.772	3907	intron1					
<i>Phgdh</i>	3-phosphoglycerate dehydrogenase pseudogene//3-phosphoglycerate dehydro NM_016966 chr3 98117093 98143892 - chr18 B2 18 chr3 3 E1	NM_016966				98139921	98139941	TAACCTGCCAATCATCTGCTT	RC	8.3	0.805	3971	intron1	1.98	
						98140052	98140072	CCTGGCTGAGTCTGTCTTAA	FW	6.9	0.79	3840	intron1		
			98140800	98140820	AACTGTGCTAAGTCAAGTGAA	RC	9.6	0.842	3092	intron1					
			98141524	98141544	AGAATATGAAGCAGCAGAGGC	FW	7.4	0.828	2368	intron1					
			98141745	98141765	CAGCCAGCCAAAGTCAGCGCA	RC	7.5	0.832	2147	intron1					
			98142178	98142198	TGACTAGCTGTCTCAGAGTTG	RC	7.8	0.811	1714	intron1					
			98142332	98142352	TaggcatgagccagCCAGCTC	FW	8.4	0.803	1560	intron1					
			98142821	98142841	AAGTGTCTACAAGCAGAAAC	FW	6.8	0.776	1071	intron1					
			98143833	98143853	CTCCGGTGAATGGCAGGGTT	FW	9.8	0.871	59	UTR5					
			98145038	98145058	TATCAATGATCCAGCGGGGGT	FW	7	0.798	-1146	upstream					
			98147284	98147304	AACCCCTGACTATGTGCGAGA	FW	6.9	0.833	-3392	upstream					
			<i>Phyh</i>	phytanoyl-CoA hydroxylase NM_010726 chr2 4840041 4859789 + chr2 A1 2	NM_010726	4835142	4835162	ccccctctaaactctgcccctctc	FW	6.4	0.764	-4899	upstream		1.79
						4836751	4836771	gacaggtgactaaagcatgtgg	FW	12.5	0.916	-3290	upstream		
						4837016	4837036	CAGAGAGCAGCGTCAGGGTGC	RC	9.6	0.847	-3025	upstream		
4837243	4837263	CATTTTGTGCTCTCACAGGTG				RC	12.9	0.853	-2798	upstream					
4837664	4837684	agagagtgactgagaaaactctg				FW	7	0.793	-2377	upstream					
4842292	4842312	GGTCATCTGGGTCTCACAGCTT				RC	7.1	0.784	2251	intron1					
4843132	4843152	caggcctgacaatgcacacact				FW	9.6	0.84	3091	intron1					
4844168	4844188	gcaggctgagaaaagccatggg				FW	9	0.804	4127	intron2					
<i>Pkm</i>	pyruvate kinase, muscle NM_011099 chr9 59504174 59527182 + chr9 B 9 52.0 cM 1-Ese14 Mafk chr9:59501181-59501609 Mel Mafk chr9:59501228-59501579 Mel Nrf2 chr9:59500015-59501972 2-Ese14 Mafk chr9:59501181-59501609 Mel Mafk chr9:59501228-59501579 Mel Nrf2 chr9:59500015-59501972 3-Ch12 Mafk chr9:59504823-59505744 4-Ch12 Mafk chr9:59504823-59505744 5-Ch12 Mafk chr9:59506743-59507873 6-Ch12 Mafk chr9:59506743-59507873	NM_011099				59501325	59501345	TGGCCATGACTCAGTTTGTGG	FW	9.6	0.8	-2849	¹ upstream	1.24	
						59501417	59501437	TCTGCTGCTGACTCACTFACTG	RC	15.1	0.939	-2757	² upstream		
			59505528	59505548	GTAATAACCCAGTCATAGTAA	RC	6.8	0.769	1354	³ intron1					
			59505690	59505710	TCTGGTCTGTGTCACTCCAG	RC	8.7	0.791	1516	⁴ intron1					
			59507037	59507057	AGTGAATGACTGGCACAATTT	FW	12.4	0.879	2863	⁵ intron1					
			59507481	59507501	ACTGTATGACGAAGAACAATTC	FW	6.4	0.769	3307	⁶ intron1					
			59502245	59502265	TGCCCTGACTTAGCAGCAAAA	FW	14.1	0.92	-1929	upstream					
			59503172	59503192	CCATAATAACCAAGCATTTAC	FW	8.9	0.8	-1002	upstream					
			59508565	59508585	ACTTCTGCAAAAGTCACTCCCT	RC	11.8	0.876	4391	intron1					
			59508821	59508841	TACCCCTGATACCAGCACAATTT	FW	8.1	0.794	4647	intron1					
			<i>Pla2g16</i>	phospholipase A2, group XVI NM_139269 chr19 7631948 7663035 + chr19 A 19	NM_139269	7627235	7627255	AAATTGGCATATTCACCGAGC	RC	9.3	0.794	-4713	upstream		1.61
						7627730	7627750	ggagagtgactgagcagaagcc	FW	10.9	0.909	-4218	upstream		
7628156	7628176	ccagcagctgactcaagacaga				RC	8.4	0.831	-3792	upstream					
7628769	7628789	GCTATTGCCATGTTATGGTGC				RC	10.3	0.777	-3179	upstream					
7629280	7629300	agagaaTGAGAATGCATTTgt				FW	9.5	0.792	-2668	upstream					
7632788	7632808	TGAAGTTGATTTCTGCTTATTT				FW	6.6	0.792	840	intron2					
7633330	7633350	ATAGCAGCAGAGTCACTCCAG				RC	9.7	0.86	1382	intron2					
7636254	7636274	GGCTTTGCAGAGTGAGACTGA				RC	9.2	0.804	4306	intron2					
<i>Plin4</i>	perilipin 4 NM_020568 chr17 56240013 56249225 - chr17 17 D	NM_020568				56247203	56247223	CTGGGGTGACACAGATGTGTT	FW	7	0.763	2022	intron4	2.74	
			56248455	56248475	CAGAATGCTGTGTATCCCGAG	RC	8.9	0.808	770	intron3					
			56249131	56249151	TCTGGGTGACACAGCAGCTCG	FW	14.9	0.924	94	UTR5					
			56250166	56250186	GTGAAGTGACTGGGGCAGAGTG	FW	8.1	0.861	-941	upstream					
			56251522	56251542	GGATCTGCAGACTCAGCCCTCC	RC	10	0.828	-2297	upstream					
<i>Plin5</i>	perilipin 5 NM_001077348 chr17 56251023 56256721 - NM_025874	NM_001077348 NM_025874	56253925	56253945	TAAAGTTCAGGTGcatggtag	RC	10.3	0.776	2796	intron5	2.80				
			56254519	56254539	GCTCAGCCCTCAGTCATGGGCA	RC	7.3	0.773	2202	exon5					
			56254949	56254969	CCAAGGCCCTGGTCACTCTTA	RC	7.1	0.807	1772	intron4					

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)				
	chr17 D 17		56256970	56256990	CCCACCTGAGTCAGCCCTCCG	FW	8.7	0.834	1	UTR5					
			56258090	56258110	taaatgctgctttaatcctga	RC	12.1	0.773	-1119	upstream					
			56258220	56258240	AGTTTGGCCAGTcatatgct	RC	9	0.863	-1249	upstream					
			56258490	56258510	gccagcttacagagcaagttc	FW	7.2	0.783	-1519	upstream					
			56260162	56260182	CGGGCAGCTGCGTCAGGTTGG	RC	7.9	0.87	-3191	upstream					
			56260270	56260290	CCGACTGCAGTATCAGGCATT	RC	6.9	0.784	-3299	upstream					
			56260818	56260838	TCGTGTTCACTTCGCAAGCC	FW	6.6	0.785	-3847	upstream					
			56261401	56261421	CCCAGGGCCGGTCAACATTG	RC	6.6	0.822	-4430	upstream					
			56261563	56261583	AGGACTGAGTTGCAATAAG	FW	8.2	0.797	-4592	upstream					
			<i>Pln</i>	phospholamban NM_023129 chr10 53057491 53065805 + chr10 B3 10	NM_001141927 NM_023129	53052965	53052985	taaagtctggaatcaatgct	RC	14.8		0.895	-4526	upstream	10.13
53054283	53054303	ATGCTGTGCATAGTAATATA				FW	8.2	0.78	-3208	upstream					
53055136	53055156	CCCAGGGCATGTCACCGATT				RC	6.8	0.808	-2355	upstream					
53055467	53055487	ACTCCATCAGAGTCATATGA				RC	8.4	0.767	-2024	upstream					
53059460	53059480	GTTGCCGAGTGTCAATTCCT				RC	8.3	0.828	1969	intron1					
53059670	53059690	TATAAATTACACAGCATAAGC				FW	9.7	0.808	2179	intron1					
53060796	53060816	ggacactgatatagctgtctc				FW	6.6	0.791	3305	intron1					
53061015	53061035	aagatggcctagtcagccatc				RC	9.1	0.839	3524	intron1					
53062321	53062341	tcagcttaactctgctctccg				FW	7.5	0.775	4830	intron1					
<i>Pnpla3</i>	patatin-like phospholipase domain containing 3 NM_054088 chr15 83998245 84019951 + chr15 15 E3	NM_054088				83993594	83993614	TCACAGTGACTCTGTTTCCCA	FW	6.7	0.765	-4651	upstream	3.03	
			83997432	83997452	gtccagctggaatcactgaag	RC	10.3	0.901	-813	upstream					
			83997598	83997618	ctactcttacagagcaccaga	FW	6.5	0.785	-647	upstream					
			83998730	83998750	CTGTGAGCTGGGTCAATCCCTG	RC	10	0.867	485	intron1					
			61107968	61107988	catgatgactgtagctgca	FW	8.4	0.863	-3400	upstream					
<i>Ppa1</i>	pyrophosphatase (inorganic) 1 NM_026438 chr10 61111368 61136913 + chr10 B4 10 36.0 cM	NM_026438	61108526	61108546	aaatagtgactgggatgctt	FW	6.9	0.763	-2842	upstream	1.85				
			61108813	61108833	tctggttgactaaagaacaa	FW	7.6	0.798	-2555	upstream					
			61109258	61109278	AAACCAATACCAAGCAGTGA	FW	10.3	0.804	-2110	upstream					
			61111713	61111733	GAAACCACTGAGTCAACCTTA	RC	13.4	0.824	345	intron1					
			61112515	61112535	ACTCCTTGACTTTGGATTAGG	FW	6.6	0.762	1147	intron1					
			61113885	61113905	tcaaatgacagagcactttt	FW	11.3	0.816	2517	intron1					
			61114916	61114936	GGTTGGTAGTTGCAACAG	FW	6.4	0.792	3548	intron2					
			61115004	61115024	GAAATCTAACTTAGCAGATTG	FW	8.5	0.815	3636	intron2					
			<i>Pparg1a</i>	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha NM_008904 chr5 51845487 51945160 - chr5 C1 5	NM_008904 NR_027710	51943427	51943447	GAATTCTGACTTAAGCAAAATC	FW	7.8		0.776	1733	intron1	1.76
						51945151	51945171	GTCACATGACAAAGCTATTAA	FW	8.9		0.855	9	UTR3	
51945487	51945507	TGTTACTGACACAGTAACCTAC				FW	7.5	0.78	-327	upstream					
51946291	51946311	GTCGTTCTGAGTCAATGAGG				RC	9.3	0.821	-1131	upstream					
51947355	51947375	ACTAGATAACTCTGCATTATT				FW	9.5	0.802	-2195	upstream					
51947525	51947545	agaaaCTAACCCAGCAGTCC				FW	6.6	0.794	-2365	upstream					
51948427	51948447	TATGGTGTGTTGTAACCTAAT				RC	9.4	0.807	-3267	upstream					
51950151	51950171	AAAGTGTGACTGTGCCCAA				FW	8.6	0.848	-4991	upstream					
<i>Pparg1b</i>	peroxisome proliferative activated receptor, gamma, coactivator 1 beta NM_133249 chr18 61457789 61560085 - chr18 E1 18	NM_133249				61555869	61555889	Ltcttcttgacagagcaatttc	FW	10	0.884	4216	intron1	1.50	
						61556555	61556575	ggactctgcttatataatgt	RC	7.6	0.777	3530	intron1		
			61557447	61557467	ccaggatcaccagccagaga	FW	8.6	0.789	2638	intron1					
			61557554	61557574	tgggtggctctgtcaccacct	RC	7.7	0.848	2531	intron1					
			61560041	61560061	CGTGCCGCGAGTCAGCGCG	RC	8.4	0.852	44	UTR5					
			61560990	61561010	ACTCCATCTGAGTCACTCTGT	RC	10.8	0.814	-905	upstream					
			61562687	61562707	GCTGCTGTAATCAACTTGG	RC	11	0.874	-2602	upstream					
			61562913	61562933	TCAAGGGCTTTATCACTGATC	RC	7.7	0.794	-2828	upstream					
			61563480	61563500	CAATAGGCTGAATCACACTAT	RC	9.9	0.847	-3395	upstream					
			61564110	61564130	Acccggctctgctcacttagt	RC	7.6	0.852	-4025	upstream					
<i>Ppp1r3a</i>	protein phosphatase 1, regulatory (inhibitor) subunit 3A NM_080464 chr6 14663821 14705274 - chr6 A2 6	NM_080464	14700724	14700744	aaagtggcctagtcagccatc	RC	8.6	0.836	4550	intron1	1.44				
			14705336	14705356	TACAGTTGACATTGCAAAAAGA	FW	7.8	0.831	-62	upstream					
			14707073	14707093	gatggctgactagccactctt	FW	9.1	0.839	-1799	upstream					
			14707210	14707230	CCTCTGTGAATGAGCTCTCCT	FW	6.6	0.818	-1936	upstream					
			14707834	14707854	AGCAGTACAGAGTCAATAATA	RC	6.8	0.772	-2560	upstream					
			14708980	14709000	AAAAGAGCTTTGTCACCAAAA	RC	10.1	0.862	-3706	upstream					
			<i>Prdx3</i>	peroxiredoxin 3 NM_007452 chr19 60939968 60950441 - chr19 D3 19 50.0 cM 1-Mel Mafk chr19:60947838-60948795	NM_007452	60948005	60948025	actgactgacttagctctcac	FW	9.5		0.881	2436	¹ intron2	1.34
						60945992	60946012	TCATTGGCTTTGTCAGTAAA	RC	10.9		0.867	4449	exon4	
60949405	60949425	CTAACTGCTGCATCATGTAGC				RC	9.3	0.837	1036	intron1					
60950563	60950583	TGTTTGTGACTTAGGGGAGAA				FW	6.6	0.768	-122	upstream					
60951160	60951180	ctttatgcttaactcattttaa				RC	6.9	0.811	-719	upstream					
60952414	60952434	tctacttgactctgctcccaag				FW	7	0.85	-1973	upstream					
60952929	60952949	ggcaatgcaaaactcaccatca				RC	8.4	0.812	-2488	upstream					
60953193	60953213	TTATATGACAGTGTGAAAGTCA				RC	6.8	0.769	-2752	upstream					
60954740	60954760	cttgctctctgctcatgatgt				RC	8.5	0.784	-4299	upstream					
60954776	60954796	aaacctgactaagcaactgt				FW	9.3	0.788	-4335	upstream					
60954917	60954937	CCAACTGAAGCAGCATATGA	FW	10.9	0.851	-4476	upstream								
<i>Pxmp2</i>	peroxisomal membrane protein 2 NM_008993 chr5 110703304 110715187 - chr5 F 5 59.0 cM	NM_008993	110718820	110718840	ACAACCGCTTAGTCAGCGCGG	RC	14.7	0.909	-3633	¹ upstream	1.50				
			110710346	110710366	AGGTAGTGACTCAAGTGGACTG	FW	7.5	0.787	4841	exon3					
			110713082	110713102	TAACCTTGCTAAGTAGGTAAA	RC	6.5	0.8	2105	intron1					
			110715858	110715878	GTATGGTGCAAAAGGAACCTG	FW	8.5	0.784	-671	upstream					

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	1-Ch12 Mafk chr5:110718654-110719040		110718404	110718424	GACACTGCTTGCTCATCTTT	RC	10.2	0.827	-3217	upstream		
			110718476	110718496	GATGAGTATAGAGCAGAGGA	FW	6.5	0.806	-3289	upstream		
			110719707	110719727	ACGTGTTACTTAGCAGCTct	FW	9.5	0.819	-4520	upstream		
Qsox1	quiescin Q6 sulfhydryl oxidase 1 NM_001024945 chr1 15765284 157660029 - chr1 G3 1 1-Ese14 Mafk chr1:157659760-157659981	NM_001024945 NM_023268	157659782	157659802	CATCCAGCAGCGTCAAGCGGT	RC	7.1	0.825	247	exon1	1.56	
			157655399	157655419	GGAGAATGACTCAGAGCAACA	FW	9.8	0.805	4630	intron1		
			157655849	157655869	TCCAGCGCTGAGTCAAGAGGA	RC	8.2	0.793	4180	intron1		
			157656042	157656062	CACAGTCCCAAGTCACTCA	RC	8	0.784	3987	intron1		
			157656232	157656252	cagcactgatacggcagctca	FW	6.9	0.785	3797	intron1		
			157657061	157657081	GCTTTGTGACTCAGTAAATAT	FW	11.5	0.833	2968	intron1		
			157657519	157657539	CTGCTCGTGTTCAGGCCAA	RC	6.7	0.796	2510	intron1		
			157657769	157657789	AAACAGGCTGTGTCAGTGCT	RC	11.9	0.88	2260	intron1		
			157657832	157657852	AGCATGTGACTCAGCTGGAAG	FW	7	0.824	2197	intron1		
			157662218	157662238	ATAGTTGCTGGTCAAGTCC	RC	9.9	0.872	-2189	upstream		
Ryr2	ryanodine receptor 2, cardiac NM_023868 chr13 11645369 12199212 - chr13 A1-A2 13 7.0 cM	NM_023868	12200005	12200025	CTCCCGTGAAGAGCAAGTT	FW	9.9	0.826	-793	upstream	5.16	
			12200283	12200303	TAACATGACTAAGAATAAA	FW	13.2	0.832	-1071	upstream		
			12201718	12201738	aatattgctatgagatccatg	RC	9.9	0.794	-2506	upstream		
			12201794	12201814	caactatgcaAGTCAATGTA	RC	7.1	0.853	-2582	upstream		
			12202748	12202768	acagctctgagtaagcagag	RC	11.5	0.841	-3536	upstream		
			12202780	12202800	ttgccatgaccaagctcttga	FW	10.2	0.861	-3568	upstream		
			74484180	74484200	gccagatgactcagtgaggca	FW	6.9	0.789	3508	intron1		
			74485502	74485522	GAGGAATCACTGAGCACCAGC	FW	7.7	0.807	2186	intron1		
Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp) NM_023281 chr13 74459702 74487688 - chr13 C1 13	NM_023281	74485706	74485726	tcaacttgacacggctggagt	FW	9.5	0.845	1982	intron1	1.31	
			74485870	74485890	gcaggctgagaaagccagtg	FW	8.7	0.802	1818	intron1		
			74486031	74486051	cttgctcttggctcaatgat	RC	8.5	0.784	1657	intron1		
			74486066	74486086	aaacctgactaagacaCCAG	FW	7.8	0.78	1622	intron1		
			74487166	74487186	TGCAACCTGAGTCACTGTGT	RC	11.5	0.823	522	intron1		
			74488758	74488778	laticggtgacttagagataaa	FW	9.4	0.785	-1070	upstream		
			74491359	74491379	acatcatgaccaagaagcaag	FW	8.5	0.784	-3671	upstream		
			74491925	74491945	AGTGAGTGAAGTCAAGCTTGAG	FW	8.2	0.831	-4237	upstream		
			140520759	140520779	ccctgctgaccagcatgggg	FW	10.2	0.891	3574	intron1		
			140512526	140512546	caagttgcttagtatacaatg	RC	8.5	0.813	-4659	upstream		
			140512837	140512857	CTGGTCTGACACAGCAGGCC	FW	7.2	0.857	-4348	upstream		
			Sdhb	succinate dehydrogenase complex, subunit B, iron sulfur (lp) NM_023374 chr4 140517185 140535107 + chr4 4 E1 1-Ch12 Mafk chr4:140520561-140521124	NM_023374	140513523	140513543	GAAAGCTGACCAGCCAGTG	FW	9.1		0.868
140514562	140514582	ATACACTGAGTCAAGTGGAGG				FW	8.4	0.836	-2623	upstream		
140516119	140516139	GGACCAGCAAAAGTCACTGGGT				RC	8.6	0.849	-1066	upstream		
140516410	140516430	CTCAGGTGACTAAGGAAACTG				FW	8.3	0.799	-775	upstream		
140517932	140517952	AAGCGTGTATTTCAGGGGTG				RC	10.6	0.847	747	intron1		
140518027	140518047	GTAGTAGCTCTGTATAGTTC				RC	8.1	0.852	842	intron1		
140518600	140518620	aaaggctgatgacagcaagatc				FW	9.4	0.834	1415	intron1		
140519134	140519154	CGTTGCTGAGGCAGCAGTGA				FW	7.3	0.817	1949	intron1		
140519995	140520015	TTGGTGGCTGTGTCATCTGT				RC	9.6	0.869	2810	intron1		
173075826	173075846	TCTACTGCCTTTTCATGAGAA				RC	6.5	0.772	4908	intron2		
173078535	173078555	GCCCAGTCACTCAGTACCCA				FW	7.5	0.809	2199	intron1		
Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein NM_025321 chr1 173059287 173080734 - chr1 H3 1	NM_025321										
Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein NM_025848 chr9 50404444 50411954 - chr9 9 B	NM_025848	50408619	50408639	aACTCCTGACAAAGCTGAGGC	FW	7.7	0.843	3335	intron2	1.34	
			50410590	50410610	TCCTACTGACACAGTCTCTTA	FW	11.1	0.878	1364	intron1		
			50412911	50412931	TACTGGTGAACAAGTAAAGAA	FW	8.1	0.774	-957	upstream		
			50413236	50413256	GACTTGTACCAAGCAGATTG	FW	7.3	0.78	-1282	upstream		
			50413327	50413347	AAAAGATTAACAGAGCAAATGT	FW	8.8	0.797	-1373	upstream		
			50415529	50415549	TCTCCACTTAGTCACTCTCC	RC	8.4	0.783	-3575	upstream		
			50416660	50416680	aatccctgacctggcagcgtt	FW	7.3	0.828	-4706	upstream		
Sds1	serine dehydratase-like NM_133902 chr5 120908210 120922772 - chr5 F 5 1-Ch12 Mafk chr5:120927470-120929055 Mel Mafk chr5:120927480-120928441 2-Ch12 Mafk chr5:120927470-120929055 Mel Mafk chr5:120927480-120928441	NM_133902	120927563	120927583	CCAAAGGCTCTCTCACTGCCA	RC	7.2	0.789	-4791	upstream	1.34	
			120927668	120927688	GTGGCAGCTGTGTGATGGGGT	RC	7.2	0.782	-4896	upstream		
			120918708	120918728	cccattgtgacagggccagatg	FW	6.6	0.813	4064	intron1		
			120919358	120919378	tgaagatgacactgaacattt	FW	10.2	0.769	3414	intron1		
			120921215	120921235	CAGAAATGAACAGCAGACTA	FW	10	0.835	1557	intron1		
			120923969	120923989	AAACATGCTTTGTAaaccaaga	RC	8.5	0.792	-1197	upstream		
Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1 NM_009196 chr3 104442586 104462385 + chr3 F2.2 3 1-Ch12 Mafk chr3:104442253-104442611 Ch12 Nrf2 chr3:104442072-104442665	NM_009196	104442374	104442394	CGCGGCGCGGGTCACTGGCC	RC	6.5	0.825	-212	upstream	1.33	
			104437783	104437803	taactttcttagtcaactgaac	RC	7.3	0.799	-4803	upstream		
			104437871	104437891	ggctctgcccgtgaaccaata	RC	7.2	0.762	-4715	upstream		
			104441193	104441213	tgggtgtgagtgagcaccatgc	FW	6.5	0.804	-1393	upstream		
			104441811	104441831	CAGTGTCTTACTAGCATGCAA	FW	6.9	0.799	-775	upstream		
			104442703	104442723	CGCCCGCCGCGTCAAGCATA	RC	6.4	0.82	117	UTR5		
			104445662	104445682	GTCACTCTGTGTATCGCTA	RC	12.2	0.809	3076	intron1		
			104446900	104446920	AGATTGTCTAagtcaccatac	RC	6.7	0.777	4314	intron1		
			104446974	104446994	gtattctgactaagctacagc	FW	8.3	0.878	4388	intron1		
			104447359	104447379	ACAGAAATGAGCTAGTCACTT	FW	7.4	0.795	4773	intron1		

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)	
<i>Slc25a18</i>	solute carrier family 25 (mitochondrial carrier), member 18 NM_001081048 chr6 120723785 120744000 + chr6 F1 6 54.0 cM	NM_001081048	120718918	120718938	TCACGTGTGACCTTGCTAGTAT	FW	9.5	0.833	-4867	upstream	1.44	
			120720071	120720091	CTTAATCCAGAGTCAAGATCA	RC	9.2	0.787	-3714	upstream		
			120720429	120720449	aagctctgcttggctcaggcccaa	RC	11	0.879	-3356	upstream		
			120720667	120720687	CTAAGATCTGTGTCAGCTCTTG	RC	8.1	0.769	-3118	upstream		
			120721041	120721061	TTCCCTGTCTGTTTCACTGAGA	RC	11.3	0.85	-2744	upstream		
			120722012	120722032	AAATACGGTGTGTCACTTTAT	RC	12.5	0.894	-1773	upstream		
			120724617	120724637	TATGTTGCTGACTAAATGGTA	RC	8.3	0.767	832	intron1		
			120724699	120724719	CCACCCTGACTTAGGCCACCT	FW	9.4	0.792	914	intron1		
			120725003	120725023	TGTGTACCTGTGTCACTTAGGG	RC	6.4	0.762	1218	intron1		
			120725790	120725810	TAAACTGCCAATTCAGTTCCT	RC	6.9	0.792	2005	intron1		
			120726308	120726328	CCCCCATTACCCTGCAGCTGTG	FW	10	0.779	2523	intron1		
			120726883	120726903	CACccctgactctgcttcttta	FW	10.3	0.861	3098	intron1		
			120727121	120727141	TATGGGTTACTGAGCAGTCTT	FW	11.1	0.825	3336	intron1		
			120727416	120727436	aggtcagcttggctcatagcaa	RC	6.9	0.845	3631	intron1		
			120728722	120728742	CAAAACCTCAAGCAGTTAT	FW	10.5	0.825	4937	intron1		
<i>Slc27a1</i>	solute carrier family 27 (fatty acid transporter), member 1 NM_011977 chr8 74092825 74110607 + chr8 B3.3 8 1-Mel Mafk chr8:74097381-74097403	NM_011977	74097386	74097406	CTCAGTTCGACTCACTCCTGT	RC	10.5	0.777	4561	intron3	1.57	
			74087928	74087948	ggatgatgagctgagcaccctcc	FW	6.5	0.801	-4897	upstream		
			74088167	74088187	ttgacttccagctccacatctc	RC	6.7	0.772	-4658	upstream		
			74088920	74088940	tggaggggcgaTGCTACTGAGA	RC	6.9	0.819	-3905	upstream		
			74091650	74091670	GAGCAGTACTGTGCTAGCTT	FW	7	0.831	-1175	upstream		
<i>Slc27a2</i>	solute carrier family 27 (fatty acid transporter), member 2 NM_011978 chr2 126378759 126413979 + chr2 F1 2	NM_011978	126374054	126374074	AAGAGGTGACCCCTGCAGAAC	FW	9.4	0.854	-4705	upstream	3.50	
			126374290	126374310	TTCCCTGTACTAGCAGGCTT	FW	11.3	0.844	-4469	upstream		
			126376713	126376733	CCGAGTGCAGAAAGTTAACTGA	RC	7.4	0.782	-2046	upstream		
			126376762	126376782	CTGTGTGACTGAGCTTCTGT	FW	8.4	0.877	-1997	upstream		
			126377258	126377278	CAGTCTTGACACAGGAAAGGG	FW	8.1	0.785	-1501	upstream		
			126377833	126377853	TGGACATGACAAAGAAATCACC	FW	6.7	0.769	-926	upstream		
			126377869	126377889	CCTCAGTGAACAAGCATGAAA	FW	7.9	0.817	-890	upstream		
			126378475	126378495	GGTACTTGATTAAGCAAAGGC	FW	6.6	0.828	-284	upstream		
			126380768	126380788	TTTAAATGACTAAGGAGTTTG	FW	9.1	0.803	2009	intron1		
			126381337	126381357	AGCTCCTGAGAGAGCAAAACA	FW	6.5	0.802	2578	intron1		
			126381565	126381585	CTGACTGACTCAGGATTGTA	FW	11.5	0.83	2806	intron1		
			126382124	126382144	aactaggctatgctcaagaat	RC	6.8	0.843	3365	intron1		
			126383442	126383462	cctcaactcaactgcaqgtttt	FW	9.3	0.776	4683	intron1		
126383728	126383748	atgctgctctgctcaactatgg	RC	9.4	0.783	4969	intron1					
<i>Slc2a4</i>	solute carrier family 2 (facilitated glucose transporter), member 4 NM_009204 chr11 69755787 69761692 - chr11 C-E1 11 40.0 cM	NM_009204	69756863	69756883	TTTGCCCTCAGTCACTTCTCA	RC	8.4	0.782	4829	UTR3	2.18	
			69759251	69759271	GAAAAGTACTTTGCTCTTCC	FW	8.8	0.85	2441	intron5		
			69763958	69763978	GAGAATGCCTATTCATCCTCC	RC	9.5	0.817	-2266	upstream		
			69765551	69765571	CTATTTGCTGAGTTAATGAAT	RC	7.9	0.824	-3859	upstream		
<i>Slc47a1</i>	solute carrier family 47, member 1 NM_026183 chr11 61156901 61191577 - chr11 B2 11	NM_026183	61188650	61188670	GCACAATAACACAGCTGACCA	FW	8.1	0.794	2927	intron1	4.02	
			61190846	61190866	GAAGTGGCTTCTCACCCCTTG	RC	10	0.808	731	intron1		
			61190881	61190901	CCAACTGACAGAGAACAGAA	FW	6.5	0.774	696	intron1		
			61191097	61191117	AGGAGCTGACACAGGATGCTT	FW	7.2	0.779	480	intron1		
			61191329	61191349	AACCCGCCCAAGTCAGACCCCT	RC	7.2	0.829	248	intron1		
			61192971	61192991	AGACTgctcttagctagtgctt	RC	7.9	0.78	-1394	upstream		
			61193264	61193284	ccctgatgactaagcattcca	FW	13.3	0.925	-1687	upstream		
			61194872	61194892	CTGAGTTCCTGGTCAACAGGC	RC	6.5	0.769	-3295	upstream		
			61196394	61196414	aaaccctgactaagatggttg	FW	8.4	0.784	-4817	upstream		
<i>Slc4a3</i>	solute carrier family 4 (anion exchanger), member 3 NM_009208 chr1 75542840 75556006 + chr1 C4 1 41.0 cM	NM_009208	75540935	75540955	AAGTTAGCTGGCTCAGGGTGA	RC	11.1	0.827	-1905	upstream	1.73	
			75545031	75545051	CAGCCCTCACTGAGCAGAACCC	FW	8.5	0.811	2191	intron5		
			75545281	75545301	ACAAGCTGAGCCAGCGAGTGG	FW	7.9	0.809	2441	intron5		
			75545722	75545742	TTCACTGACTAAGCCACCCTG	FW	6.8	0.863	2882	intron6		
			75546378	75546398	GCCAGGGCTGAGTGAGGCCCTT	RC	8.4	0.8	3538	intron6		
			75546628	75546648	TGTGAGTAAC TAGGCACTAG	FW	6.9	0.77	3788	intron6		
			75546684	75546704	GGAAGATGACCAAGCAACCCCT	FW	10.4	0.885	3844	intron6		
			75546874	75546894	TTGTTGTGACTTGGCCAGTGC	FW	7.2	0.834	4034	intron6		
<i>Sucla2</i>	succinate-Coenzyme A ligase, ADP-forming, beta subunit NM_011506 chr14 73952592 73995949 + chr14 D3 14	NM_011506	73950382	73950402	gtcaaccactgagctcaatccc	RC	7.2	0.788	-2210	upstream	1.35	
			73952372	73952392	GAAATGACAGCGTCAAGTTC	RC	8.7	0.841	-220	upstream		
			73956660	73956680	gggcactgagatagcagagatc	FW	8.5	0.812	4068	intron1		
			73956974	73956994	CAGACTGCTGTTtaattatgat	RC	10.9	0.771	4382	intron1		
			73957108	73957128	tcaacttgacacagctggaat	FW	12	0.892	4516	intron1		
			73957431	73957451	cttgcctcttggctcatgatgt	RC	8.5	0.784	4839	intron1		
			73957466	73957486	acaccctgactaagcactgg	FW	10.1	0.796	4874	intron1		
<i>Sult1d1</i>	sulfotransferase family 1D, member 1 NM_016771 chr5 87983674 87998031 - chr5 E1 5	NM_016771	87993195	87993215	AAATGGCTCTTTCACTTCTT	RC	8.7	0.8	4836	intron3	4.77	
			87998504	87998524	AAAAATGAGATAGCATTGTG	FW	10.4	0.831	-473	upstream		
			87999858	87999878	ttattgcttactcaatgtctt	RC	9.5	0.821	-1827	upstream		
			88000027	88000047	AAGGCCACTTTGTCATTATGA	RC	8.1	0.764	-1996	upstream		
			88001627	88001647	GTTTGTCTGTGTCACCTGGT	RC	10	0.802	-3596	upstream		
			88002509	88002529	CCGGTTGCTGTTTCAAGTTTG	RC	8.5	0.834	-4478	upstream		
			88002703	88002723	ATAGATCTGTTTCAACCACCTC	RC	10.2	0.837	-4672	upstream		

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<i>Tecrl</i>	trans-2,3-enoyl-CoA reductase-like NM_153801 chr5 83707146 83784220 - chr5 E1 5	NM_153801	83781611	83781631	CCTGGGTGACTTAGACATATAA	FW	8.9	0.784	2609	intron1	2.28				
			83781856	83781876	TTTCATGCATCTTCATCGTGA	RC	7.6	0.789	2364	intron1					
			83781936	83781956	aaATAATCACAGAGCAACTCC	FW	6.5	0.786	2284	intron1					
			83783024	83783044	GTAATATTACCTAGCAATCCA	FW	6.5	0.788	1196	intron1					
			83784433	83784453	GAATCATAACCGCTGGCAAAATA	FW	7.5	0.768	-213	upstream					
<i>Tff2</i>	trefoil factor 2 (spasmolytic protein 1) NM_009363 chr17 31278006 31281227 - chr17 A3.3 17 17.0 cM	NM_009363	31276275	31276295	CGSTTGGCTAGGTCAAGTGTGG	RC	9.7	0.864	4952	downstream	5.61				
			31279316	31279336	TCCAAGGCTTTGTCAAGGCTGG	RC	12.3	0.879	1911	intron2					
			31279372	31279392	GGACACTGAATTTGCAAGGCTC	FW	7.3	0.803	1855	intron2					
			31281391	31281411	ACATGGGCTGGGTCAAGGCTGG	RC	14.1	0.896	-164	upstream					
			31282337	31282357	gcagactgagtaagccatggg	FW	10.2	0.833	-1110	upstream					
			31284440	31284460	gctttacctttagtcagccgca	RC	7.4	0.766	-3213	upstream					
			31284531	31284551	TCAGCCTGATGAAGCAAAACT	FW	10.5	0.831	-3304	upstream					
			31285007	31285027	agcatggctccatccatggtg	RC	7.6	0.803	-3780	upstream					
			<i>Thrsp</i>	thyroid hormone responsive SPOT14 homolog (Rattus) NM_009381 chr7 104561442 104566060 - chr7 7 E3	NM_009381	104561880	104561900	TAAAGGTGAGCCTGCAACCAA	FW	7.4		0.793	4180	UTR3	4.11
104562264	104562284	tttgttgcacttccatagctg				RC	6.8	0.806	3796	intron1					
104565566	104565586	GAACCTGCCCTGTCAATTCCT				RC	8.1	0.836	494	exon1					
104567140	104567160	gtcctatgagagagcaaaaaag				FW	7.1	0.812	-1080	upstream					
104567241	104567261	CAGGGCTGACTTGCAGCAGTG				FW	11	0.861	-1181	upstream					
104569335	104569355	ATCAGGGCTAAGTCAGACTCA				RC	12.4	0.896	-3275	upstream					
104570170	104570190	TGGAGTCTTATGCATACCGA				RC	10.5	0.816	-4110	upstream					
104570437	104570457	ACACTGTGACTGTGGAGCAGG				FW	8.5	0.779	-4377	upstream					
<i>Tnnc1</i>	troponin C, cardiac/slow skeletal NM_009393 chr14 32021497 32024897 + chr14 B 14 10.0 cM	NM_009393				32018028	32018048	gcccagtgaggcagaccagct	FW	10.4	0.843	-3469	upstream	4.85	
						32018185	32018205	gCGGTGGCTCAATCAGCTCA	RC	7	0.812	-3312	upstream		
			32019895	32019915	CAGGGGGGGGGGTCAAGCTCC	RC	6.5	0.824	-1602	upstream					
			32020165	32020185	AACTCTCCGAAGTCACTCTGC	RC	8.9	0.778	-1332	upstream					
			32020362	32020382	TTGTGGTGTCTCTGAGTGTCT	FW	8.5	0.82	-1135	upstream					
			32020700	32020720	AATGCAGCTGACTCAAACCCG	RC	7.3	0.823	-797	upstream					
			32022490	32022510	GGCTCTGAGGCGAGCACCAGT	FW	7.1	0.815	993	intron1					
			32025721	32025741	GAACAGTGACTAGGGAGGGGA	FW	8.3	0.773	4224	downstream					
			32026042	32026062	CCAGAGTGACCAGCAAGGCT	FW	14.7	0.926	4545	downstream					
			<i>Tnni3</i>	troponin I, cardiac 3 NM_009406 chr7 4469909 4474045 - chr7 A1 7 9.0 cM	NM_009406	4471398	4471418	tcaacttgacacagctgagat	FW	12	0.892	2647	intron6		6.94
4471722	4471742	tttgcttctgtgcatgatgt				RC	8.4	0.784	2323	intron6					
4471757	4471777	aaacctgactaaagacgCGT				FW	9.8	0.794	2288	intron6					
4472678	4472698	CAATCTGCAGATCAGAGTCT				RC	7.2	0.792	1367	exon5					
4474550	4474570	CAGAGGTGACCTGCGCTTTT				FW	10.3	0.836	-505	upstream					
4475939	4475959	agaccctgagcttgcaccag				FW	8.1	0.807	-1894	upstream					
4477059	4477079	gagacagctatatacagggtcc				RC	7.5	0.795	-3014	upstream					
4477483	4477503	acctttactgagctcatctctc				RC	10.8	0.823	-3438	upstream					
4478106	4478126	CGTTGTGCTGCGTGAATCTGC				RC	7.1	0.799	-4061	upstream					
<i>Tnnt2</i>	troponin T2, cardiac NM_001130174 chr1 137732910 137748845 + chr1 E4 1 60.0 cM	NM_001130174 NM_001130175 NM_001130176 NM_001130177 NM_001130178 NM_001130179 NM_001130180 NM_001130181 NM_001136083 NM_011619				137727895	137727915	GGCCCTTGATTTGGCATATGT	FW	6.7	0.795	-5015	upstream	4.66	
			137729252	137729272	CCAATGCAGAGTTACATGTC	RC	7.6	0.789	-3658	upstream					
			137730188	137730208	CCAGTCTCTCAGTCAATGGCTA	RC	8.8	0.781	-2722	upstream					
			137735511	137735531	CAAGGGGCATTTGTCAACATTT	RC	6.6	0.812	-1926	upstream					
			137735861	137735881	GCATCCGCTCAATCATATCTG	RC	6.4	0.806	-1576	upstream					
			137736097	137736117	GGACTATTACCGAGCTCAAT	FW	8.3	0.788	-1340	upstream					
			137739213	137739233	ACCTGTCTGAGTCATGTGGC	RC	12.1	0.834	1776	intron1					
			137740197	137740217	GAGGAGTGAAGGCTGCCATTT	FW	6.6	0.762	2760	intron1					
			137741225	137741245	CGCCAAGCTGAGTCAATGGTCT	RC	13.1	0.921	3788	intron2					
			137741973	137741993	AGCATTCTCTGTCAATTTGGG	RC	7.3	0.775	4536	intron2					
			<i>Tomm5</i>	translocase of outer mitochondrial membrane 5 homolog (yeast) NM_001099675 chr4 45118081 45120985 - chr4 B1 4 1-Ch12 Mafk chr4:45119011-45119604 Ese14 Mafk chr4:45119169-45119672 Mel Mafk chr4:45119196-45119947	NM_001099675 NM_001134646	45119389	45119409	tagagatgactcagcagttca	FW	16.3	0.948	1596	¹ intron1		1.36
						45116107	45116127	TCTCTGTAACCTAAGCAGGTGG	FW	10.9	0.834	4878	downstream		
						45118759	45118779	CATACTGCACAGTATAATGG	RC	8.5	0.779	2226	intron1		
45121891	45121911	ccagggtagacacagaaaaatc				FW	14.3	0.83	-906	upstream					
45124949	45124969	ATTGTTCTGTGTGACAGAAATG				RC	6.9	0.777	-3964	upstream					
<i>Tpm1</i>	tropomyosin 1, alpha NM_001164253 chr9 66870399 66891678 - chr9 C 9 40.0 cM	NM_001164248 NM_001164249 NM_001164250 NM_001164251 NM_001164252 NM_001164253 NM_001164254 NM_001164255 NM_001164256 NM_024427				66886659	66886679	GGCAGGACTGAGTCACTAGGG	RC	8.1	0.796	5019	intron1	1.69	
			66888813	66888833	CCAAGTGAATTAGGGCCAAG	FW	8.9	0.79	2865	intron1					
			66889543	66889563	CTCATGGCTTTGTCTACTAAAC	RC	7.8	0.85	2135	intron1					
			66891611	66891631	AGGCCGGCTTTGTAAAGCCCG	RC	7.8	0.77	67	UTR5					
			66891953	66891973	CCTGAAGCTGAGTAAGGCTAG	RC	8.8	0.813	-275	upstream					
			66892564	66892584	AACCTGTGACAGAGCTCTCTG	FW	8.2	0.854	-886	upstream					
			66893314	66893334	GATAAGCTGAGTCACTACTAC	RC	8.1	0.791	-1636	upstream					
			66893376	66893396	CAATCAGCTACATCACAGTTA	RC	7	0.795	-1698	upstream					
			66894257	66894277	TGGGGTGAAGTGGGCTATCTC	FW	10.4	0.872	-2579	upstream					
			66895572	66895592	GCAGTGTGAGCTGCACTTAC	FW	6.9	0.784	1448	intron2					
			66895778	66895798	GCAGCGTATCCCGCAAGTGT	FW	8.3	0.804	1242	intron1					
			66900711	66900731	acatctgactaaatcttggc	FW	6.4	0.779	-3691	upstream					
			66901079	66901099	CAAGTAGCCAAGTAAGTGG	RC	9.9	0.776	-4059	upstream					
			<i>Trf</i>	transferrin NM_133977	NM_133977	103128342	103128362	TGGGGATGACCCAGCCTGCAG	FW	9.7	0.866	4274	exon4		1.29
						103128953	103128973	GATGCTGACTCAGAGAGTCC	FW	8.5	0.81	3663	intron3		

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	NM_133977 chr9 103111205 103132616 - chr9 F1-F3 9 56.0 cM		103129207	103129227	GGTTGTCGGAGTCAGGCCGG	RC	7.7	0.777	3409	exon3	
			103130523	103130543	CAGTCATGACAGGACAGGG	FW	11.6	0.886	2093	intron1	
			103130819	103130839	GTTTGTCTACAGTCATCATGT	RC	8.1	0.781	1797	intron1	
			103131463	103131483	lccccagcTGGGTCAACCAGT	RC	8.4	0.861	1153	intron1	
			103131575	103131595	ACTTACTGACTCAGCAAGCCC	FW	12.1	0.929	1041	intron1	
			103131772	103131792	CTTGGTCCGGTGTCACTGTGC	RC	9	0.773	844	intron1	
			103132687	103132707	CCAATTGCCCAATCACCCCGC	RC	9.9	0.816	-71	upstream	
Uox	urate oxidase NM_009474 chr3 146260112 146294447 + chr3 H2 3 75.0 cM 1-Ch12 Mafk chr3:146261596-146261969	NM_009474	146261740	146261760	GTTTGTGACTAAGGAATCTG	FW	6.7	0.788	1628	¹ intron1	1.64
			146255101	146255121	CAGCTACAGAGTCATTTTAA	RC	7.2	0.78	-5011	upstream	
			146255512	146255532	TAACGGCTTTGTTCATCCCTT	RC	11.2	0.863	-4600	upstream	
			146255742	146255762	ATGAGTGTGAGTGAAGTTGGC	RC	9.7	0.833	-4370	upstream	
			146255919	146255939	GTTTTCTCTGTGCATCATCT	RC	9.2	0.777	-4193	upstream	
			146256543	146256563	TAAACCTAACAGAGCAAAAAG	FW	8.4	0.791	-3569	upstream	
			146257440	146257460	ACATCATTACAATGCAATGGT	FW	10.5	0.775	-2672	upstream	
			146259535	146259555	CCAGTGTGACTCTGGAGCCT	FW	8.1	0.768	-577	upstream	
			146260275	146260295	TGTCATGCTTAGTCACTTCAT	RC	10.1	0.907	163	intron1	
			146260952	146260972	GGCAGTGCAGGTTTCATCTTAA	RC	6.7	0.792	840	intron1	
			146263779	146263799	CACAGTCTAAGTCAATGTTG	RC	14.4	0.932	3667	intron1	
			146264739	146264759	CAGAAGCCTATGTAAGTGAAGT	RC	7.8	0.773	4627	intron1	
			146264777	146264797	CCCCCTCCTCTGTCAGAGTCA	RC	7.4	0.776	4665	intron1	
			146264856	146264876	GGACTGTGACAAAGGGTTAAA	FW	8.3	0.766	4744	intron1	
Uqcr10	ubiquinol-cytochrome c reductase, complex III subunit X NM_197979 chr11 4601970 4604347 - chr11 A1 11	NM_197979	4599856	4599876	gagagatgactcagtgattaa	FW	9.1	0.795	4491	downstream	1.44
			4606506	4606526	TTAATTACTTAGTCAATTTAA	RC	7.9	0.804	-2159	upstream	
			4608057	4608077	caaatgaccttttcaacagggg	RC	7.7	0.764	-3710	upstream	
Uqcr11	ubiquinol-cytochrome c reductase, complex III subunit XI NM_025650 chr10 79865741 79869566 - chr10 C1 10	NM_025650	79865282	79865302	cagctcttacttagcatgcaa	FW	7.5	0.806	4284	downstream	1.50
			79865915	79865935	AAAGGGTGAAGTCAAGCA	FW	9	0.827	3651	intron2	
			79865982	79866002	ATGCCAGCAGTGTCACTAC	RC	7.2	0.833	3584	intron2	
			79867062	79867082	TGCTGGTAACTAGCCTTTGA	FW	7.1	0.784	2504	intron1	
			79868172	79868192	GTTGGGGCTGATTCATCAGAA	RC	7.7	0.826	1394	intron1	
			79869162	79869182	AAGACTGCAAAATCAAAAGCCA	RC	7.1	0.798	404	intron1	
			79870464	79870484	AGAGTGTGACTACATCAGGGCG	RC	6.4	0.801	-898	upstream	
			79872692	79872712	TTTTCTGCTTGGTCACTGGGG	RC	13.7	0.901	-3126	upstream	
			79873363	79873383	TGTACTGTGGTTCACAGCAC	RC	11.6	0.905	-3797	upstream	
			79874267	79874287	AAGGCCCTTAGGTCAAGGTGC	RC	8.2	0.764	-4701	upstream	
Uqcr1	ubiquinol-cytochrome c reductase core protein 1 NM_025407 chr9 108838660 108851686 + chr9 F2 9 57.0 cM	NM_025407	108836261	108836281	acagtgtagcttaagttgtag	FW	8.2	0.789	-2399	upstream	1.55
			108836580	108836600	cacaagccttagttacactctg	RC	7	0.785	-2080	upstream	
			108838067	108838087	TTTTTTGCTTAGTATTTTAT	RC	9.1	0.822	-593	upstream	
			108842821	108842841	ltgctttgacacagaaattca	FW	6.6	0.826	4161	intron2	
Uqcrf51	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 NM_025710 chr13 30632180 30637185 - chr13 13 A3.3	NM_025710	30633397	30633417	CAAATTGCTGTGGACCATTT	RC	12.8	0.832	3788	intron1	1.58
			30633653	30633673	AAATCGCAAAgtaattatta	RC	11.1	0.794	3532	intron1	
			30635167	30635187	ATCTTTCCATAGTCACCCAGA	RC	9.7	0.775	2018	intron1	
			30636773	30636793	TCACCGTGAGCCCGCTGTCT	FW	6.7	0.778	412	intron1	
			30640051	30640071	TCTACTGCAGAGTATGCTTC	RC	11.6	0.814	-2866	upstream	
			30641648	30641668	acctctgctaggtcacatcac	RC	7.7	0.867	-4463	upstream	
Uqcrh	ubiquinol-cytochrome c reductase hinge protein NM_025641 chr4 115739569 115747675 - chr4 4 C7	NM_025641	115743020	115743040	CAACTTGCAAAGTCAGAAAAA	RC	7.8	0.855	4655	intron2	1.38
			115743732	115743752	gattaagcttgttcaacctgac	RC	6.6	0.795	3943	intron1	
			115746246	115746266	GAAAATCCAAAGTCACACTGA	RC	11	0.791	1429	intron1	
			115750264	115750284	AGAACTTGACTCTGTAAGAAC	FW	6.9	0.776	-2589	upstream	
			115750315	115750335	AGCGTCTGCTTTCAGAGGGA	RC	9.5	0.838	-2640	upstream	
			115750951	115750971	gtgtgtgctgaetcaacctg	RC	11.9	0.869	-3276	upstream	
			115751878	115751898	CCTCAGTGAGCAAGCAGCTTA	FW	9.5	0.825	-4203	upstream	
Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII NM_025352 chr11 53242449 53244333 - chr11 B1.3 11	NM_025352	53240128	53240148	ACACTGTCCACAGCTCAGAC	FW	8.7	0.798	4205	downstream	1.50
			53240184	53240204	ACACTGTCCACAGCTCAGAC	FW	8.7	0.798	4149	downstream	
			53240244	53240264	ACACTGTTCACAGCTCAGAC	FW	10.1	0.804	4089	downstream	
			53240362	53240382	GAACACTCACACAGCTCAGAG	FW	6.9	0.778	3971	downstream	
			53240451	53240471	ATCAGAGCCGATTCACAAATGC	RC	8.3	0.808	3882	downstream	
Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII NM_025352 chr11 53242449 53244333 - chr11 B1.3 11	NM_025352	53242348	53242368	tcgcatgacatagcaggcaag	FW	14.6	0.909	1985	downstream	1.50
			53243209	53243229	ccgaggtgactaagggaagtaa	FW	8.9	0.784	1124	intron1	
			53245389	53245409	TTTTATCCTGTGCTAATGATG	RC	9.2	0.791	-1056	upstream	
			53246055	53246075	tttaactgccaggtcatccatc	RC	8.6	0.835	-1722	upstream	
			53247167	53247187	ACTACATGAAAAGCTCTATA	FW	7.5	0.795	-2834	upstream	
			53247836	53247856	tctctgctcagtcactctag	RC	12.9	0.925	-3503	upstream	
Usp13	ubiquitin specific peptidase 13 (isopeptidase T-3) NM_001013024 chr3 32716547 32834179 + chr3 A3 3	NM_001013024	32714214	32714234	ATGCAGTAACTAGCAATAGC	FW	6.7	0.781	-2333	upstream	1.36
			32714935	32714955	GGCTGATGACAGTGCAGAGTG	FW	8.1	0.834	-1612	upstream	
			32716441	32716461	CCCGCTGACGCTGCAGCTGG	FW	9.9	0.857	-106	upstream	
			32717502	32717522	GATTCGTGACCCCGCAGGAGG	FW	7.7	0.846	955	intron1	
			32717658	32717678		FW	15.8	0.937	1111	intron1	
			32718670	32718690	cttgettccttagtcatgatgt	RC	8.5	0.784	2123	intron1	
			32718705	32718725	aaacctgactaagacaACAC	FW	8.6	0.784	2158	intron1	

Gene symbol	Gene title/Transcript Info/Chromosomal location/ChIP-seq	RefSeq Transcript ID	ARE_start(mm9)	ARE_end(mm9)	ARE_seq	Orientation	PWM	MS	Dist_TSS	Location	FI (SFN vs PBS)
			32720177	32720197	taaatagctggatcacagatc	RC	7.9	0.806	3630	intron1	
			32720905	32720925	ggagttgctccttcatgctgt	RC	8	0.824	4358	intron1	

Table E4. Pathway analysis of lung transcriptome changes by hyperoxia in *Nrf2*^{+/+} mice (n = 7162, *p* < 0.01 Moderate *t*-test).

A. Top networks

	Genes (SFN-altered in bold)	Score	Disease and Functions
1	<i>Actr10, Actr1b, Ankrd1, Anxa8/Anxa8l1, Arhgdib, Ccdc137, Cep76, Chrac1, Cspp1, Ddit4l, Gdap2, Gnb2, Ifitm5, Ipo13, Irx3, Klhl13, Mad2l2, Mdh1, Mpp3, Mterf2, Myl6b, Nhlrc2</i> , etc.	31	DNA Replication, Recombination, and Repair, Cell Cycle, Developmental Disorder
2	<i>Aass, Ap4e1, Ap4m1, Ap4s1, Atp11a, Bicap, Clec2d (Includes Others), Eny2, Esr1, Fgd5, Gcsh, Kcnj13, Kenk6, Lypd1, Macrod1, Marc2, Mphosph9, Mta, Ncaph, Rp2, Rtn4rl1, Scube2</i> , etc.	29	Hematological Disease, Metabolic Disease, Hereditary Disorder
3	<i>Clpp, Cluh, Denr, Dpp8, Farsb, Malsu1, Mapk, Mecr, Mettl1, Mrpl2, Mrpl3, Mrpl9, Mrpl13, Mrpl14, Mrpl16, Mrpl17, Mrpl19, Mrpl20, Mrpl27, Mrpl32, Mrpl37, Mrpl45, Mrps30, Mtif2</i> , etc.	29	Cancer, Organismal Injury and Abnormalities, Gastrointestinal Disease

B. Top upstream regulators

Regulators	Molecule Type	Predicted Activation State	<i>p</i>
<i>Tp53</i>	transcription regulator	Activated	3.34E-10
<i>Pdgfbb</i>	complex	Activated	3.35E-09
<i>Cd40lg</i>	cytokine	-	5.98E-09
<i>F2</i>	peptidase	Activated	3.90E-08
<i>Hgf</i>	growth factor	Activated	5.47E-08
<i>Tnf</i>	cytokine	Activated	1.63E-07
Lipopolysaccharide	chemical drug	Activated	1.72E-07
ERK	group	Activated	2.44E-07
<i>Nfe2l2</i>	transcription regulator	Activated	3.38E-07

C. Top canonical pathways

Pathway	-Log(<i>p</i>)	Genes
NRF2-mediated Oxidative Stress Response	4.47	<i>Sqstm1, Gsto2, Pik3c2a, Mras, Prkcq, Dnajc5, Ube2e3, Enc1, Dnajc21, Actg1, Cct7, Actb, Dnajc15, Gsr, Cat, Aox1, Gpx2</i> , etc.
tRNA Charging	3.98	<i>Cars2, Yars, Sars, Tars12, Yars2, Farsb, Farsa, Wars2, Gars, Eprs, Tars, Mars2, Hars, Cars, Nars2, Rars, Aars2, Vars</i> , etc.
ILK Signaling	3.55	<i>Pik3c2a, Tnfrsf1a, Ppp2r4, Itgb2, Myh9, Rps6ka5, Arhgef6, Actg1, Ppp2r5a, Creb3, Snai2, Actb, Ppp2cb, Actn2, Flnc</i> , etc.
Crosstalk between Dendritic Cells and Natural Killer Cells	3.57	<i>Ccr7, Il15, Itgal, Csf2, Actc1, Il6, Tln2, Trem2, Tlr4, Cd83, Actg1, Actb, Hla-Drb5, Cd80, Fscn1, Ltb, Nfkb1, Faslg, Tln1</i> , etc.
Actin Nucleation by ARP-WASP Complex	3.35	<i>Rhoh, Itga3, Rhod, Mras, Rhoc, Wipf1, Arpc5l, Rock2, Wasf1, Was, Itgb1, Rnd3, Arpc1a, Rras2, Vasp, Ppp1r12c, Rhoj, Actr3</i> , etc.
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	3.16	<i>Csf2, Dkk3, Pik3c2a, Tlr1, Tnfrsf1a, Mras, Prkcq, Smo, Dkk1, Plce1, Il1r2, Nfkbie, Il16, Mapkapk2, Tlr4, Tnfsf13b, Pik3r3, Ccl5, Pik3r4, Traf5, Fzd4, Plcd3, Pdgc, Mmp3, Il18, Prkcd, Calm1</i> , etc.
p53 Signaling	2.67	<i>Pik3c2a, Ccng1, E2f1, Gadd45b, Pias1, Thbs1, Tp53inp1, Gnl3, Topbp1, Dram1, Pik3ca, Snai2, Tp53bp2, Atr, Pidd1, Gadd45g</i> , etc.
NF-κB Activation by Viruses	2.62	<i>Eif2ak2, Traf2, Itgal, Tnfrsf14, Pik3c2a, Itga3, Mras, Itgb2, Nfkbie, Itga1, Pik3ca, Cr2, Itgb1, Prkcb, Nfkb1, Rela, Itga5</i> , etc.

Table E5. Nrf2^{-/-} mice: Air vs Hyperoxia

Moderated T-Test (p-value cut-off:0.01)/Fold Change 2

*Fold change (FC) in red indicates increased and in blue decreased by hyperoxia.

RefSeq	Transcript	IE Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_007950		<i>Ereg</i>	104.283	3.40E-05	epiregulin
NM_011315		<i>Saa3</i>	95.127	1.21E-04	serum amyloid A 3
NM_031168		<i>Il6</i>	86.566	1.24E-04	interleukin 6
NM_001044384	///N	<i>Timp1</i>	57.112	3.40E-05	tissue inhibitor of metalloproteinase 1
NM_011333		<i>Ccl2</i>	44.161	6.57E-05	chemokine (C-C motif) ligand 2
NM_011819		<i>Gdf15</i>	43.117	6.30E-05	growth differentiation factor 15
NM_009890		<i>Ch25h</i>	23.631	3.89E-04	cholesterol 25-hydroxylase
NM_008176		<i>Cxcl1</i>	22.824	4.52E-05	chemokine (C-X-C motif) ligand 1
NM_009117		<i>Saa1</i>	22.778	0.002576101	serum amyloid A 1
NM_009627		<i>Adm</i>	22.591	5.78E-05	adrenomedullin
NM_172845		<i>Adams4</i>	22.263	2.94E-04	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4
NM_009252		<i>Serpina3n</i>	20.860	5.15E-05	serine (or cysteine) peptidase inhibitor, clade A, member 3N
NM_008726		<i>Nppb</i>	20.599	6.71E-04	natriuretic peptide type B
NM_013654		<i>Ccl7</i>	20.081	5.59E-05	chemokine (C-C motif) ligand 7
NM_011607		<i>Tnc</i>	19.457	2.80E-04	tenascin C
NM_133731		<i>Prss22</i>	18.406	0.004186718	protease, serine, 22
NM_010555		<i>Il1r2</i>	18.044	0.006343347	interleukin 1 receptor, type II
NM_010171		<i>F3</i>	17.742	4.79E-05	coagulation factor III
NM_007697		<i>Chl1</i>	16.255	2.05E-04	cell adhesion molecule with homology to L1CAM
NM_008630		<i>Mt2</i>	16.140	4.26E-05	metallothionein 2
NM_008871		<i>Serpine1</i>	16.133	5.36E-05	serine (or cysteine) peptidase inhibitor, clade E, member 1
NM_007825		<i>Cyp7b1</i>	15.246	3.40E-05	cytochrome P450, family 7, subfamily b, polypeptide 1
NM_013602		<i>Mt1</i>	13.987	5.78E-05	metallothionein 1
NM_011331	///XM_1	<i>Ccl12</i> ///LOC100862578	13.652	2.41E-04	chemokine (C-C motif) ligand 12///c-c motif chemokine 12-like
NM_001177352	///N	<i>Myc</i>	13.504	3.40E-05	myelocytomatosis oncogene
NM_010809		<i>Mmp3</i>	13.381	6.52E-05	matrix metallopeptidase 3
NM_008638		<i>Mthfd2</i>	12.763	3.40E-05	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase
NM_011452		<i>Serpina9b</i>	12.344	2.83E-04	serine (or cysteine) peptidase inhibitor, clade B, member 9b
NM_028889		<i>Efh1</i>	11.866	5.78E-05	EF hand domain containing 1
NM_001111099	///N	<i>Cdkn1a</i>	11.449	3.40E-05	cyclin-dependent kinase inhibitor 1A (P21)
NM_134102		<i>Pla1a</i>	11.408	7.68E-05	phospholipase A1 member A
NM_009141		<i>Cxcl5</i>	11.223	2.88E-04	chemokine (C-X-C motif) ligand 5
NM_008987		<i>Ptx3</i>	11.202	7.66E-04	pentraxin related gene
NM_009140		<i>Cxcl2</i>	11.035	0.001773256	chemokine (C-X-C motif) ligand 2
NM_008611		<i>Mmp8</i>	10.968	0.002842004	matrix metallopeptidase 8
NM_001163525	///N	<i>S100a14</i>	10.698	7.96E-05	S100 calcium binding protein A14
NM_009404		<i>Tnfrsf9</i>	10.580	3.40E-05	tumor necrosis factor (ligand) superfamily, member 9
NM_021342		<i>Kcne4</i>	10.497	6.57E-05	potassium voltage-gated channel, Isk-related subfamily, gene 4
NM_001039562		<i>Ankrd37</i>	10.477	0.001198963	ankyrin repeat domain 37
NM_011347		<i>Selp</i>	10.403	6.74E-05	selectin, platelet
NM_001161746	///N	<i>Tnfrsf12a</i>	9.863	3.40E-05	tumor necrosis factor receptor superfamily, member 12a
NM_008491		<i>Lcn2</i>	9.794	6.36E-04	lipocalin 2
NM_203320		<i>Cxcl3</i>	9.782	0.001372295	chemokine (C-X-C motif) ligand 3
NM_001039537	///N	<i>Lif</i>	9.740	7.43E-05	leukemia inhibitory factor
NM_008381		<i>Inhbb</i>	9.606	8.83E-05	inhibin beta-B
NM_013468		<i>Ankrd1</i>	9.579	3.07E-04	ankyrin repeat domain 1 (cardiac muscle)
NM_007695		<i>Chi3l1</i>	9.254	4.05E-04	chitinase 3-like 1
NM_009912		<i>Ccr1</i>	9.141	0.004920226	chemokine (C-C motif) receptor 1
NM_011817		<i>Gadd45g</i>	8.713	7.38E-05	growth arrest and DNA-damage-inducible 45 gamma
NM_007390		<i>Chrna7</i>	8.653	7.94E-05	cholinergic receptor, nicotinic, alpha polypeptide 7
NM_001109914		<i>Apol1</i>	8.482	8.88E-04	apolipoprotein I domain containing 1
NM_017373		<i>Nfil3</i>	8.413	1.13E-04	nuclear factor, interleukin 3, regulated
NM_022415		<i>Ptges</i>	8.392	0.002804473	prostaglandin E synthase
NM_026835		<i>Ms4a6d</i>	8.262	1.52E-04	membrane-spanning 4-domains, subfamily A, member 6D
NM_015798		<i>Fbxo15</i>	8.166	1.01E-04	F-box protein 15
NM_010755		<i>Maff</i>	8.085	3.40E-05	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)
NM_001081249	///N	<i>Vcan</i>	8.020	1.50E-04	versican
NM_007836		<i>Gadd45a</i>	8.017	3.40E-05	growth arrest and DNA-damage-inducible 45 alpha
NM_001081957	///X	<i>LOC100504934</i> ///Wfcd17	7.968	0.001044687	extracellular peptidase inhibitor-like///WAP four-disulfide core domain 17
NM_018865		<i>Wisp1</i>	7.961	8.74E-04	WNT1 inducible signaling pathway protein 1
NM_009899	///NM_	<i>Cla1</i> ///Cla2	7.904	7.45E-05	chloride channel calcium activated 1///chloride channel calcium activated 2
NM_024495		<i>Car13</i>	7.863	1.68E-04	carbonic anhydrase 13
NM_001161432	///N	<i>Eda2r</i>	7.817	2.76E-04	ectodysplasin A2 receptor
NM_020581		<i>Angptl4</i>	7.791	0.001826737	angiopoietin-like 4
NM_007930		<i>Enc1</i>	7.770	3.40E-05	ectodermal-neural cortex 1
NM_028216		<i>Pscs</i>	7.750	6.90E-05	prostate stem cell antigen
NM_026862		<i>Cd177</i>	7.713	3.40E-05	CD177 antigen
NM_011332		<i>Ccl17</i>	7.659	8.42E-04	chemokine (C-C motif) ligand 17
NM_009253		<i>Serpina3m</i>	7.576	2.22E-04	serine (or cysteine) peptidase inhibitor, clade A, member 3M
NM_009704		<i>Areg</i>	7.571	1.29E-04	amphiregulin
NM_010118		<i>Egr2</i>	7.546	7.24E-04	early growth response 2
NM_009903		<i>Cldn4</i>	7.364	0.006593674	claudin 4
NM_001113326	///N	<i>Msr1</i>	7.244	7.57E-05	macrophage scavenger receptor 1
NM_001161714	///N	<i>Tgms1</i>	7.142	1.14E-04	transglutaminase 1, K polypeptide
NM_009971		<i>Csf3</i>	7.095	0.004375011	colony stimulating factor 3 (granulocyte)
NM_020610		<i>Nrip3</i>	6.914	1.97E-04	nuclear receptor interacting protein 3
NM_007707		<i>Socs3</i>	6.815	6.57E-05	suppressor of cytokine signaling 3
NM_001162939	///N	<i>Aen</i>	6.798	6.13E-05	apoptosis enhancing nuclease
NM_027399		<i>Steap1</i>	6.742	9.86E-05	six transmembrane epithelial antigen of the prostate 1
NM_011227		<i>Rab20</i>	6.720	2.24E-04	RAB20, member RAS oncogene family

RefSeq Transcript ID	Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_001205339	LOC100047252//Psat1	6.698	4.26E-05	phosphoserine aminotransferase-like//phosphoserine aminotransferase 1
NM_001276455	Slc19a2	6.682	3.40E-05	solute carrier family 19 (thiamine transporter), member 2
NM_001172472	Sphk1	6.598	1.75E-04	sphingosine kinase 1
NM_010902	Nfe2l2	6.586	0.004835362	nuclear factor, erythroid derived 2, like 2
NM_009899	Clca1//Clca2	6.540	7.57E-05	chloride channel calcium activated 1//chloride channel calcium activated 2
NM_026473	Tubb6	6.514	3.40E-05	tubulin, beta 6 class V
NM_029796	Lrg1	6.484	2.83E-04	leucine-rich alpha-2-glycoprotein 1
NM_010235	Fosl1	6.437	7.45E-05	fos-like antigen 1
NM_008147	Gp49a//Lilrb4	6.408	0.007934198	glycoprotein 49 A//leukocyte immunoglobulin-like receptor, subfamily B, member 4
NR_029468	Snhg12	6.370	1.37E-04	small nucleolar RNA host gene 12
NM_027519	Medag	6.247	8.16E-04	mesenteric estrogen dependent adipogenesis
NM_001164197	Mmp19	6.190	0.007614046	matrix metalloproteinase 19
NM_144554	Trib3	6.112	7.45E-05	tribbles homolog 3 (Drosophila)
NM_019738	Nupr1	5.950	2.55E-04	nuclear protein transcription regulator 1
NR_002896	Snhg1	5.939	4.26E-05	small nucleolar RNA host gene (non-protein coding) 1
NM_021274	Cxcl10	5.914	1.21E-04	chemokine (C-X-C motif) ligand 10
NM_001135151	Slc39a14	5.897	1.15E-04	solute carrier family 39 (zinc transporter), member 14
NM_007539	Bdkrb1	5.858	4.26E-05	bradykinin receptor, beta 1
NM_019568	Cxcl14	5.746	0.002195939	chemokine (C-X-C motif) ligand 14
NM_007431	Alpl	5.713	2.35E-04	alkaline phosphatase, liver/bone/kidney
NM_009711	Artn	5.634	6.45E-04	artemin
NM_001190161	Psrc1	5.605	2.80E-04	proline/serine-rich coiled-coil 1
NM_011404	Slc7a5	5.598	1.58E-04	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
NM_008605	Mmp12	5.555	0.001380294	matrix metalloproteinase 12
NM_011337	Ccl3	5.386	5.26E-04	chemokine (C-C motif) ligand 3
NM_183160	Tmem252	5.382	1.21E-04	transmembrane protein 252
NM_011075	Abcb1b	5.376	1.68E-04	ATP-binding cassette, sub-family B (MDR/TAP), member 1B
NM_199447	Rrp12	5.290	5.92E-05	ribosomal RNA processing 12 homolog (S. cerevisiae)
NM_010220	Fkbp5	5.261	0.0017525	FK506 binding protein 5
NM_175307	Fam46b	5.235	2.76E-04	family with sequence similarity 46, member B
NM_001038604	Clec5a	5.199	0.009944347	C-type lectin domain family 5, member a
NM_001081328	Chsy3	5.163	0.003958511	chondroitin sulfate synthase 3
NM_173036	Gpr97	5.114	8.08E-04	G protein-coupled receptor 97
NM_205820	Tlr13	5.111	8.74E-04	toll-like receptor 13
NM_007403	Adam8	5.094	6.52E-05	a disintegrin and metalloproteinase domain 8
NM_011338	Ccl9	5.008	3.63E-04	chemokine (C-C motif) ligand 9
NM_007408	Plin2	4.997	9.11E-05	perilipin 2
NM_001172205	Arid5a	4.997	7.45E-05	AT rich interactive domain 5A (MRF1-like)
NM_009705	Arg2	4.978	0.002089744	arginase type II
NM_008350	Il11	4.961	8.86E-04	interleukin 11
NM_008046	Fst	4.940	9.09E-04	follicle-stimulating hormone receptor
NM_178595	Ptrh1	4.877	1.52E-04	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)
NM_028351	Rspa3	4.850	0.003096426	R-spondin 3 homolog (Xenopus laevis)
NM_007498	Atf3	4.812	1.39E-04	activating transcription factor 3
NM_027514	Pvr	4.805	3.17E-04	poliovirus receptor
NM_021406	Trem1	4.744	0.007444954	triggering receptor expressed on myeloid cells 1
NM_011267	Rgs16	4.717	2.77E-04	regulator of G-protein signaling 16
NM_001082960	Itgam	4.697	0.008168832	integrin alpha M
NM_153543	Aldh1l2	4.692	2.56E-04	aldehyde dehydrogenase 1 family, member L2
NM_010664	Krt18	4.610	7.96E-05	keratin 18
NM_013473	Anxa8	4.603	0.001603919	annexin A8
NM_001099792	Trtm61a	4.583	1.16E-04	tRNA methyltransferase 61A
NM_199223	Rtn4r12	4.568	1.21E-04	reticulon 4 receptor-like 2
NM_009364	Tfpi2	4.564	2.05E-04	tissue factor pathway inhibitor 2
NM_010441	Hmga2	4.558	5.12E-04	high mobility group AT-hook 2
NM_021362	Pappa	4.558	1.14E-04	pregnancy-associated plasma protein A
NM_008416	Junb	4.551	5.14E-04	Jun-B oncogene
NM_011498	Bhlhe40	4.510	1.04E-04	basic helix-loop-helix family, member e40
NM_013750	Phlda3	4.501	6.71E-04	pleckstrin homology-like domain, family A, member 3
NM_023716	Tubb2a-ps2//Tubb2b	4.495	2.11E-04	tubulin, beta 2a, pseudogene 2//tubulin, beta 2B class IIB
NM_001024619	Tsku	4.486	1.50E-04	tsukushi
NM_023731	Ccdc86	4.484	1.58E-04	coiled-coil domain containing 86
NM_010050	Dio2	4.435	6.05E-04	deiodinase, iodothyronine, type II
NM_019967	Dbc1	4.383	7.07E-04	deleted in bladder cancer 1 (human)
NM_153287	Csrnp1	4.352	1.08E-04	cysteine-serine-rich nuclear protein 1
NM_025878	Mrps18b	4.348	4.26E-05	mitochondrial ribosomal protein S18B
NM_025310	Ftsj3	4.342	2.79E-04	FtsJ homolog 3 (E. coli)
NM_153547	Gnl3	4.300	5.78E-05	guanine nucleotide binding protein-like 3 (nucleolar)
NM_001136079	Ptger4	4.296	1.68E-04	prostaglandin E receptor 4 (subtype EP4)
NM_009841	Cd14	4.292	0.00129915	CD14 antigen
NM_028810	Rnd3	4.284	1.29E-04	Rho family GTPase 3
NM_013614	Odc1	4.218	4.72E-05	ornithine decarboxylase, structural 1
NM_011580	Palad1//Thbs1	4.205	7.57E-05	phosphatase domain containing, paladin 1//thrombospondin 1
NM_010104	Edn1	4.199	2.91E-04	endothelin 1
NM_001159394	Nfkbiz	4.195	0.001026998	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta
NM_027193	Dph5	4.185	7.96E-05	DPH5 homolog (S. cerevisiae)
NM_013529	Gjpt2	4.157	4.26E-05	glutamine fructose-6-phosphate transaminase 2
NM_008872	Plat	4.145	1.40E-04	plasminogen activator, tissue
NM_008773	P2ry2	4.141	0.001198904	purinergic receptor P2Y, G-protein coupled 2
NM_145495	Rin1	4.138	1.29E-04	Ras and Rab interactor 1
NM_009779	C3ar1	4.114	2.39E-04	complement component 3a receptor 1
NM_001163346	Cdc42ep4	4.082	1.63E-04	CDC42 effector protein (Rho GTPase binding) 4
NM_029665	Xm1//Ipo11//LOC100504500	4.059	0.005588106	importin 11//leucine-rich repeat-containing protein 70-like

RefSeq Transcript ID	Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_001110809	<i>Gpatch4</i>	4.049	1.29E-04	G patch domain containing 4
NM_021560	<i>Bhlhe22</i>	4.033	3.90E-04	basic helix-loop-helix family, member e22
NM_009831	<i>Ccng1</i>	4.024	1.29E-04	cyclin G1
NM_013737	<i>Pla2g7</i>	3.998	0.007231838	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)
NM_011400	<i>Slc2a1</i>	3.940	2.89E-04	solute carrier family 2 (facilitated glucose transporter), member 1
NM_009272	<i>Srm</i>	3.928	1.12E-04	spermidine synthase
NM_016748	<i>Ctps</i>	3.921	1.08E-04	cytidine 5'-triphosphate synthase
NM_018868	<i>Nop58</i>	3.918	5.00E-04	NOP58 ribonucleoprotein
NM_010516	<i>Cyr61</i>	3.908	7.73E-05	cysteine rich protein 61
NM_009853	<i>Cd68</i>	3.885	0.001188299	CD68 antigen
NM_053110	<i>Gpnmb</i>	3.877	6.98E-04	glycoprotein (transmembrane) nmb
NM_007527	<i>Bax</i>	3.877	7.57E-05	BCL2-associated X protein
NM_001142706	<i>C2</i>	3.876	0.001561041	complement component 2 (within H-2S)///complement factor B
NM_011113	<i>Plaur</i>	3.861	5.25E-04	plasminogen activator, urokinase receptor
NM_010045	<i>Darc</i>	3.847	9.17E-05	Duffy blood group, chemokine receptor
NM_001166402	<i>Tnfrsf3</i>	3.835	1.96E-04	tumor necrosis factor, alpha-induced protein 3
NM_197982	<i>Ddx39</i>	3.819	4.26E-05	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
NM_001134385	<i>Gpr160</i>	3.817	1.27E-04	G protein-coupled receptor 160
NM_025443	<i>Pno1</i>	3.813	1.68E-04	partner of NOB1 homolog (S. cerevisiae)
NM_001170785	<i>Mthfd1l</i>	3.801	2.69E-04	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
NM_026963	<i>Lzic</i>	3.780	6.57E-05	leucine zipper and CTNBP1 domain containing
NM_001271705	<i>Pgf</i>	3.779	7.38E-05	placental growth factor
NM_011087	<i>Pira1</i>	3.771	0.00984946	paired-Ig-like receptor A1
NM_001077189	<i>Fcgr2b</i>	3.770	0.001867556	Fc receptor, IgG, low affinity IIb
NR_051981	<i>H2-Q5</i>	3.761	0.00129915	histocompatibility 2, Q region locus 5///histocompatibility 2, K1, K region
NM_009747	<i>Bdkrb2</i>	3.751	2.42E-04	bradykinin receptor, beta 2
NM_001093749	<i>Mpz13</i>	3.741	6.80E-04	myelin protein zero-like 3
NM_021511	<i>Rrs1</i>	3.736	7.45E-05	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
NM_010728	<i>Lox</i>	3.726	5.78E-05	lysyl oxidase
NM_153419	<i>Grwd1</i>	3.725	7.96E-05	glutamate-rich WD repeat containing 1
NM_011314	<i>Saa2</i>	3.723	0.008600426	serum amyloid A 2
NM_031170	<i>Krt8</i>	3.715	1.03E-04	keratin 8
NM_012055	<i>Asns</i>	3.708	8.78E-05	asparagine synthetase
NM_053108	<i>Glrx</i>	3.684	0.006439096	glutaredoxin
NM_023158	<i>Cxcl16</i>	3.658	6.52E-05	chemokine (C-X-C motif) ligand 16
NM_011898	<i>Spry4</i>	3.651	1.58E-04	sprouty homolog 4 (Drosophila)
NM_175314	<i>Adamts9</i>	3.641	0.001160721	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 9
NM_001145953	<i>Lgals3</i>	3.637	7.45E-05	lectin, galactose binding, soluble 3
NM_031185	<i>Akap12</i>	3.602	1.14E-04	A kinase (PRKA) anchor protein (gravin) 12
NM_019980	<i>Litaf</i>	3.583	1.33E-04	LPS-induced TN factor
NM_001272052	<i>Ada</i>	3.574	2.29E-04	adenosine deaminase
NM_010188	<i>Fcgr3</i>	3.552	0.006187574	Fc receptor, IgG, low affinity III
NM_008651	<i>Mybl1</i>	3.532	0.00204319	myeloblastosis oncogene-like 1
NM_134156	<i>Actn1</i>	3.524	2.41E-04	actinin, alpha 1
NM_013898	<i>Timm8a1</i>	3.521	7.43E-05	translocase of inner mitochondrial membrane 8A1
NM_001164074	<i>Tgjf1</i>	3.518	3.17E-04	TGFB-induced factor homeobox 1
NM_010212	<i>Fhl2</i>	3.504	7.57E-05	four and a half LIM domains 2
NM_001166391	<i>F13a1</i>	3.494	1.14E-04	coagulation factor XIII, A1 subunit
NM_145610	<i>Ppan</i>	3.485	1.79E-04	peter pan homolog (Drosophila)
NM_026816	<i>Gtf2f2</i>	3.478	5.52E-04	general transcription factor IIF, polypeptide 2
NM_001103156	<i>Steap2</i>	3.471	5.00E-04	six transmembrane epithelial antigen of prostate 2
NM_201367	<i>Gpr176</i>	3.470	0.006621157	G protein-coupled receptor 176
NR_003964	<i>Tubb2a-ps2</i>	3.469	9.30E-04	tubulin, beta 2a, pseudogene 2///tubulin, beta 2B class IIB
NM_022811	<i>Polr1e</i>	3.461	7.43E-05	polymerase (RNA) I polypeptide E
NM_001159631	<i>Nek6</i>	3.450	9.27E-04	NIMA (never in mitosis gene a)-related expressed kinase 6
NM_053113	<i>Ear11</i>	3.449	1.68E-04	eosinophil-associated, ribonuclease A family, member 11
NM_011955	<i>Nubp1</i>	3.440	1.33E-04	nucleotide binding protein 1
NM_001164733	<i>Mpp6</i>	3.404	2.39E-04	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)
NR_040721	<i>Snhg5</i>	3.401	3.40E-04	small nucleolar RNA host gene 5
NM_177364	<i>Sh3pxd2b</i>	3.401	0.001733131	SH3 and PX domains 2B
NM_144810	<i>Klhdc8a</i>	3.397	3.74E-04	kelch domain containing 8A
NM_145535	<i>Sdcbp2</i>	3.395	1.29E-04	syndecan binding protein (syntenin) 2
NM_008012	<i>Akr1b8</i>	3.390	1.07E-04	aldo-keto reductase family 1, member B8
NM_026929	<i>Chac1</i>	3.385	0.002199478	ChaC, cation transport regulator 1
NM_009716	<i>Atf4</i>	3.385	1.29E-04	activating transcription factor 4
NM_020047	<i>Tacstd2</i>	3.382	0.008238319	tumor-associated calcium signal transducer 2
NM_011175	<i>Lgmn</i>	3.374	1.68E-04	legumain
NM_001163478	<i>Rabggtb</i>	3.367	1.29E-04	RAB geranylgeranyl transferase, b subunit
NM_198664	<i>Tbc1d2</i>	3.360	2.76E-04	TBC1 domain family, member 2
NM_001276301	<i>Ampd3</i>	3.358	0.001810649	adenosine monophosphate deaminase 3
NM_001252588	<i>Tspan4</i>	3.348	7.25E-04	tetraspanin 4
NM_001029842	<i>Slc16a6</i>	3.347	8.90E-05	solute carrier family 16 (monocarboxylic acid transporters), member 6
NM_007513	<i>Slc7a1</i>	3.343	6.27E-04	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
NM_134139	<i>Wdr74</i>	3.322	9.11E-05	WD repeat domain 74
NM_010401	<i>Hal</i>	3.316	0.006537725	histidine ammonia lyase
NM_011656	<i>Tuft1</i>	3.303	6.66E-04	tuftelin 1
NR_024067	<i>Snhg6</i>	3.293	1.46E-04	small nucleolar RNA host gene (non-protein coding) 6
NR_002840	<i>Gas5</i>	3.291	0.006950962	growth arrest specific 5///small nucleolar RNA, C/D box 47
NM_023044	<i>Slc15a3</i>	3.273	7.02E-04	solute carrier family 15, member 3
NM_026631	<i>Nhp2</i>	3.267	7.45E-05	NHP2 ribonucleoprotein
NM_008471	<i>Krt19</i>	3.256	2.92E-04	keratin 19
NM_009396	<i>Tnfrsf2</i>	3.255	6.99E-04	tumor necrosis factor, alpha-induced protein 2
NM_001013389	<i>Mrs2</i>	3.254	1.17E-04	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)

RefSeq Transcript ID	Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_018781	<i>Egr3</i>	3.247	2.89E-04	early growth response 3
NM_020275	<i>Tnfrsf10b</i>	3.234	2.39E-04	tumor necrosis factor receptor superfamily, member 10b
NM_007679	<i>Cebpd</i>	3.228	4.79E-04	CCAAT/enhancer binding protein (C/EBP), delta
NM_007771	<i>Cry1</i>	3.223	7.13E-05	cryptochrome 1 (photolyase-like)
NM_022032	<i>Perp</i>	3.213	7.45E-05	PERP, TP53 apoptosis effector
NM_009917	<i>Ccr5</i>	3.210	6.55E-04	chemokine (C-C motif) receptor 5
NM_019501	<i>Pdss1</i>	3.206	7.23E-04	prenyl (solaneyl) diphosphate synthase, subunit 1
NM_009448//NR_C Gm6682//Tuba1c		3.199	8.77E-05	tubulin, alpha 1C pseudogene//tubulin, alpha 1C
NM_033601	<i>Bcl3</i>	3.191	9.21E-04	B cell leukemia/lymphoma 3
NM_028798	<i>Crct1</i>	3.185	6.02E-04	cysteine-rich C-terminal 1
NM_153065	<i>Ddx27</i>	3.184	1.74E-04	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27
NM_031380	<i>Fstl3</i>	3.177	1.71E-04	folliculin-like 3
NM_001113478//N Frs1		3.172	5.01E-04	ferric-chelate reductase 1
NM_009369	<i>Tgfb1</i>	3.168	6.99E-04	transforming growth factor, beta induced
NM_023579	<i>Ipo5</i>	3.165	7.43E-05	importin 5
NM_001114087//N Pdlim7		3.163	3.72E-04	PDZ and LIM domain 7
NM_013743	<i>Pdk4</i>	3.158	7.66E-04	pyruvate dehydrogenase kinase, isoenzyme 4
NM_001166672//N Lira6//Pira1		3.145	0.005276636	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 receptor A11
NM_001271607//N Cxcr7		3.144	8.94E-04	chemokine (C-X-C motif) receptor 7
NM_001130457//N Tbrg4		3.138	7.96E-05	transforming growth factor beta regulated gene 4
NM_026041	<i>Rrp15</i>	3.133	8.04E-05	ribosomal RNA processing 15 homolog (<i>S. cerevisiae</i>)
NM_008967	<i>Ptgir</i>	3.131	0.001501375	prostaglandin I receptor (IP)
NM_019432	<i>Tmem37</i>	3.128	2.47E-04	transmembrane protein 37
NM_011414	<i>Slpi</i>	3.115	0.001914019	secretory leukocyte peptidase inhibitor
NM_009921	<i>Camp</i>	3.102	0.002404555	cathelicidin antimicrobial peptide
NM_019670	<i>Diap3</i>	3.099	0.005023152	diaphanous homolog 3 (<i>Drosophila</i>)
NM_183029	<i>Igf2bp2</i>	3.099	6.57E-05	insulin-like growth factor 2 mRNA binding protein 2
NM_001168333//N Tinaql1		3.088	3.72E-04	tubulointerstitial nephritis antigen-like 1
NM_175259	<i>Shisa4</i>	3.076	6.13E-04	shisa homolog 4 (<i>Xenopus laevis</i>)
NM_009994	<i>Cyp1b1</i>	3.070	7.05E-04	cytochrome P450, family 1, subfamily b, polypeptide 1
NM_010792	<i>Mettl1</i>	3.060	2.76E-04	methyltransferase like 1
NM_020010	<i>Cyp51</i>	3.045	3.77E-04	cytochrome P450, family 51
NM_145404	<i>Prmt7</i>	3.037	6.55E-04	protein arginine N-methyltransferase 7
NM_153561	<i>Nudt6</i>	3.035	3.06E-04	nudix (nucleoside diphosphate linked moiety X)-type motif 6
NM_009448//NR_C Gm6682//Tuba1c//LOC101i		3.026	9.20E-05	tubulin, alpha 1C pseudogene//tubulin, alpha 1C//tubulin alpha-1C chain-like//tubulin, alpha 1A
NM_010120//NM_Ejfla//BB287469//Gm4027		3.021	3.72E-04	eukaryotic translation initiation factor 1A//expressed sequence BB287469//predicted gene 4027
NM_011198	<i>Ptgs2</i>	3.016	4.95E-04	prostaglandin-endoperoxide synthase 2
NM_183168	<i>P2ry6</i>	3.014	1.41E-04	pyrimidinergic receptor P2Y, G-protein coupled, 6
NM_009121	<i>Sat1</i>	3.010	2.34E-04	spermidine/spermine N1-acetyl transferase 1
NM_009046	<i>Relb</i>	3.009	2.88E-04	avian reticuloendotheliosis viral (v-rel) oncogene related B
NM_010481	<i>Hspa9</i>	2.996	8.97E-05	heat shock protein 9
NM_023040//NM_Gfer		2.985	7.82E-05	growth factor, erv1 (<i>S. cerevisiae</i>)-like (augmenter of liver regeneration)
NM_018820	<i>Sertad1</i>	2.985	3.67E-04	SERTA domain containing 1
NM_001004140	<i>Ckap2</i>	2.984	2.83E-04	cytoskeleton associated protein 2
NM_001039185//N Ceacam1//Ceacam2		2.977	1.83E-04	carcinoembryonic antigen-related cell adhesion molecule 1
NM_008006	<i>Fgf2</i>	2.975	0.00130335	fibroblast growth factor 2
NM_001024945//N Qsox1		2.973	5.85E-04	quiescin Q6 sulfhydryl oxidase 1
NM_029614	<i>Prss23</i>	2.965	3.77E-04	protease, serine, 23
NM_029662	<i>Mfsd2a</i>	2.964	0.00984946	major facilitator superfamily domain containing 2A
NM_024215	<i>Zfp593</i>	2.962	2.06E-04	zinc finger protein 593
NM_177325	<i>Tsr1</i>	2.958	8.83E-05	TSR1 20S rRNA accumulation
NM_001199060//N Wdr12		2.958	1.27E-04	WD repeat domain 12
NM_007793	<i>Cstb</i>	2.954	1.14E-04	cystatin B
NM_028766	<i>Tmem43</i>	2.954	2.64E-04	transmembrane protein 43
NM_008519	<i>Ltb4r1</i>	2.950	0.001985311	leukotriene B4 receptor 1
NM_178605	<i>Nop16</i>	2.940	7.96E-05	NOP16 nucleolar protein
NM_027450	<i>Glipr2</i>	2.936	0.001501375	GLI pathogenesis-related 2
NM_001205173//N Iffa2		2.929	3.77E-04	intermediate filament family orphan 2
NM_011019	<i>Osmr</i>	2.924	4.76E-04	oncostatin M receptor
NM_001164357//N Slc25a25		2.923	2.39E-04	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25
NM_026072	<i>Cwc27</i>	2.912	9.34E-05	CWC27 spliceosome-associated protein homolog (<i>S. cerevisiae</i>)
NM_001109657//N Gas7		2.910	1.85E-04	growth arrest specific 7
NM_001033187//N Btb19		2.908	1.05E-04	BTB (POZ) domain containing 19
NM_178890	<i>Abtb2</i>	2.908	0.004193235	ankyrin repeat and BTB (POZ) domain containing 2
NM_009855	<i>Cd80</i>	2.891	4.65E-04	CD80 antigen
NM_153159	<i>Zc3h12a</i>	2.884	0.008351559	zinc finger CCCH type containing 12A
NM_178591	<i>Nrg1</i>	2.880	3.49E-04	neuregulin 1
NM_146041	<i>Gm5s</i>	2.870	3.51E-04	GDP-mannose 4, 6-dehydratase
NM_027985	<i>Mad2l2</i>	2.859	1.29E-04	MAD2 mitotic arrest deficient-like 2
NM_153507	<i>Cpne2</i>	2.853	7.68E-04	copine II
NM_008889	<i>Ppp1r14b</i>	2.851	7.45E-05	protein phosphatase 1, regulatory (inhibitor) subunit 14B
NM_013899	<i>Timm10</i>	2.830	8.49E-05	translocase of inner mitochondrial membrane 10
NM_013868	<i>Hspb7</i>	2.830	6.30E-04	heat shock protein family, member 7 (cardiovascular)
NM_010798	<i>Mif</i>	2.816	1.68E-04	macrophage migration inhibitory factor
NM_179203	<i>Atad3a</i>	2.813	9.66E-05	ATPase family, AAA domain containing 3A
NM_008102	<i>Gch1</i>	2.811	7.20E-04	GTP cyclohydrolase 1
NM_008037	<i>Fosl2</i>	2.810	2.86E-04	fos-like antigen 2
NM_026438	<i>Ppa1</i>	2.810	6.03E-04	pyrophosphatase (inorganic) 1
NM_175096	<i>Stbd1</i>	2.808	6.75E-04	starch binding domain 1
NM_007984	<i>Fscn1</i>	2.807	4.42E-04	fascin homolog 1, actin bundling protein (<i>Strongylocentrotus purpuratus</i>)
NM_011574	<i>Cirha1</i>	2.805	1.01E-04	cirrhosis, autosomal recessive 1A (human)
NM_009026	<i>Rasd1</i>	2.797	0.007411147	RAS, dexamethasone-induced 1
NM_145419	<i>Hkd1</i>	2.790	0.004679649	hexokinase domain containing 1

RefSeq Transcript ID	Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_001082976	Tc2n	2.787	0.006999408	tandem C2 domains, nuclear
NM_012048	Polk	2.784	0.00198089	polymerase (DNA directed), kappa
NM_008013	Fgl2	2.780	6.30E-04	fibrinogen-like protein 2
NM_025297	Mecr	2.778	2.39E-04	mitochondrial trans-2-enoyl-CoA reductase
NM_029005	Mkl1	2.771	9.06E-04	mixed lineage kinase domain-like
NM_178403	Pus7	2.768	0.001967898	pseudouridylyl synthase 7 homolog (S. cerevisiae)
NM_145987	Tmem82	2.766	1.63E-04	transmembrane protein 82
NM_175639	Wdr43	2.758	7.57E-05	WD repeat domain 43
NM_030244	Ier5l	2.755	0.00150021	immediate early response 5-like
NM_026578	Gar1	2.751	9.27E-05	GAR1 ribonucleoprotein homolog (yeast)
NM_011311	S100a4	2.751	1.89E-04	S100 calcium binding protein A4
NM_008690	Nfkbie	2.748	2.76E-04	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon
NM_175113	Trmt6	2.747	2.59E-04	tRNA methyltransferase 6
NM_030701	Niacr1	2.742	0.005598428	niacin receptor 1
NM_018754	Sfn	2.739	0.001169223	stratifin
NM_153570	Noc4l	2.738	1.40E-04	nucleolar complex associated 4 homolog (S. cerevisiae)
NM_001080940	Gm6484	2.736	1.68E-04	predicted gene 6484
NM_001042606	Sstr2	2.734	0.001277622	somatostatin receptor 2
NM_007484	Rhoc	2.727	1.16E-04	ras homolog gene family, member C
NM_001109748	Tomm40	2.725	0.001044687	translocase of outer mitochondrial membrane 40 homolog (yeast)
NM_001193309	Morc4	2.712	4.02E-04	microorchidia 4
NM_013562	Ifrd1	2.708	7.10E-04	interferon-related developmental regulator 1
NM_011580	Palad1	2.708	2.39E-04	phosphatase domain containing, paladin 1
NM_175270	Sowahb	2.706	8.64E-04	sonosdown ankryrin repeat domain family member B
NM_153566	Yrdc	2.704	2.39E-04	yrnC domain containing (E.coli)
NM_013594	Mbd1	2.702	1.68E-04	methyl-CpG binding domain protein 1
NM_028762	Rbm19	2.701	1.97E-04	RNA binding motif protein 19
NM_025897	Rrp8	2.698	0.001770565	ribosomal RNA processing 8, methyltransferase, homolog (yeast)
NM_007913	Egr1	2.693	0.003242609	early growth response 1
NM_001113368	Ceacam2	2.690	1.11E-04	carcinoembryonic antigen-related cell adhesion molecule 2
NM_030724	Uck2	2.687	2.71E-04	uridine-cytidine kinase 2
NM_015796	Fbxo17	2.681	2.19E-04	F-box protein 17
NM_008969	Ptgs1	2.681	8.18E-04	prostaglandin-endoperoxide synthase 1
NM_029546	Pwp2	2.676	3.51E-04	PWP2 periodic tryptophan protein homolog (yeast)
NM_133993	Pwp1	2.670	1.68E-04	PWP1 homolog (S. cerevisiae)
NM_001161329	Nol11	2.670	7.41E-04	nucleolar protein 11
NM_028925	Polr3c	2.660	1.09E-04	polymerase (RNA) III (DNA directed) polypeptide C
NM_013807	Plk3	2.652	2.59E-04	polo-like kinase 3
NM_001042534	Capg	2.639	0.001113707	capping protein (actin filament), gelsolin-like
NM_007991	Fbl	2.633	9.66E-05	fibrillarlin/rRNA 2'-O-methyltransferase fibrillarlin-like
NM_007788	Csnk2a1	2.632	0.00156432	casein kinase 2, alpha 1 polypeptide/casein kinase II subunit alpha-like
NM_019553	Dax21	2.628	4.46E-04	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
NM_013463	Gla	2.628	6.71E-04	galactosidase, alpha
NM_028404	Top1mt	2.628	3.91E-04	DNA topoisomerase 1, mitochondrial
NM_001024604	Ankrd28	2.627	2.76E-04	ankryrin repeat domain 28
NM_001008700	Il4ra	2.620	8.86E-04	interleukin 4 receptor, alpha
NM_007994	Fbp2	2.620	0.001792886	fructose bisphosphatase 2
NM_013671	Sod2	2.618	0.002407445	superoxide dismutase 2, mitochondrial
NM_001204979	Sars	2.615	2.39E-04	seryl-aminoacyl-tRNA synthetase
NM_025380	Eef1e1	2.611	2.50E-04	eukaryotic translation elongation factor 1 epsilon 1
NM_001025561	Pus1	2.611	7.96E-05	pseudouridine synthase 1
NM_001164107	Ripk3	2.598	7.24E-04	receptor-interacting serine-threonine kinase 3
NM_001164426	Kcnk13	2.595	8.66E-04	potassium channel, subfamily K, member 13
NM_011448	Sox9	2.591	2.56E-04	SRY-box containing gene 9
NM_026796	Smyd2	2.582	4.49E-04	SET and MYND domain containing 2
NM_009517	Zmat3	2.577	1.32E-04	zinc finger matrin type 3
NM_001161413	Slc3a2	2.576	1.69E-04	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
NM_026472	Mki67ip	2.575	1.88E-04	Mki67 (FHA domain) interacting nucleolar phosphoprotein
NM_010415	Hbegf	2.571	4.66E-04	heparin-binding EGF-like growth factor
NM_033073	Krt7	2.565	5.07E-04	keratin 7
NM_177388	Slc41a2	2.564	2.88E-04	solute carrier family 41, member 2
NM_133974	Cdcp1	2.555	6.29E-04	CUB domain containing protein 1
NM_010658	Mafb	2.554	2.02E-04	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)
NM_019511	Ramp3	2.540	0.002974334	receptor (calcitonin) activity modifying protein 3
NM_001252629	Smn1	2.535	0.003288299	survival motor neuron 1
NM_026993	Ddah1	2.535	0.001867556	dimethylarginine dimethylaminohydrolase 1
NM_007686	Cfi	2.534	0.00376992	complement component factor i
NM_001164472	Nip7	2.534	1.44E-04	nuclear import 7 homolog (S. cerevisiae)
NM_009848	Entpd1	2.532	0.001490762	ectonucleoside triphosphate diphosphohydrolase 1
NM_001111277	Eif2b3	2.530	0.001250645	eukaryotic translation initiation factor 2B, subunit 3
NM_001159593	Slc20a1	2.530	1.31E-04	solute carrier family 20, member 1
NM_008842	Pim1	2.527	7.13E-04	proviral integration site 1
NM_026545	Psmc8	2.523	0.001149367	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
NM_028315	Dis3	2.513	0.002015146	DIS3 mitotic control homolog (S. cerevisiae)
NM_172713	Sdad1	2.510	6.66E-04	SDA1 domain containing 1
NM_001024703	Mctp2	2.508	0.009495543	multiple C2 domains, transmembrane 2
NM_001081214	Pprc1	2.508	2.41E-04	peroxisome proliferative activated receptor, gamma, coactivator-related 1
NM_001039515	Arl4a	2.504	0.00135958	ADP-ribosylation factor-like 4A
NM_011345	Sele	2.502	6.01E-04	selectin, endothelial cell
NM_026268	Dusp6	2.497	6.14E-04	dual specificity phosphatase 6
NM_016966	Gm8096	2.496	0.002043013	3-phosphoglycerate dehydrogenase pseudogene/3-phosphoglycerate dehydrogenase
NM_198937	Hn1l	2.495	8.24E-04	hematological and neurological expressed 1-like
NM_001032727	Sybu	2.495	0.006600949	syntabulin (syntaxin-interacting)

RefSeq Transcript	IC Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_013789	<i>Sergef</i>	2.491	1.26E-04	secretion regulating guanine nucleotide exchange factor
NM_027460//XM_ <i>Slc25a33</i>		2.490	2.66E-04	solute carrier family 25, member 33
NM_025465	<i>Tma16</i>	2.488	0.001376601	translation machinery associated 16 homolog (S. cerevisiae)
NM_133787	<i>Nmd3</i>	2.488	2.76E-04	NMD3 homolog (S. cerevisiae)
NM_172930	<i>Tmem255a</i>	2.487	0.002438871	transmembrane protein 255A
NM_015816	<i>Lsm4</i>	2.487	1.96E-04	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)
NM_145632	<i>Polr2h</i>	2.486	2.76E-04	polymerase (RNA) II (DNA directed) polypeptide H
NM_025431//XM_ <i>Gm12952//Gm14535//Lph</i>		2.484	1.33E-04	predicted gene 12952//predicted pseudogene 14535//LLP homolog, long-term synaptic facilitation
NM_145706	<i>Nup43</i>	2.483	1.87E-04	nucleoporin 43
NM_016723//NM_ <i>Uchl3//Uchl4</i>		2.483	2.55E-04	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)//ubiquitin carboxyl-terminal esterase L4
NM_007426	<i>Angpt2</i>	2.482	9.08E-04	angiopoietin 2
NM_016776	<i>Mybbp1a</i>	2.482	2.26E-04	MYB binding protein (P160) 1a
NM_008873	<i>Plau</i>	2.482	0.001912931	plasminogen activator, urokinase
NM_026053//XM_ <i>Gemin6//Gm6253</i>		2.481	1.46E-04	gem (nuclear organelle) associated protein 6//predicted pseudogene 6253
NM_026464	<i>Wdr55</i>	2.479	1.01E-04	WD repeat domain 55
NM_027000	<i>Gtpbp4</i>	2.478	1.68E-04	GTP binding protein 4
NM_009373	<i>Tgm2</i>	2.477	1.67E-04	transglutaminase 2, C polypeptide
NM_145431	<i>Nle1</i>	2.470	8.65E-04	notchless homolog 1 (Drosophila)
NM_008654	<i>Ppp1r15a</i>	2.466	0.003629632	protein phosphatase 1, regulatory (inhibitor) subunit 15A
NM_001039824//N <i>Fdx1//Raver1-fdx1</i>		2.464	1.01E-04	ferredoxin 1-like//Raver1-Fdx1 readthrough
NM_013470	<i>Anxa3</i>	2.461	1.89E-04	annexin A3
NM_001025427//N <i>Hmga1//Hmga1-rs1</i>		2.461	0.006787071	high mobility group AT-hook 1//high mobility group AT-hook 1, related sequence 1
NM_016966//NR_C <i>Gm8096//Phgdh//Gm6756</i>		2.457	0.002244629	3-phosphoglycerate dehydrogenase pseudogene//3-phosphoglycerate dehydrogenase
NM_010786	<i>Mdm2</i>	2.452	2.64E-04	transformed mouse 3T3 cell double minute 2
NM_133662	<i>Ier3</i>	2.450	1.31E-04	immediate early response 3
NM_001039351//N <i>Nolc1</i>		2.447	6.49E-04	nucleolar and coiled-body phosphoprotein 1
NM_001002008	<i>Zfp948</i>	2.446	0.003603296	zinc finger protein 948
NM_010139	<i>Epha2</i>	2.445	0.005758154	Eph receptor A2
NM_010276	<i>Gem</i>	2.445	2.39E-04	GTP binding protein (gene overexpressed in skeletal muscle)
NM_021329	<i>Rangrf</i>	2.443	0.002084006	RAN guanine nucleotide release factor
NM_053247	<i>Lyve1</i>	2.439	0.003320745	lymphatic vessel endothelial hyaluronan receptor 1
NM_010431	<i>Hif1a</i>	2.434	5.32E-04	hypoxia inducible factor 1, alpha subunit
NM_033398	<i>Jmj6</i>	2.431	4.36E-04	jumonji domain containing 6
NM_144866	<i>Etf1</i>	2.430	2.94E-04	eukaryotic translation termination factor 1
NM_152817	<i>Ttc27</i>	2.425	8.16E-04	tetratricopeptide repeat domain 27
NM_173426	<i>Fam110b</i>	2.420	0.001575869	family with sequence similarity 110, member B
NM_009344	<i>Phld1</i>	2.419	8.02E-04	pleckstrin homology-like domain, family A, member 1
NM_001042556//N <i>Rpf2</i>		2.416	1.33E-04	ribosome production factor 2 homolog (S. cerevisiae)
NM_180678	<i>Gars</i>	2.414	1.37E-04	glycyl-tRNA synthetase
NM_009044	<i>Rel</i>	2.413	0.001769273	reticuloendotheliosis oncogene
NM_175158	<i>Utp20</i>	2.412	3.29E-04	UTP20, small subunit (SSU) processome component, homolog (yeast)
NM_009897	<i>Ckmt1</i>	2.412	0.002492751	creatine kinase, mitochondrial 1, ubiquitous
NM_001160012//N <i>Gjb3</i>		2.412	0.003248493	gap junction protein, beta 3
NM_177603	<i>Frat2</i>	2.410	4.98E-04	frequently rearranged in advanced T cell lymphomas 2
NM_029993	<i>Mlana</i>	2.409	6.27E-04	melan-A
NM_010324	<i>Got1</i>	2.409	0.004969221	glutamate oxaloacetate transaminase 1, soluble
NM_001190473//N <i>Dapk3</i>		2.408	0.001093517	death-associated protein kinase 3
NM_001141922//N <i>Bean1</i>		2.408	0.004566726	brain expressed, associated with Neddd4, 1
NM_178798	<i>Slc706</i>	2.406	0.001205589	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
NM_023536//XM_ <i>Gm5633//Gm9178//Mrto4</i>		2.406	2.29E-04	predicted gene 5633//predicted gene 9178//MRT4, mRNA turnover 4, homolog (S. cerevisiae)
NM_011192	<i>Psme3</i>	2.404	1.57E-04	proteasome (prosome, macropain) 28 subunit, 3
NM_010191	<i>Fdft1</i>	2.403	0.001553634	farnesyl diphosphate farnesyl transferase 1
NM_201362	<i>Ccdc68</i>	2.402	7.18E-04	coiled-coil domain containing 68
NM_023196//NM_ <i>Pla2g12a</i>		2.402	0.001445296	phospholipase A2, group X1A
NM_027532	<i>Anapc15</i>	2.401	1.87E-04	anaphase promoting complex C subunit 15
NM_001164627//N <i>Arhgap8</i>		2.400	0.00177771	Rho GTPase activating protein 8
NM_016859	<i>Bysl</i>	2.395	2.76E-04	bystin-like
NM_029083	<i>Ddit4</i>	2.393	0.001165501	DNA-damage-inducible transcript 4
NM_010186	<i>Fcgr1</i>	2.391	0.002794191	Fc receptor, IgG, high affinity I
NM_010158	<i>Khdrbs3</i>	2.389	0.001770565	KH domain containing, RNA binding, signal transduction associated 3
NM_153416	<i>Aaas</i>	2.382	6.77E-04	achalasia, adrenocortical insufficiency, alacrimia
NM_001012396//N <i>Ptpla</i>		2.377	8.66E-04	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a
NM_001039710//N <i>Coq10b</i>		2.376	6.37E-04	coenzyme Q10 homolog B (S. cerevisiae)
NM_001161515//N <i>Dctd</i>		2.376	0.003346541	dCMP deaminase
NM_019696	<i>Cpxm1</i>	2.371	0.009013065	carboxypeptidase X 1 (M14 family)
NM_028307	<i>Tdrkh</i>	2.371	8.18E-04	tudor and KH domain containing protein
NM_020049	<i>Slc6a14</i>	2.370	0.002365604	solute carrier family 6 (neurotransmitter transporter), member 14
NM_011222//NR_C <i>Pvt1</i>		2.370	5.17E-04	plasmacytoma variant translocation 1
NM_181470	<i>Ltv1</i>	2.369	4.10E-04	LTV1 homolog (S. cerevisiae)
NM_027250	<i>Selc1</i>	2.369	2.40E-04	Sel1 repeat containing 1
NM_001168250//N <i>Mtbp</i>		2.367	2.39E-04	Mdm2, transformed 3T3 cell double minute p53 binding protein
NM_178891//NR_C <i>Prrt6</i>		2.366	1.29E-04	protein arginine N-methyltransferase 6
NM_028749	<i>Npl</i>	2.363	0.005317851	N-acetylneuraminase pyruvate lyase
NM_027911//NR_C <i>Raver1//Raver1-fdx1//Fdx</i>		2.363	1.08E-04	ribonucleoprotein, PTB-binding 1//Raver1-Fdx1 readthrough//ferredoxin 1-like
NM_013845	<i>Ror1</i>	2.358	0.005102613	receptor tyrosine kinase-like orphan receptor 1
NM_028943	<i>Sgms2</i>	2.355	0.001844777	sphingomyelin synthase 2
NM_010880	<i>Ncl</i>	2.355	2.30E-04	nucleolin
NM_008857	<i>Prkci</i>	2.352	1.50E-04	protein kinase C, iota
NM_008152	<i>Gpr65</i>	2.352	0.001654325	G-protein coupled receptor 65
NM_010864	<i>Myo5a</i>	2.349	3.22E-04	myosin VA
NM_001013375	<i>Utp18</i>	2.348	2.24E-04	UTP18, small subunit (SSU) processome component, homolog (yeast)
NM_001164735//N <i>Crif2</i>		2.342	4.09E-04	cytokine receptor-like factor 2
NM_175016	<i>Alkbh2</i>	2.333	0.00158859	alkB, alkylation repair homolog 2 (E. coli)

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NM_001164370	<i>Mipol1</i>	2.333	6.75E-04	mirror-image polydactyly gene 1 homolog (human)
NM_026855	<i>Arv1</i>	2.327	0.001127156	ARV1 homolog (yeast)
NM_053080	<i>Aldh1a3</i>	2.327	5.61E-04	aldehyde dehydrogenase family 1, subfamily A3
NM_008311	<i>Htr2b</i>	2.326	0.001303626	5-hydroxytryptamine (serotonin) receptor 2B
NM_009743	<i>Bcl2l1</i>	2.325	0.001286065	BCL2-like 1
NM_001099217///N	<i>Ly6c1///Ly6c2</i>	2.320	2.76E-04	lymphocyte antigen 6 complex, locus C1///lymphocyte antigen 6 complex, locus C2
NM_181848	<i>Optn</i>	2.319	2.24E-04	optineurin
NM_145354	<i>Nsun2</i>	2.318	5.47E-04	NOL1/NOP2/Sun domain family member 2
NM_001033476///X	<i>Ahnak2///LOC101055828</i>	2.318	0.003263333	AHNAK nucleoprotein 2///protein AHNAK2-like
NM_001081224	<i>Prr16</i>	2.316	0.004164954	proline rich 16
NM_133990	<i>Il13ra1</i>	2.316	0.006537725	interleukin 13 receptor, alpha 1
NM_133807	<i>Lrrc59</i>	2.313	3.89E-04	leucine rich repeat containing 59
NR_037996	<i>Hmga2-ps1</i>	2.312	3.51E-04	high mobility group AT-hook 2, pseudogene 1
NM_010288	<i>Gja1</i>	2.311	0.001337127	gap junction protein, alpha 1
NM_007573	<i>C1qbp</i>	2.309	2.55E-04	complement component 1, q subcomponent binding protein
NM_028599	<i>Wdr75</i>	2.306	2.41E-04	WD repeat domain 75
NM_177613	<i>Cdc34</i>	2.300	0.001678436	cell division cycle 34
NM_133740	<i>Prmt3</i>	2.300	1.74E-04	protein arginine N-methyltransferase 3
NM_027198	<i>Zswim7</i>	2.299	8.94E-04	zinc finger SWIM-type containing 7
NM_001079847///N	<i>Gpr64</i>	2.298	0.002377753	G protein-coupled receptor 64
NM_025748	<i>Adat2</i>	2.291	3.71E-04	adenosine deaminase, tRNA-specific 2
NM_007544	<i>Bid</i>	2.288	2.76E-04	BH3 interacting domain death agonist
NM_007737	<i>Col5a2</i>	2.286	3.58E-04	collagen, type V, alpha 2
NM_021888	<i>Qtrt1</i>	2.286	8.11E-04	queuine tRNA-ribosyltransferase 1
NM_173014	<i>Lpcat2</i>	2.285	2.97E-04	lysophosphatidylcholine acyltransferase 2
NM_025462///NM	<i>Ece2</i>	2.285	1.74E-04	endothelin converting enzyme 2
NM_133753	<i>Errf1</i>	2.284	8.14E-04	ERBB receptor feedback inhibitor 1
NM_001168253///N	<i>Fam83h</i>	2.282	4.86E-04	family with sequence similarity 83, member H
NM_008704///XM	<i>Nme1///LOC100047753</i>	2.281	1.68E-04	NME/NM23 nucleoside diphosphate kinase 1///nucleoside diphosphate kinase A-like
NM_053015	<i>Mlph</i>	2.280	0.00380293	melanophilin
NM_001252316///N	<i>Shmt2</i>	2.274	8.16E-04	serine hydroxymethyltransferase 2 (mitochondrial)
NM_001082483	<i>Efr3b</i>	2.269	3.49E-04	EFR3 homolog B (<i>S. cerevisiae</i>)
NM_145585	<i>Thumpd1</i>	2.262	8.03E-04	THUMP domain containing 1
NM_021557	<i>Rdh11</i>	2.257	0.006202221	retinol dehydrogenase 11
NM_001252470///N	<i>Cpt1c</i>	2.257	0.005425115	carnitine palmitoyltransferase 1c
NM_025824	<i>Bzw1</i>	2.256	3.65E-04	basic leucine zipper and W2 domains 1
NM_001177371///N	<i>Dbn1</i>	2.254	9.52E-04	drebrin 1
NM_009011	<i>Rad23b</i>	2.254	1.68E-04	RAD23b homolog (<i>S. cerevisiae</i>)
NM_001100449	<i>Taf4b</i>	2.254	2.89E-04	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor
NM_026453	<i>Mak16</i>	2.252	1.68E-04	MAK16 homolog (<i>S. cerevisiae</i>)
NM_001172146///N	<i>Aimp2</i>	2.252	5.01E-04	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2
NM_019683	<i>Ankrd49</i>	2.250	0.008708203	ankyrin repeat domain 49
NM_001113529///N	<i>Csf1</i>	2.248	7.29E-04	colony stimulating factor 1 (macrophage)
NM_024193	<i>Nop56</i>	2.248	2.29E-04	NOP56 ribonucleoprotein
NM_181593	<i>Itpkc</i>	2.247	0.001413234	inositol 1,4,5-trisphosphate 3-kinase C
NM_008612	<i>Mnat1</i>	2.247	2.06E-04	menage a trois 1
NM_026114	<i>Eif2s1</i>	2.246	1.93E-04	eukaryotic translation initiation factor 2, subunit 1 alpha
NM_008608	<i>Mmp14</i>	2.242	0.001506803	matrix metalloproteinase 14 (membrane-inserted)
NM_145822	<i>Cd3eap</i>	2.242	3.82E-04	CD3E antigen, epsilon polypeptide associated protein
NM_001005767	<i>Parl</i>	2.242	3.34E-04	presenilin associated, rhomboid-like
NM_138747	<i>Nop2</i>	2.241	0.001083616	NOP2 nucleolar protein
NM_027106	<i>Avp11</i>	2.241	4.43E-04	arginine vasopressin-induced 1
NM_001111051///N	<i>Dclk1</i>	2.241	8.60E-04	doublecortin-like kinase 1
NM_025599///NM	<i>Cms5///Pgap2</i>	2.241	4.83E-04	cms small ribosomal subunit 1///post-GPI attachment to proteins 2
NM_001146708///N	<i>Fas</i>	2.238	0.003935241	Fas (TNF receptor superfamily member 6)
NM_130881///NM	<i>Pabpc4</i>	2.237	5.71E-04	poly(A) binding protein, cytoplasmic 4
NM_025281	<i>Lyar</i>	2.234	3.33E-04	Ly1 antibody reactive clone
NM_001001981///N	<i>Utp14b</i>	2.230	0.004545432	UTP14, U3 small nucleolar ribonucleoprotein, homolog B (yeast)
NM_025531	<i>Slmo2</i>	2.230	6.75E-04	slowmo homolog 2 (<i>Drosophila</i>)
NM_022889	<i>Pes1</i>	2.230	2.16E-04	pescadillo homolog 1, containing BRCT domain (<i>zebrafish</i>)
NM_026792	<i>Agpat5</i>	2.229	1.76E-04	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)
NM_001164561///N	<i>Exosc1</i>	2.229	0.00705132	exosome component 1
NM_011604	<i>Tlr6</i>	2.228	0.00230658	toll-like receptor 6
NM_001160149///N	<i>Cgref1</i>	2.227	0.004690172	cell growth regulator with EF hand domain 1
NM_146247	<i>Mettl22</i>	2.226	5.24E-04	methyltransferase like 22
NM_001159375///N	<i>Ejf4a1</i>	2.226	6.02E-04	eukaryotic translation initiation factor 4A1
NM_028453	<i>Otud3</i>	2.224	2.31E-04	OTU domain containing 3
NM_008723///NR	<i>C Npm3///Npm3-ps1</i>	2.223	0.001561041	nucleoplasmin 3///nucleoplasmin 3, pseudogene 1
NM_001113553///N	<i>Irak2</i>	2.223	0.001481983	interleukin-1 receptor-associated kinase 2
NM_016847	<i>Avpr1a</i>	2.223	0.003876133	arginine vasopressin receptor 1A
NM_013872	<i>Pmm1</i>	2.222	0.008187106	phosphomannomutase 1
NM_001008421	<i>Nol10</i>	2.220	2.39E-04	nucleolar protein 10
NM_001163481///N	<i>Fkbp10</i>	2.217	0.00232895	FK506 binding protein 10
NM_028276	<i>Utp14a</i>	2.216	4.24E-04	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
NM_007918	<i>Eif4ebp1</i>	2.211	2.76E-04	eukaryotic translation initiation factor 4E binding protein 1
NM_173376	<i>Rbmx2</i>	2.208	2.24E-04	RNA binding motif protein, X-linked 2
NM_001146211///N	<i>Mrps10</i>	2.207	3.71E-04	mitochondrial ribosomal protein S10
NM_001004150///N	<i>A4galt</i>	2.206	8.60E-04	alpha 1,4-galactosyltransferase
NM_001039934///N	<i>A730034C02///Map2</i>	2.203	4.16E-04	uncharacterized protein A730034C02///microtubule-associated protein 2
NM_001033306	<i>Shb</i>	2.198	0.001163322	src homology 2 domain-containing transforming protein B
NM_138599	<i>Tom70a</i>	2.197	3.71E-04	translocase of outer mitochondrial membrane 70 homolog A (yeast)
NM_001252476///N	<i>Prmt1</i>	2.196	2.39E-04	protein arginine N-methyltransferase 1
NM_010217	<i>Ctgf</i>	2.196	2.84E-04	connective tissue growth factor

RefSeq Transcript	IC Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_144886	Exosc2	2.196	2.89E-04	exosome component 2
NM_053191	Pi15	2.194	0.006341125	peptidase inhibitor 15
NM_025475	Haus2	2.188	0.004225463	HAUS augmin-like complex, subunit 2
NM_029891	Nkrf	2.188	3.49E-04	NF-kappaB repressing factor
NM_170592	Ntm1	2.188	4.30E-04	N-terminal Xaa-Pro-Lys N-methyltransferase 1
NM_026152	Hoga1	2.187	9.31E-04	4-hydroxy-2-oxoglutarate aldolase 1
NM_178069	Lsg1	2.186	6.03E-04	large subunit GTPase 1 homolog (S. cerevisiae)
NM_001081094	Znhit6	2.186	3.07E-04	zinc finger, HIT type 6
NM_008380	Inhba	2.185	8.04E-04	inhibin beta-A
NM_001177794///N Sertad4		2.184	0.003525739	SERTA domain containing 4
NM_026742	Ndujaf4	2.183	2.41E-04	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4
NM_001199271///N Slc19a1		2.182	0.002086022	solute carrier family 19 (folate transporter), member 1
NM_026040///XM_1 Srfbp1		2.181	2.80E-04	serum response factor binding protein 1
NM_145154	Angptl6	2.177	0.008775103	angiopoietin-like 6
NM_001277875///N Tpm2		2.176	0.004191475	tropomyosin 2, beta
NM_011561///NM_1 Tdg		2.176	1.58E-04	thymine DNA glycosylase pseudogene
NM_030704	Hspb8	2.174	7.47E-04	heat shock protein 8
NM_009554	Zfp37	2.174	0.006180156	zinc finger protein 37
NM_019428	Rpp30	2.171	4.09E-04	ribonuclease P/MRP 30 subunit
NM_008359	Il17ra	2.170	0.002864797	interleukin 17 receptor A
NM_175507	Slc35g1	2.170	8.41E-04	solute carrier family 35, member G1
NM_026247///NR_1 C Alg13		2.168	0.00123716	asparagine-linked glycosylation 13
NM_028261	Tmem173	2.168	3.31E-04	transmembrane protein 173
NM_027652	Ept1	2.167	1.70E-04	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)
NM_001166409///N Gm15453///Rbm3		2.167	6.90E-04	predicted gene 15453//RNA binding motif protein 3
NR_030708///NM_1 C 6820431F20Rik///2610005L07		2.167	0.001912931	cadherin 11 pseudogene
NM_001163511///N Spata5		2.167	3.17E-04	spermatogenesis associated 5
NM_001081047	Cnksr1	2.167	6.83E-04	connector enhancer of kinase suppressor of Ras 1
NM_009453///NM_1 Zrsr2		2.165	0.001769273	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2
NM_029278	Nop14	2.165	0.001321322	NOP14 nucleolar protein
NM_001163476///N Gins1		2.165	0.002920305	GINS complex subunit 1 (Psf1 homolog)
NM_001025444///N Aptx		2.163	0.001830343	aprataxin
NM_001033194	Gtf3c3	2.162	8.54E-04	general transcription factor IIIC, polypeptide 3
NM_170758	Cd300a	2.160	0.002323181	CD300A antigen
NM_153143	Kctd11	2.159	5.00E-04	potassium channel tetramerisation domain containing 11
NM_028108	Naa50	2.158	7.12E-04	N(alpha)-acetyltransferase 50, NatE catalytic subunit
NM_181590	Shq1	2.157	7.02E-04	SHQ1 homolog (S. cerevisiae)
NM_001272041///N Acta1		2.153	9.00E-04	actin, alpha 1, skeletal muscle
NM_008655	Gadd45b	2.151	0.004444553	growth arrest and DNA-damage-inducible 45 beta
NM_053085	Tcf23	2.149	0.003876133	transcription factor 23
NM_172437	Pus7l	2.148	9.62E-04	pseudouridylyl synthase 7 homolog (S. cerevisiae)-like
NM_144549	Trib1	2.146	5.74E-04	tribbles homolog 1 (Drosophila)
NM_001252593///N Cars		2.145	5.98E-04	cysteinyl-tRNA synthetase
NM_001163847///N Tbc1d24		2.143	0.004920226	TBC1 domain family, member 24
NM_001162924///N Pkp3		2.142	2.76E-04	plakophilin 3
NM_010807	Marcks1	2.142	8.04E-04	MARCKS-like 1
NM_001146012	R3hcc1	2.141	8.86E-04	R3H domain and coiled-coil containing 1
NM_144907	Sesn2	2.140	0.002740392	sestrin 2
NM_009687	Apex1	2.138	2.42E-04	apurinic/apyrimidinic endonuclease 1
NM_026932	Ebna1bp2	2.137	3.72E-04	EBNA1 binding protein 2
NM_001164201	Cers3	2.137	0.003887256	ceramide synthase 3
NM_007553	Bmp2	2.136	0.001321322	bone morphogenetic protein 2
NM_018736	Mre11a	2.134	2.81E-04	meiotic recombination 11 homolog A (S. cerevisiae)
NM_021303	Noc2l	2.131	4.44E-04	nucleolar complex associated 2 homolog (S. cerevisiae)
NM_001166376///N Ms406c		2.130	0.00733393	membrane-spanning 4-domains, subfamily A, member 6C
NM_025716	Spryd4	2.128	6.20E-04	SPRY domain containing 4
NM_001277305///N Adamts2		2.128	0.001334864	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2
NM_020493	Srf	2.127	6.29E-04	serum response factor
NM_001190717///N Dbf4		2.126	0.001491779	DBF4 homolog (S. cerevisiae)
NM_007413	Adora2b	2.124	0.005008493	adenosine A2b receptor
NM_001001297///N Thns1		2.121	0.003039222	threonine synthase-like 1 (bacterial)
NM_028870	Citb	2.120	3.58E-04	clathrin, light polypeptide (Lcb)
NM_025779	Ccdc109b	2.120	0.002864969	coiled-coil domain containing 109B
NM_028228	Pinx1	2.119	4.75E-04	PIN2/TERF1 interacting, telomerase inhibitor 1
NM_172704	Dnajc11	2.119	2.17E-04	Dnaj (Hsp40) homolog, subfamily C, member 11
NM_001042513///N Txnrd1		2.117	8.23E-04	thioredoxin reductase 1
NM_009298	Surf6	2.116	2.76E-04	surfeit gene 6
NM_021336	Snrpa1	2.116	2.53E-04	small nuclear ribonucleoprotein polypeptide A'
NM_001127177///N Ptpn2		2.116	8.96E-04	protein tyrosine phosphatase, non-receptor type 2
NM_145939	Alg3	2.115	0.001960379	asparagine-linked glycosylation 3 (alpha-1,3-mannosyltransferase)
NM_023048	Asb4	2.114	0.001480785	ankyrin repeat and SOCS box-containing 4
NM_026277	Nob1	2.113	9.38E-04	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)
NM_170593	Disp2	2.112	0.00517247	dispatched homolog 2 (Drosophila)
NM_175112	Rae1	2.111	0.001338532	RAE1 RNA export 1 homolog (S. pombe)
NM_011639	Trip6	2.111	0.001376601	thyroid hormone receptor interactor 6
NM_013745	Nufip1	2.109	4.03E-04	nuclear fragile X mental retardation protein interacting protein 1
NM_025782///NM_1 Ttc39b		2.108	0.001636828	tetratricopeptide repeat domain 39B
NM_011133	Pole2	2.106	0.001937505	polymerase (DNA directed), epsilon 2 (p59 subunit)
NM_001161844///N Cblc		2.105	0.001945286	Casitas B-lineage lymphoma c
NM_026856///XM_1 Gm8350///Zfp644		2.104	8.84E-04	predicted gene 8350//zinc finger protein 644
NM_134133	Smim3	2.100	0.002343752	small integral membrane protein 3
NM_133800	Nol12	2.098	6.96E-04	nucleolar protein 12
NM_001038607///N Kcnh1		2.096	1.96E-04	potassium voltage-gated channel, subfamily H (eag-related), member 1

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NM_008466	Kpna3	2.094	6.20E-04	karyopherin (importin) alpha 3
NM_025772	Dtnbp1	2.093	8.87E-04	dystrobrevin binding protein 1
NM_025846	Rras2	2.093	6.21E-04	related RAS viral (r-ras) oncogene homolog 2
NM_021315	Noc3l	2.092	4.78E-04	nucleolar complex associated 3 homolog (S. cerevisiae)
NM_009163	Sgpl1	2.090	6.04E-04	sphingosine phosphate lyase 1
NM_178918	Utp15	2.087	2.24E-04	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)
NM_026396	Brix1	2.085	2.94E-04	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)
NM_016767	Batf	2.082	3.69E-04	basic leucine zipper transcription factor, ATF-like
NM_013768	Prmt5	2.081	0.001264891	protein arginine N-methyltransferase 5
NM_001190461	Hilpda	2.081	0.001174438	hypoxia inducible lipid droplet associated
NM_026195	Atic	2.080	0.001822205	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
NM_145508	Dyrk3	2.080	0.001010932	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3
NM_173363	Ejf5	2.077	5.11E-04	eukaryotic translation initiation factor 5/eukaryotic translation initiation factor 5-like
NM_025546	Rsl1d1	2.075	0.002871729	ribosomal L1 domain containing 1
NM_001025388	Eno1	2.075	2.80E-04	enolase 1, alpha non-neuron/predicted gene 5506/alpha-enolase-like
NM_203319	Dhx37	2.075	0.002404555	DEAH (Asp-Glu-Ala-His) box polypeptide 37
NM_172480	Mtrr	2.075	4.05E-04	5-methyltetrahydrofolate-homocysteine methyltransferase reductase
NM_148933	Slco4a1	2.074	8.71E-04	solute carrier organic anion transporter family, member 4a1
NM_027204	Mrp12	2.072	5.97E-04	mitochondrial ribosomal protein L12
NM_009836	Cct3	2.070	3.77E-04	chaperonin containing Tcp1, subunit 3 (gamma)
NM_178668	Pde12	2.069	2.39E-04	phosphodiesterase 12
NM_009086	Polr1b	2.069	2.38E-04	polymerase (RNA) I polypeptide B
NM_026344	Dph2	2.068	0.001990845	DPH2 homolog (S. cerevisiae)
NM_026660	Mfsd10	2.067	9.11E-04	major facilitator superfamily domain containing 10
NM_028850	Chic2	2.065	8.05E-04	cysteine-rich hydrophobic domain 2/RIKEN cDNA B930098A02 gene
NM_028341	Ttc39c	2.065	4.26E-04	tetratricopeptide repeat domain 39C
NM_021322	Wdr4	2.064	7.15E-04	WD repeat domain 4
NM_033572	Wbscr16	2.063	6.71E-04	Williams-Beuren syndrome chromosome region 16 homolog (human)
NM_028444	Prkcdbp	2.063	0.002271578	protein kinase C, delta binding protein
NM_013692	Klf10	2.063	0.001216768	Kruppel-like factor 10
NM_145480	Rfc4	2.062	0.001859592	replication factor C (activator 1) 4
NM_001025388	Eno1	2.061	3.89E-04	enolase 1, alpha non-neuron/predicted gene 5506/alpha-enolase-like
NM_146215	Ftsj1	2.060	0.001356925	FtsJ methyltransferase domain containing 1
NM_029092	Trmt10c	2.060	0.002257306	tRNA methyltransferase 10C
NM_053074	Nup62	2.060	3.51E-04	nucleoporin 62
NM_001190786	Ddx19b	2.059	2.83E-04	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b/DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a
NM_183358	Gadd45gip1	2.058	0.001990845	growth arrest and DNA-damage-inducible, gamma interacting protein 1
NR_030711	Mir22hg	2.050	0.006537725	Mir22 host gene (non-protein coding)
NM_008255	Hmgcr	2.049	5.47E-04	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
NM_024250	L0C106740	2.048	0.001918135	uncharacterized LOC106740/PHD finger protein 10
NM_021297	Tlr4	2.047	0.001200894	toll-like receptor 4
NM_030250	Nus1	2.044	0.001378578	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)
NM_153126	Nat10	2.044	2.39E-04	N-acetyltransferase 10
NM_009698	Aprt	2.044	0.001085979	adenine phosphoribosyl transferase
NM_001104529	Gpr35	2.042	0.00448045	G protein-coupled receptor 35
NM_026637	Ggct	2.042	0.001043494	gamma-glutamyl cyclotransferase
NM_133757	Pgs1	2.039	6.77E-04	phosphatidylglycerophosphate synthase 1
NM_011499	Strap	2.038	4.41E-04	serine/threonine kinase receptor associated protein
NM_008044	Fxn	2.038	0.001191939	frataxin
NM_028607	Bloc1s2	2.038	0.001832486	biogenesis of lysosome-related organelles complex-1, subunit 2
NM_030720	Gpr84	2.037	0.006206421	G protein-coupled receptor 84
NM_001025570	Prrx1	2.033	0.002088393	paired related homeobox 1
NM_173363	Ejf5	2.032	6.46E-04	eukaryotic translation initiation factor 5/eukaryotic translation initiation factor 5-like
NM_001081682	Gnb1l	2.032	0.002255388	guanine nucleotide binding protein (G protein), beta polypeptide 1-like
NM_028115	Trub1	2.031	6.64E-04	TruB pseudouridine (psi) synthase homolog 1 (E. coli)
NM_009883	Cebpb	2.031	4.40E-04	CCAAT/enhancer binding protein (C/EBP), beta
NM_054056	Pawr	2.030	2.69E-04	PRKC, apoptosis, WT1, regulator
NM_033373	Krt23	2.029	5.32E-04	keratin 23
NM_007961	Etv6	2.029	0.001988984	ets variant gene 6 (TEL oncogene)
NM_011590	Timm17a	2.028	4.39E-04	translocase of inner mitochondrial membrane 17a
NM_023876	Elp4	2.027	7.19E-04	elongation protein 4 homolog (S. cerevisiae)
NM_028355	Tmem48	2.027	3.10E-04	transmembrane protein 48
NM_028292	Ppme1	2.027	9.62E-04	protein phosphatase methylesterase 1
NM_026538	Ddx56	2.025	4.42E-04	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56
NM_026295	Ctdp1	2.025	8.96E-04	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1
NM_009423	Traf4	2.023	0.006347864	TNF receptor associated factor 4
NM_009391	L0C100045999	2.023	2.76E-04	GTP-binding nuclear protein Ran-like/RAN, member RAS oncogene family
NM_025436	Sc4mol	2.022	0.001723029	sterol-C4-methyl oxidase-like
NM_028234	Rbm33	2.022	0.00600567	RNA binding motif protein 33
NM_001177776	Ahi1	2.022	9.22E-04	Abelson helper integration site 1
NM_053169	Trim16	2.020	0.001264761	tripartite motif-containing 16
NM_016966	Gm6756	2.019	0.007138217	3-phosphoglycerate dehydrogenase pseudogene/3-phosphoglycerate dehydrogenase
NM_198246	Yars2	2.018	6.74E-04	tyrosyl-tRNA synthetase 2 (mitochondrial)
NM_018757	Nme6	2.017	0.006537725	NME/NM23 nucleoside diphosphate kinase 6
NM_025927	Mrpl45	2.017	0.003269561	mitochondrial ribosomal protein L45
NM_001083341	Mboat2	2.016	5.51E-04	membrane bound O-acyltransferase domain containing 2
NM_146217	Aars	2.016	0.001055065	alanyl-tRNA synthetase/exosome component 6
NM_011486	Stat3	2.016	0.001055065	signal transducer and activator of transcription 3
NM_173757	Mrps27	2.016	0.002324157	mitochondrial ribosomal protein S27
NM_001253883	Pkm	2.016	0.002575949	pyruvate kinase, muscle
NM_026603	Denr	2.014	3.28E-04	density-regulated protein
NM_023203	Dctpp1	2.014	8.03E-04	dCTP pyrophosphatase 1
NM_025635	Zwint	2.012	0.002685749	ZW10 interactor

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NM_008909	<i>Ppl</i>	2.012	0.002519995	periplakin
NM_013678	<i>Surf2</i>	2.012	2.82E-04	surfeit gene 2
NM_144835	<i>Heatr1</i>	2.011	7.80E-04	HEAT repeat containing 1
NM_030713	<i>Zfp202</i>	2.011	0.001165849	zinc finger protein 202
NM_001130456///N	<i>Sema6b</i>	2.011	0.001931946	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B
NM_011239	<i>Ranbp1</i>	2.010	0.001513254	RAN binding protein 1
NM_028572	<i>Vgll3</i>	2.010	0.009275182	vestigial like 3 (Drosophila)
NM_134188///NM_	<i>Acot2///Acot1</i>	2.009	0.007231838	acyl-CoA thioesterase 2///acyl-CoA thioesterase 1
NM_024199	<i>Cstf1</i>	2.009	3.17E-04	cleavage stimulation factor, 3' pre-RNA, subunit 1
NM_008729	<i>Ctnd2</i>	2.005	8.93E-04	catenin (cadherin associated protein), delta 2
NM_001144855	<i>Ppfa4</i>	2.005	0.002456469	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4
NM_001159748///N	<i>Serpnb8</i>	2.005	0.0013881	serine (or cysteine) peptidase inhibitor, clade B, member 8
NM_172541	<i>Tmem120a</i>	2.005	0.007270044	transmembrane protein 120A
NM_010579	<i>Ejfb</i>	2.004	3.19E-04	eukaryotic translation initiation factor 6
NM_019715	<i>Kcmf1</i>	2.004	5.14E-04	potassium channel modulatory factor 1
NM_025317	<i>Mrpl54</i>	2.003	7.53E-04	mitochondrial ribosomal protein L54
NM_145575	<i>Cald1</i>	2.002	2.82E-04	caldesmon 1
NM_007617	<i>Cav3</i>	2.002	0.004482651	caveolin 3
NM_025942///NM_	<i>Ola1</i>	2.001	6.70E-04	Obg-like ATPase 1
NM_011119	<i>Pa2g4</i>	2.000	6.80E-04	proliferation-associated 2G4
NM_026851	<i>Mrpl52</i>	2.000	4.10E-04	mitochondrial ribosomal protein L52
NM_001010836	<i>Ppp1r13l</i>	1.998	4.98E-04	protein phosphatase 1, regulatory (inhibitor) subunit 13 like
NM_001013365	<i>Osm</i>	1.998	0.004345239	oncostatin M
NM_001243748///N	<i>Rassf1</i>	1.998	9.19E-04	Ras association (RalGDS/AF-6) domain family member 1
NM_028679	<i>Irak3</i>	1.994	0.001450804	interleukin-1 receptor-associated kinase 3
NM_010851	<i>Myd88</i>	1.994	0.001960379	myeloid differentiation primary response gene 88
NM_176933	<i>Dusp4</i>	1.991	9.36E-04	dual specificity phosphatase 4
NM_145144	<i>Aif1</i>	1.991	0.003178401	allograft inflammatory factor 1-like
NM_008186	<i>Gtf2h1</i>	1.990	7.13E-04	general transcription factor II H, polypeptide 1
NM_011278	<i>Rnf4</i>	1.989	5.39E-04	ring finger protein 4
NM_007609	<i>Casp4</i>	1.989	0.00201471	caspase 4, apoptosis-related cysteine peptidase
NM_011193	<i>Pstpip1</i>	1.987	0.004871914	proline-serine-threonine phosphatase-interacting protein 1
NM_198620	<i>Rundc3b</i>	1.984	0.003979686	RUN domain containing 3B
NM_025485	<i>Mrps22</i>	1.982	6.72E-04	mitochondrial ribosomal protein S22
NM_030116	<i>Mrpl9</i>	1.981	0.001655251	mitochondrial ribosomal protein L9
NM_144918	<i>Smyd5</i>	1.980	5.77E-04	SET and MYND domain containing 5
NM_028042	<i>Erc8</i>	1.980	5.78E-04	excision repair cross-complementing rodent repair deficiency, complementation group 8
NM_001013780	<i>Slc25a34</i>	1.975	0.001750939	solute carrier family 25, member 34
NM_010757	<i>Mafk</i>	1.975	0.003958511	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)
NM_080848	<i>Wdr5</i>	1.975	4.83E-04	WD repeat domain 5
NM_026500///NM_	<i>Ddx59</i>	1.974	0.002595066	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59
NM_001039157///N	<i>Ube2j2</i>	1.973	2.39E-04	ubiquitin-conjugating enzyme E2J 2
NM_025500	<i>Mrpl37</i>	1.973	0.003853279	mitochondrial ribosomal protein L37
NM_173400	<i>Haus6</i>	1.970	0.001089375	HAUS augmin-like complex, subunit 6
NM_027529	<i>6330409D20Rik</i>	1.969	7.33E-04	RIKEN cDNA 6330409D20 gene
NM_145742	<i>Dhx35</i>	1.967	0.004319004	DEAH (Asp-Glu-Ala-His) box polypeptide 35
NM_019425	<i>Gnpnat1</i>	1.967	0.001769273	glucosamine-phosphate N-acetyltransferase 1
NM_008681	<i>Ndrp1</i>	1.963	7.15E-04	N-myc downstream regulated gene 1
NM_009932	<i>Col4a2</i>	1.961	0.003584707	collagen, type IV, alpha 2
NM_152804	<i>Plk2</i>	1.960	3.69E-04	polo-like kinase 2
NM_001162921	<i>Zc3h12c</i>	1.959	0.003554222	zinc finger CCCH type containing 12C
NM_010907	<i>Nfkbia</i>	1.957	6.75E-04	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha
NM_015817	<i>Ppap2c</i>	1.955	7.47E-04	phosphatidic acid phosphatase type 2C
NM_001015889///N	<i>Gm12372///Taf9</i>	1.955	3.29E-04	predicted gene 12372///TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor
NM_001081212	<i>Irs2</i>	1.954	9.22E-04	insulin receptor substrate 2
NM_172814	<i>Lrp12</i>	1.951	0.0040227	low density lipoprotein-related protein 12
NM_007863	<i>Mpp3</i>	1.950	0.001605832	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)
NM_033074	<i>Tars</i>	1.949	5.39E-04	threonyl-tRNA synthetase
NM_026467	<i>Rps27l</i>	1.949	4.47E-04	ribosomal protein S27-like
NM_001080979///N	<i>Tead4</i>	1.947	0.001234603	TEA domain family member 4
NM_026894	<i>Tamm41</i>	1.946	5.01E-04	TAM41, mitochondrial translocator assembly and maintenance protein, homolog (S. cerevisiae)
NM_025301	<i>Mrpl17</i>	1.945	8.79E-04	mitochondrial ribosomal protein L17
NM_001025378///N	<i>Orc2</i>	1.945	2.75E-04	origin recognition complex, subunit 2
NM_001045550///N	<i>Mup1</i>	-49.478	0.008887862	major urinary protein 1
NM_009406	<i>Tnni3</i>	-26.589	6.44E-04	troponin I, cardiac 3
NM_009827	<i>Cckar</i>	-25.920	0.002935268	cholecystokinin A receptor
NM_025540	<i>Sln</i>	-23.507	4.56E-05	sarcoplipin
NM_001164171///N	<i>Myh6///Myh7</i>	-22.114	5.78E-05	myosin, heavy polypeptide 6, cardiac muscle, alpha///myosin, heavy polypeptide 7, cardiac muscle, beta
NM_001252591///N	<i>Smpx</i>	-18.659	4.36E-04	small muscle protein, X-linked
NM_023617	<i>Aox3</i>	-17.123	3.88E-05	aldehyde oxidase 3
NM_198415	<i>Ckmt2</i>	-14.757	5.92E-05	creatine kinase, mitochondrial 2
NM_010858	<i>Myl4</i>	-13.278	1.15E-04	myosin, light polypeptide 4
NM_001198841///N	<i>Csrp3</i>	-12.345	3.77E-04	cysteine and glycine-rich protein 3
NM_001110227	<i>Kcnj13</i>	-11.068	7.43E-05	potassium inwardly-rectifying channel, subfamily J, member 13
NM_007641	<i>Ms4a1</i>	-11.058	9.86E-05	membrane-spanning 4-domains, subfamily A, member 1
NM_001141927///N	<i>Pln</i>	-10.927	2.40E-04	phospholamban
NM_022879	<i>Myl7</i>	-10.627	5.77E-04	myosin, light polypeptide 7, regulatory
NM_001012324	<i>Ecm2</i>	-10.398	2.65E-04	extracellular matrix protein 2, female organ and adipocyte specific
NM_009944	<i>Cox7a1</i>	-10.248	6.20E-04	cytochrome c oxidase subunit VIIa 1
NM_023624	<i>Lrat</i>	-9.864	1.24E-04	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)
NM_174857	<i>Mamdc2</i>	-9.422	3.40E-05	MAM domain containing 2
NM_021503	<i>Myoz2</i>	-9.231	6.21E-04	myozenin 2
NM_011784	<i>Aplnr</i>	-9.087	6.52E-05	apelin receptor

RefSeq Transcript ID	Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_018732	<i>Scn3a</i>	-8.940	2.41E-04	sodium channel, voltage-gated, type III, alpha
NM_008182///NM_009608	<i>Gsta2///Gm3776///Gsta1</i>	-8.593	3.17E-04	glutathione S-transferase, alpha 2 (Yc2)///predicted gene 3776///glutathione S-transferase, alpha 1 (Ya)
NM_009608	<i>Actc1</i>	-8.281	9.61E-04	actin, alpha, cardiac muscle 1
NM_001164047///NM_009393	<i>Mb</i>	-8.243	2.89E-04	myoglobin
NM_026671	<i>Tnnc1</i>	-8.141	0.001404422	troponin C, cardiac/slow skeletal
NM_001130174///NM_011606	<i>Lypd2</i>	-7.862	0.004108078	Ly6/Plaur domain containing 2
NM_011606	<i>Tnnt2</i>	-7.854	4.69E-04	troponin T2, cardiac
NM_001002900///NM_145219	<i>Clec3b</i>	-7.853	0.002604679	C-type lectin domain family 3, member b
NM_145219	<i>Higd1c///Mettl7a1</i>	-7.625	3.40E-05	HIG1 domain family, member 1C///methyltransferase like 7A1
NM_152839	<i>Lgi3</i>	-7.406	4.26E-05	leucine-rich repeat LGI family, member 3
NM_025786	<i>Igj</i>	-7.308	0.005861272	immunoglobulin joining chain
NM_146017	<i>Rnf186</i>	-7.182	4.49E-04	ring finger protein 186
NM_001136059///NM_017394	<i>Gabbrp</i>	-7.137	0.004560471	gamma-aminobutyric acid (GABA) A receptor, pi
NM_017394	<i>Cyp11a1</i>	-7.079	0.004515543	cytochrome P450, family 1, subfamily a, polypeptide 1
NM_011540	<i>Slc7a10</i>	-7.041	4.79E-05	solute carrier family 7 (cationic amino acid transporter, y+ system), member 10
NM_020052	<i>Tcap</i>	-7.029	6.52E-05	titin-cap
NM_007621	<i>Scube2</i>	-6.790	4.16E-04	signal peptide, CUB domain, EGF-like 2
NM_008760	<i>Igk-V28</i>	-6.704	3.77E-04	immunoglobulin kappa chain variable 28 (V28)
NM_018778	<i>Cbr2</i>	-6.568	6.03E-04	carbonyl reductase 2
NM_029894	<i>Ogn</i>	-6.564	1.68E-04	osteoglycin
NM_001142952	<i>Cldn8</i>	-6.460	6.77E-04	claudin 8
NM_001166067	<i>Fam162b</i>	-6.435	3.29E-04	family with sequence similarity 162, member B
NM_001130513///NM_026831	<i>Fam46c</i>	-6.300	0.001941726	family with sequence similarity 46, member C
NM_026831	<i>Slc4a5</i>	-6.279	1.01E-04	solute carrier family 4, sodium bicarbonate cotransporter, member 5
NM_080462	<i>Ace2</i>	-6.254	1.58E-04	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
NM_011921	<i>Mybphl</i>	-6.170	5.25E-04	myosin binding protein H-like
NM_178118	<i>Hnmt</i>	-6.164	1.68E-04	histamine N-methyltransferase
NM_001081346///NM_019866	<i>Aldh1a7</i>	-6.160	0.001195612	aldehyde dehydrogenase family 1, subfamily A7
NM_019866	<i>Dixdc1</i>	-6.112	3.45E-04	DIX domain containing 1
NM_182839	<i>Rtkn2</i>	-6.110	0.001198963	rhotekin 2
NM_023868	<i>Spib</i>	-6.080	1.68E-04	Spi-B transcription factor (Spi-1/PU.1 related)
NM_008664	<i>Tppp</i>	-6.047	5.78E-05	tubulin polymerization promoting protein
NM_022983	<i>Ryr2</i>	-6.034	7.66E-04	ryanodine receptor 2, cardiac
NM_001025364///NM_032541	<i>Myom2</i>	-5.823	1.33E-04	myomesin 2
NM_032541	<i>Lpar3</i>	-5.817	4.40E-04	lysophosphatidic acid receptor 3
NM_178405	<i>Rtn2</i>	-5.767	0.001149089	reticulon 2 (Z-band associated protein)
NM_175347	<i>Hamp</i>	-5.696	0.001645654	hepcidin antimicrobial peptide
NM_001033350	<i>Atp1a2</i>	-5.586	2.82E-04	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide
NM_153529	<i>Srl</i>	-5.580	1.76E-04	sarcalumenin
NM_008829	<i>Bank1</i>	-5.575	1.58E-04	B cell scaffold protein with ankyrin repeats 1
NM_175692	<i>Nrn1</i>	-5.560	6.52E-05	neuritin 1
NM_177793	<i>Pgr</i>	-5.492	5.33E-04	progesterone receptor
NM_010406	<i>Snhg11</i>	-5.460	0.001019461	small nucleolar RNA host gene 11
NM_001008501	<i>Mettl24</i>	-5.422	8.00E-04	methyltransferase like 24
NM_010370	<i>Hc</i>	-5.408	7.11E-04	hemolytic complement
NM_009170	<i>Zfp760</i>	-5.401	1.82E-04	zinc finger protein 760
NM_021896	<i>Gzma</i>	-5.398	2.08E-04	granzyme A
NM_011136	<i>Shh</i>	-5.359	9.86E-05	sonic hedgehog
NM_080575	<i>Gucy1a3</i>	-5.337	0.001515375	guanylate cyclase 1, soluble, alpha 3
NM_007751	<i>Pou2af1</i>	-5.320	6.59E-04	POU domain, class 2, associating factor 1
NM_001045481///NM_010570	<i>Acss1</i>	-5.270	5.89E-04	acyl-CoA synthetase short-chain family member 1
NM_010570	<i>Cox8b</i>	-5.224	0.002212501	cytochrome c oxidase subunit VIIIb
NM_054077	<i>Gm16340///Ifi203///LOC1006</i>	-5.215	0.001340871	predicted gene 16340///interferon activated gene 203///uncharacterized LOC100862473
NM_011449	<i>Irs1</i>	-5.146	4.26E-05	insulin receptor substrate 1
NM_029620	<i>Prelp</i>	-5.143	1.91E-04	proline arginine-rich end leucine-rich repeat
NM_001003671///NM_010389	<i>Spa17</i>	-5.135	0.007006854	sperm autoantigenic protein 17
NM_010389	<i>Pcolce2</i>	-5.111	3.40E-05	procollagen C-endopeptidase enhancer 2
NM_009135	<i>Pcdha1</i>	-5.110	4.26E-05	protocadherin alpha 16
NM_001080814	<i>H2-Ob</i>	-4.917	2.82E-04	histocompatibility 2, O region beta locus
XM_001472541	<i>Scn7a</i>	-4.867	8.49E-05	sodium channel, voltage-gated, type VII, alpha
NM_001198914///NM_026976	<i>Fat3</i>	-4.823	1.14E-04	FAT tumor suppressor homolog 3 (Drosophila)
NM_026976	<i>Ighm</i>	-4.791	0.00373231	immunoglobulin heavy constant mu
NM_001081064	<i>Myb</i>	-4.757	0.009976391	myeloblastosis oncogene
NM_001042451///NM_026976	<i>Sema4f</i>	-4.746	3.35E-04	sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic domain
NM_026976	<i>Faim3</i>	-4.737	8.18E-04	Fas apoptotic inhibitory molecule 3
NM_001081064	<i>Pdzd2</i>	-4.718	1.96E-04	PDZ domain containing 2
NM_172471	<i>Snca</i>	-4.709	0.004845291	synuclein, alpha
NM_021718	<i>Itih5</i>	-4.703	0.005071465	inter-alpha (globulin) inhibitor H5
NM_001161665///NM_007735	<i>Ms4a4b</i>	-4.698	0.001128292	membrane-spanning 4-domains, subfamily A, member 4B
NM_007735	<i>Kif26b</i>	-4.677	0.001690585	kinesin family member 26B
NM_001081198	<i>Col4a4</i>	-4.639	1.15E-04	collagen, type IV, alpha 4
NM_001160096///NM_024263	<i>Tmem182</i>	-4.616	3.28E-04	transmembrane protein 182
NM_024263	<i>Cldn10</i>	-4.570	9.72E-04	claudin 10
NM_033268	<i>Mxra8</i>	-4.534	4.56E-04	matrix-remodelling associated 8
NM_008492	<i>Actn2</i>	-4.525	0.002720153	actinin alpha 2
NM_025817	<i>Ldhb</i>	-4.478	8.09E-04	lactate dehydrogenase B
NM_023821///NM_080846	<i>Tril</i>	-4.462	9.20E-05	TLR4 interactor with leucine-rich repeats
NM_080846	<i>Higd1b</i>	-4.442	3.36E-04	cardiomyopathy associated 5
NM_009425	<i>Tnfrsf10</i>	-4.418	0.001608569	HIG1 domain family, member 1B
NM_013691	<i>Thbs3</i>	-4.406	1.50E-04	tumor necrosis factor (ligand) superfamily, member 10
NM_011403	<i>Thbs3</i>	-4.374	7.57E-05	thrombospondin 3
NM_026481	<i>Slc4a1</i>	-4.310	9.34E-05	solute carrier family 4 (anion exchanger), member 1
	<i>Tppp3</i>	-4.253	0.005707828	tubulin polymerization-promoting protein family member 3

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NM_011652//NM_	Ttn	-4.248	0.001311058	titin
NM_008609	Mmp15	-4.236	0.002118693	matrix metalloproteinase 15
NM_001102446//N	Alas2	-4.221	0.008583684	aminolevulinic acid synthase 2, erythroid
NM_001243092//N	Gm3776//Gsta1//Gsta2	-4.195	6.95E-04	predicted gene 3776//glutathione S-transferase, alpha 1 (Ya)//glutathione S-transferase, alpha 2 (Yc2)
NM_001033217	Prickle1	-4.180	4.00E-04	prickle homolog 1 (Drosophila)
NM_012038	Vsnl1	-4.153	2.48E-04	visinin-like 1
NM_011125	Pltp	-4.145	4.30E-04	phospholipid transfer protein
NM_001170669//N	Pde8b	-4.111	9.20E-05	phosphodiesterase 8B
NM_001271708//N	Lrrn3	-4.098	1.86E-04	leucine rich repeat protein 3, neuronal
NM_198171	Ces2b	-4.067	6.96E-04	carboxylesterase 2B
NM_001252563//N	Matn4	-4.062	1.29E-04	matrilin 4
NM_146013	Sec14l4	-4.062	7.45E-05	SEC14-like 4 (S. cerevisiae)
NM_008339	Cd79b	-4.061	0.004846103	CD79B antigen
NM_027391	lyd	-4.057	9.07E-04	iodotyrosine deiodinase
NM_145463	Shisa2	-4.053	0.001055663	shisa homolog 2 (Xenopus laevis)
NM_153422	Pde5a	-3.999	7.43E-05	phosphodiesterase 5A, cGMP-specific
NM_009844	Cd19	-3.985	0.001578967	CD19 antigen
NM_015760	Nox4	-3.984	2.62E-04	NADPH oxidase 4
NM_011415	Snai2	-3.982	2.76E-04	snail homolog 2 (Drosophila)
NM_153574	Fam13a	-3.975	4.08E-04	family with sequence similarity 13, member A
NR_028264	Dleu2	-3.943	5.64E-04	deleted in lymphocytic leukemia, 2
NM_007551	Cxcr5	-3.938	8.42E-04	chemokine (C-X-C motif) receptor 5
NM_008086	Gas1	-3.920	7.27E-04	growth arrest specific 1
NM_153803	Glb1l2	-3.915	2.39E-04	galactosidase, beta 1-like 2
NM_011397	Slc23a1	-3.912	5.34E-04	solute carrier family 23 (nucleobase transporters), member 1
NM_001136062//N	Eno3	-3.895	2.93E-04	enolase 3, beta muscle
NM_172479	Slc38a5	-3.874	4.58E-04	solute carrier family 38, member 5
NM_010654	Klrtd1	-3.872	0.001412184	killer cell lectin-like receptor, subfamily D, member 1
NM_030203	Tsply4	-3.859	7.13E-05	TSPY-like 4
NM_175446	Zmat1	-3.855	0.001859716	zinc finger, matrin type 1
NM_001045481//N	Gm16340//Ifi203//LOC1006	-3.841	9.30E-04	predicted gene 16340//interferon activated gene 203//uncharacterized LOC100862473
NM_133485//NR_C	Ppp1r14c//Gm14057	-3.837	2.53E-04	protein phosphatase 1, regulatory (inhibitor) subunit 14c//Ppp1r14c pseudogene
NM_183312//NM_	Synn	-3.833	5.51E-04	synemin, intermediate filament protein
NM_176846	Exph5	-3.831	0.002179117	exophilin 5
NM_013930	Aass	-3.831	0.001355728	aminoadipate-semialdehyde synthase
NM_001043317//N	Cd22	-3.824	1.21E-04	CD22 antigen
NM_133969	Cyp4v3	-3.822	1.74E-04	cytochrome P450, family 4, subfamily v, polypeptide 3
NM_009749	Bex2	-3.816	0.001044687	brain expressed X-linked 2
NM_016854	Ppp1r3c	-3.789	1.39E-04	protein phosphatase 1, regulatory (inhibitor) subunit 3C
NM_175522	Elfn1	-3.764	3.03E-04	leucine rich repeat and fibronectin type III, extracellular 1
NM_177368	Tmtc2	-3.740	5.24E-04	transmembrane and tetratricopeptide repeat containing 2
NM_025877	Slc25a23	-3.738	0.001089407	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23
NM_181728	Art3	-3.720	1.16E-04	ADP-ribosyltransferase 3
NM_026512	Bphl	-3.708	0.005724517	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)
NM_175441	Mylk3	-3.689	1.68E-04	myosin light chain kinase 3
NM_197999	Ces2g	-3.687	0.00253697	carboxylesterase 2G
NM_001113283//N	Fam214a	-3.681	7.38E-05	family with sequence similarity 214, member A
	Igk2	-3.678	0.002983615	immunoglobulin lambda constant 2
NM_027468	Cpm	-3.646	2.41E-04	carboxypeptidase M
NM_028075	Tnfrsf13c	-3.633	2.17E-04	tumor necrosis factor receptor superfamily, member 13c
NM_001122733//N	Kit	-3.618	1.08E-04	kit oncogene
NM_178256	Reps2	-3.596	7.13E-05	RALBP1 associated Eps domain containing protein 2
NM_001099774	Krtap17-1	-3.583	8.04E-04	keratin associated protein 17-1
NM_001081756//N	Nckap5	-3.581	3.28E-04	NCK-associated protein 5
NM_010197	Fgf1	-3.570	7.43E-05	fibroblast growth factor 1
NM_009623	Adcy8	-3.569	0.009643979	adenylate cyclase 8
NM_001267796//N	6330403M23Rik//Pura	-3.560	5.90E-04	RIKEN cDNA 6330403M23 gene//purine rich element binding protein A
NM_001114385//N	Chrd1	-3.560	0.00155429	chordin-like 1
NM_009804	Cat	-3.541	1.29E-04	catalase
NM_011545	Tcf21	-3.532	9.66E-05	transcription factor 21
NM_001001309	Itga8	-3.529	3.70E-04	integrin alpha 8
NM_013653	Ccl5	-3.525	6.17E-04	chemokine (C-C motif) ligand 5
NM_134042	Aldh6a1	-3.521	7.13E-05	aldehyde dehydrogenase family 6, subfamily A1
NM_013794	Klra16	-3.508	7.15E-04	killer cell lectin-like receptor, subfamily A, member 16
NM_001164155//N	Tnfrsf19	-3.499	4.44E-04	tumor necrosis factor receptor superfamily, member 19
NM_080728//NM_	Myh7//Myh6	-3.499	5.00E-04	myosin, heavy polypeptide 7, cardiac muscle, beta//myosin, heavy polypeptide 6, cardiac muscle, alpha
NM_001252627//N	Cdh16	-3.498	3.22E-04	cadherin 16
NM_009676	Aox1	-3.478	3.94E-04	aldehyde oxidase 1
NM_175366	Mex3b	-3.478	0.001605832	mex3 homolog B (C. elegans)
NM_001024720	Hmcn1	-3.457	1.01E-04	hemicentin 1
NM_007934	Enpep	-3.455	8.83E-05	glutamyl aminopeptidase
NM_133994	Gstt3	-3.422	6.71E-04	glutathione S-transferase, theta 3
NM_138741	Sdpr	-3.421	2.64E-04	serum deprivation response
NM_011542	Tcea3	-3.413	0.004638682	transcription elongation factor A (SII), 3
NM_053200	Ces1d	-3.406	3.45E-04	carboxylesterase 1D
NM_008057	Fzd7	-3.383	7.96E-05	frizzled homolog 7 (Drosophila)
NM_026950	Oclad2	-3.377	7.96E-05	OCIA domain containing 2
NM_178214	Hist2h2be	-3.366	9.62E-05	histone cluster 2, H2be
NM_007664	Cdh2	-3.362	0.002797552	cadherin 2
NM_009378	Thbd	-3.360	1.29E-04	thrombomodulin
NM_001271599//N	Sort1	-3.360	2.41E-04	sortilin 1
NM_001014399//N	Abi3bp	-3.349	8.04E-05	ABI gene family, member 3 (NESH) binding protein
NM_011416//NM_	Smarca2	-3.347	2.41E-04	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2

RefSeq Transcript ID	Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_001029836	<i>Npnt</i>	-3.338	1.68E-04	nephronectin
NM_030018	<i>Tmem50b</i>	-3.273	6.57E-05	transmembrane protein 50B
NM_020259	<i>Hhip</i>	-3.270	4.80E-04	Hedgehog-interacting protein
NM_001253867	<i>Tmem205</i>	-3.266	5.01E-04	transmembrane protein 205
NM_001076791	<i>Zfp874b</i>	-3.258	2.76E-04	zinc finger protein 874b
NM_172907	<i>Olfml1</i>	-3.257	0.00241148	olfactomedin-like 1
NM_001159986	<i>Sec16b</i>	-3.256	6.66E-04	SEC16 homolog B (S. cerevisiae)
NM_177566	<i>Arhgef15</i>	-3.254	2.76E-04	Rho guanine nucleotide exchange factor (GEF) 15
NM_027222	<i>Mzb1</i>	-3.241	6.38E-04	marginal zone B and B1 cell-specific protein 1
NM_027629	<i>Pgm2l1</i>	-3.240	0.008711767	phosphoglucomutase 2-like 1
NM_178748	<i>Egflam</i>	-3.240	2.89E-04	EGF-like, fibronectin type III and laminin G domains
NM_029541	<i>Arxes1</i>	-3.238	0.002865075	adipocyte-related X-chromosome expressed sequence 1
NM_183183	<i>Gprin3</i>	-3.236	0.003020603	GPRIN family member 3
NM_001039039	<i>Kctd21</i>	-3.236	0.001620157	potassium channel tetramerisation domain containing 21
NM_172913	<i>Tox3</i>	-3.235	9.47E-04	TOX high mobility group box family member 3
NM_153100	<i>Rtp3</i>	-3.234	8.05E-04	receptor transporter protein 3
NM_017378	<i>Pcdh12</i>	-3.220	0.002212424	protocadherin 12
NM_011707	<i>Vtn</i>	-3.216	3.95E-04	vitronectin
NM_023665	<i>D4Wsu53e</i>	-3.204	0.004027749	DNA segment, Chr 4, Wayne State University 53, expressed
NM_001033301	<i>Fhdc1</i>	-3.195	3.29E-04	FH2 domain containing 1
NM_013486	<i>Cd2</i>	-3.187	0.001686255	CD2 antigen
NM_001145857	<i>Lrp4</i>	-3.175	1.82E-04	low density lipoprotein receptor-related protein 4
NM_001080707	<i>Gpr155</i>	-3.174	0.002033981	G protein-coupled receptor 155
NM_001163336	<i>Atp2a3</i>	-3.173	2.50E-04	ATPase, Ca++ transporting, ubiquitous
NM_008344	<i>Igf1bp6</i>	-3.167	8.66E-04	insulin-like growth factor binding protein 6
NM_016704	<i>C6</i>	-3.166	1.39E-04	complement component 6
NM_028235	<i>Ttc30b</i>	-3.157	0.004482193	tetratricopeptide repeat domain 30B
NM_172778	<i>Maob</i>	-3.149	5.78E-05	monoamine oxidase B
NM_001159850	<i>Kcnk2</i>	-3.146	4.49E-04	potassium channel, subfamily K, member 2
NM_009349	<i>Inmt</i>	-3.146	0.003108903	indoethylamine N-methyltransferase
NM_018870	<i>Pgam2</i>	-3.136	0.001578967	phosphoglycerate mutase 2
NM_153145	<i>Abca8a</i>	-3.135	0.005864564	ATP-binding cassette, sub-family A (ABC1), member 8a
NM_007758	<i>Cr2</i>	-3.124	0.001299643	complement receptor 2
NM_001081416	<i>Fndc1</i>	-3.121	0.007422347	fibronectin type III domain containing 1
NM_009421	<i>Traf1</i>	-3.116	1.88E-04	TNF receptor-associated factor 1
NM_001114174	<i>Fam189a2</i>	-3.113	0.001784032	family with sequence similarity 189, member A2
NM_175523	<i>Ppm1k</i>	-3.110	7.43E-05	protein phosphatase 1K (PP2C domain containing)
NM_001177503	<i>Plekhd1</i>	-3.107	0.001879665	pleckstrin homology domain containing, family D (with coiled-coil domains) member 1
NM_001163154	<i>Etv1</i>	-3.101	9.47E-04	ets variant gene 1/predicted gene 5454
NM_001252401	<i>Tie2</i>	-3.091	0.002039599	transducin-like enhancer of split 2, homolog of Drosophila E(spl)
NM_001159745	<i>St8sia4</i>	-3.083	5.59E-05	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 4
NM_001159632	<i>Atp6v1c2</i>	-3.081	1.74E-04	ATPase, H+ transporting, lysosomal V1 subunit C2
NM_054041	<i>Antxr1</i>	-3.077	1.58E-04	anthrax toxin receptor 1
NM_001145813	<i>Elf5</i>	-3.067	0.005771829	E74-like factor 5
NM_001161763	<i>Fmo5</i>	-3.066	2.80E-04	flavin containing monooxygenase 5
NM_011395	<i>Slc22a3</i>	-3.061	0.001657702	solute carrier family 22 (organic cation transporter), member 3
NM_001083906	<i>Nr3c2</i>	-3.051	2.41E-04	nuclear receptor subfamily 3, group C, member 2
NM_153594	<i>Pcmdt2</i>	-3.047	1.16E-04	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2
NM_013811	<i>Dnah8</i>	-3.042	0.001928523	dynein, axonemal, heavy chain 8
NM_001081567	<i>Mapk10</i>	-3.030	0.004139287	mitogen-activated protein kinase 10
NM_009789	<i>S100g</i>	-3.020	0.002522721	S100 calcium binding protein G
NM_001003914	<i>Obscn</i>	-3.019	0.003496041	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
NM_010621	<i>Stard9</i>	-3.016	2.98E-04	START domain containing 9
NM_007563	<i>Bpgm</i>	-3.000	0.002602705	2,3-bisphosphoglycerate mutase
NM_018734	<i>Gbp3</i>	-2.997	0.001597892	guanylate binding protein 3
NM_178874	<i>Tmcc2</i>	-2.991	7.51E-04	transmembrane and coiled-coil domains 2
NM_054103	<i>Stk33</i>	-2.983	0.006537725	serine/threonine kinase 33
NM_173788	<i>Npr2</i>	-2.972	3.82E-04	natriuretic peptide receptor 2
NM_007511	<i>Atp7b</i>	-2.966	0.00123706	ATPase, Cu++ transporting, beta polypeptide
NM_001083312	<i>Gbp7</i>	-2.966	3.29E-04	guanylate binding protein 7
NM_001277903	<i>Tnnt1</i>	-2.963	3.28E-04	troponin T1, skeletal, slow
NM_024264	<i>Cyp27a1</i>	-2.959	1.27E-04	cytochrome P450, family 27, subfamily a, polypeptide 1
NM_177775	<i>Esy3</i>	-2.941	6.59E-04	extended synaptotagmin-like protein 3
NM_001136061	<i>Ednrb</i>	-2.938	4.85E-04	endothelin receptor type B
NM_001161842	<i>Il18r1</i>	-2.937	0.001678562	interleukin 18 receptor 1
NM_010680	<i>Lama3</i>	-2.927	1.54E-04	laminin, alpha 3
NM_001033322	<i>Gucy1a2</i>	-2.925	9.89E-04	guanylate cyclase 1, soluble, alpha 2
NM_001110009	<i>Apoc1</i>	-2.919	0.005123673	apolipoprotein C-I
NM_001081154	<i>Marf1</i>	-2.901	0.004587661	meiosis arrest female 1
NM_007868	<i>Dmd</i>	-2.883	4.86E-04	dystrophin, muscular dystrophy
NM_134110	<i>Kcne2</i>	-2.879	0.005823636	potassium voltage-gated channel, Isk-related subfamily, gene 2
NM_172872	<i>Kank4</i>	-2.874	0.002877965	KN motif and ankyrin repeat domains 4
NM_174995	<i>Mgst2</i>	-2.872	0.004264744	microsomal glutathione S-transferase 2
NM_027626	<i>Psd3</i>	-2.867	3.16E-04	pleckstrin and Sec7 domain containing 3
NM_133660	<i>Ces1e</i>	-2.865	0.005288303	carboxylesterase 1E
NM_001034863	<i>Tmem136</i>	-2.859	7.05E-04	transmembrane protein 136
NM_001013370	<i>Sesn1</i>	-2.858	1.50E-04	sestrin 1
NM_139269	<i>Pla2g16</i>	-2.857	5.77E-04	phospholipase A2, group XVI
NM_019503	<i>Fxyd1</i>	-2.854	0.003178824	FXD domain-containing ion transport regulator 1
NM_013712	<i>Itgb1bp2</i>	-2.850	1.72E-04	integrin beta 1 binding protein 2
NM_001122756	<i>Corin</i>	-2.839	0.004162732	corin
NM_001109661	<i>Bach2</i>	-2.832	1.68E-04	BTB and CNC homology 2
NM_029398	<i>Tmem14a</i>	-2.827	0.004279444	transmembrane protein 14A

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NM_177756	<i>Colgalt2</i>	-2.827	0.001240698	collagen beta(1-O)galactosyltransferase 2
NM_001166493///N	<i>Rasgrp3</i>	-2.826	0.001890957	RAS, guanyl releasing protein 3
NM_001113323	<i>Glb1l3</i>	-2.821	0.001596298	galactosidase, beta 1 like 3
NM_001114339///N	<i>Pank1</i>	-2.802	0.006714245	pantothenate kinase 1
NM_016678	<i>Reck</i>	-2.802	6.20E-04	reversion-inducing-cysteine-rich protein with kazal motifs
NM_012050	<i>Omd</i>	-2.799	4.03E-04	osteomodulin
NM_178899	<i>Hepacam2</i>	-2.798	2.85E-04	HEPACAM family member 2
NM_001252458///N	<i>Prkd2</i>	-2.796	2.18E-04	protein kinase D2
NM_172543	<i>Fam117a</i>	-2.792	1.16E-04	family with sequence similarity 117, member A
NM_146126	<i>Sord</i>	-2.787	2.41E-04	sorbitol dehydrogenase
NM_010151	<i>Nr2f1</i>	-2.783	0.001378992	nuclear receptor subfamily 2, group F, member 1
NM_026793	<i>Myct1</i>	-2.779	2.77E-04	myc target 1
NM_029619	<i>Msrb2</i>	-2.779	0.002044925	methionine sulfoxide reductase B2
NM_013462	<i>Adrb3</i>	-2.774	1.68E-04	adrenergic receptor, beta 3
NM_146015	<i>Efemp1</i>	-2.768	0.009804216	epidermal growth factor-containing fibulin-like extracellular matrix protein 1
NM_028626	<i>Mcee</i>	-2.767	0.001501518	methylmalonyl CoA epimerase
NM_001159965///N	<i>Ralgps2</i>	-2.765	9.47E-04	Ral GEF with PH domain and SH3 binding motif 2
NM_026192	<i>Calcoco1</i>	-2.763	0.00145978	calcium binding and coiled coil domain 1
NM_029555	<i>Gstk1</i>	-2.763	0.001033408	glutathione S-transferase kappa 1
NM_007639	<i>Cd1d1</i>	-2.762	8.68E-04	CD1d1 antigen
NM_007710	<i>Ckm</i>	-2.761	0.002401592	creatine kinase, muscle
NM_153578	<i>Nipa1</i>	-2.760	2.80E-04	non imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)
NM_023653	<i>Wnt2</i>	-2.757	8.62E-04	wingless-related MMTV integration site 2
NM_001039071///N	<i>Ldb3</i>	-2.755	0.005516979	LIM domain binding 3
NM_001109988///N	<i>Nrep</i>	-2.746	4.62E-04	neuronal regeneration related protein
NM_175429	<i>Kctd12b</i>	-2.745	0.002274961	potassium channel tetramerisation domain containing 12b
NM_008520	<i>Ltbp3</i>	-2.741	0.001083616	latent transforming growth factor beta binding protein 3
NM_001113386///N	<i>Lifr</i>	-2.739	2.76E-04	leukemia inhibitory factor receptor
NM_008011	<i>Fgfr4</i>	-2.738	4.80E-04	fibroblast growth factor receptor 4
NM_001267846///N	<i>Fign</i>	-2.737	4.88E-04	fidgetin
NM_028306	<i>Hspa12b</i>	-2.736	8.72E-04	heat shock protein 12B
NM_023785	<i>Ppbp</i>	-2.734	0.009913875	pro-platelet basic protein
NM_182805	<i>Gpt</i>	-2.726	2.11E-04	glutamic pyruvic transaminase, soluble
NM_178767	<i>Agmo</i>	-2.721	0.001524561	alkylglycerol monooxygenase
NM_177157	<i>Gchfr</i>	-2.713	6.70E-04	GTP cyclohydrolase I feedback regulator
	<i>Iglc1///Iglv1</i>	-2.712	6.46E-04	immunoglobulin lambda constant 1///immunoglobulin lambda variable 1
NM_001039546///N	<i>Myo6</i>	-2.712	0.00123908	myosin VI
NM_019641	<i>Stmn1///Gm11223</i>	-2.711	0.002303129	stathmin 1///stathmin 1 pseudogene
NM_025807	<i>Slc16a9</i>	-2.710	3.41E-04	solute carrier family 16 (monocarboxylic acid transporters), member 9
NM_145220	<i>App12</i>	-2.707	2.24E-04	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2
NM_001253737///N	<i>Fcer2a</i>	-2.704	7.11E-04	Fc receptor, IgE, low affinity II, alpha polypeptide
NM_001170853///N	<i>Mndal</i>	-2.701	2.76E-04	myeloid nuclear differentiation antigen like
NM_001040085///N	<i>Sytl2</i>	-2.695	5.98E-04	synaptotagmin-like 2
NM_001081433	<i>Ankrd44</i>	-2.692	3.65E-04	ankyrin repeat domain 44
NM_133236	<i>Giccl1</i>	-2.692	9.86E-05	glucocorticoid induced transcript 1
NM_001081006///N	<i>Etl4</i>	-2.687	1.15E-04	enhancer trap locus 4
NM_031392	<i>Wdr6</i>	-2.686	7.10E-04	WD repeat domain 6
NM_011825	<i>Grem2</i>	-2.678	7.02E-04	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)
NM_001172481///N	<i>Aspn</i>	-2.677	0.002377753	asporin
NM_011923	<i>Angptl2</i>	-2.674	7.67E-04	angiopoietin-like 2
NM_145394	<i>Slc44a3</i>	-2.674	0.002086022	solute carrier family 44, member 3
NM_177699	<i>Fhod1</i>	-2.671	3.30E-04	formin homology 2 domain containing 1
NR_024097///NM_1	<i>Gm14057///Ppp1r14c</i>	-2.670	0.002221199	Ppp1r14c pseudogene///protein phosphatase 1, regulatory (inhibitor) subunit 14c
NM_007988	<i>Fasn</i>	-2.669	0.005758877	fatty acid synthase
NM_019684	<i>Srpk3</i>	-2.668	3.63E-04	serine/arginine-rich protein specific kinase 3
NM_009850	<i>Cd3g</i>	-2.668	0.001474285	CD3 antigen, gamma polypeptide
NM_029726	<i>Trdn</i>	-2.663	0.001836494	triadin
NM_001135172///N	<i>C1qtnf7</i>	-2.660	4.16E-04	C1q and tumor necrosis factor related protein 7
NM_199446	<i>Phkb</i>	-2.658	0.002986362	phosphorylase kinase beta
NM_025347///NM_	<i>Ypel3</i>	-2.657	2.71E-04	yippee-like 3 (Drosophila)
NM_019790	<i>Tmeff2</i>	-2.649	7.68E-04	transmembrane protein with EGF-like and two follistatin-like domains 2
NM_011129		4-Sep -2.649	2.24E-04	septin 4
NM_008306	<i>Ndst1</i>	-2.638	6.53E-04	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1
NM_001205085///N	<i>Tbx20</i>	-2.635	5.07E-04	T-box 20
NM_001037719///N	<i>Btla</i>	-2.633	0.006824015	B and T lymphocyte associated
NM_023051	<i>Clstn1</i>	-2.629	2.35E-04	calsyntenin 1
NM_010859	<i>My13</i>	-2.628	0.006537725	myosin, light polypeptide 3
NM_001145830///N	<i>Plcb1</i>	-2.625	1.01E-04	phospholipase C, beta 1
NM_001164785///N	<i>Adamts20</i>	-2.618	1.33E-04	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 20
NM_172588	<i>Serinc5</i>	-2.613	3.77E-04	serine incorporator 5
NM_007548	<i>Prdm1</i>	-2.613	0.005759039	PR domain containing 1, with ZNF domain
NM_007592	<i>Car8</i>	-2.606	2.65E-04	carbonic anhydrase 8
NR_003513	<i>Neat1</i>	-2.599	1.85E-04	nuclear paraspeckle assembly transcript 1 (non-protein coding)
NM_027526	<i>Rasgef1a</i>	-2.598	0.003177782	RasGEF domain family, member 1A
NM_001166553///N	<i>Rnf145</i>	-2.595	9.86E-05	ring finger protein 145
NM_170778	<i>Dpyd</i>	-2.592	0.00289723	dihydropyrimidine dehydrogenase
NM_009324	<i>Tbx2</i>	-2.587	4.89E-04	T-box 2
NM_144942	<i>Csad</i>	-2.580	1.04E-04	cysteine sulfinic acid decarboxylase
NM_001163155///N	<i>Col4a5</i>	-2.579	0.008702599	collagen, type IV, alpha 5
NM_010260	<i>Gbp2</i>	-2.579	9.06E-04	guanylate binding protein 2
NM_175260	<i>Myh10</i>	-2.578	1.46E-04	myosin, heavy polypeptide 10, non-muscle
NM_020559	<i>Alas1</i>	-2.574	2.83E-04	aminolevulinic acid synthase 1
NM_001190333///N	<i>Ccr6</i>	-2.574	6.06E-04	chemokine (C-C motif) receptor 6

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NM_008591	Met	-2.570	3.84E-04	met proto-oncogene
NM_178111	Trp53inp2	-2.567	0.00145598	transformation related protein 53 inducible nuclear protein 2
NM_001159543///N	Dpp4	-2.565	1.97E-04	dipeptidylpeptidase 4
NM_021452	Kcnmb4	-2.550	0.003208843	potassium large conductance calcium-activated channel, subfamily M, beta member 4
NM_011067	Per3	-2.546	0.004606443	period circadian clock 3
NM_026146	Eps8l1	-2.546	3.72E-04	EPS8-like 1
NM_001142335///N	Lmo2	-2.545	0.001560419	LIM domain only 2
NM_008287	Hrsp12	-2.544	0.003026003	heat-responsive protein 12
NM_001146690///N	Chpt1	-2.539	8.52E-04	choline phosphotransferase 1
NM_199018	Stard8	-2.538	2.76E-04	START domain containing 8
NM_001114879///N	D14Abb1e	-2.538	7.69E-04	DNA segment, Chr 14, Abbott 1 expressed
NM_001145959///N	Ndrq2	-2.538	3.64E-04	N-myc downstream regulated gene 2
NM_172463	Sned1	-2.535	4.86E-04	sushi, nidogen and EGF-like domains 1
NM_007914	Ehf	-2.532	9.08E-04	ets homologous factor
NM_001163533///N	Rtdr1	-2.529	0.00760186	rhabdoid tumor deletion region gene 1
NM_009219	Sstr4	-2.529	0.001546612	somatostatin receptor 4
NM_001163557///N	Ppfbp2	-2.528	5.91E-04	PTPRF interacting protein, binding protein 2 (liprin beta 2)
NM_001014288///N	Ptprd	-2.528	3.29E-04	protein tyrosine phosphatase, receptor type, D
NM_018826	Irx5	-2.527	0.001832486	Iroquois related homeobox 5 (Drosophila)
NM_019427	Epb4.114b	-2.527	7.93E-04	erythrocyte protein band 4.1-like 4b
NM_001029937	Sec14l3	-2.525	0.001187766	SEC14-like 3 (S. cerevisiae)
NM_153801	Tecrl	-2.525	0.002047945	trans-2,3-enoyl-CoA reductase-like
NM_001160215///N	Fcrla	-2.517	0.007491329	Fc receptor-like A
NM_001081977///N	Rnf144a	-2.514	4.58E-04	ring finger protein 144A
NM_007419	Adrb1	-2.510	0.005517647	adrenergic receptor, beta 1
NM_009955	Dpysl2	-2.509	9.34E-05	dihydropyrimidinase-like 2
NM_024253	Nkg7	-2.507	0.004040194	natural killer cell group 7 sequence
XM_977361	Tcrb-1///Trbv1	-2.505	0.009810162	T-cell receptor beta-2 chain C region-like
NM_177355	Plcx3	-2.504	9.36E-04	phosphatidylinositol-specific phospholipase C, X domain containing 3
NM_001039581///N	Abca3	-2.504	2.93E-04	ATP-binding cassette, sub-family A (ABC1), member 3
NM_178711	Plscr4	-2.500	4.20E-04	phospholipid scramblase 4
NM_175026	Pyhin1	-2.497	0.001149367	pyrin and HIN domain family, member 1
NM_001007220///N	Adam22	-2.494	4.34E-04	a disintegrin and metallopeptidase domain 22
NM_019759	Dpt	-2.493	0.006780631	dermatopontin
NM_001113527///N	Isg20	-2.493	2.17E-04	interferon-stimulated protein
NM_172145	Eva1b	-2.490	2.79E-04	eva-1 homolog B (C. elegans)
NM_009150	Selenbp1	-2.489	0.006994343	selenium binding protein 1
NM_021472///NM_	Rnase4	-2.489	1.29E-04	ribonuclease, RNase A family 4
NM_021345	Ptplad1	-2.487	2.76E-04	protein tyrosine phosphatase-like A domain containing 1
NM_010473	Hrc	-2.486	2.07E-04	histidine rich calcium binding protein
NM_011770	Ikarf2	-2.480	0.00507514	IKAROS family zinc finger 2
NM_021320	Ntn4	-2.479	3.33E-04	netrin 4
NM_009437	Tst	-2.479	0.007463692	thiosulfate sulfurtransferase, mitochondrial
NM_133746	Calhm2	-2.476	3.88E-04	calcium homeostasis modulator 2
NM_010207///NM_	Fgfr2	-2.475	3.77E-04	fibroblast growth factor receptor 2
NM_021355	Fmod	-2.473	0.001755369	fibromodulin
NM_020567	Gmn	-2.471	8.08E-04	geminin
NM_001252555///N	Gstz1	-2.470	0.002339523	glutathione transferase zeta 1 (maleylacetoacetate isomerase)
NM_013478	Azgp1	-2.469	0.009629243	alpha-2-glycoprotein 1, zinc
NM_144812///NM_	Tnrc6b	-2.468	1.31E-04	trinucleotide repeat containing 6b
NM_001195431///N	Islr	-2.468	0.006786901	immunoglobulin superfamily containing leucine-rich repeat
NM_023186	Chia	-2.459	5.32E-04	chitinase, acidic
NM_007981	Acs1l	-2.459	0.001377418	acyl-CoA synthetase long-chain family member 1
NM_013476	Ar	-2.458	9.25E-04	androgen receptor
NM_008259	Foxa1	-2.456	8.04E-04	forkhead box A1
NM_027823	Arhgap42	-2.455	0.00112995	Rho GTPase activating protein 42
NM_001145164///N	Tgtp1///Tgtp2	-2.453	0.005057073	T cell specific GTPase 1///T cell specific GTPase 2
NM_008417	Kcna2	-2.452	2.38E-04	potassium voltage-gated channel, shaker-related subfamily, member 2
NM_009006	Map4k2	-2.450	2.17E-04	mitogen-activated protein kinase kinase kinase kinase 2
NM_153170	Slc36a2	-2.449	0.003370586	solute carrier family 36 (proton/amino acid symporter), member 2
NM_023873	Cep70	-2.444	1.96E-04	centrosomal protein 70
NM_023134	Sftpa1	-2.443	0.008285309	surfactant associated protein A1
NM_001013013	Dhrs7c	-2.442	0.004752389	dehydrogenase/reductase (SDR family) member 7C
NM_029077	Trim14	-2.440	0.002520105	tripartite motif-containing 14
NM_007642	Cd28	-2.440	5.52E-04	CD28 antigen
NM_001037723///N	Adcy7	-2.437	8.03E-04	adenylate cyclase 7
NM_173749	Pamr1	-2.436	0.003285761	peptidase domain containing associated with muscle regeneration 1
NM_027265///NM_	Il17rd	-2.434	2.40E-04	interleukin 17 receptor D
NM_026346	Fbxo32	-2.433	3.71E-04	F-box protein 32
NM_146008	Tcp112	-2.431	9.10E-04	t-complex 11 (mouse) like 2
NM_001083895///N	Srpax2	-2.429	7.66E-04	sushi-repeat-containing protein, X-linked 2
NM_138956	Rassf3	-2.426	0.00198089	Ras association (RalGDS/AF-6) domain family member 3
NM_019811	Acss2	-2.426	0.001378992	acyl-CoA synthetase short-chain family member 2
NM_145382	Fam193b	-2.426	0.001806099	family with sequence similarity 193, member B
NM_201361	Rmdn2	-2.424	0.001158827	regulator of microtubule dynamics 2
NM_001252105///N	Cadps2	-2.420	0.001066288	Ca2+-dependent activator protein for secretion 2
NM_009275///NM_	Srprb///Trf	-2.420	0.002179589	signal recognition particle receptor, B subunit///transferrin
NM_019588	Plce1	-2.419	9.16E-04	phospholipase C, epsilon 1
NM_023184	Klf15	-2.416	0.001443687	Kruppel-like factor 15
NM_013605	Muc1	-2.414	0.003351672	mucin 1, transmembrane
NM_007671	Cdkn2c	-2.412	5.00E-04	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
NM_008989///NM_	Pura///6330403M23Rik	-2.411	5.58E-04	purine rich element binding protein A///RIKEN cDNA 6330403M23 gene
NM_026178	Mmd	-2.402	9.04E-04	monocyte to macrophage differentiation-associated

RefSeq Transcript ID Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_001165939//N Tshb	-2.397	0.005496437	thyroid stimulating hormone, beta subunit
NM_011077 Phex	-2.397	0.003288299	phosphate regulating gene with homologies to endopeptidases on the X chromosome
NM_139144 Ogt	-2.395	1.45E-04	O-linked N-acetylglucosamine (GlcNAc) transferase
NM_172435 P2ry10	-2.394	0.006720671	purinergic receptor P2Y, G-protein coupled 10
NM_009236 Sox18	-2.392	0.008887862	SRY-box containing gene 18
NM_172448 Rnf43	-2.390	0.008478482	ring finger protein 43
NM_080793 Setd7	-2.389	2.02E-04	SET domain containing (lysine methyltransferase) 7
NM_009911 Cxcr4	-2.387	6.75E-04	chemokine (C-X-C motif) receptor 4
NM_001098233//N Purg	-2.385	6.50E-04	purine-rich element binding protein G
NM_138313 Bmf	-2.382	0.001723029	BCL2 modifying factor
NM_001085415//N Zfp467	-2.382	0.001999964	zinc finger protein 467
NM_144847 Nrbp2	-2.378	4.16E-04	nuclear receptor binding protein 2
NM_029999 Lbh	-2.377	0.005640974	limb-bud and heart
NM_010358 Gstm1	-2.375	0.00198089	glutathione S-transferase, mu 1
NM_001013786 Zscan26	-2.375	0.001093711	zinc finger and SCAN domain containing 26
NM_008916 Inpp5k	-2.375	8.09E-04	inositol polyphosphate 5-phosphatase K
NM_001162492//N Mpst	-2.374	0.006537725	mercaptopyruvate sulfurtransferase
NM_011465 Spta1	-2.371	0.002919029	spectrin alpha, erythrocytic 1
NM_145376 Lpcat1	-2.369	0.001171902	lysophosphatidylcholine acyltransferase 1
NM_178600 Vkorc1	-2.365	0.005917811	vitamin K epoxide reductase complex, subunit 1
NM_177687 Crebl2	-2.363	1.58E-04	cAMP responsive element binding protein-like 2
NM_010923//NM_ Nnat	-2.363	0.003284936	neuronatin
NM_177733//NM_ E2f2	-2.359	3.62E-04	E2F transcription factor 2
NM_007549 Blk	-2.359	4.68E-04	B lymphoid kinase
NM_181595 Ppp1r9a	-2.359	1.52E-04	protein phosphatase 1, regulatory (inhibitor) subunit 9A
NM_133245 Ahsp	-2.355	6.80E-04	alpha hemoglobin stabilizing protein
NM_080555 Ppap2b	-2.354	3.77E-04	phosphatidic acid phosphatase type 2B
NM_011204 Ptpn13	-2.352	4.56E-04	protein tyrosine phosphatase, non-receptor type 13
NM_173378 Trp53bp2	-2.351	1.69E-04	transformation related protein 53 binding protein 2
NM_172397//XM_ Limd2//LOC632329	-2.350	2.40E-04	LIM domain containing 2//LIM domain-containing protein 2-like
NM_026516 Tmem178	-2.349	0.002713842	transmembrane protein 178
NM_007998 Fech	-2.347	0.001239535	ferrochelatase
NM_029057 Tbc1d30	-2.345	9.41E-04	TBC1 domain family, member 30
NM_030697 Kank3	-2.345	4.20E-04	KN motif and ankyrin repeat domains 3
NM_001014996 Cenpj	-2.344	0.005575034	centromere protein J
NM_010656 Sspn	-2.340	0.004020363	sarcospan
NM_134054 Sptssa	-2.339	4.48E-04	serine palmitoyltransferase, small subunit A
NM_023245 Palmd	-2.329	3.05E-04	palmdelphin
NM_144550 Spice1	-2.328	0.005060671	spindle and centriole associated protein 1
NM_001083810//N Prr5l	-2.326	3.28E-04	proline rich 5 like
NM_001040398//N Setd1b	-2.326	1.74E-04	SET domain containing 1B
NM_153781 Pygb	-2.324	0.005139725	brain glycogen phosphorylase
NM_001033198//N Ankrd50	-2.323	3.90E-04	ankyrin repeat domain 50
NM_028995 Nipal3	-2.322	5.53E-04	NIPA-like domain containing 3
NM_146236 Tceal1	-2.315	2.59E-04	transcription elongation factor A (SII)-like 1
NM_133738 Antxr2	-2.315	1.89E-04	anthrax toxin receptor 2
NM_001253822//N Irx3	-2.312	6.71E-04	Iroquois related homeobox 3 (Drosophila)
NM_001039056//N Kcnj15	-2.311	2.28E-04	potassium inwardly-rectifying channel, subfamily J, member 15
NM_007655 Cd79a	-2.311	3.72E-04	CD79A antigen (immunoglobulin-associated alpha)
NM_029436 Klhl24	-2.310	0.006731548	kelch-like 24
XM_977361 LOC665506//Tcrb-J//Trbv1	-2.309	0.008020304	T-cell receptor beta-2 chain C region-like
NM_001162532 Fam174b	-2.309	2.91E-04	family with sequence similarity 174, member B
NM_008212 Hadh	-2.309	4.78E-04	hydroxyacyl-Coenzyme A dehydrogenase
NM_008059 G0s2	-2.305	5.68E-04	G0/G1 switch gene 2
NM_027445 Rnf167	-2.301	0.001269958	ring finger protein 167
NM_013881 Ulk2	-2.296	3.71E-04	unc-51 like kinase 2
NM_001005510 Syne2	-2.295	3.05E-04	spectrin repeat containing, nuclear envelope 2
NM_001166213 Fam129c	-2.295	0.006339997	family with sequence similarity 129, member C
NM_001005863//N Mtus1	-2.294	4.62E-04	mitochondrial tumor suppressor 1
NM_025331 Gng11	-2.293	6.17E-04	guanine nucleotide binding protein (G protein), gamma 11
NM_010062 Dnase2a	-2.293	0.001349824	deoxyribonuclease II alpha
NM_016712 Tmod4	-2.293	8.78E-04	tropomodulin 4
NM_007678 Cebpa	-2.289	4.56E-04	CCAAT/enhancer binding protein (C/EBP), alpha
NM_008207 H2-T24	-2.287	0.004685006	histocompatibility 2, T region locus 24
NM_028765 Acox1	-2.284	0.001450804	acyl-Coenzyme A oxidase-like
NM_001271676//N Ifi47	-2.284	0.001810734	interferon gamma inducible protein 47
NM_007620 Cbr1	-2.280	4.56E-04	carbonyl reductase 1
NM_001177881//N Mfap3l	-2.279	0.008403818	microfibrillar-associated protein 3-like
NM_183116 Slc18b1	-2.279	0.003301159	solute carrier family 18, subfamily B, member 1
NM_009210//NM_ Hltf	-2.276	2.48E-04	helicase-like transcription factor
NM_172656//NM_ Stradb	-2.276	4.34E-04	STE20-related kinase adaptor beta
NM_175480 Zfp612	-2.275	0.006179562	zinc finger protein 612
NM_008695 Nid2	-2.275	0.003006224	nidogen 2
NM_028763 Cbx6	-2.274	0.003162149	chromobox 6
NM_007719 Ccr7	-2.273	0.002015146	chemokine (C-C motif) receptor 7
NM_178929 Kazal1	-2.272	0.004742138	Kazal-type serine peptidase inhibitor domain 1
NM_153403 Ago1	-2.271	0.00176573	argonaute RISC catalytic subunit 1
NM_001168620//N Enpp5	-2.261	8.38E-04	ectonucleotide pyrophosphatase/phosphodiesterase 5
NM_019826 Ivd	-2.260	0.002125425	isovaleryl coenzyme A dehydrogenase
NM_008278 Hpgd	-2.260	0.001160332	hydroxyprostaglandin dehydrogenase 15 (NAD)
NM_001146119//N Fam49a	-2.259	7.06E-04	family with sequence similarity 49, member A
NM_001163522//N Emcn	-2.254	0.001908361	endomucin
NM_181418 Ushbp1	-2.253	4.44E-04	Usher syndrome 1C binding protein 1

RefSeq Transcript	IC Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_023794	<i>Etv5</i>	-2.252	0.004515543	ets variant gene 5
NM_025951//NM_024288	<i>Pi4k2b</i>	-2.249	0.002800664	phosphatidylinositol 4-kinase type 2 beta
NM_024288	<i>Rmnd5a</i>	-2.249	3.72E-04	required for meiotic nuclear division 5 homolog A (S. cerevisiae)
NM_145562	<i>Parm1</i>	-2.248	0.002038784	prostate androgen-regulated mucin-like protein 1
NM_001141933//NM_025370	<i>Nkain4</i>	-2.248	0.006591699	Na ⁺ /K ⁺ transporting ATPase interacting 4
NM_025370	<i>Aaed1</i>	-2.246	6.77E-04	AhpC/TSA antioxidant enzyme domain containing 1
NM_001001980//NM_001162941//NM_001167983//NM_019394	<i>Limch1</i>	-2.246	3.10E-04	LIM and calponin homology domains 1
NM_001162941//NM_001167983//NM_019394	<i>Mapre2</i>	-2.241	0.001794255	microtubule-associated protein, RP/EB family, member 2
NM_001167983//NM_019394	<i>Sipa11</i>	-2.236	1.71E-04	signal-induced proliferation-associated 1 like 1
NM_019394	<i>Mia</i>	-2.235	0.002287676	melanoma inhibitory activity
NM_011074	<i>Cdk14</i>	-2.233	2.85E-04	cyclin-dependent kinase 14
NM_025359	<i>Tspan13</i>	-2.232	3.90E-04	tetraspanin 13
NM_001111320//NM_001253885//NM_199025	<i>Idh1</i>	-2.232	0.001344785	isocitrate dehydrogenase 1 (NADP ⁺), soluble
NM_001253885//NM_199025	<i>Appb1</i>	-2.231	0.002829249	amyloid beta (A4) precursor protein-binding, family B, member 1
NM_199025	<i>Zbtb26</i>	-2.231	0.001782064	zinc finger and BTB domain containing 26
NM_029938	<i>H2afv</i>	-2.231	2.76E-04	H2A histone family, member V
NM_181394	<i>Anapc13</i>	-2.230	3.62E-04	anaphase promoting complex subunit 13
NM_007556	<i>Bmp6</i>	-2.227	0.006732636	bone morphogenetic protein 6
NM_011663	<i>Zrsr1</i>	-2.224	9.32E-04	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1
NM_007734	<i>Col4a3</i>	-2.216	6.01E-04	collagen, type IV, alpha 3
NM_001005341	<i>Ypel2</i>	-2.215	7.44E-04	yippe-like 2 (Drosophila)
NM_001168304//NM_029522	<i>Cdk19</i>	-2.215	0.001378992	cyclin-dependent kinase 19
NM_029522	<i>Gpsm2</i>	-2.212	0.006340119	G-protein signalling modulator 2 (AGS3-like, C. elegans)
NM_001199136//NM_001007596//NM_001114098//NM_001077696//NM_001025600//NM_027506//NM_009027	<i>Macf1</i>	-2.210	0.002325118	microtubule-actin crosslinking factor 1
NM_001007596//NM_001114098//NM_001077696//NM_001025600//NM_027506//NM_009027	<i>Rasgrf2</i>	-2.208	0.00232895	RAS protein-specific guanine nucleotide-releasing factor 2
NM_001170537//NM_008385	<i>Mef2c</i>	-2.207	3.57E-04	myocyte enhancer factor 2C
NM_008385	<i>Inpp5b</i>	-2.200	6.98E-04	inositol polyphosphate-5-phosphatase B
NM_001277265//NM_001038609//NM_173368	<i>Tbxa2r</i>	-2.199	0.001022452	thromboxane A2 receptor
NM_001038609//NM_173368	<i>Mapt</i>	-2.199	2.76E-04	microtubule-associated protein tau
NM_173368	<i>Chd6</i>	-2.194	0.001402105	chromodomain helicase DNA binding protein 6
NM_010019	<i>Dapk2</i>	-2.193	3.72E-04	death-associated protein kinase 2
NM_001097621	<i>Kif26a</i>	-2.193	0.002006382	kinesin family member 26A
NM_013657	<i>Sema3c</i>	-2.193	3.82E-04	sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C
NM_001167997//NM_008409	<i>Tex11</i>	-2.191	0.006537725	testis expressed gene 11
NM_008409	<i>Itm2a</i>	-2.190	9.07E-04	integral membrane protein 2A
NM_138628	<i>Txlnb</i>	-2.189	0.004548972	taxilin beta
NM_007763	<i>Crip1</i>	-2.189	3.05E-04	cysteine-rich protein 1 (intestinal)
NM_001033228	<i>Itga1</i>	-2.188	3.45E-04	integrin alpha 1
NM_001025576	<i>Ccdc141</i>	-2.187	3.42E-04	coiled-coil domain containing 141
NM_001033240//NM_175324	<i>Wjfd6a</i>	-2.183	0.003178824	WAP four-disulfide core domain 6A
NM_175324	<i>Acad11</i>	-2.182	0.005749376	acyl-Coenzyme A dehydrogenase family, member 11
NR_015456	<i>D7Ert715e</i>	-2.181	5.53E-04	DNA segment, Chr 7, ERATO Doi 715, expressed
NM_008506	<i>Mycl1</i>	-2.180	0.001349824	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)
NM_015775	<i>Tmprss2</i>	-2.175	0.003464903	transmembrane protease, serine 2
NM_007554	<i>Bmp4</i>	-2.175	8.38E-04	bone morphogenetic protein 4
NM_001042752//NM_011436	<i>Neo1</i>	-2.168	6.77E-04	neogenin
NM_011436	<i>Sorl1</i>	-2.166	1.82E-04	sortilin-related receptor, LDLR class A repeats-containing
NM_026979	<i>C1qtnf2</i>	-2.166	3.54E-04	C1q and tumor necrosis factor related protein 2
NM_019419	<i>Arl6ip1</i>	-2.164	8.13E-04	ADP-ribosylation factor-like 6 interacting protein 1
NM_172467	<i>Zc3hav1</i>	-2.163	9.72E-04	zinc finger CCCH-type, antiviral 1-like
NM_029870	<i>Crebrf</i>	-2.163	0.001687169	CREB3 regulatory factor
NM_001081087	<i>Klhl41</i>	-2.162	0.00179363	kelch-like 41
NM_001005740//NM_146162	<i>Phactr1//Chst11</i>	-2.162	6.88E-04	phosphatase and actin regulator 1//carbohydrate sulfotransferase 11
NM_146162	<i>Tmem119</i>	-2.160	0.002015146	transmembrane protein 119
NM_001276481//NM_144552	<i>Dag1</i>	-2.158	0.001226607	dystroglycan 1
NM_144552	<i>Stxbp6</i>	-2.158	5.37E-04	syntaxin binding protein 6 (amisyn)
NM_028593	<i>Cybrd1</i>	-2.157	5.58E-04	cytochrome b reductase 1
NM_010181//XM_001111110//NM_001081490//NM_026347	<i>Fbn2//LOC100047082</i>	-2.157	3.96E-04	fibrillin 2//fibrillin-2-like
NM_001111110//NM_001081490//NM_026347	<i>Cmah</i>	-2.156	2.83E-04	cytidine monophospho-N-acetylneuraminic acid hydroxylase
NM_001081490//NM_026347	<i>Fbxo9</i>	-2.155	5.75E-04	f-box protein 9
NM_026347	<i>Iah1</i>	-2.154	8.94E-04	isoamyl acetate-hydrolyzing esterase 1 homolog (S. cerevisiae)
NM_001048204//NM_177351	<i>Zfp455</i>	-2.152	3.89E-04	zinc finger protein 455
NM_177351	<i>Aghpd1</i>	-2.151	9.07E-04	aminoglycoside phosphotransferase domain containing 1
NM_030719	<i>Gatsl2</i>	-2.151	0.004020363	GATS protein-like 2
NM_008966	<i>Ptgif</i>	-2.149	0.001810369	prostaglandin F receptor
NM_139300	<i>Myik</i>	-2.149	6.78E-04	myosin, light polypeptide kinase
NM_021715	<i>Chst7</i>	-2.148	6.55E-04	carbohydrate (N-acetylglucosamine) sulfotransferase 7
NM_013630	<i>Pkd1</i>	-2.146	0.002438871	polycystic kidney disease 1 homolog
NM_001122952//NM_194336	<i>Nfia</i>	-2.142	2.83E-04	nuclear factor I/A
NM_194336	<i>Gbp6</i>	-2.142	0.001943574	guanylate binding protein 6
NM_175432	<i>Tmem132c</i>	-2.141	0.004321892	transmembrane protein 132C
NM_001160378//NM_026162	<i>Fam46a</i>	-2.141	7.77E-04	family with sequence similarity 46, member A
NM_026162	<i>Plxdc2</i>	-2.141	9.29E-04	plexin domain containing 2
NM_001038621//NM_001048179//NM_011372	<i>Rabgap1</i>	-2.141	6.57E-04	RAB GTPase activating protein 1-like
NM_001048179//NM_011372	<i>Ccl27a//Ccl27b//Gm13306</i>	-2.139	4.46E-04	chemokine (C-C motif) ligand 27A
NM_011372	<i>St6galnac3</i>	-2.139	5.69E-04	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3
NM_025654	<i>Rdm1</i>	-2.137	0.004303742	RAD52 motif 1
NM_021422	<i>Dnaja4</i>	-2.136	0.00336258	DnaJ (Hsp40) homolog, subfamily A, member 4

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NM_007382	Acadm	-2.134	9.00E-04	acyl-Coenzyme A dehydrogenase, medium chain
NM_001134457	Nxpe3	-2.134	2.89E-04	neuralexophilin and PC-esterase domain family, member 3
NM_026385	Plip	-2.133	0.001428592	plasma membrane proteolipid
NM_028977	Lrrc17	-2.133	9.03E-04	leucine rich repeat containing 17
NM_001177995///N Prdm16		-2.133	0.001119699	PR domain containing 16
NM_023055///NM_Slc9a3r2		-2.132	0.00129915	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
NM_001136236///N Fcrl1		-2.131	4.02E-04	Fc receptor-like 1
NM_212457	Bex4	-2.125	0.003246647	brain expressed gene 4
NM_001037743///X 4921506M07Rik///Ttc6		-2.125	0.002968934	RIKEN cDNA 4921506M07 gene///tetratricopeptide repeat domain 6
NR_001461	Kcnq1ot1	-2.123	0.001936572	KCNQ1 overlapping transcript 1
NM_010745	Ly86	-2.123	0.008698097	lymphocyte antigen 86
NM_212445	Kdelc2	-2.120	0.001025225	KDEL (Lys-Asp-Glu-Leu) containing 2
NM_178934	Slc2a12	-2.119	0.009670761	solute carrier family 2 (facilitated glucose transporter), member 12
NM_008835///NR_C Phxr4		-2.119	5.01E-04	per-hexamer repeat gene 4
NM_010952	Oaz2	-2.118	5.17E-04	ornithine decarboxylase antizyme 2
NM_145525	Osbpl6	-2.116	0.003165932	oxysterol binding protein-like 6
NM_008584	Meox2	-2.115	7.06E-04	mesenchyme homeobox 2
NM_011402	Slc34a2	-2.113	0.002794191	solute carrier family 34 (sodium phosphate), member 2
NM_008737	Nrp1	-2.113	3.88E-04	neuropilin 1
NM_172900	Siglec9	-2.113	0.0096586	sialic acid binding Ig-like lectin G
NM_001033251///N Gpr174		-2.111	0.005344273	G protein-coupled receptor 174
NM_001024950	Zfp563	-2.107	5.53E-04	zinc finger protein 563
NM_024437///NM_Nudt7		-2.107	0.002114211	nudix (nucleoside diphosphate linked moiety X)-type motif 7
NM_011158	Prkar2b	-2.106	0.007640117	protein kinase, cAMP dependent regulatory, type II beta
NM_001033257///N Phacr2		-2.106	3.29E-04	phosphatase and actin regulator 2
NM_001145826///N Specc1l		-2.103	0.001430434	sperm antigen with calponin homology and coiled-coil domains 1-like
NM_053195	Slc24a3	-2.103	0.001356925	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
NM_001042489///N Hvcn1		-2.099	0.001810649	hydrogen voltage-gated channel 1
NM_011250	Rbl2	-2.099	0.002817239	retinoblastoma-like 2
NM_016753	Lxn	-2.097	0.004395806	latexin
NM_008514	2210419D22Rik///Lrp6	-2.093	7.81E-04	RIKEN cDNA 2210419D22 gene///low density lipoprotein receptor-related protein 6
NM_194334	Tbc1d2b	-2.092	0.001750872	TBC1 domain family, member 2B
NM_001077410///N Gimap8		-2.092	2.82E-04	GTPase, IMAP family member 8
NM_001172424///N Dhrs3		-2.092	0.001541005	dehydrogenase/reductase (SDR family) member 3
NM_010648///NM_Klra3///Klra9///LOC1008624		-2.091	0.002426628	killer cell lectin-like receptor, subfamily A, member 3
NM_019516	Lgals12	-2.090	0.00232895	lectin, galactose binding, soluble 12
NM_013548///NM_Hist1h3b///Hist1h3c///Hist1h		-2.089	0.004167333	histone cluster 1, H3b
NM_010279	Gfra1	-2.087	0.008463806	glial cell line derived neurotrophic factor family receptor alpha 1
NM_009640	Angpt1	-2.087	6.59E-04	angiopoietin 1
NM_027878	Dram1	-2.086	8.64E-04	DNA-damage regulated autophagy modulator 1
NM_001267622///N Ttc28		-2.086	9.10E-04	tetratricopeptide repeat domain 28
NM_133229	Ripply3	-2.085	0.002715577	rippy3 homolog (zebrafish)
NM_172628	Sh3tc2	-2.084	0.005366257	SH3 domain and tetratricopeptide repeats 2
NM_175013	Pgm5	-2.084	0.007678451	phosphoglucomutase 5
NM_017367	Ccni	-2.082	6.03E-04	cyclin I
NM_009223	Snn	-2.081	0.00154566	stannin
NM_019975	Hacl1	-2.079	7.45E-04	2-hydroxyacyl-CoA lyase 1
NM_026046	Zfp329	-2.078	7.18E-04	zinc finger protein 329
NM_001082414///N Sh3d19		-2.077	0.0075961	SH3 domain protein D19
NM_175526	Clec1a	-2.075	0.004526648	C-type lectin domain family 1, member a
NM_001195084///N Plscr2		-2.074	4.49E-04	phospholipid scramblase 2
NM_001083922///N Wbp1		-2.073	9.32E-04	WW domain binding protein 1
NM_177899	Zfp866	-2.073	7.78E-04	zinc finger protein 866
NM_001122899///N Lepr		-2.073	0.00155429	leptin receptor
NM_009856	Cd83	-2.072	6.77E-04	CD83 antigen
NM_146115	Tor4a	-2.072	0.00347863	torsin family 4, member A
NM_001081499	Tbc1d8b	-2.072	5.37E-04	TBC1 domain family, member 8B
NM_013626	Pam	-2.072	0.003868885	peptidylglycine alpha-amidating monooxygenase
NM_031874	Rab3d	-2.071	5.17E-04	RAB3D, member RAS oncogene family
NM_019440	Irgm2	-2.070	0.003892792	immunity-related GTPase family M member 2
NM_001014995	Fam189b	-2.069	6.17E-04	family with sequence similarity 189, member B
NM_018881	Fmo2	-2.069	3.41E-04	flavin containing monooxygenase 2
NM_010612	Kdr	-2.069	0.001425611	kinase insert domain protein receptor
NM_001099738///N Dnajc28		-2.068	2.83E-04	DnaJ (Hsp40) homolog, subfamily C, member 28
NM_011246	Rasgrp1	-2.068	0.001742034	RAS guanyl releasing protein 1
NM_021455	Mxipl	-2.068	0.009639582	MLX interacting protein-like
NM_010746	Ncr1	-2.068	6.02E-04	natural cytotoxicity triggering receptor 1
NM_001042605///N Cd74		-2.067	0.002405635	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)
NM_008206	H2-Oa	-2.067	0.003849075	histocompatibility 2, O region alpha locus
NM_001111060///N Cd59a		-2.066	7.61E-04	CD59a antigen
NM_153533	Tenc1	-2.066	0.003914276	tensin like C1 domain-containing phosphatase
NM_026514	Cdc42ep3	-2.065	2.44E-04	CDC42 effector protein (Rho GTPase binding) 3
NM_198967	Tmtc1	-2.064	5.11E-04	transmembrane and tetratricopeptide repeat containing 1
NM_010378	H2-Aa	-2.064	0.00232895	histocompatibility 2, class II antigen A, alpha
NM_001172216///N Fam221a		-2.063	6.75E-04	family with sequence similarity 221, member A
	Trav9d-3	-2.062	0.005751283	T cell receptor alpha variable 9D-3
NM_008518	Ltb	-2.062	0.006886334	lymphotoxin B
NM_012033	Tinag	-2.061	2.18E-04	tubulointerstitial nephritis antigen
NM_001048179///N Ccl27a///Ccl27b///Gm13306/		-2.059	5.01E-04	chemokine (C-C motif) ligand 27A
NM_133670	Sult1a1	-2.059	0.005167726	sulfotransferase family 1A, phenol-preferring, member 1
NM_175291	Dock10	-2.058	0.006494219	dedicator of cytokinesis 10
NM_011159	Prkdc	-2.055	9.36E-04	protein kinase, DNA activated, catalytic polypeptide
NM_023053	Twsg1	-2.054	5.64E-04	twisted gastrulation homolog 1 (Drosophila)

RefSeq Transcript ID	Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_001004359	Gprasp1	-2.053	8.05E-04	G protein-coupled receptor associated sorting protein 1
NM_028372	Mblac2	-2.049	0.001120056	metallo-beta-lactamase domain containing 2
NM_001033167	Slc22a23	-2.049	6.98E-04	solute carrier family 22, member 23
NM_010231	Fmo1	-2.048	0.00225009	flavin containing monooxygenase 1
NM_001001183	Tmem204	-2.041	3.45E-04	transmembrane protein 204
NM_018815	Nup210	-2.041	0.003026003	nucleoporin 210
NM_021462	Mknk2	-2.040	6.37E-04	MAP kinase-interacting serine/threonine kinase 2
NM_028375	Cx1c	-2.040	0.002260302	CAAX box 1C
NM_080285	Cttnbp2	-2.040	4.41E-04	cortactin binding protein 2
NM_001163290	Adck3	-2.038	0.002078079	aarF domain containing kinase 3
NM_019697	Kcnd2	-2.037	0.003096426	potassium voltage-gated channel, Shal-related family, member 2
NM_001163394	Evl	-2.032	8.84E-04	Ena-vasodilator stimulated phosphoprotein
NM_080595	Emid1	-2.026	0.003389474	EMI domain containing 1
NM_018874	Pnliprp1	-2.026	0.005315011	pancreatic lipase related protein 1
NM_019730	Mrps34	-2.025	8.82E-04	mitochondrial ribosomal protein S34
NM_027924	Pdgfd	-2.025	0.004660305	platelet-derived growth factor, D polypeptide
NM_008957	Ptch1	-2.025	6.66E-04	patched homolog 1
NM_178920	Mal2	-2.024	0.002829249	mal, T cell differentiation protein 2
NM_133821	Phlpp1	-2.024	8.95E-04	PH domain and leucine rich repeat protein phosphatase 1
NM_182995	Ccp110	-2.023	0.00394273	centriolar coiled coil protein 110
NM_011056	Pde4d	-2.023	0.001086998	phosphodiesterase 4D, cAMP specific
NM_011828	Hs2t1	-2.022	9.16E-04	heparan sulfate 2-O-sulfotransferase 1
NM_001159538	Fgd2	-2.020	0.001198963	FYVE, RhoGEF and PH domain containing 2
NM_053090	Fam126a	-2.020	0.001605911	family with sequence similarity 126, member A
NM_025476	Rmdn1	-2.019	2.64E-04	regulator of microtubule dynamics 1
NM_001039530	Parp14	-2.017	3.96E-04	poly (ADP-ribose) polymerase family, member 14
NM_001033122	Cd69	-2.016	0.009130292	CD69 antigen
NM_183028	Pcmtd1	-2.014	7.69E-04	protein-L-isopartate (D-aspartate) O-methyltransferase domain containing 1
NM_019641	Gm11223	-2.013	0.003239767	stathmin 1 pseudogene
NM_010636	Klf12	-2.013	4.34E-04	Kruppel-like factor 12
NM_023580	Epha1	-2.013	3.05E-04	Eph receptor A1
NM_010102	S1pr4	-2.012	2.72E-04	sphingosine-1-phosphate receptor 4
NM_010225	Foxf2	-2.011	0.001269162	forkhead box F2
NM_001113549	Ltbp4	-2.009	0.003891582	latent transforming growth factor beta binding protein 4
NM_001166597	Dgkz	-2.009	2.83E-04	diacylglycerol kinase zeta
NM_172694	Megf9	-2.009	0.001378605	multiple EGF-like-domains 9
NM_028064	Slc39a4	-2.007	0.00355201	solute carrier family 39 (zinc transporter), member 4
NM_001038999	Atp8a1	-2.007	9.30E-04	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1
NM_028194	Fryl	-2.006	2.85E-04	furry homolog-like (Drosophila)
NM_013548	Hist1h3b	-2.006	0.005660404	histone cluster 1, H3b
NM_025421	Acyp1	-2.006	0.002303129	acylphosphatase 1, erythrocyte (common) type
NM_001253857	Tet1	-2.005	0.001057821	tet methylcytosine dioxygenase 1
NM_026700	Dopey2	-2.002	5.85E-04	dopey family member 2
NM_009275	Srprb	-2.001	0.004879819	signal recognition particle receptor, B subunit
NM_177561	Usp46	-2.000	0.001245336	ubiquitin specific peptidase 46
NM_001110826	Ddx6	-1.998	0.003629632	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
NM_026420	Paip2	-1.998	3.67E-04	polyadenylate-binding protein-interacting protein 2
NM_001252584	Zmynd8	-1.997	3.12E-04	zinc finger, MYND-type containing 8
NM_001081278	Tbc1d4	-1.996	0.001899942	TBC1 domain family, member 4
NM_001252094	Mettl20	-1.995	0.001537402	methyltransferase like 20
NM_175437	Gsap	-1.995	0.006752007	gamma-secretase activating protein
NM_177231	Arb1	-1.992	0.001134317	arrestin, beta 1
NM_001159289	Bcl11a	-1.991	9.90E-04	B cell CLL/lymphoma 11A (zinc finger protein)
NM_178061	Mob3b	-1.990	5.49E-04	MOB kinase activator 3B
NM_001172154	Dnase1l1	-1.990	5.01E-04	deoxyribonuclease 1-like 1
NM_001199296	Acly	-1.989	8.05E-04	ATP citrate lyase
NM_001205253	Thsd1	-1.989	0.002794191	thrombospondin, type I, domain 1
NM_008514	2210419D22Rik	-1.989	6.66E-04	RIKEN cDNA 2210419D22 gene
NM_001037842	Cml3	-1.988	0.001996096	camello-like 3
NM_001002268	Gpr126	-1.987	6.71E-04	G protein-coupled receptor 126
NM_021299	Ak3	-1.984	0.002691781	adenylate kinase 3
NM_011946	Map3k2	-1.984	0.001867556	mitogen-activated protein kinase kinase kinase 2
NR_045164	Slc2a4rg-ps	-1.984	0.002401592	Slc2a4 regulator, pseudogene
NM_178407	Arap2	-1.984	0.002790515	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
NM_028713	Rftn2	-1.982	7.59E-04	raftlin family member 2
NM_001044720	Abcc9	-1.981	0.007997302	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
NM_001243199	Gimap4	-1.980	3.17E-04	GTPase, IMAP family member 4
NM_021356	Gab1	-1.980	2.98E-04	growth factor receptor bound protein 2-associated protein 1
NM_177839	Tnn	-1.979	3.52E-04	tenascin N
NM_001039509	Pnkd	-1.978	0.001177222	paroxysmal nonkinesigenic dyskinesia
NM_027326	Mllt3	-1.978	4.56E-04	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3
NM_001114328	Ccpg1	-1.977	5.32E-04	cell cycle progression 1
NM_011226	Rab19	-1.977	5.56E-04	RAB19, member RAS oncogene family
NM_145412	Chtf8	-1.977	0.004879819	CTF8, chromosome transmission fidelity factor 8
NM_001277106	Crjf3	-1.974	5.36E-04	cytokine receptor-like factor 3
NM_009238	Sox4	-1.973	0.003689988	SRY-box containing gene 4
NM_133218	Zfp704	-1.971	8.93E-04	zinc finger protein 704
NM_009128	Scd2	-1.969	0.001899942	stearoyl-Coenzyme A desaturase 2
NM_138742	Nap1l3	-1.969	0.004871914	nucleosome assembly protein 1-like 3
NM_001170848	LOC100861853	-1.969	0.006276889	uncharacterized LOC100861853
NM_001080819	Arid1a	-1.968	9.61E-04	AT rich interactive domain 1A (SWI-like)
NM_001004363	Nuak1	-1.967	4.16E-04	NUAK family, SNF1-like kinase, 1
NM_001079883	Bcl11b	-1.967	0.00119185	B cell leukemia/lymphoma 11B

RefSeq Transcript ID	Gene Symbol	*FC (Air vs O ₂)	p (Corr)	Gene Title
NM_133838	Ehd4	-1.966	0.001274417	EH-domain containing 4
NM_001033633	Slc2a13	-1.966	0.009415985	solute carrier family 2 (facilitated glucose transporter), member 13
NM_001081014///N	Dennd4c	-1.964	4.66E-04	DENN/MADD domain containing 4C
NM_009712	Arsb	-1.963	0.006347864	arylsulfatase B
	Igk1///Iglv1	-1.963	0.001311582	immunoglobulin lambda constant 1///immunoglobulin lambda variable 1
NM_010153	ErbB3	-1.962	0.001628247	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
NM_001164557///N	Pdzk1ip1	-1.962	0.001399721	PDZK1 interacting protein 1
NM_008149	Gpam	-1.959	2.94E-04	glycerol-3-phosphate acyltransferase, mitochondrial
NM_153590	Klre1	-1.959	5.58E-04	killer cell lectin-like receptor family E member 1
NM_028841	Tspan17	-1.958	0.001372295	tetraspanin 17
	Tcrg-C1///Tcrg-C2	-1.957	0.003593694	T cell receptor gamma, constant 1///T-cell receptor gamma, constant 2
NM_001110253///N	Fyco1	-1.957	4.56E-04	FYVE and coiled-coil domain containing 1
NM_001082485///N	Zfp266	-1.956	0.00119982	zinc finger protein 266
NM_001163608///N	Plxdc1	-1.955	3.54E-04	plexin domain containing 1
NM_010174	Fabp3	-1.955	0.004088384	fatty acid binding protein 3, muscle and heart
NM_175251	Arid2	-1.954	0.001044687	AT rich interactive domain 2 (ARID, RFX-like)
NM_001079686///N	Syne1	-1.954	0.001384595	spectrin repeat containing, nuclear envelope 1
NM_027294	Cmtm8	-1.954	0.009374986	CKLF-like MARVEL transmembrane domain containing 8
NM_172630	Mppe1	-1.953	0.001158827	metallophosphoesterase 1
NM_025760	Ptplad2	-1.952	0.009038386	protein tyrosine phosphatase-like A domain containing 2
NM_053262	Hsd17b11	-1.949	0.002183938	hydroxysteroid (17-beta) dehydrogenase 11
NM_018854	Ift20	-1.949	6.29E-04	intraflagellar transport 20
NM_001204134///N	C1qtnf3	-1.948	0.009551567	C1q and tumor necrosis factor related protein 3
NM_011383	Six5	-1.948	0.001234603	sine oculis-related homeobox 5
NM_001164275///N	Prrg1	-1.945	0.00220432	proline rich Gla (G-carboxyglutamic acid) 1
NM_001177945///N	AamdC	-1.945	0.004676728	adipogenesis associated Mth938 domain containing

Table E6. Pathway analysis of Nrf2-dependently changed lung genes by hyperoxia (n = 816, P < 0.01 2-Way ANOVA).

A. Top networks

	Genes (SFN-altered in bold)	Score	Disease and Functions
1	<i>Acox1, Adh7, Akap5, Cat, Cbr1, Ces1g, Coq7, Gstp1, Hcls1, Kcnk2, Kcnmb4, Keap1, Khdrbs3, Metrnl, Msr1, Nfe2l2, Nqo1, Pgd, Psm5, Slc1a1, Spr, Srxn1, Sub1</i>	35	Cellular Movement, Immune Cell Trafficking, Dermatological Diseases and Conditions
2	<i>Adamts15, Appl2, Axin2, Ccl7, Cd44, Cxcl12, Fhl2, Frat1, Hey1, Ipo5, Jag1, Kctd10, Klf15, Myo6, Nme2, Pdlim2, Prrx1, Rbpj, Rhob, Rnf146, Rspo3, Rtn4rl2, Tgfb1, Tnc, Vcan</i>	34	Cell-To-Cell Signaling and Interaction, Cellular Movement, Cardiovascular System Development and Function
3	<i>Cald1, Cd93, Cdk1, Ckap2, Dkc1, Gar1, Hmbox1, Kif11, Kif22, Kif4a, Ncapg, Nusap1, Pink1, Polr1b, Polr1e, Reps2, Rfwd3, Rrm2, Sele, Ssr1, Taf12, Taf1c, Thbd, Wdr12</i>	33	DNA Replication, Recombination, and Repair, Cell Cycle, Cellular Movement
4	<i>Angpt1, Apex1, Birc5, Cdr2, Cdt1, Cenpa, Col5a2, Dclre1c, Dst, Hlcs, Limd1, Mcm5, Mms22l, Neo1, Nlrp3, Pole, Pole2, Psm10, Rad50, Rec8, Rfc3, Rfc4, Sema3c, Tfdp1</i>	33	DNA Replication, Recombination, and Repair, Cancer, Gastrointestinal Disease

B. Top upstream regulators

Regulators	Molecule Type	Predicted Activation State	p
Lipopolysaccharide	chemical drug	Activated	1.35E-12
<i>Csf2</i>	cytokine	Activated	8.94E-11
<i>Tgfb1</i>	growth factor	Activated	4.04E-09
<i>Nfe2l2</i>	transcription regulator	Inhibited	5.33E-09
IL-17A	cytokine	Activated	7.55E-09
<i>Tnf</i>	cytokine	Activated	9.11E-09
STAT3	transcription regulator	Activated	1.11E-07

C. Top canonical pathways

Pathway	-Log(p)	Genes
phagosome formation	6.41	<i>Rhoh, Plcd4, Fcgr1a, Msr1, Fcgr2a, Pik3cg, Tlr4, Syk, Fcgr2b, Rhob, Tlr13, Plcg1, Plcl2, Rnd3, Pik3c3</i>
NRF2-mediated Oxidative Stress Response	5.01	<i>Gsta3, Gclc, Dnajc13, Cbr1, Sod1, Txnrd1, Nqo1, Enc1, Pik3cg, Cct7, Gstm5, Gsr, Cat, Gstp1, Keap1, Gclm, Pik3c3, Nfe2l2</i>
Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	3.88	<i>Cxcl12, Osm, Plcd4, Jak2, Fcgr1a, Fgf2, Sele, Rock2, Irak3, Pik3cg, Tlr4, Ikbkg, Il17ra, Nos2, C5ar1, Tlr13, Plcg1, Plcl2, Traf1, Mif, Vegfc, Pik3c3</i>
TREM1 Signaling	2.99	<i>Tlr4, Lat2, Fcgr2b, Jak2, Nlrp3, Tlr13, Plcg1, Cd86</i>
Dendritic Cell Maturation	2.98	<i>Plcd4, Jak2, Fcgr1a, Fcgr2a, Pik3cg, Tlr4, Ikbkg, Fcgr2b, Cd80, Plcg1, Plcl2, Cd86, Pik3c3</i>
Superoxide Radicals Degradation	2.76	<i>Cat, Sod1, Nqo1</i>
Sphingosine-1-phosphate Signaling	2.72	<i>Rhoh, Plcd4, Rhob, Plcg1, Plcl2, Rnd3, Adcy9, Pik3c3, Slpr5, Pik3cg</i>

Table E7. Nrf2+/- mice: Pretreatment and Exposure 264 genes

2-WAY ANOVA (Benjamini-Hochberg Correction, p-value cut-off: 0.05)

*Fold change (FC) in red incates increased and in blue decreased by SFN, compared to PBS, after O2 exposure.

RefSeq	Transcript	ID	p	(Pretreatment-Exposure)	FC	- O2:PBS vs O2:SFN	Gene Symbol
NM_008949			9.25E-05		3.16		<i>Psmc3ip</i>
XM_144292//XM_914571			1.18E-04		2.71		<i>Tmem156</i>
NM_001161515//NM_001161515			4.46E-04		2.65		<i>Dctd</i>
NM_013762//XM_00147575			1.04E-04		2.65		<i>Gm12816//Gm5879//f</i>
NR_002904//NR_003270			3.34E-04		2.16		<i>Snhg3</i>
NM_026993			2.39E-05		2.08		<i>Ddah1</i>
NM_175406			4.49E-04		1.89		<i>Atp6v0d2</i>
NM_178403			1.03E-04		1.85		<i>Pus7</i>
NM_001142943//NM_001142943			6.01E-05		1.82		<i>Zfp949</i>
NM_001177843//NM_001177843			3.31E-04		1.67		<i>Frdm4a</i>
NM_145930			4.75E-04		1.67		<i>AW549877</i>
NM_001159317//NM_001159317			2.82E-04		1.66		<i>Il1rap</i>
NM_015754			1.15E-04		1.65		<i>Rbbp9</i>
NM_007901			2.50E-04		1.65		<i>S1pr1</i>
NM_008517			3.86E-05		1.65		<i>Lta4h</i>
NM_010167			2.74E-04		1.62		<i>Eya4</i>
NM_025447			4.50E-05		1.62		<i>Dimt1</i>
NM_025635			1.21E-04		1.62		<i>Zwint</i>
NM_172990			5.14E-04		1.59		<i>Pank4</i>
NM_007554			1.48E-04		1.58		<i>Bmp4</i>
NM_009542			3.55E-04		1.57		<i>Zfp101</i>
NM_001271019//NM_145510			4.95E-04		1.57		<i>Siglec5</i>
NM_027270			3.87E-04		1.57		<i>Exoc1</i>
NM_001013372			5.68E-05		1.57		<i>Nrp</i>
NM_175112			1.77E-04		1.56		<i>Rae1</i>
NM_016693			5.12E-04		1.54		<i>Map3k6</i>
NM_001009949			2.11E-04		1.52		<i>Slc25a51</i>
NM_201372			1.65E-05		1.50		<i>Ccdc84</i>
NM_001003898//NM_001003898			3.63E-04		1.47		<i>Tarabdp</i>
NM_011083			2.66E-04		1.47		<i>Pik3c2a</i>
			1.04E-04		1.46		<i>9430013L17Rik</i>
NM_009740			1.75E-04		1.46		<i>Bcl10</i>
NM_029949			3.27E-05		1.46		<i>Snop3</i>
NM_009517			4.24E-04		1.46		<i>Zmat3</i>
NM_001161797//NM_175301			1.19E-04		1.45		<i>Phactr4</i>
NM_001271797//NM_026501			6.52E-05		1.44		<i>Rchy1</i>
NM_133854			2.90E-05		1.44		<i>Snapiin</i>
NM_001001986//NM_0011001986			1.67E-04		1.43		<i>8430427H17Rik</i>
NM_178694			1.14E-04		1.42		<i>Zer1</i>
XM_003945523//XM_003945523			1.64E-05		1.42		<i>3021401N23Rik</i>
NR_029555			4.11E-04		1.40		<i>A430104N18Rik//Mir142</i>
NR_035472//NR_038073			3.69E-04		1.40		<i>Mir1949//Snhg4</i>
NM_172742			2.33E-04		1.39		<i>Mtmr10</i>
NM_027193			5.11E-05		1.39		<i>Dph5</i>
NM_001177792//NM_001177792			1.73E-05		1.38		<i>Snop23</i>
NM_001111279//NM_027001			2.82E-05		1.36		<i>Wdfy1</i>
NM_001080387//NM_0101080387			2.18E-04		1.36		<i>Srsf10</i>
NM_011157			3.15E-04		1.36		<i>Srgn</i>
NM_027861			8.87E-05		1.36		<i>Brox</i>
NM_001276292//NM_177301			1.05E-04		1.36		<i>Wwp1</i>
NM_001037723//NM_001037723			3.15E-04		1.35		<i>Adcy7</i>
NM_145612			4.78E-04		1.35		<i>Zfp810</i>
NM_144866			9.07E-05		1.33		<i>Etf1</i>
NM_212450			3.63E-04		1.32		<i>Ctdsp2</i>
NM_001159595//NM_178101			3.74E-04		1.32		<i>Ints8</i>
NM_018829			1.28E-04		1.32		<i>Ap3m1</i>
NM_011669			3.28E-05		1.32		<i>Usp12</i>
NM_177992			4.84E-04		1.31		<i>Gmpr2</i>
NM_025356			4.43E-04		1.31		<i>Ube2d3</i>
NM_001172073//NM_028201			3.62E-04		1.31		<i>Ttc4</i>
NM_027276			2.69E-04		1.30		<i>Cdc16</i>
NM_153423			2.73E-04		1.30		<i>Wasf2</i>
NM_001161456//NM_001161456			3.69E-04		1.30		<i>Cbfb</i>
NM_026040//XM_00394600			2.41E-04		1.30		<i>Srfbp1</i>
NM_001002846//NM_013901			3.53E-04		1.29		<i>Fbxl12</i>
NM_133887			2.81E-04		1.29		<i>Stx12</i>
NM_001033441			3.50E-04		1.29		<i>Alg10b</i>
NM_019570			3.33E-04		1.29		<i>Rev1</i>
NM_001159908//NM_133301			4.93E-04		1.28		<i>Zfand2a</i>
NM_001164580			2.23E-04		1.28		<i>BC030336</i>
NM_026662			2.75E-04		1.28		<i>Prps2</i>
NM_009047			9.27E-05		1.28		<i>Rem1</i>
NM_009976			1.82E-04		1.28		<i>Cst3</i>
NM_001081119//NM_026801			3.83E-04		1.28		<i>Abhd13</i>
NM_001159518//NM_008001			1.61E-04		1.28		<i>Igfbp7</i>
NM_009543			1.48E-04		1.27		<i>Rnf103</i>
NM_001163354//NM_001163354			1.56E-04		1.27		<i>Rhot1</i>
NM_009628			4.68E-04		1.27		<i>Adnp</i>
NM_028151			2.42E-04		1.27		<i>Skiv2l2</i>
NM_028731			4.66E-04		1.27		<i>Eys2</i>
NM_020050			3.78E-05		1.27		<i>Tmem9b</i>
NM_027946			9.62E-05		1.26		<i>Dcaf7</i>
NM_009632			2.28E-04		1.25		<i>Parp2</i>
NM_001077507//NM_001077507			1.30E-05		1.25		<i>Gnas</i>
NM_175465			1.37E-05		1.24		<i>Sestd1</i>
NM_175552			2.75E-05		1.24		<i>Wdr3</i>
NM_145416			4.09E-04		1.24		<i>Kri1</i>
NM_026217			4.71E-04		1.23		<i>Atg12</i>
NM_001145779//NM_008401			3.95E-04		1.23		<i>Kif2a</i>
NM_022331			3.19E-04		1.23		<i>Herpud1</i>
NM_001199004//NM_013701			1.87E-04		1.23		<i>Golga5</i>
NM_029491//NM_177038			5.66E-05		1.22		<i>Trappc8</i>

RefSeq Transcript ID	p (Pretreatment-Exposure)	FC - O2:PBS vs O2:SFN	Gene Symbol	Gene Title
NM_009840		4.31E-04	1.21 <i>Cct8</i>	chaperonin containing Tcp1, subunit 8 (theta)
NM_030016		1.61E-05	1.21 <i>Trmt13</i>	tRNA methyltransferase 13
NM_001177806//NM_0137:		1.50E-04	1.21 <i>Ejzka4</i>	eukaryotic translation initiation factor 2 alpha kinase 4
NM_021512		1.73E-04	1.21 <i>Nup160</i>	nucleoporin 160
NM_025283		2.46E-04	1.20 <i>Mob4</i>	MOB family member 4, phocein
NM_153198//NM_177993		1.75E-04	1.20 <i>Hbp1</i>	high mobility group box transcription factor 1
NM_023740		4.01E-05	1.20 <i>Zdhhc16</i>	zinc finger, DHHC domain containing 16
NM_177390		3.08E-04	1.19 <i>Myo1d</i>	myosin ID
NM_007636		3.72E-04	1.19 <i>Cct2</i>	chaperonin containing Tcp1, subunit 2 (beta)
NM_001099319//NM_1774:		3.91E-04	1.19 <i>Gm12942//Zmym6</i>	predicted gene 12942//zinc finger, MYM-type 6
NM_144802		3.23E-04	1.18 <i>Hnrpl</i>	heterogeneous nuclear ribonucleoprotein L-like
NM_145943		3.05E-04	1.18 <i>Sde2</i>	SDE2 telomere maintenance homolog (S. pombe)
NM_009076//XM_0039456:		4.46E-04	1.18 <i>LOC101055925//LOC63:</i>	60S ribosomal protein L12-like//ribosomal protein L12
NM_001097644		3.12E-04	1.18 <i>Cnly1</i>	cyclin Y-like 1
NM_212484		5.07E-04	1.18 <i>Cnot6</i>	CCR4-NOT transcription complex, subunit 6
NM_172839		1.97E-04	1.18 <i>Cnjl</i>	cyclin J
NM_029645		5.69E-05	1.18 <i>Gatc</i>	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)
NM_198631		2.70E-04	1.17 <i>Zc3h4</i>	zinc finger CCHC-type containing 4
NM_001024622		2.77E-04	1.17 <i>Pcnp</i>	PEST proteolytic signal containing nuclear protein
NM_001081430		1.85E-04	1.17 <i>Naa30</i>	N(alpha)-acetyltransferase 30, NatC catalytic subunit
NM_027000		3.49E-04	1.17 <i>Gtbbp4</i>	GTP binding protein 4
NM_009076//XM_0039456:		4.52E-04	1.17 <i>LOC101055925//LOC63:</i>	60S ribosomal protein L12-like//ribosomal protein L12
NM_053263//NM_146130//		1.95E-04	1.17 <i>Hnrnpa3//Gm6793</i>	heterogeneous nuclear ribonucleoprotein A3//heterogeneous nuclear ribonucleoprotein A3 pseudogene
NM_001168281//NM_1337:		1.45E-04	1.16 <i>Wwtr1</i>	WW domain containing transcription regulator 1
NM_001001144//NM_0011:		4.39E-04	1.16 <i>Scap</i>	SREBF chaperone
NM_172601		3.58E-04	1.16 <i>Rab2b</i>	RAB2B, member RAS oncogene family
NM_001080706		1.28E-04	1.16 <i>Rta1</i>	BTA1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)
NM_001205367//NM_0098:		1.06E-04	1.16 <i>Sep7</i>	septin 7
NM_024213		4.58E-04	1.16 <i>Anapc4</i>	anaphase promoting complex subunit 4
NM_001159645//NM_0097:		4.88E-04	1.15 <i>Araf</i>	v-rat murine sarcoma 3611 viral oncogene homolog
NM_028599		9.72E-05	1.15 <i>Wdr75</i>	WD repeat domain 75
NM_001168248//NM_0289:		2.46E-04	1.14 <i>Rmi1</i>	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)
NM_019995		1.36E-04	1.13 <i>Supt20</i>	suppressor of Ty 20
NM_00114131//NM_1460:		3.45E-04	1.12 <i>Ppp4r1</i>	protein phosphatase 4, regulatory subunit 1
NM_010239//NR_073181		1.03E-04	1.12 <i>Fth1</i>	ferritin heavy chain 1
NM_001001491		1.67E-04	1.12 <i>Tpm4</i>	tropomyosin 4
NM_025975		2.97E-04	1.12 <i>Dynl1t3</i>	dynein light chain Tctex-type 3
NM_178610		4.11E-04	1.11 <i>Krr1</i>	KRR1, small subunit (SSU) processome component, homolog (yeast)
NM_145441		2.62E-04	1.10 <i>Ubx2a</i>	UBX domain protein 2A
NM_080561//NM_207110		3.08E-04	1.10 <i>Rnf216</i>	ring finger protein 216
NM_026444		4.33E-04	1.09 <i>Cs</i>	citrate synthase
NM_001099319//NM_1774:		4.86E-04	1.06 <i>Gm12942//Zmym6</i>	predicted gene 12942//zinc finger, MYM-type 6
NR_003292		3.00E-04	1.03 <i>Zxda</i>	zinc finger, X-linked, duplicated A
NM_028123		4.61E-05	1.02 <i>Zlc37a3</i>	solute carrier family 37 (glycerol-3-phosphate transporter), member 3
NM_001159571//NM_0101:		3.56E-04	-2.22 <i>Ephb4</i>	Eph receptor B4
NM_008369		3.27E-04	-2.20 <i>Il3ra</i>	interleukin 3 receptor, alpha chain
NM_008512		3.22E-05	-1.93 <i>Lrp1</i>	low density lipoprotein receptor-related protein 1
NM_001081342//NM_1777:		4.46E-04	-1.90 <i>Gpr133</i>	G protein-coupled receptor 133
NM_026158		4.81E-04	-1.87 <i>Iso2b</i>	isochorismatase domain containing 2b
NM_138672		4.13E-04	-1.82 <i>Stab1</i>	stabilin 1
NM_010517		1.54E-04	-1.80 <i>Igfbp4</i>	insulin-like growth factor binding protein 4
NM_010180		5.09E-04	-1.77 <i>Fbln1</i>	fibulin 1
NM_053272		1.62E-04	-1.74 <i>Dhcr24</i>	24-dehydrocholesterol reductase
NM_030238		2.18E-05	-1.69 <i>Dync1h1</i>	dynein cytoplasmic 1 heavy chain 1
NM_001038612//NM_0010:		4.44E-04	-1.67 <i>Olfm1</i>	olfactomedin 1
NM_011989		1.23E-05	-1.63 <i>Zlc27a4</i>	solute carrier family 27 (fatty acid transporter), member 4
NM_001101448//NM_0011:		7.31E-05	-1.63 <i>Mgat1</i>	mannoside acetylglucosaminyltransferase 1
NM_019776		3.45E-04	-1.62 <i>Snd1</i>	staphylococcal nuclease and tudor domain containing 1
NM_153088		4.62E-04	-1.62 <i>Ctdsp1</i>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1
NM_139139		3.09E-04	-1.61 <i>Dnajc17</i>	Dnaj (Hsp40) homolog, subfamily C, member 17
NM_153781		2.57E-04	-1.60 <i>Pygb</i>	brain glycogen phosphorylase
NM_177301		1.29E-04	-1.59 <i>Hnrpl</i>	heterogeneous nuclear ribonucleoprotein L
NM_008551		9.68E-05	-1.59 <i>Mapkapk2</i>	MAP kinase-activated protein kinase 2
NM_013700		1.40E-04	-1.59 <i>Usp5</i>	ubiquitin specific peptidase 5 (isopeptidase T)
NM_011814		4.99E-04	-1.56 <i>Fxr2</i>	fragile X mental retardation, autosomal homolog 2
NM_010950		2.67E-04	-1.56 <i>Numbl</i>	numb-like
NM_178919		4.23E-04	-1.56 <i>Lmf2</i>	lipase maturation factor 2
NM_133949		4.72E-05	-1.54 <i>Ptvl1</i>	prostate tumor over expressed gene 1
NM_001130450//NM_0011:		3.16E-04	-1.54 <i>Nfe2l1</i>	nuclear factor, erythroid derived 2,-like 1
NM_001172205//NM_0011:		3.44E-04	-1.52 <i>Arid5a</i>	AT rich interactive domain 5A (MRF1-like)
NM_001271402//NM_0012:		1.69E-05	-1.51 <i>Ephx2</i>	epoxide hydrolase 2, cytoplasmic
NM_080728//NM_0011641:		1.95E-04	-1.49 <i>Myh7//Myh6</i>	myosin, heavy polypeptide 7, cardiac muscle, beta//myosin, heavy polypeptide 6, cardiac muscle, alpha
NM_001127363//NM_1831:		1.18E-04	-1.47 <i>Ipp5a</i>	inositol polyphosphate-5-phosphatase A
NM_001001565//NM_0010:		7.34E-05	-1.45 <i>Chpf</i>	chondroitin polymerizing factor
NM_031874		2.21E-04	-1.45 <i>Rab3d</i>	RAB3D, member RAS oncogene family
NM_019649		1.45E-06	-1.44 <i>Clptm1</i>	cleft lip and palate associated transmembrane protein 1
NM_001024458//NM_0011:		1.53E-04	-1.44 <i>Add1</i>	adducin 1 (alpha)
NM_001252282//NM_0012:		4.10E-04	-1.43 <i>Ogdh</i>	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)
NM_011349		2.56E-04	-1.42 <i>Sema3f</i>	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F
NM_027402		5.17E-04	-1.42 <i>Fndc5</i>	fibronectin type III domain containing 5
NM_145396		4.06E-04	-1.41 <i>Tbl3</i>	transducin (beta)-like 3
NM_001146318//NM_0099:		5.25E-04	-1.40 <i>Cnp</i>	2',3'-cyclic nucleotide 3' phosphodiesterase
NM_001162998		2.49E-04	-1.40 <i>Ssm16</i>	small integral membrane protein 6
NM_001159328//NM_0082:		2.83E-04	-1.39 <i>Hgs</i>	HGF-regulated tyrosine kinase substrate
NM_016860		2.02E-05	-1.39 <i>Actr1a</i>	ARP1 actin-related protein 1A, contractin alpha
NM_001083921//NM_0197:		6.96E-05	-1.38 <i>Rbck1</i>	RanBP-type and C3HC4-type zinc finger containing 1
NM_175356		2.47E-04	-1.38 <i>Pi4kb</i>	phosphatidylinositol 4-kinase, catalytic, beta polypeptide
NM_013863		1.68E-04	-1.38 <i>Bag3</i>	BCL2-associated athanogene 3
NM_001136085//NM_0012:		1.49E-04	-1.37 <i>Uba1</i>	ubiquitin-like modifier activating enzyme 1
NM_001110504//NM_0076:		1.69E-05	-1.36 <i>Capn1</i>	calpain 1
NM_001112722//NM_0011:		1.82E-05	-1.35 <i>Arhgef10</i>	Rho guanine nucleotide exchange factor (GEF) 10-like
NM_024227		4.93E-04	-1.35 <i>Mrp128</i>	mitochondrial ribosomal protein L28
NM_026938		3.32E-04	-1.35 <i>Tmem160</i>	transmembrane protein 160
NM_001163571//NM_0307:		3.58E-04	-1.33 <i>Senp3</i>	SUMO/sentrin specific peptidase 3
NM_022995		3.05E-04	-1.33 <i>Pmepa1</i>	prostate transmembrane protein, androgen induced 1

RefSeq Transcript ID	p (Pretreatment-Exposure)	FC - O2:PBS vs O2:SFN	Gene Symbol	Gene Title
NM_024256	3.59E-04	-1.32	B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)
NM_001122736//NM_0011:	6.23E-05	-1.32	Igf2	insulin-like growth factor 2
NM_001163452//NM_0198:	8.19E-05	-1.31	Trpc4ap	transient receptor potential cation channel, subfamily C, member 4 associated protein
NM_001177759//NM_0011:	3.52E-04	-1.30	Tnfrsf8	tumor necrosis factor, alpha-induced protein 8
NM_138748	1.73E-04	-1.29	Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)
NM_001159521//NM_1387:	2.69E-04	-1.28	Plexnb2	plexin B2
NM_001243043//NM_0012:	1.47E-04	-1.26	Ap1b1	adaptor protein complex AP-1, beta 1 subunit
NM_026017	2.16E-05	-1.26	Ctdnep1	CTD nuclear envelope phosphatase 1
NM_001164184//NM_0011:	3.77E-04	-1.26	Lsr	lipolysis stimulated lipoprotein receptor
NM_009439	4.71E-04	-1.26	Psmc3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3
NM_001081158	2.93E-04	-1.25	Cluh	clustered mitochondria (cluA/CLU1) homolog
NM_027088	2.59E-04	-1.24	Bap1	Brca1 associated protein 1
NM_025954	2.12E-04	-1.24	Pgp	phosphoglycolate phosphatase
NM_001145970//NM_1449:	3.46E-04	-1.23	Map7d1	MAP7 domain containing 1
NM_026759	2.00E-04	-1.21	Mrpl13	mitochondrial ribosomal protein L13
NM_001253883//NM_0110:	3.21E-04	-1.20	Pkm	pyruvate kinase, muscle
NM_181650	1.86E-05	-1.20	Prdm4	PR domain containing 4
NM_001109995//NM_0114:	2.80E-04	-1.19	Eftud2	elongation factor Tu GTP binding domain containing 2
NM_133204	2.95E-04	-1.19	Zscan5b	zinc finger and SCAN domain containing 5B
NM_019443	2.46E-04	-1.19	Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1
NM_024166//XM_0014726:	2.48E-05	-1.18	Chchd2//Gm13202//LC	coiled-coil-helix-coiled-coil-helix domain containing 2
NM_134151	5.41E-05	-1.18	Yars	tyrosyl-tRNA synthetase
NM_001037722//NM_0096:	3.84E-04	-1.18	Adam15	a disintegrin and metallopeptidase domain 15 (metargidin)
NM_172793	8.31E-05	-1.17	Btn19	butyrophilin-like 9
NM_021383	5.23E-04	-1.16	Racd1	rcd1 (required for cell differentiation) homolog 1 (S. pombe)
NM_001146196//NM_0091:	8.52E-05	-1.16	Scin	scinderin
NM_007533	9.84E-05	-1.13	Bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide
NM_024220//XM_910031//	3.29E-04	-1.13	LOC635087//LOC675851	NADH dehydrogenase [ubiquinone] 1 subunit C2-like//NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2
NM_011292//XM_0039455:	4.95E-04	-1.13	Gms451//LOC10105602	predicted gene 5451//60S ribosomal protein L9-like//ribosomal protein L9
NM_009642	2.72E-05	-1.13	Agtrap	angiotensin II, type I receptor-associated protein
NM_009304	1.28E-05	-1.12	Syngn2	synaptogyrin 2
NM_010163	2.08E-04	-1.10	Ext2	exostoses (multiple) 2
NM_175102	4.82E-04	-1.10	Sf3b5	splicing factor 3b, subunit 5
	9.71E-07	-1.09	AA511254	expressed sequence AA511254
NM_001122739//NM_0105:	2.69E-04	-1.08	Inpp1	inositol polyphosphate phosphatase-like 1
NM_145383	2.92E-04	-1.08	Rho	rhodopsin
NM_024437//NM_024446	6.13E-05	-1.05	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7

Table E8. Selected genes and pathway analysis of Nrf2-dependent lung transcriptome changes by sulforaphane during hyperoxia exposure (n = 1,007, $P < 0.01$ 2-Way ANOVA).

A. Selected gene list

Functional Category	RefSeq ID	p^{\dagger}	FD [‡]	Gene Symbol	Gene Title
Mitochondrial Function and Energy Metabolism	NM_016966	0.00823	5.37	<i>Phgdh</i>	3-phosphoglycerate dehydrogenase pseudogene
	NM_028765	0.00232	2.99	<i>Acox1</i>	acyl-Coenzyme A oxidase-like
	NM_008512	0.00159	2.47	<i>Lrp1</i>	low density lipoprotein receptor-related protein 1
	NM_173371	8.27E-04	1.50	<i>H6pd</i>	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)
	NM_010324	2.90E-04	-5.86	<i>Got1</i>	glutamate oxaloacetate transaminase 1, soluble
	NM_009731	0.00321	-3.79	<i>Akr1b7</i>	aldo-keto reductase family 1, member B7
	NM_011399	0.00875	-2.31	<i>Slc25a17</i>	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane)
	NM_173011	0.00727	-2.30	<i>Iah2</i>	isocitrate dehydrogenase 2 (NADP+), mitochondrial
	NM_001009949	0.00110	-2.05	<i>Mcart1</i>	mitochondrial carrier triple repeat 1
	NM_025835	4.40E-05	-2.01	<i>Pccb</i>	propionyl Coenzyme A carboxylase, beta polypeptide
	NM_025485	0.00558	-1.82	<i>Mrps22</i>	mitochondrial ribosomal protein S22
	NM_029673	4.35E-04	-1.79	<i>Immt</i>	inner membrane protein, mitochondrial
	NM_001135112	0.00418	-1.67	<i>Dnaja3</i>	DnaJ (Hsp40) homolog, subfamily A, member 3
	NM_016774	0.00356	-1.66	<i>Atp5b</i>	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit
Antioxidant and Defense	NM_021456	0.00702	-7.42	<i>Ces1g</i>	carboxylesterase 1G
	NM_016903	2.02E-04	-5.44	<i>Esd</i>	esterase D/formylglutathione hydrolase
	NM_010363	0.00360	-4.68	<i>Gstz1</i>	glutathione transferase zeta 1 (maleylacetoacetate isomerase)
	NM_183165	5.27-E04	-1.98	<i>Pyroxd1</i>	pyridine nucleotide-disulphide oxidoreductase domain 1
	NM_008049	0.00930	-1.78	<i>Ftl</i>	ferritin light chain 1
Immunity, Injury, and Development	NM_001110146	0.00713	5.76	<i>Prg4</i>	proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone)
	NM_001123382	0.00142	2.96	<i>Il1r1</i>	interleukin 1 receptor, type 1
	NM_013605	0.00659	2.74	<i>Muc1</i>	mucin 1, transmembrane
	NM_001038612	9.41E-07	2.58	<i>Olfm1</i>	olfactomedin 1
	NM_008608	0.00607	2.48	<i>Mmp14</i>	matrix metalloproteinase 14 (membrane-inserted)
	NM_001079908	0.00701	2.37	<i>Fgfr1</i>	fibroblast growth factor receptor 1
	NM_001146268	0.00946	2.26	<i>Pdgfrb</i>	platelet derived growth factor receptor, beta polypeptide
	NM_033574	0.00910	1.62	<i>Pcdhga1</i>	protocadherin gamma subfamily A, 1
	NM_001163522	0.00563	-4.49	<i>Emcn</i>	endomucin
	NM_010393	7.58E-04	-2.91	<i>H2-Q5</i>	histocompatibility 2, Q region locus 5
Other Cellular Process and Signaling	NM_008209	3.90-E04	-2.79	<i>Mrl1</i>	major histocompatibility complex, class I-related
	NM_011957	0.00884	3.76	<i>Creb3l1</i>	cAMP responsive element binding protein 3-like 1
	NM_001098799	0.00634	3.07	<i>Tox2</i>	TOX high mobility group box family member 2
	NM_020047	0.00592	-7.13	<i>Tacstd2</i>	tumor-associated calcium signal transducer 2
	NM_008949	9.66E-05	-3.83	<i>Psmc3ip</i>	proteasome 26S subunit, ATPase 3, interacting protein
	NM_133977	0.00685	-2.85	<i>Trf</i>	transferrin
	NM_011068	0.00497	-2.11	<i>Pex11a</i>	peroxisomal biogenesis factor 11 alpha
	NM_181410	4.64-E04	-1.79	<i>Gtf2h3</i>	general transcription factor IIH, polypeptide 3

[†]Two-way ANOVA (Genotype, pretreatment) of hyperoxia-exposed mice. [‡]Fold difference in SFN-treated/O₂-exposed *Nrf2*^{-/-} mice vs SFN-treated/O₂-exposed *Nrf2*^{+/+} mice (positive values indicate higher expression in *Nrf2*^{-/-}, negative values lower expression in *Nrf2*^{-/-}).

B. Top networks

	Genes (SFN-altered in bold)	Score	Disease and Functions
1	<i>Atg2a, Bre, Chd8, Commd5, Commd7, Ddost, Dnttip1, Faf1, Fam175a, Fucal, Got1, Got2, Ilkap, Itpkb, Kpna1, Kpna3, Nkiras1, Nsf1c, Nxt1, Pak1ip1, Pdlim1, Pnpt1, Sar1a, Slbp, Snip1, Tmem120a, Trim13, Ttc28, Uba3, Zfand6</i>	45	Amino Acid Metabolism, Small Molecule Biochemistry, Auditory Disease
2	<i>Aasdhppt, Atg13, Atp2a3, Bzw1, Cct3, Ddx18, Dlgap4, Eif2ak1, Eif2b2, Gabarapl2, Gfm1, Gstz1, Hccs, Hmcn1, Kcnq5, Mlx, Nck1, Nit1, Nova2, Pcbp2, Rnf103, Rrp36, Shmt1, Sumo3, Tardbp, Tbc1d2b, Thyn1, Tmpo, Trmt5, Wdr43</i>	43	Dermatological Diseases and Conditions, Developmental Disorder, Hereditary Disorder
3	<i>Acp6, Adipor1, Aig1, Arpc5, Asb8, Camk2g, Cdk18, Diaph1, Ilk, Jdp2, Kctd5, Larpl, Mapkapk2, Mtch2, Nckap1, Nfib, Nfx1, Parvb, Rasgrp2, Rchyl, Rhob, Rusc1, Saa3, Sertad1, Smpd2, Tns1, Vars, Wdr74, Znf746</i>	42	Cell Morphology, Cellular Assembly and Organization, Cellular Function and Maintenance
4	<i>Afg3l2, Arl16, Atp5a1, Cbfa2t3, Dctd, Hip1, Hmg20b, Homer2, Itp2, Lrp12, Mark3, Mprp, Nif3l1, Nol11, Pcgf5, Pde12, Pde6d, Phc2, Phf21a, Rab8a, Rhbdf2, Rnf146, Snapin, Ssx2ip, Stx7, Tbc1d10a, Tsc22d4, Vamp2, Zbtb4</i>	42	Cellular Assembly and Organization, Cellular Function and Maintenance, Cellular Movement
5	<i>Arfgap1, Arid5a, Dmap1, Emg1, Gcn1l1, Gtf2a1, Gtf2f1, Gtf2h3, H6pd, Med4, Med7, Med10, Med24, Med27, Pex12, Pex19, Pex11a, Polr2d, Rad1, Rela, Rfc3, Rfwd3, Rpa2, Slc25a17, Snapc4, Supt6h, Taf12, Tmem9b, Ubac2</i>	42	Cellular Assembly and Organization, Cellular Function and Maintenance, Gene Expression

C. Top canonical pathways and toxicity lists

Pathway	-Log(p)	Genes
Oxidative Phosphorylation/Mitochondrial Dysfunction	2.54-1.78	<i>Sdhb, Cox11, Uqcrc1, Ndufa8, Ndufs3, Atp5a1, Cox8a, Uqcrfs1, Pdha1, Atp5b, Casp8, Ndufs1</i>
Glutamate Degradation II/ Aspartate Biosynthesis/ L-cysteine Degradation I/ Aspartate Degradation II	2.3-2.01	<i>Got2, Got1</i>
Hypoxia-Inducible Factor Signaling	2.24	<i>Cops5, Flt4, Kdr, Plcg1, Mdm2, Elavl1, Eif2b2, Hsp90aa1</i>
TCA Cycle II (Eukaryotic)	2.0	<i>Idh3a, Sdhb, Idh3b, Suclg1</i>
NF-κB Signaling	1.8	<i>Map2k7, Fgfr1, Pdgrb, Flt4, Kdr, Ube2v1, Traf3, Rela, Pik3cd, Il1r1, Bcl10, Bmp4, Casp8</i>
RAN Signaling	1.74	<i>Kpna1, Kpna3, Ranbp1</i>
Huntington's Disease Signaling	1.73	<i>Map2k7, Dnajb1, Map3k10, Hspa14, Sdhb, Dnm1l, Pdpk1, Pik3cd, Polr2d, Hip1, Casp2, Atp5b, Capn7, Casp8, Casp7, Gna15</i>
PPARγ/RXR activation	1.7	<i>Map2k7, Acadl, Got2, Adipor1, Med24, Rela, Il1r1, Nr2f1, Adipor2, Rxra, Plcg1, Hsp90aa1, Gna15</i>
PI3K/AKT Signaling	1.61	<i>Ppp2r5b, Pdpk1, Pik3cd, Inpp5d, Ppp2cb, Mdm2, Eif4e, Ilk, Hsp90aa1, Rela</i>
Superpathway of Serine and Glycine Biosynthesis I	1.5	<i>Ubac2, Shmt1</i>
Biogenesis of Mitochondria	1.32	<i>Dnaja3, Pted2, Cxadr</i>
Pro-Apoptosis	1.15	<i>Traf3, Casp2, Casp8, Casp7</i>
Mechanism of Gene Regulation by Peroxisome Proliferators via PPARγ	1.04	<i>Pdgrb, Il1r1, Hsd17b4, Nr2f1, Rxra, Hsp90aa1, Rela</i>