Supplementary File 4:

GENES REGULATED IN SAME DIRECTION

		FOLD CHANGE	
mgi_symbol	mgi_description	KO versus WT	Old versus Young
Kcng4	potassium voltage-gated channel, subfamily G, member 4	-1.922	-1.361
Glrx	glutaredoxin	-1.264	-0.283
Hsbp1l1	heat shock factor binding protein 1-like 1	-1.147	-0.585
1810014F10Rik	RIKEN cDNA 1810014F10 gene	-1.099	-0.348
Fndc5	fibronectin type III domain containing 5	-1.030	-0.793
Tm6sf1	transmembrane 6 superfamily member 1	-0.923	-1.112
Kcnn2	K+ intermediate/small conductanceCa++-activated channel, N2	-0.877	-0.507
Pigy	phosphatidylinositol glycan anchor biosynthesis, class Y	-0.745	-0.246
Ung	uracil DNA glycosylase	-0.733	-0.613
Endog	endonuclease G	-0.702	-0.436
Tecta	tectorin alpha	-0.685	-0.712
Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	-0.670	-0.408
Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	-0.599	-0.289
2310061C15Rik	RIKEN cDNA 2310061C15 gene	-0.573	-0.495
Ngp	neutrophilic granule protein	-0.569	-0.269
Fdx1	ferredoxin 1	-0.565	-0.255
Fam195a	family with sequence similarity 195, member A	-0.554	-0.320
Vav2	vav 2 oncogene	-0.544	-0.630
Alas1	aminolevulinic acid synthase 1	-0.544	-0.176
Slc25a39	solute carrier family 25, member 39	-0.537	-0.449
Mrpl12	mitochondrial ribosomal protein L12	-0.531	-0.333
Nrtn	neurturin	-0.529	-0.502
Spsb4	splA/ryanodine receptor domain and SOCS box containing 4	-0.526	-0.676
Mrpl47	mitochondrial ribosomal protein L47	-0.525	-0.437
Zfp827	zinc finger protein 827	-0.524	-0.274
Aifm1	apoptosis-inducing factor, mitochondrion-associated 1	-0.476	-0.180
Uqcr10	ubiquinol-cytochrome c reductase, complex III subunit X	-0.474	-0.418
Sox5	SRY-box containing gene 5	-0.469	-0.336
Mut	methylmalonyl-Coenzyme A mutase	-0.462	-0.270
Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	-0.454	-0.230
Cldn18	claudin 18	-0.450	-0.267
Cox10	COX10 homolog, cyto c oxidase assembly, heme A: farnesyltransferase (yeast)	-0.450	-0.246
Ptges2	prostaglandin E synthase 2	-0.450	-0.155

Gbp1	guanylate binding protein 1	-0.441	-0.317
Dnajc6	DnaJ (Hsp40) homolog, subfamily C, member 6	-0.437	-0.250
Timm44	translocase of inner mitochondrial membrane 44	-0.429	-0.376
D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	-0.424	-0.236
Ndufaf4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	-0.404	-0.419
Paqr4	progestin and adipoQ receptor family member IV	-0.404	-0.547
Acads	acyl-Coenzyme A dehydrogenase, short chain	-0.395	-0.440
Krt12	keratin 12	-0.394	-0.252
Brp44	brain protein 44	-0.387	-0.171
Ushbp1	Usher syndrome 1C binding protein 1	-0.384	-0.344
Mrpl34	mitochondrial ribosomal protein L34	-0.357	-0.227
Leng1	leukocyte receptor cluster (LRC) member 1	-0.356	-0.318
Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	-0.355	-0.482
Glud1	glutamate dehydrogenase 1	-0.349	-0.410
Ncapd2	non-SMC condensin I complex, subunit D2	-0.346	-0.192
Inpp1	inositol polyphosphate-1-phosphatase	-0.344	-0.394
Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	-0.340	-0.135
Lpgat1	lysophosphatidylglycerol acyltransferase 1	-0.337	-0.250
Ak3	adenylate kinase 3	-0.333	-0.737
1110017D15Rik	RIKEN cDNA 1110017D15 gene	-0.321	-0.229
Efna2	ephrin A2	-0.320	-0.352
Fam82b	family with sequence similarity 82, member B	-0.307	-0.344
Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	-0.306	-0.186
Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	-0.305	-0.190
Dnase2a	deoxyribonuclease II alpha	-0.305	-0.225
Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	-0.302	-0.257
Epdr1	ependymin related protein 1 (zebrafish)	-0.302	-0.389
Pcyt2	phosphate cytidylyltransferase 2, ethanolamine	-0.301	-0.248
Sidt1	SID1 transmembrane family, member 1	-0.299	-0.182
Cep68	centrosomal protein 68	-0.296	-0.529
Ap1g2	adaptor protein complex AP-1, gamma 2 subunit	-0.294	-0.248
Fam115c	family with sequence similarity 115, member C	-0.291	-0.290
Cox4i1	cytochrome c oxidase subunit IV isoform 1	-0.290	-0.132
Trpt1	tRNA phosphotransferase 1	-0.286	-0.255
C1qbp	complement component 1, q subcomponent binding protein	-0.278	-0.162
Aph1a	anterior pharynx defective 1a homolog (C. elegans)	-0.278	-0.421
Psg16	pregnancy specific glycoprotein 16	-0.263	-0.140
Csrnp3	cysteine-serine-rich nuclear protein 3	-0.260	-0.212

Naa20	N(alpha)-acetyltransferase 20, NatB catalytic subunit	-0.246	-0.231
Cybasc3	cytochrome b, ascorbate dependent 3	-0.240	-0.304
Gcnt3	glucosaminyl (N-acetyl) transferase 3, mucin type	-0.235	-0.281
Mrrf	mitochondrial ribosome recycling factor	-0.230	-0.134
Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1	-0.227	-0.161
3110056O03Rik	RIKEN cDNA 3110056O03 gene	-0.226	-0.192
Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	-0.221	-0.308
Aars2	alanyl-tRNA synthetase 2, mitochondrial (putative)	-0.213	-0.131
Mrpl20	mitochondrial ribosomal protein L20	-0.204	-0.179
Tdp2	tyrosyl-DNA phosphodiesterase 2	-0.198	-0.259
Hdhd1a	haloacid dehalogenase-like hydrolase domain containing 1A	-0.159	-0.176
Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	-0.146	-0.224
Ift52	intraflagellar transport 52 homolog (Chlamydomonas)	0.128	0.129
Fxr1	fragile X mental retardation gene 1, autosomal homolog	0.155	0.141
Akr1a1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	0.156	0.207
Gmppa	GDP-mannose pyrophosphorylase A	0.186	0.419
Sar1a	SAR1 gene homolog A (S. cerevisiae)	0.187	0.228
Cd164	CD164 antigen	0.193	0.216
Frg1	FSHD region gene 1	0.202	0.198
Celf5	CUGBP, Elav-like family member 5	0.203	0.202
Smyd2	SET and MYND domain containing 2	0.207	0.425
P4hb	prolyl 4-hydroxylase, beta polypeptide	0.208	0.526
Cfl2	cofilin 2, muscle	0.210	0.386
Usp47	ubiquitin specific peptidase 47	0.211	0.326
Ptpn4	protein tyrosine phosphatase, non-receptor type 4	0.217	0.234
Daf2	decay accelerating factor 2	0.218	0.225
Skp1a	S-phase kinase-associated protein 1A	0.222	0.251
Copg	coatomer protein complex, subunit gamma	0.225	0.233
Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0.226	0.563
Apex1	apurinic/apyrimidinic endonuclease 1	0.230	0.325
Bcap31	B cell receptor associated protein 31	0.236	0.172
Zwilch	Zwilch, kinetochore associated, homolog (Drosophila)	0.244	0.301
Zfp623	zinc finger protein 623	0.249	0.182
D11Wsu99e	DNA segment, Chr 11, Wayne State University 99, expressed	0.250	0.164
Senp5	SUMO/sentrin specific peptidase 5	0.261	0.363
Zfp828	zinc finger protein 828	0.262	0.144
Tbcb	tubulin folding cofactor B	0.262	0.373
Atp6v1g1	ATPase, H+ transporting, lysosomal V1 subunit G1	0.266	0.100

Tbcd	tubulin-specific chaperone d	0.274	0.470
Pyroxd1	pyridine nucleotide-disulphide oxidoreductase domain 1	0.274	0.367
Suz12	suppressor of zeste 12 homolog (Drosophila)	0.276	0.193
St7l	suppression of tumorigenicity 7-like	0.287	0.274
Egf	epidermal growth factor	0.296	0.524
Zc3h15	zinc finger CCCH-type containing 15	0.299	0.382
Nagk	N-acetylglucosamine kinase	0.317	0.317
Serpinb6a	serine (or cysteine) peptidase inhibitor, clade B, member 6a	0.318	0.293
Sbno1	sno, strawberry notch homolog 1 (Drosophila)	0.319	0.270
Cand2	cullin-associated and neddylation-dissociated 2 (putative)	0.331	0.303
Ifi27l1	interferon, alpha-inducible protein 27 like 1	0.337	0.734
Scd3	stearoyl-coenzyme A desaturase 3	0.338	0.345
Ppap2a	phosphatidic acid phosphatase type 2A	0.341	0.523
Vps37c	vacuolar protein sorting 37C (yeast)	0.344	0.158
Nedd4	neural precursor cell expressed, developmentally down-regulated 4	0.348	0.660
Ankle2	ankyrin repeat and LEM domain containing 2	0.360	0.637
Phf20	PHD finger protein 20	0.371	0.320
Vezt	vezatin, adherens junctions transmembrane protein	0.374	0.732
Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2	0.376	0.631
St13	suppression of tumorigenicity 13	0.377	0.261
Dtna	dystrobrevin alpha	0.385	0.436
Heatr6	HEAT repeat containing 6	0.392	0.383
Taf4b	TAF4B RNA polymerase II, TATA box binding, (TBP)-associated factor	0.397	0.291
Btbd9	BTB (POZ) domain containing 9	0.407	0.465
Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)	0.411	0.439
Uevld	UEV and lactate/malate dehyrogenase domains	0.415	0.431
Lsm10	U7 snRNP-specific Sm-like protein LSM10	0.425	0.333
Twsg1	twisted gastrulation homolog 1 (Drosophila)	0.435	0.684
Derl1	Der1-like domain family, member 1	0.438	0.594
Psmd10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	0.444	0.337
Hn1	hematological and neurological expressed sequence 1	0.456	0.629
Yap1	yes-associated protein 1	0.461	0.459
Tdrd7	tudor domain containing 7	0.475	0.339
Srpk3	serine/arginine-rich protein specific kinase 3	0.477	0.397
Slk	STE20-like kinase (yeast)	0.495	0.532
Chrna1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	0.506	1.096
Lonrf1	LON peptidase N-terminal domain and ring finger 1	0.509	0.592
Fam48a	family with sequence similarity 48, member A	0.512	0.249

Trp53	transformation related protein 53	0.515	0.758
Mdm4	transformed mouse 3T3 cell double minute 4	0.517	0.393
Mtap1b	microtubule-associated protein 1B	0.546	1.150
Cpd	carboxypeptidase D	0.548	1.141
Chrnb1	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	0.549	0.588
2010106G01Rik	RIKEN cDNA 2010106G01 gene	0.550	0.218
Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	0.585	0.441
Relb	avian reticuloendotheliosis viral (v-rel) oncogene related B	0.600	0.402
Wls	wntless homolog (Drosophila)	0.604	0.603
Sel1l	sel-1 suppressor of lin-12-like (C. elegans)	0.651	0.437
Rai14	retinoic acid induced 14	0.664	1.417
Lrp11	low density lipoprotein receptor-related protein 11	0.702	0.860
Fbxo17	F-box protein 17	0.714	0.441
R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	0.719	0.591
Chchd6	coiled-coil-helix-coiled-coil-helix domain containing 6	0.767	0.627
Tph1	tryptophan hydroxylase 1	0.970	0.509
Cpne2	copine II	1.040	2.847
Snapc3	small nuclear RNA activating complex, polypeptide 3	1.244	1.212

Total genes: 165

GENES REGULATED IN OPPOSITE DIRECTION

mgi_symbol	mgi_description	KO versus WT	Old versus Young
Pdha1	pyruvate dehydrogenase E1 alpha 1	-0.508	0.323
Gca	grancalcin	-0.484	0.937
Apol6	apolipoprotein L 6	-0.417	0.333
Sh2d4a	SH2 domain containing 4A	-0.394	0.478
1300010F03Rik	RIKEN cDNA 1300010F03 gene	-0.377	0.373
Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma	-0.370	0.169
Prdx5	peroxiredoxin 5	-0.357	0.474
Iscu	IscU iron-sulfur cluster scaffold homolog (E. coli)	-0.356	0.199
Trap1	TNF receptor-associated protein 1	-0.308	0.340
Ciapin1	cytokine induced apoptosis inhibitor 1	-0.270	0.183
Gsto1	glutathione S-transferase omega 1	-0.248	0.205
Eci1	enoyl-Coenzyme A delta isomerase 1	-0.240	0.163
Nudt13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	-0.239	0.243

Mrps31	mitochondrial ribosomal protein S31	-0.223	0.076
Ces4a	carboxylesterase 4A	-0.206	0.111
Poldip2	polymerase (DNA-directed), delta interacting protein 2	-0.202	0.099
Srsf11	serine/arginine-rich splicing factor 11	-0.191	0.190
Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	-0.140	0.144
Csnk1a1	casein kinase 1, alpha 1	0.146	-0.265
B3gnt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	0.154	-0.160
H2afx	H2A histone family, member X	0.220	-0.302
Mapk1	mitogen-activated protein kinase 1	0.221	-0.590
Rdx	radixin	0.252	-0.586
Fam167a	family with sequence similarity 167, member A	0.270	-0.216
Gpx7	glutathione peroxidase 7	0.275	-0.517
Smurf2	SMAD specific E3 ubiquitin protein ligase 2	0.279	-0.560
Nck2	non-catalytic region of tyrosine kinase adaptor protein 2	0.285	-0.184
Nup153	nucleoporin 153	0.295	-0.191
Zfp532	zinc finger protein 532	0.302	-0.241
Mapt	microtubule-associated protein tau	0.315	-0.194
Gm266	predicted gene 266	0.322	-0.278
Cpeb3	cytoplasmic polyadenylation element binding protein 3	0.349	-0.148
Rell1	RELT-like 1	0.354	-0.385
E2f3	E2F transcription factor 3	0.375	-0.385
Ttyh2	tweety homolog 2 (Drosophila)	0.383	-0.417
Atp7a	ATPase, Cu++ transporting, alpha polypeptide	0.391	-0.296
Ccnk	cyclin K	0.427	-0.303
Afap1l1	actin filament associated protein 1-like 1	0.434	-0.328
2210011C24Rik	RIKEN cDNA 2210011C24 gene	0.435	-0.482
Adamts3	disintegrin-like and metallopeptidase, thrombospondin type 1 motif, 3	0.499	-0.934
Tceal8	transcription elongation factor A (SII)-like 8	0.647	-1.186

Total genes: 41