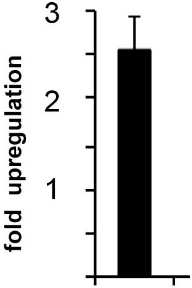

Fig. S1. gata1 is 2.57-fold upregulated in the rpl11 mutant in comparison to siblings at 48 hpf. qPCR RNA was pooled from 30 mutant or sibling embryos

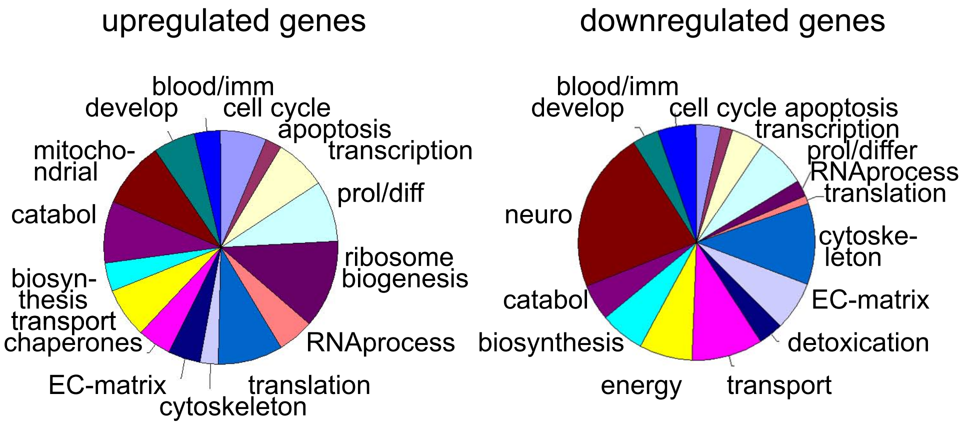

Fig. S2. rpl11 mutant had changes in expression of hundreds of genes. Among upregulated genes, the biggest fraction was represented by genes involved in ribosome biogenesis, RNA processing, and translation. Also, genes involved in catabolism and mitochondrial functions were mostly upregulated. Among downregulated genes the largest group were genes participating in the development and function of the nervous system, and followed by structural genes involved in cytoskeleton and extracellular matrix. Cutoff of 1.5 fold was used to make the chart..

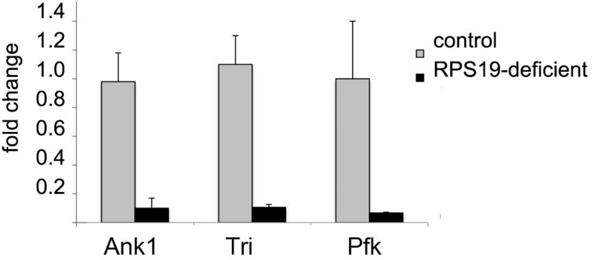

Fig. S3. RPS19-deficient mouse fetal liver cells downregulated expression of a structural protein ank1 and glycolytic enzymes Tri and Pfk

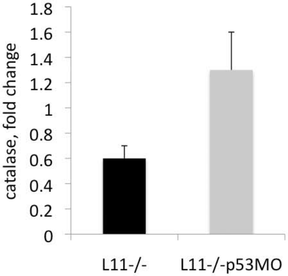

Fig. S4 Inhibition of p53 resulted in normalization of expression of many dysregulated genes.

Expresssion of a detoxifying enzyme catalase was downregulated in the mutant. p53 inhibition led to increase in catalase expression.

Figure legend to Supplementary tables 1-6.

To uncover pathways affected in the rpl11 mutant we manually analyzed microarray data using different cutoffs. Unfortunately, programs for finding pathways such as Ingenuity, do not work on zebrafish data because of insufficient annotation of zebrafish genes. We started from cutoff 3, then 2, 1.5, and 1.3. After finding that a particular pathway was affected, we used lower cutoff to see what happens with other genes from the same pathway. Often, genes from the same pathway showed changes in the same direction, and then we included them into the tables. For example, 3 mitochondrial ribosomal proteins show upregulation >2 fold but another 29 are upregulated from 1.3 to 1.9 fold. We think that it is more informative to show all these 32 genes instead of showing only 3, then you can see a trend. Another example eIFs, 21 from 23 present on the array show upregulation, only 3 are upregulated >2 fold. Again, we included all, even with smaller changes since it reveals the trend. The same is true for other pathways; some of them are discussed in the paper.

Supplementary Table 1.

Changes in expression of genes involved in regulation of cell cycle, transcription, proliferation, and apoptosis

genes	fold	function
CELL CYCLE, CHROMATIN, REPLICATION		
ccnd1 /// LOC562165: cyclin D1	+1.9	promotes cell cycle
ccng1: cyclin G1	+2.1	inhibit cell cycle
ccng2: cyclin G2	-3.1	inhibitor, suppressed by mitogenic factors
ccni: cyclin I	-2.1	function unknown, increased in cancer
ccnl1: cyclin L1	+1.3	affects splicing
cdc25b: cell division cycle 25 homolog B (S. pombe)	+2	promotes cell cycle
cdc34: cell division cycle 34 homolog (S. cerevisiae)	-1.7	
cdc2: cell division cycle 2	-1.4	G1 to S and G2 to M transition
clk4: CDC-like kinase 4	-1.7	
orc3l: origin recognition complex, subunit 3-like (yeast)	+2	DNA replication
tipin: timeless interacting protein	+2	progression of S-phase
skp2: S-phase kinase-associated protein 2 (p45)	+2	ubiquitination CDKN1B/p27kip G1/S trans
drg2: developmentally regulated GTP binding protein 2	+2	inhibits C2/M progression
tfdp2: transcription factor Dp-2	+1.9	E2F partner, G1 to S phase control
tfdp1: transcription factor Dp-1	+1.5	
cdc123: cell division cycle 123 homolog (S. cerevisiae)	+1.8	required for S phase entry
plk3: polo-like kinase 3 (Drosophila)	+1.8	M phase, phosphorylate CDC25C
rcc1: regulator of chromosome condensation 1	+1.6	chromosome condensation in the S phase
smarcd1: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1	+1.3	regulator of chromatin
gspt1: G1 to S phase transition 1	+1.6	cell cycle, translation
e2f4: E2F transcription factor 4, p107/p130-binding	+1.4	cell cycle
rcc2: regulator of chromosome condensation 2	-1.6	required for completion of mitosis and cytokinesis
pak2: p21 protein (Cdc42/Rac)-activated kinase 2	+1.3	replication
orc3l: origin recognition complex, subunit 3-like (yeast)	+2	chromosome condensation
snhg3-rcc1: SNHG3-RCC1 readthrough transcript	+1.6	early step in replication initiation
rpa1: replication protein A1, 70kDa	+1.3	initiation of eukaryotic genome replication
mcm3: minichromosome maintenance complex comp. 3	+1.3	
mcm4: minichromosome maintenance complex comp. 4	+1.4	
pwp2: PWP2 periodic tryptophan protein homolog	+2.3	a role in the early G1 phase of the cell cycle
pwp1: PWP1 homolog (S. cerevisiae)	+2.4	
ppapdc1b: phosphatidic acid phosphatase type 2 domain containing 1B	-1.7	negative regulation of cell cycle
pds5a: PDS5, regulator of cohesion maintenance, hom. A	+1.3	regulation of sister chromatid cohesion
nuf2: NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	+1.7	centromere
ncapg: non-SMC condensin I complex, subunit G	+1.6	conversion of interphase chromatin into mitotic-like
ncapd: non-SMC condensin I complex, subunit D	+1.5	condense chromosomes
hp1bp3: heterochromatin protein 1, binding protein 3	-1.3	chromatin structure and function
hmgb1: high-mobility group box 1	-1.3	binds s.s.DNA, unwind double strand
fzr1: fizzy/cell division cycle 20 related 1 (Drosophila)	+1.3	regulates ubiquitin ligase activity of the anaphase
chd4: chromodomain helicase DNA binding protein 4	-1.7	component of the nucleosome remodeling and deacetylase complex
pinx1: pin2/trf1-interacting protein 1	+2.8	inhibits telomerase
set: SET nuclear oncogene	+1.4	stimulate DNA replication
hcfc1: host cell factor C1 (VP16-accessory protein)	+1.4	nuclear co-activator, controls cell cycle
nap1l4 (nucleosome assembly protein 1-like 4)	+2.1	chromatin, tumor-suppressor
tp53: tumor protein p53	+3.3	tumor supressor
mdm2: transformed 3T3 cell double minute 2 homolog	+2.8	p53 ubiquitinase
rchy1: ring finger and CHY zinc finger domain containing 1	+1.7	promotes the ubiquitin-mediated proteosomal degradation of p53

rassf1: Ras association (RalGDS/AF-6) domain family 1	+2.5	tumor suppressor, inhibit mdm2, andcyclin D1
khdrbs: KH domain containing, RNA binding, signal transduction associated 1	-1.4	expressed in growth-arrested cells only, inhibits S phase
ptp4a3: protein tyrosine phosphatase, type 4a, member 3	+1.3	stimulates progression from G1 to S phase at mitosis
btg2: BTG family, member 2	+1.5	G1/S transition, anti-proliferative
mapk14: mitogen-activated protein kinase 14	+1.8	activated by stress, substrate p53, role in cell cycle/apopt
APOPTOSIS		
gadd45a:growth arrest and DNA-damage-inducible alpha	+3	pro-apoptotic
gadd45b: growth arrest and DNA-damage-inducible, beta	+2.4	pro-apoptotic
thyn1: thymocyte nuclear protein 1	+2.2	induction of apoptosis
bax: bcl2-associated X protein /// similar to Bax	+1.6	pro-apoptotic
tmem49: transmembrane protein 49	+1.6	stress induced, vacuolization and cell death
dapk3: death-associated protein kinase 3	+1.5	positive regulator of apoptosis
tsc22d3: TSC22 domain family, member 3	+1.9	suppress apoptosis by inhibiting FOXO3a
optn: optineurin	+1.8	part of the TNFa pathway, induces cell death
diablo: diablo homolog (Drosophila)	+1.8	promotes apoptosis
hint1: histidine triad nucleotide binding protein 1	+1.3	pro-apoptotic
casp3a: caspase 3, apoptosis-related cysteine protease a	-1.6	effector caspase pro-apoptotic
caspb: caspase b	-1.7	pro-apoptotic, inflammatory response
aplp:amyloid beta (A4) precursor-like protein	-1.7	enhancer of neuronal apoptosis
appb: amyloid beta (A4) precursor protein b	-1.7	enhancer of neuronal apoptosis
tia1: cytotoxic granule-associated RNA binding protein 1	-1.7	binds poly(A)homopolymers, DNA fragmentation
pdcd6ip: programmed cell death 6 interacting protein	-1.5	
ndrg1l: N-myc downstream regulated gene 1, like	-5.6	hydrolase, p53-mediated caspase activation/apoptosis
aifm2: apoptosis-inducing factor, mitochondrion-associated, 2	+1.4	oxidoreductase, which may play a role in mediating a p53-dependent apoptosis
ankhd1: ankyrin repeat and KH domain containing 1	+1.3	antiapoptotic, regulation of caspases
birc2: baculoviral IAP repeat-containing 2	+1.5	apoptotic suppressor
aatf: apoptosis antagonizing transcription factor	+2.7	anti-apoptotic
asns: asparagine synthetase	+1.8	anti-apoptotic
cks2: CDC28 protein kinase regulatory subunit 2	+2	essential for cyclin dependent kinases function
TRANSCRIPTION		
atf7ip: activating transcription factor 7 interacting protein	-1.9	recruit TF to general transcription apparatus
nfia: nuclear factor I/A	-4.8	activates transcription and replication
camta1: calmodulin binding transcription activator 1	-2.6	transcription activator, tumor suppressor
nr2f2: nuclear receptor subfamily 2, group F, member 2	-1.4	initiation of transcription.
top2b: topoisomerase (DNA) II beta 180kDa	-1.8	control of topological DNA states by transient breakage
g3bp2: GTPase activating protein (SH3 domain) binding protein 2	-2.9	may be involved in mRNA transport
thrap6: thyroid hormone receptor associated protein	-2.1	TRAP/Mediator complex, pol II transcription
med30: mediator complex subunit 30	-2.1	component of the Mediator complex, coactivator
rybpa: RING1 and YY1 binding protein a	-1.8	repressor of the transcriptional activity of E4TF1
tfap2b: transcription factor AP-2 beta	-2.7	transcription regulator
tfap2a; transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	-1.4	transcription regulator
hmgn3: high mobility group nucleosomal binding domain 3	-1.7	enhances transcription in the presence of thyroid hormone
prmt6: protein arginine methyltransferase 6	+2.2	modifies histones, inhibits transcription
insm1b: insulinoma-associated 1b	+1.7	transcriptional repression, CNS, pancreas
nsd1a: Nuclear receptor binding SET domain protein 1a	+2	bifunctional transcriptional regulator, methyltransferase
nat10: N-acetyltransferase 10	+2	histone acetyltransferase hTERT activation
rpap3: RNA polymerase II associated protein 3	+2	interface between RNA pol II and scaffolding proteins
rfc5: replication factor C (activator 1) 5, 36.5kDa	+1.5	elongation of DNA by DNA pol. delta and epsilon
mych: myelocytomatosis oncogene homolog	+2.2	transcription regulator, immediate early gene
mycb: myelocytomatosis oncogene b	+1.9	transcription regulator
mycn: myelocytomatosis oncogene, homolog	+1.7	transcription regulator
minal: MYC induced nuclear antigen-like	+2.3	increases after c-myc after serum activation

mybbp1a: myb-binding protein 1a	+2.5	c-myb supressor
fos: v-fos FBJ murine osteosarcoma	+8	transcription regulator, immediate early gene
fosl2: FOS-like antigen 2	+6.4	transcription regulator
junbl: jun B, like	+4.6	transcription regulator
junb: jun B	+3.6	transcription regulator
jun: v-jun sarcoma virus 17	+1.5	transcription regulator
atf1: activating transcription factor 1	+1.4	transcription regulator
atf3: activating transcription factor 3	+7.3	transcription regulator
atf4: activating transcription factor 4 (tax-responsive enhancer element B67)	+3.1	transcriptional activator, binds cAMP response element
polr2e:polymerase (RNA) II (DNA directed) polypept. E	+1.5	component of polymerase
atf5: activating transcription factor 5	+3.3	transcription regulator
cnbp:CCHC-type zinc finger, nucl acid binding protein	+2.1	sterol-mediated repression
cebpb: CCAAT/enhancer binding protein (C/EBP), beta	+3.1	transcription regulator
cebpg: CCAAT/enhancer binding prot (C/EBP), gamma	+3.1	transcription regulator
cebpz: CCAAT/enhancer binding protein zeta	+2	transcription regulator
cebpa: CCAAT/enhancer binding protein (C/EBP), alpha	+1.5	transcription regulator
htatsf1: HIV TAT specific factor 1	+1.6	transcription elongation
litaf: lipopolysaccharide-induced TNF factor	+1.6	transcription polII Charcot/Marie/Tooth disease
h1fx: H1 histone family, member X	+2.3	histone
h1fo: H1 histone family, member 0	+1.4	histone
h2afy2: H2A histone family, member Y2	-1.6	histone
h2afx: H2A histone family, member X	+1.4	histone
yy1b: YY1 transcription factor b	+1.7	may act as activator or a repressor
tceb3: transcription elongation factor B (SIII), polypeptide 3 (elongin A)	+1.6	transcription elongation
tbp: TATA box binding protein	+1.5	the core of the DNA-binding multiprotein factor TFIID
znf593: zinc finger protein 593	+2.4	negatively modulates DNA binding activity of Oct-2
zfp36: zinc finger protein 36, C3H type, homolog (mse)	+1.8	transcription regulator, response to growth factors
taf5: TAF5 RNA polymerase II, TATA box binding prtn	+1.3	(TBP)-associated factor
taf8: TAF8 RNA polymerase II, TATA box binding prtn	+1.4	(TBP)-associated factor
poldip2: polymerase (DNA-directed), delta interacting protein 2	+1.4	transcription regulator
sirtuin: (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	+1.6	deacetylates p53, TAF1b, represses transcription
sin3b: SIN3 homolog B, transcription regulator (yeast)	-1.3	transcriptional repressor, antagonize MYC
rbbp7: retinoblastoma binding protein 7	+1.5	histone-binding subunit, chromatin assembly, transcript
ets2:v-ets erythroblastosis virus E26 oncogene homolog2	+2.7	transcription regulator
gpn1: GPN-loop GTPase 1	+1.7	links pol II and chaperone/scaffolding proteins
aebp1: AE (adipocyte enhancer) binding protein 1	-2.4	transcriptional repressor, promotes proliferation
med28: mediator complex subunit 28	+1.4	component of the Mediator complex
epc2: enhancer of polycomb homolog 2 (Drosophila)	+1.5	part of NuA4 histone acetyltransferase (HAT) complex
ing3: inhibitor of growth family, member 3	+1.3	component of the NuA4 histone acetyltransferase
hif1an: hypoxia-inducible factor 1, alpha subunit inhibitor	+1.9	regulator of the adaptive response to hypoxia
esrrg: estrogen-related receptor gamma	-1.9	orphan rec, transcription activator in ligand' absence
fubp1: far upstream element (FUSE) binding protein 1	-1.4	stimulates expression of c-myc in undifferentiated cells
jarid1b: jumonji, AT rich interactive domain 1B	-1.8	histone demethylase, demethylates 'Lys-4' of histone H3
whsc2: Wolf-Hirschhorn syndrome candidate 2	+1.9	component of NELF complex, that negatively regulates the elongation of transcription by RNA polymerase II
pabpc4: poly(A) binding protein, cytoplasmic 4 (inducible form)	-1.7	bind to the poly(A), increased in activated T cells and platelets
pabpc3: poly(A) binding protein, cytoplasmic 3	+1.3	bind to the poly(A)
ndpkz2: nucleoside diphosphate kinase-Z2	-1.6	transcriptional activator of the c-Myc gene
PROLIFERATION/DIFFERENTIATION/SIGNALING		
ptena: phosphatase and tensin homolog A	-1.5	inositol phosphatase opposing PI3 kinase
ptenb: phosphatase and tensin homolog B	-1.5	inositol phosphatase opposing PI3 kinase
rbbp9: retinoblastoma binding protein 9	+2.1	confers resistance to growth-inhibitory effect of TGFb

igf2: insulin-like growth factor 2 (somatomedin A)	+1.6	growth factor
hbegf: heparin-binding EGF-like growth factor	+3.5	growth factor
igfbp1: insulin-like growth factor binding protein 1	+3.9	inhibition of proliferation
igf2bp1: insulin-like growth factor 2 mRNA binding pr 1	+1.4	inhibition of proliferation
rogbi: rogdi homolog (Drosophila)	-1.5	may act as a positive regulator of cell proliferation
grb2: growth factor receptor-bound protein	-2.2	suppressing proliferative signals
pdgfab: platelet derived growth factor alpha b	+2	growth factor
pdgfra: platelet derived growth factor receptor alpha	-1.5	growth factor receptor
pdgfrl: platelet-derived growth factor receptor-like	-2.9	tumor suppressor, inhibits proliferation
agr2/LOC799364:anterior gradient homolog 2 (Xenopus)	-2.1	differentiation
bhlhb5: basic helix-loop-helix domain contain, class B, 5	-1.7	inhibit DNA binding to TCF3/E47
rasgef1bb: RasGEF domain family, member 1Bb	+2.3	guanine nucleotide exchange factor for Ras
arl4c: ADP-ribosylation factor-like 4C	+1.5	binds/exchanges GTP and GDP, induced by cholesterol
arl5b: ADP-ribosylation factor-like 5B	+1.3	binds/exchanges GTP and GDP
arl8a: ADP-ribosylation factor-like 8A	-1.4	binds/exchanges GTP and GDP
rasd1: RAS, dexamethasone-induced 1	+2.9	morphology, growth, extracellular matrix interactions
hig1: hypoxia induced gene 1	+2.7	over expressed in cancer
csrp1: cysteine and glycine-rich protein 1	+1.8	suppresses proliferation, stress response/ development
drg1: developmentally regulated GTP binding protein 1	+1.8	suppress proliferation
pdap1: pdgfa associated protein 1	+1.7	regulate pdgfa
dusp1: dual specificity phosphatase 1	+1.7	dephosphorylates ERK2, suppress growth
ptpn12:protein tyrosine phosphatase,non-receptor type 12	+1.7	ABL-kinase regulation, cytoskeleton
ywhag1: 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide 1	+1.7	14-3-3 family, adapter protein signal transduction
fkbp5: FK506 binding protein 5	+2	progesterone receptor-associated, calcineurin inhibition
map3k7ip1: mitogen-activated protein kinase kinase kinase 7 interacting protein 1	+2	intermediate between TGFb and MAP3K7/TAK1, embryogenesis
dnajc11:DnaJ(Hsp40) homolog, subfamily C, member 11	+1.9	deleted in neuroblastoma,, tumor supressor
lyricl: lyric-like = astrocyte elevated gene-1	+1.5	promote metastasis by activating NF-kB
ywhah: tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	-1.7	conserved 14-3-3 family phosphoserine or phosphothreonine motif recognition
id1: inhibitor of DNA binding 1,	+1.5	negatively regulates cell differentiation
id2: inhibitor of DNA binding 2, dominant negative helix-loop-helix protein, a	-1.7	dominant negative helix-loop-helix protein
id4: inhibitor of DNA binding 4	-2.3	dominant negative helix-loop-helix protein
chn1: chimerin (chimaerin) 1	-1.7	GTPase-activating protein for p21-rac and a phorbol ester receptor, axon pathfinding
ldb3: LIM-domain binding factor 3, like	-1.7	couple PKC-mediated signal via its LIM domains to the cytoskeleton
stam: signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	-1.6	cytokine and growth factors signaling
egfl6: EGF-like-domain, multiple 6	-1.6	member of the EGF repeat superfamily
fzd2: frizzled homolog 2	-1.6	receptor for Wnt proteins, fetal kidney
fzd7: frizzled homolog 7 (Drosophila)	+1.3	receptor for Wnt proteins
wif1: WNT inhibitory factor 1	+2.6	inhibition of wnt pathway
ctnnbip1: catenin, beta interacting protein 1	-1.7	inhibition of wnt pathway
map2k6: mitogen-activated protein kinase kinase 6	+1.4	inflammatory cytokines,environmental stress, p38 pathw
map2k4:mitogen-activated protein kinase kinase kinase 4	+1.3	activates JUN kinases T cell development, organogenesis
map3k7ip1: mitogen-activated protein kinase kinase kinase 7 interacting protein 1	+2	mediate various signaling pathways, embryogenesis
mapkapk2: mitogen-activated protein kinase-activated protein kinase 2	+1.5	regulated through phosph. by p38 MAP kinase, stress, inflammation, nuclear export, expression, proliferation.
stat3: signal transducer and activator of transcription 3 (acute-phase response factor)	+1.9	signaling
arhgdib: Rho GDP dissociation inhibitor (GDI) beta	-1.4	GDP/GTP exchange reaction of Rho proteins, endosome, cytoskeleton, cell-matrix, suppress metastases.
arhgef4:Rho guanine nucleotide exchange factor 4	-1.6	exchange factor for RhoA and RAC1cell adhesion
ppp2r2c: protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	-2.4	negative control of cell growth and division

ywhae: tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	+1.4	adapter protein binds phosphoserine or phosphothreonin cell-cyle checkpoints,signal transd,inhibitor of apoptosis
tnip1: TNFAIP3 interacting protein 1	-1.4	inhibits TNF-induced NFkB-dependent gene expression
tifa: TRAF-interacting protein with forkhead-associated domain	+2.3	mediates IRAK1/TRAF6 interaction resulting in activation of NF-kappa-B and AP-1 pathways
rasgef: RasGEF domain family, member 1B	+1.3	GEF for KRAS, HRAS, NRAS role in cell migration
cry2: cryptochrome 2 (photolyase-like)	+1.9	blue light-dependent regulator of circadian feedback loop
reps1: RALBP1 associated Eps domain containing 1	+1.9	coordinate the cellular actions of activated EGF receptors and Ral-GTPases
ranbp1: RAN binding protein 1	+1.4	Inhibits GTP exchange on Ran.
pelp1: proline, glutamate and leucine rich protein 1	+1.4	coactivator of estrogen receptor
pdcl3: phosducin-like 3	+1.6	modulate heterotrimeric G proteins,apoptosis, cytoskelet
mtdh: metadherin	+1.6	promotes survival through PI3K-Akt
ms4a4a: membrane-spanning 4-domains, subfamily A, member 4	+1.8	signaling
hdgf2: hepatoma-derived growth factor-related protein 2	+1.5	member hepatoma-derived growth factor (HDGF) family
gps1: G protein pathway suppressor 1	+1.5	component of the COP9 signalosome complex
fgfbp1: fibroblast growth factor binding protein 1	+1.8	carry FGFs from extracellular matrix (EM) storage
ebf2: early B-cell factor 2	+1.3	Olf/EBF family transcription factors, differentiation
cops3: COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	+1.3	COP9 signalosome complex
cd81: CD81 molecule	+1.5	regulation of lymphoma cell growth
cav1: caveolin 1, caveolae protein, 22kDa	+1.5	links integrin subunits to the tyrosine kinase FYN
angptl4: angiopoietin-like 4	+1.5	hypoxia-induced. glucose metablzm, inhibit proliferation
akap1: A kinase (PRKA) anchor protein 1	+1.4	binds PKA confining it to discrete locations
adcyap1: adenylate cyclase activating polypeptide 1 (pituitary)	-1.4	stimulates adenylate cyclase increasing camp levels
limk2: LIM domain kinase 2	+1.4	phosphorylation of myelin basic protein and histone
epha2: EPH receptor A2	+1.9	receptor for ephrin-A1, -A3, -A4 and -A5
csnk2a1: casein kinase 2, alpha 1 polypeptide	+1.4	participates in Wnt signaling.
chuk: conserved helix-loop-helix ubiquitous kinase	+1.5	phosphorylates inhibitors of NF-kappa-B
gpr85: G protein-coupled receptor 85	-2.8	orphan receptor
vcp: valosin-containing protein	-1.5	mitosis, membrane fusion, spindle pole body function, and ubiquitin-dependent protein degradation
snd1: staphylococcal nuclease and tudor domain containing 1	-1.3	bridging factor between STAT6 and the basal transcription factor
sdcbp: syndecan binding protein (syntenin)	-1.3	syndecan-mediated signaling to the cytoskeleton
gtpbp1: GTP binding protein 1	+3.0	microtubule-based movement immune response
gng7: guanine nucleotide binding protein (G protein), gamma 7	-1.7	modulator or transducer in various transmembrane signaling systems, gamma subunit confers specificity
gng3: guanine nucleotide binding protein (G protein), gamma 3	-2	
gng13: guanine nucleotide binding protein (G protein), gamma 13	-6.3	
gnao1: guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	-1.4	interacts with progesterone receptor, folding, trafficking modulation of ryanodine receptor isoform-1
fkbp5: FK506 binding protein 5	+2	cis-trans prolyl isomerase modul. ryanodine receptor
fkbp1a: FK506 binding protein 1A, 12kDa	-1.3	hydroxylates HIF-1 alpha at 'Pro-564', and HIF-2 alpha.
fkbp1b: FK506 binding protein 1B, 12.6 kDa	-1.5	Functions as a cellular oxygen sensor
egln3: egl nine homolog 3 (C. elegans)	+4.5	ubiquitination of tyrosine-phosphorylated CDH1
cbll1: Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	+1.6	control of angiogenesis, inflammation, and wound healing

Supplementary table 2

Changes in expression of genes functioning in metabolism, transport, chaperones, organelles

genes	fold	function
CHAPERONES		
hsp47: heat shock protein 47	+4.5	chaperone protein for collagen
hspa9: heat shock protein 9	+2.6	centrosome duplication, cell proliferation, chaperone
hspa14: heat shock protein 14	+2.4	complex LAP2 - chromosomes
hsp90a.1: heat shock protein 90-alpha 1	+2.3	molecular chaperone, folding, degradation
dnajc11: DnaJ (Hsp40) homolog, subfamily C, member 11	+1.9	chaperone
dnajc21: DnaJ (Hsp40) homolog, subfamily C, member 21	+1.7	chaperone
hspb8: Heat shock protein, alpha-crystallin-related, b8	+1.7	chaperone
hspb1: heat shock protein, alpha-crystallin-related, 1	+1.5	chaperone
hspd1: heat shock 60kD protein 1 (chaperonin)	+1.4	chaperone
hspa4: heat shock protein 4	+1.3	chaperone
pfdn5: prefoldin 5	+1.7	a subunit of chaperone prefoldin
pfdn4: prefoldin subunit 4	+1.9	a subunit of chaperone prefoldin
dnajc21: DnaJ (Hsp40) homolog, subfamily C, member 21	+1.7	may act as co-chaperone for HSP70
unc45b: unc-45 homolog B (C. elegans)	+1.6	may act as HSP90 co-chaperone, myosin folding
xbp1: X-box binding protein 1 /// hypothetical protein LOC793034	+1.7	folding, transporting, glycosylation, degradation
calr: calreticulin	-4.1	ER, prevents export misfolded proteins
hsp90b1: heat shock protein 90kDa beta (grp94), member 1	-4.3	ER, processing, transport secreted proteins, in complex
pdia4: protein disulfide isomerase associated 4	-1.9	part of ER chaperone complex together with hsp90b1
pda6: protein disulfide isomerase family A, member 6	-1.7	part of the same complex
ppib: peptidylprolyl isomerase B (cyclophilin B)	-1.5	part of the same complex
hspa5: heat shock 70kDa protein 5 (glucose-regulated protein)	-1.8	part of the same complex
derl3: derlin 3 homolog, BQ260790	-11	degradation of misfolded glycoproteins in the ER
derl2: Der1-like domain family, member 2	-10.6	degradation of misfolded proteins in the ER
gdi1: GDP dissociation inhibitor 1	-2.1	GDP-GTP exchange reaction of rab proteins
sgta: small glutamine-rich tetratricopeptide repeat (TPR)-containing	+1.4	co-chaperone that binds directly to HSC70 and HSP70
cct7: chaperonin containing TCP1, subunit 7 (eta)	+1.5	assist the folding of proteins upon ATP hydrolysis
cct5: chaperonin containing TCP1, subunit 5 (epsilon)	+1.5	assist the folding of proteins upon ATP hydrolysis
cct2: chaperonin containing TCP1, subunit 2 (beta)	+1.3	assist the folding of proteins upon ATP hydrolysis
xbp1: X-box binding protein 1	+1.7	activates unfolded protein response
pscd1: pleckstrin homology, Sec7 and coiled-coil domains 1(cytohesin 1)	+1.5	GDP with GTP exchange, protein sorting
DETOXICATION		
sod2: superoxide dismutase 2, mitochondrial	-1.4	turn superoxide radicals into hydrogen peroxide
sod1:superoxide dismutase 1, soluble,amyotrophic lateral sclerosis 1	-1.4	turn superoxide radicals into hydrogen peroxide
cat: catalase	-1.9	destroys hydrogen peroxide
prdx2: peroxiredoxin 2	-1.3	reduces hydrogen peroxide and alkyl hydroperoxides
prdx1: peroxiredoxin 1	+1.8	
prdx5: peroxiredoxin 5	-1.3	
txndc9: thioredoxin domain containing 9	-1,4	
txnl4a: thioredoxin-like 4A	-1.3	
txnrd3: thioredoxin reductase 3	+1.3	
txn: thioredoxin	+1.8	reduction of overoxidized peroxiredoxins
txnrd1: thioredoxin reductase 1	+1.3	reduces thioredoxins
txnip: thioredoxin interacting protein	+1.9	inhibits thioredoxin activity
glrx3: glutaredoxin 3	+1.7	reduction of protein thiols, antioxidant
gstp1: glutathione S-transferase pi	+1.7	conjugation of reduced glutathione
gsr: glutathione reductase	+1.9	
gstm3: glutathione S-transferase M3 (brain)	+1.3	
sesn3: sestrin 3	+1.9	antioxidant modulators of peroxiredoxins
aldh2b: aldehyde dehydrogenase 2b	-2.1	oxidases aldehydes , acetaldehyde oxidation
adh8b: aldehydel dehydrogenase 8b	-1.8	oxidases aldehydes
aldh1b1: aldehyde dehydrogenase 1 family, member B1	-2.1	oxidases aldehydes acetaldehyde oxidation

aldh7a1: aldehyde dehydrogenase 7 family, member A1	-1.6	oxidases aldehydes, lysine catabolism,
aldh91a1: aldehyde dehydrogenase 9 family, member A1	-1.4	oxidases aldehydes, GABA biosynthesis
TRANSPORT		
mvp, major vault protein	+2.3	nucleo-cytoplasmic transport
nup43: nucleoporin 43	+2.2	nucleo-cytoplasmic transport
nup50: nucleoporin 50	+1.7	nucleo-cytoplasmic transport
nupl1: nucleoporin like 1	+1.8	nucleo-cytoplasmic transport
nup62: nucleoporin 62	+1.8	nucleo-cytoplasmic transport
nup35: nucleoporin 35	+1.8	nucleo-cytoplasmic transport
nup88: nucleoporin 88	+1.5	nucleo-cytoplasmic transport
nip7: nuclear import 7 homolog (S. cerevisiae)	+2	
slc16a9b:solute carrier family 16(monocarboxylic acid transporters)	+3	proton-linked monocarboxylate transporter
sec22ba: SEC22 vesicle trafficking protein homolog Ba	+2.9	ER-Golgi protein trafficking
abcf1: ATP-binding cassette, sub-family F (GCN20), member 1	+2.8	ATP transporter
abce1: ATP-binding cassette, sub-family E (OABP), member 1	+1.6	ATP transporter
slc7a3: solute carrier family 7 (aa transporter, y+ system), member 3	+1.9	transport of cationic amino acids
grpel1: GrpE-like 1, mitochondrial	+1.9	protein translocation inner membrane into the mit matri
slc1a3:solute carrier family1(glial high affinity glutamate transporter	+1.7	glutamate transporter
slc1a4: solute carrier family 1 (glutamate/neutral aa transporter) 4	+1.5	glutamate transporter
slc3a2: solute carrier family 3, member 2	+1.3	activators of dibasic and neutral amino acid transport
slc20a1b: solute carrier family 20, member 1b	+1.4	transporter
slc11a2: solute carrier family 11, member 2	+1.5	proton-coupled divalent metal ion transporters
snx5: sorting nexin 5	+1.6	may be a retromer unit, endosomes to Golgi mannose-6
snx7: sorting nexin 7	+1.5	transporter
mal: T-cell differentiation protein	+1.7	transporter
ntd5: ntl-dependent gene 5= apolipoprotein H	+1.6	lipoprotein metabolism, coagulation
ldlrad2:low density lipoprotein receptor class A domain containing 2	+2.5	lipoprotein receptor
apoh: apolipoprotein H (beta-2-glycoprotein I)	+1.6	transporter extracellular space
apod: apolipoprotein D	+1.5	transporter extracellular space
ipo9: importin 9	+2.4	transporter, nucleus
ipo4: importin 4	+1.7	transporter, nucleus
ipo5: importin 5	+1.5	transporter, nucleus
ap1s1: adaptor-related protein complex 1, sigma 1 subunit	+1.4	transporter
ap1s3: adaptor-related protein complex 1, sigma 3 subunit	+1.5	transporter
abcb7: ATP-binding cassette, sub-family B (MDR/TAP), member 7	+1.3	transporter
tspo: translocator protein (18kDa)	+1.6	transmembrane protein
gpc6: glypican 6	+1.7	transmembrane protein
tnpo3: transportin 3	+2.2	transporter
magt1: magnesium transporter 1	+1.7	transporter
chac1: ChaC, cation transport regulator homolog 1 (E. coli)	+1.4	
golt1b: golgi transport 1 homolog B (S. cerevisiae)	+1.3	
vamp3: vesicle-associated membrane protein 3 (cellubrevin)	+1.3	targeting/fusion of transport vesicles to target membran
srp72: signal recognition particle 72kDa	+1.5	targets secretory proteins to rough ER membrane
rab21: RAB21, member RAS oncogene family	+1.4	integrin trafficking
yif1a: Yip1 interacting factor homolog A (S. cerevisiae)	+1.5	transport between endoplasmic reticulum and Golgi
yipf5: Yip1 domain family, member 5	+1.3	transport between endoplasmic reticulum and Golgi
prickle: prickle homolog 1 (Drosophila)	+1.5	Nuclear translocation receptor
atp2a1l:ATPase, Ca++ transporting, cardiac muscle, fast twitch 1like	-2.6	bring Ca+ to sarcoplasmic reticulum muscle contraction
atp2a1: ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	-1.7	Ca++ transporting
atp1a1b: ATPase, Na+/K+ transporting, alpha 1b polypeptide	-1.9	Vesicular transport
atp1a3a: ATPase, Na+/K+ transporting, alpha 3a polypeptide	-2.2	vesicle-mediated transport, fusion protein
atp1b2a: ATPase, Na+/K+ transporting, beta 2a polypeptide	-1.7	vesicle-mediated transport, fusion protein
atp6v1e1: ATPase, H+ transporting, lysosomal, V1 subunit E isof 1	-1.9	acidification of eukaryotic intracellular organelles
atp6v1d: ATPase, H+ transporting, V1 subunit D	-1.7	acidification of eukaryotic intracellular organelles
atp6v1h: ATPase, H+ transporting, lysosomal, V1 subunit H	-1.5	acidification of eukaryotic intracellular organelles
atp6v1g1: ATPase, H+ transporting, V1 subunit G isoform 1	-1.4	acidification of eukaryotic intracellular organelles
atp6v0d1: ATPase, H+ transporting, V0 subunit D isoform 1	-2.0	transporter
atp6v1b2: ATPase, H+ transporting, lysosomal, V1 sbunit B2	-1.6	transporter

rab3c: RAB3C, member RAS oncogene family	-2.0	vesicles transport
flot1: flotillin 1	-1.7	endocytosis
nsf: N-ethylmaleimide-sensitive factor	-2.0	fusion of transport vesicles within the Golgi cisternae
syt1: synaptotagmin I	-2.1	synaptic vesicles trafficking and exocytosis
vldlr: very low density lipoprotein receptor	-1.9	binds VLDL and transports it into cells by endocytosis
sypb /// zgc:136469: synaptophysin b	-1.9	fusion of synaptic vesicles in brain/endocrine cells
apob: novel protein similar to vertebrate apolipoprotein B	-1.8	transport of fatty acids
apom: apolipoprotein M	-1.6	associated with high density lipoproteins
apoc2: apolipoprotein C-II	-1.6	activates lipoprotein lipase hydrolyzing triglycerides
rtn1b: reticulon 1b	-1.8	neuroendocrine secretion, membrane trafficking
slc39a7: solute carrier family 39 (zinc transporter), member 7	-1.6	Zn transport
slc17a5: solute carrier family 17, member 5	-2.9	anion/sugar transporter
slc40a1: solute carrier family 40, member 1	-1.5	transporter
slc7a6os: solute carrier family 7, member 6 opposite strand	-1.4	
slc16a12: solute carrier family 16, member 12	-1.4	monocarboxylic acid transporter 12
tcn2: transcobalamin II; macrocytic anemia	-1.7	iron-regulated transporter
syt4: synaptotagmin IV	-1.6	transporter, extracellular space
ldb3: LIM-domain binding factor 3, like	-1.7	transporter
gja1: gap junction protein, alpha 1, 43kDa	-1.4	transporter
etfa: electron-transfer-flavoprotein, alpha polypeptide	-1.4	transporter
arpp19: cAMP-regulated phosphoprotein 19	-1.3	transporter
apba2: amyloid beta (A4) precursor protein-binding, family A, member 2	-1.4	transporter
ap3m2: adaptor-related protein complex 3, mu 2 subunit	-1.5	transporter
ap3s: adaptor-related protein complex 3, sigma 2 subunit	-1.4	transporter
abcd3a: ATP-binding cassette, sub-family D (ALD), member 3a	-1.4	transporter
abcc5: ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.8	transporter
sepp1: selenoprotein P, plasma, 1	-2.3	transporter
nkain1: Na+/K+ transporting ATPase interacting 1	-1.3	
vamp2: vesicle-associated membrane protein 2 (synaptobrevin 2)	-2.1	targeting/fusion of transport vesicles to target membrane
rab1b: RAB1B, member RAS oncogene family	-1.3	protein transport between the ER and Golgi
rab5a: RAB5A, member RAS oncogene family	-1.3	fusion of plasma membranes and early endosomes
rab7a: RAB7A, member RAS oncogene family	-1.5	traffic in late endosomes and lysosomes
rac3: ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	-1.6	small GTPase, cell spreading, formation of actin-based protusions including lamellipodia and membrane ruffles
CA++-BINDING PROTEINS		
calm1a/calm1b/calm2a /calm2b /calm3a /calm3b: calmodulin	-1.6	Ca ion binding
pvalb: parvalbumin	-1.8	Ca ion binding
pvalb3: parvalbumin 3	-2.0	Ca ion binding, muscle relaxation
pvalb8: parvalbumin 8	-1.8	Ca ion binding
pvalb1: parvalbumin 1	-1.6	Ca ion binding
calb2: calbindin 2, (calretinin)	-2.0	Ca ion binding, auditory neurons, cancer
rcn3: reticulocalbin 3, EF-hand calcium binding domain	-2.0	Ca ion binding
calb2l: calbindin 2, like	-1.9	intracellular Ca-binding protein troponin C superfamily
atp2b3a: ATPase, Ca++ transporting, plasma membrane 3a	-1.8	Ca membrane transport
camk2d2: Calcium/calmodulin-dependent protein kinase	-2.3	signals to histone deacetylase 4,cardiac cells
anxa1a: annexin A1a	+1.4	calcium-dependent phospholipid binding proteins
anxa1c /// zgc:86853: annexin A1c	+1.6	calcium-dependent phospholipid binding proteins
anxa4 /// LOC792474: similar to annexin A4	-2.2	calcium-dependent phospholipid binding proteins
anxa2a: annexin A2a	+2.1	calcium-dependent phospholipid binding proteins
axa11: annexin A11	-1.3	calcium-dependent phospholipid binding proteins
axa2: annexin A2	+2	calcium-dependent phospholipid binding proteins
cherp: calcium homeostasis endoplasmic reticulum protein	+1.4	
gca: grancalcin, EF-hand calcium binding protein	-1.4	
hpca: hippocalcin	-1.4	
hrc: histidine rich calcium binding protein	-1.4	
ocm: oncomodulin	+1.4	high-affinity calcium ion-binding protein
HORMONES		

ins: preproinsulin	+1.8	glucose uptake and conversion to glycogen
prl: prolactin	+4	anti-apoptotic
fst: follistatin	+2.6	opposes activin, BMP4, induces D1cyclin
sgk1: serum/glucocorticoid regulated kinase 1	+1.9	stimulates glycogenolysis and proteolysis
neurod: neurogenic differentiation	-3.9	insuin production
ENERGY PRODUCTION		
pygl: phosphorylase, glycogen (Hers/glycogen storage dis type VI)	-1.8	glycolysis, production of glucose from glycogen, liver
pygmb: phosphorylase, glycogen (muscle) b	-1.6	glycolysis, production of glucose from glycogen, muscl
gpib: glucose phosphate isomerase b	-1.9	glycolysis, glucose/fructose phosphate isomerization
pfkm: phosphofructokinase, muscle	-1.8	glycolysis, makes fructose 1.6-bisphosphate
aldoab: aldolase a, fructose-bisphosphate, b	-1.7	form dihydroxyacetone and glyceraldehyde 3-phosphate
tpi1a: triosephosphate isomerase 1a	-3	dihydroxyacetone phosphate into glyceraldehyde 3-phos
pgam2: phosphoglycerate mutase 2 (muscle)	-1.9	glycolysis, convert 3- into 2-phosphoglycerate
pklr: pyruvate kinase, liver and RBC	-1.3	glycolysis, forms pyruvate
ldha: lactate dehydrogenase A4	-1.8	covert lactate into pyruvate
pfkfb3: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	+2.6	synthesis of biphosphate that supresses glycolysis
pfkfb4: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	+1.4	synthesis of biphosphate that supresses glycolysis
fbp1: fructose-1,6-bisphosphatase 1	-1.4	hydrolysis of 1,6-bisphosphate
g6pc: glucose-6-phosphatase, catalytic subunit	+2.4	catalyses glucose-6-phosphate hydrolysis
aldoal1: aldolase A-like 1	-1.7	
idh1: isocitrate dehydrogenase 1 (NADP+), soluble	-1.3	
sogdh: oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	-1.6	citric acid cycle
mdh1a: malate dehydrogenase 1a, NAD (soluble)	-1.5	citric acid cycle
ogdh: oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	-1.6	citric acid cycle
got2b: glutamic-oxaloacetic transaminase 2b	-1.5	citric acid cycle
got1: glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	-1.4	citric acid cycle
lctla: lactase-like a	-6.4	lactose hydrolysis
gpd1b: glycerol-3-phosphate dehydrogenase 1b	-2.1	
slc25a1: solute carrier family 25, member 1	-1.6	citrate transporter
ucp2: uncoupling protein 2 (mitochondrial, proton carrier)	-1.5	transporter
mdh2: malate dehydrogenase 2, NAD (mitochondrial)	-1.4	citric acid cycle, converts malate into oxaloacetate
gatm:glycine amidinotransferase (L-arginine:glycine)	-1.7	creatine biosynthesis
ckmb: creatine kinase, muscle b	-1.3	energy homeostasis. reversibly catalyze the transfer of phosphate between ATP and various phosphogens such as creatine phosphate.
ckma: creatine kinase, muscle a	-1.3	
ckb: creatine kinase, brain	-3.2	
atp5a1:glutaryl-Coenzyme A dehydrogenase, ATP synthase	-1.3	subunit of ATP synthase
atp5j: ATP synthase, H+ transporting, mitochondrial F0 complex, F6	-1.5	subunit of ATP synthase
atp5j: ATP synthase, , subunit F6	+1.3	subunit of ATP synthase
cox17: COX17 cytochrome c oxidase assembly homolog (yeast)	+2.1	subunit of cytochrome c oxidase (COX), respiration
cox4nb: cox4 neighbor	+1.8	subunit of cytochrome c oxidase (COX), respiration
cox7a2l: cytochrome c oxidase subunit VIIa polypeptide 2 like	+1.2	subunit of cytochrome c oxidase (COX), respiration
cox6b1: cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	-1.5	
nnt: nicotinamide nucleotide transhydrogenase	-1.3	transhydrogenation between NADH and NADP
ndufs6: NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	+1.3	transfer electrons from NADH to the respiratory chain
acaa2: acetyl-Coenzyme A acyltransferase 2	-1.3	first step in mitochondrial fatty acid beta-oxidation
hadha: hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit	-1.6	beta-oxidation of fatty acids
hadhb: hydroxyacyl-Coenzyme A dehydrogenase, beta subunit	-2.1	beta-oxidation of fatty acids
acadl: acyl-Coenzyme A dehydrogenase, long chain	-1.8	beta-oxidation of straight-chain fatty acid
BIOSYNTHESIS		
me3: malic enzyme 3, NADP(+)-dependent, mitochondrial	-1.6	generate NADP+ for biosynthesis
Nme1: non-metastatic cells 1, protein (NM23A)	-1.6	synthesis of nucleoside triphosphates other than ATP
Pank3: pantothenate kinase 3	-1.5	biosynthesis of coenzyme A (CoA)
elovl4: elongation of very long chain fatty acids -like 4	-3.4	fatty acids synthesis

hsdl2: hydroxysteroid dehydrogenase like 2	-1.6	sterol synthesis, transporter
scp2: sterol carrier protein 2	-1.4	sterol synthesis, transporter
bckdk: branched chain ketoacid dehydrogenase kinase	-1.5	biosynthesis
pdip5: protein disulfide isomerase-related protein (provisional)	-1.7	formation and rearrangement of disulfide bonds
papss1: 3'-phosphoadenosine 5'-phosphosulfate synthase 1	-1.5	
papss2: 3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.7	
sulf2: sulfatase 2	-1.6	removes 6-O-sulfate groups from heparan sulfate
insig1: insulin induced gene 1	+2.1	negative regulation of cholesterol synthesis
papss2: 3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.7	sulfation
serinc1: serine incorporator 1	-1.7	incorporates serine into phosphatidylserine /sphingolipi
adsl: adenylosuccinate lyase	-1.3	synthesis of purines
gnmt: glycine N-methyltransferase	-1.3	converts S-adenosyl-L-methionine (along with glycine) to S-adenosyl-L-homocysteine and sarcosine
ces2: carboxylesterase 2 (intestine, liver)	-2.3	
ctps: CTP synthase	+1.8	CTP synthesis
cad: carbamoyl-phosphate synthetase 2, aspartate transcarbamylase	+1.9	pyrimidine nucleotides byosynthesis
uprt: uracil phosphoribosyltransferase (FUR1) homolog (S. cerev.)	+1.8	pyrimidine nucleotides byosynthesis
impdh2: IMP (inosine monophosphate) dehydrogenase 2	+1.6	guanine nucleotides synthesis
pck1: (phosphoenolpyruvate carboxykinase 1	+4	gluconeogenesis formation of phosphoenolpyruvate
elovl5: ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	+3.2	
hsd17b12a: hydroxysteroid (17-beta) dehydrogenase 12a	+1.5	3-ketoacyl-CoA to 3-hydro fatty acid/estrone to estradio
gad1: glutamate decarboxylase 1 (brain, 67kDa)	-1.9	catalyzes the production of GABA
acat1: acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	-1.6	forms acetoacetyl-CoA from two mol of acetyl-CoA deficiency - alpha-methylacetoaceticaciduria disorder
adsl: adenylosuccinate lyase	-1.3	synthesis of purines, AMP
asns: asparagine synthetase	+1.8	synthesis of asparagine
gale: UDP-galactose-4-epimerase	+1.3	UDP-glucose to UDP-galactose and UDP-N-acetylglucosamine to UDP-N-acetylgalactosamine
gmppb: GDP-mannose pyrophosphorylase B	+1.4	production of N-linked oligosaccharides
hsd17b12: hydroxysteroid (17-beta) dehydrogenase 12	+1.5	3-ketoacyl-CoA to 3-hydroxyacyl, fatty acid elongation
hsd17b8: hydroxysteroid (17-beta) dehydrogenase 8	-1.7	estrogens and androgens
kmo: kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-1.8	synthesis of quinolinic acid
ftcd: formiminotransferase cyclodeaminase	-1.8	one-carbon unit from formiminoglutamate to folate
lfng: LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	+1.6	adding an N-acetylglucosamine to the fucose in recepto
mat1a: methionine adenosyltransferase I, alpha	-1.4	forms S-adenosylmethionine from methionine and ATP
nmnat2: nicotinamide nucleotide adenylyltransferase 2	-1.6	NAD (NADP) biosynthetic pathway
sult6b1: sulfotransferase family, cytosolic, 6B, member 1	+1.8	may catalyze the sulfate conjugation
nat13: N-acetyltransferase 13	+1.6	acetylates N-ends of polypeptides
nat10: N-acetyltransferase 10	+2.0	
nat5: N-acetyltransferase 5	+1.4	
nat8l: N-acetyltransferase 8-like	+1.6	
ogt: O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	-1.4	adds N-acetylglucosamine in O-glycosidic linkage to Se or Thre residues
padi2: peptidyl arginine deiminase, type II	-1.8	post-translational deimination of proteins
phgdh: phosphoglycerate dehydrogenase	+1.3	rate-limiting step in the serine biosynthesis
ppil3: peptidylprolyl isomerase (cyclophilin)-like 3	+1.8	isomerization peptid bonds, protein folding
ppat: phosphoribosyl pyrophosphate amidotransferase	+2.2	purine nucleotide biosynthesis
psat1: phosphoribosyl pyrophosphate amidotransferase	+1.3	3-phosphohydroxypyruvate to phosphoserine
nsfl1c: NSFL1 (p97) cofactor (p47)	-1.3	regrowth of Golgi cisternae from mitotic Golgi fragmen
mboat1: membrane bound O-acyltransferase domain containing 1	+2.2	converts lysophosphatidylethanolamine/serine to phosphatidylethanolamine and phosphatidylserine
gch1: GTP cyclohydrolase 1 (dopa-responsive dystonia)	-1.3	rate-limiting enzyme in tetrahydrobiopterin (BH4) biosynthesis
odc1, ornithine decarboxylase 1	+2.4	polyamine biosynthesis ornithine to putrescine,
pcbd1: 6-pyruvoyl-tetrahydropterin synthase	+1.4	tetrahydrobiopterin biosynthesis
CATABOLISM		
cyp24a1l: cytochrome P450, family 24, subfamily A, polypeptide 1	+10.3	vitamin D catabolism

cyp27c1: cytochrome P450, family 27, subfamily C, polypeptide 1	+2.4	
cathepsin L, 1 b	+3	lysosomal cysteine proteinase
ctsl1a: cathepsin L1, a	+1.8	lysosomal cysteine proteinase
ctsll: cathepsin L, like	+5.2	lysosomal cysteine proteinase
ctsf: cathepsin F	-1.4	peptidase
tbl3: transducin (beta)-like 3	+1.7	peptidase
psap: prosaposin	+1.8	catabolize glycosphingolipids
gcdhl: glutaryl-Coenzyme A dehydrogenase, like	-6.1	degradative Lys, HLys, and Thp metabolism
6-29kD-proteinase, cathepsin K	-2.1	bone resorption
fpgs: folylpolyglutamate synthase	+2.6	folate metabolism
prmt7: protein arginine N-methyltransferase 7	+2.1	arginine methylation, ST, RNA transport, and splicing
prmt1: protein arginine methyltransferase 1	+1.3	
prmt3: protein arginine methyltransferase 3	+3.6	
prmt5: protein arginine methyltransferase 5	+1.9	
gldc /// LOC795637: glycine dehydrogenase (decarboxylating	+1.8	degradation of glycine
smfn: small fragment nuclease	+1.8	degrades DNA
mtap: methylthioadenosine phosphorylase	+1.7	salvage of adenine and methionine
cstf3: cleavage stimulation factor, 3' pre-RNA, subunit 3	+1.8	pre-mRNA 3'-end formation, polyadenilation
cbs: cystathionine-beta-synthase	+1.7	transsulfuration, first step homocysteine to cystathionin
aga: aspartylglucosaminidase	+1.7	catabolism of N-linked oligosaccharides
psme3: proteasome activator subunit 3	+1.5	cleave peptides in an ATP/ubiquitin-dependent process
psmb6: proteasome (prosome, macropain) subunit, beta type, 6	+1.3	proteasome
psmd1:proteasome (prosome macropain) 26S subunit, non-ATPase,1	-1.4	proteasome
psmd2:proteasome (prosome macropain) 26S subunit, non-ATPase,2	-1.4	proteasome
prss36: protease, serine, 36	+1.5	protease, extracellular space
aup1: ancient ubiquitous protein 1	+1.9	degradation of misfolded proteins by the proteasome
glud2: glutamate dehydrogenase 2	-1.3	glutamate recycling during neurotransmission
ppap2a: phosphatidic acid phosphatase type 2A	+1.5	phosphatase
thop1: thimet oligopeptidase 1	-1.5	oligopeptidase
dual specificity phosphatase 6	+1.4	phosphatese
st14: suppression of tumorigenicity 14 (colon carcinoma)	+1.4	peptidase
rhbdl3: rhomboid, veinlet-like 3 (Drosophila)	+2.4	peptidase
ncln: nicalin homolog (zebrafish)	+2.1	peptidase
cpn1: carboxypeptidase N, polypeptide 1	+1.3	peptidase
cpe: carboxypeptidase E	-1.7	peptidase
cast: calpastatin	+1.3	peptidase
2310051m13: RIKEN cDNA 2310051M13 gene	+2.3	peptidase
ADAM23: ADAM metallopeptidase domain 23	-2.3	peptidase
abhd14e: abhydrolase domain containing 14B	-1.5	
ardia: ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	+1.5	
asnsd1: asparagine synthetase domain containing 1	+2	
bckdha: branched chain keto acid dehydrogenase E1, alpha peptide	+1.3	dehydrogenase
enpp1: ectonucleotide pyrophosphatase/phosphodiesterase 1	-1.3	ATP hydrolysis, pyrophosphate levels
fahd2a: fumarylacetoacetate hydrolase domain containing 2A	-1.5	may have hydrolase activity
gnpda1: glucosamine-6-phosphate deaminase 1	+1.5	D-glucosamine-6-phosphate into D-fructose-6-phosphat
lipa: lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	-1.3	hydrolysis of cholesteryl esters and triglycerides
mettlb2: methyltransferase like 2B	+1.9	probable methyltransferase (by similarity)
qdpr: quinoid dihydropteridine reductase	+2.9	pterin-dependent aromatic a.a. hydroxylating systems
rexo2: REX2, RNA exonuclease 2 homolog (S. cerevisiae)	+1.8	3'-to-5' exoribonuclease on small oligoribonucleotides
rpe: ribulose-5-phosphate-3-epimerase	+1.5	pentose phosphate cycle
sardh: sarcosine dehydrogenase	-1.4	oxidative demethylation of sarcosine to glycine
sat1: spermidine/spermine N1-acetyltransferase 1	+1.5	catabolic pathway of polyamine metabolism
tdh: L-threonine dehydrogenase	+1.5	L-threonine degradation
tktl2: transketolase-like 2	+1.5	pentose phosphate pathway
hpdl: 4-hydroxyphenylpyruvate dioxygenase-like	+3	aromatic amino acid family metabolic process
ola1: Obg-like ATPase 1	+1.4	ATP catabolic process
nob1: NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	+1.8	may play a role in mRNA degradation

usp36: ubiquitin specific peptidase 36	+2.2	cleaving ubiquitin
usp1: ubiquitin specific peptidase 1	+1.4	cleaving ubiquitin
ubl5: ubiquitin-like 5	+1.3	reversible modulator of ubiquitin function
ubtd2: ubiquitin domain containing 2	-1.6	regulatory?
urm1: ubiquitin related modifier 1 homolog (S. cerevisiae)	+1.3	reversible modulator of ubiquitin function
uba: ubiquitin-like modifier activating enzyme 2	+1.4	E1 ligase for SUMO proteins
ube2v2: ubiquitin-conjugating enzyme E2 variant 2	+1.3	non-canonical poly-ubiquitin chains, activates NF-kB
uchl3: ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	+1.5	hydrolyzes bond C-term. glycine of ubiquitin or NEDD
rbx1: ring-box 1	+1.4	mediate the ubiquitination
fbxo42: F-box protein 42	+1.3	E3 ubiquitin ligase complex
fbxo28: F-box protein 28	+1.3	E3 ubiquitin ligase complex
wwp2: WW domain containing E3 ubiquitin protein ligase 2	-1.6	transfers the ubiquitin to targeted substrates
OTHER MITOCHONDRIAL		
clic4:chloride intracellular channel 4	+1.4	transporter
mthfd2: methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	+1.4	glyoxylate and dicarboxylate metabolism
slc25a33: solute carrier family 25, member 33	+1.4	transporter
hibadh: 3-hydroxyisobutyrate dehydrogenase	+1.3	dehydrogenase
auh: AU RNA binding protein/enoyl-Coenzyme A hydratase	+1.6	metabolism of RNAs and leucine
ndufab1: NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	+1.3	carrier of the growing fatty acid chain in fatty acid biosynthesis in mitochondria
crls1: cardiolipin synthase	+2.5	phosphatidyltransferase
fxn: frataxin	+2.6	iron transport and respiration
pprc1: peroxisome proliferator-activated receptor gamma, coactivator-rel 1	+2.3	activates mitochondrial biogenesis through NRF1
ptpmt1: protein tyrosine phosphatase, mitochondrial 1	+2.2	dephosphorylation of mitochondrial proteins, ATP mak
timm44: translocase of inner mitochondrial membrane 44 homolog	+2.1	component of PAM complex peptide translocation, AT
mrrf: mitochondrial ribosome recycling factor	+2	release of ribosomes from messenger RNA, translation
grpel1: GrpE-like 1, mitochondrial	+2	component of PAM complex
slc25a25: solute carrier family 25 (mitochondrial phosphate carrier)	+1.9	calcium-dependent mitochondrial solute carrier.
slc25a26: solute carrier family 25, member 26	+2.0	S-adenosylmethionine (SAM) transport
ucp4: uncoupling protein 4	+1.9	uncoupling oxidative phosphorylation
timm50: translocase of inner mitochondrial membrane 50 homolog	+1.8	component of the TIM23 complex proteins translocatio
timm9: translocase of inner mitochondrial membrane 9 homolog	+1.5	transporter
timm17a: translocase of inner mitochondrial membrane 17 homolog	+1.4	transporter
timm8b: translocase of inner mitochondrial membrane 8 homolog B	+1.6	chaperone, hydrophobic proteins into the inner membra
tomm20: translocase of outer mitochondrial membrane 20 homolog	+1.8	transport cytosolically synthesized mitochondrial protei
atpaf2: ATP synthase mitochondrial F1 complex assembly factor 2	+1.7	ATP synthase
atpaf1: ATP synthase mitochondrial F1 complex assembly factor 1	+1.5	
tomm22: translocase of outer mitochondrial membrane 22 homolog	+1.5	transport cytosolically synthesized mitochondrial protei
tomm40: translocase of outer mitochondrial membrane 40 homolog	+1.5	transport cytosolically synthesized mitochondrial protei
timm17a: translocase of inner mitochondrial membrane 17 homol A	+1.4	component of the TIM23 complex
timm44: translocase of inner mitochondrial membrane 44 homolog	+2.1	transporter
bcat2: branched chain aminotransferase 2, mitochondrial	+1.3	catabolism of leucine, isoleucine, and valine
pck2: phosphoenolpyruvate carboxykinase 2 (mitochondrial)		
atad3b: ATPase family, AAA domain containing 3B	+1.6	stabilization mtDNA-protein complexes called nucleoid
atad3a: ATPase family, AAA domain containing 3A	+1.6	H+ transporting, mitochondrial F0 complex
slc25a4: solute carrier family 25, member 4	-2.7	adenine nucleotide translocator
fastkd2: FAST kinase domains 2	+1.9	mitochondrial apoptosis, cytochrome c oxidase
phb: prohibitin	+2.1	inhibit DNA synthesis and proliferation increases 3-fold in G1 phase, respiration aging
phb2: prohibitin 2	+1.6	mediator of transcriptional repression by nuclear hormone receptors respiration aging
mrpl3: mitochondrial ribosomal protein L3	+1.4	mitochondrial ribosomal protein
mrpl9: mitochondrial ribosomal protein L9	+1.8	mitochondrial ribosomal protein
mrpl12: mitochondrial ribosomal protein L12	+1.8	mitochondrial ribosomal protein

mrpl14: mitochondrial ribosomal protein L14	+1.3	mitochondrial ribosomal protein
mrpl15: mitochondrial ribosomal protein L15	+1.8	mitochondrial ribosomal protein
mrpl18: mitochondrial ribosomal protein L18	+1.4	mitochondrial ribosomal protein
mrpl19: mitochondrial ribosomal protein L19	+1.6	mitochondrial ribosomal protein
mrpl27: mitochondrial ribosomal protein L27	+1.9	mitochondrial ribosomal protein
mrpl28: mitochondrial ribosomal protein L28	+1.4	mitochondrial ribosomal protein
mrpl30: mitochondrial ribosomal protein L30	+1.9	mitochondrial ribosomal protein
mrpl35: mitochondrial ribosomal protein L35	+1.6	mitochondrial ribosomal protein
mrpl37: mitochondrial ribosomal protein L37	+1.5	mitochondrial ribosomal protein
mrpl38: mitochondrial ribosomal protein L38	+1.4	mitochondrial ribosomal protein
mrpl42: mitochondrial ribosomal protein L42	+2.1	mitochondrial ribosomal protein
mrpl44: mitochondrial ribosomal protein L44	+1.4	mitochondrial ribosomal protein
mrpl45: mitochondrial ribosomal protein L45	+1.6	mitochondrial ribosomal protein
mrpl48: mitochondrial ribosomal protein L48	+1.5	mitochondrial ribosomal protein
mrpl52: mitochondrial ribosomal protein L52	+1.9	mitochondrial ribosomal protein
mrpl53: mitochondrial ribosomal protein L53	+1.5	mitochondrial ribosomal protein
mrpl54: mitochondrial ribosomal protein L54	+1.3	mitochondrial ribosomal protein
mrpl55: mitochondrial ribosomal protein L55	+1.5	mitochondrial ribosomal protein
mrp63: mitochondrial ribosomal protein 63	+1.6	mitochondrial ribosomal protein
mrps5: mitochondrial ribosomal protein S5	+1.5	mitochondrial ribosomal protein
mrps6: mitochondrial ribosomal protein S6	+1.3	mitochondrial ribosomal protein
mrps10: mitochondrial ribosomal protein S10	+1.8	mitochondrial ribosomal protein
mrps15: mitochondrial ribosomal protein S15	+1.8	mitochondrial ribosomal protein
mrps18a: mitochondrial ribosomal protein S18A	+1.9	mitochondrial ribosomal protein
mrps18b: mitochondrial ribosomal protein S18B	+2.1	mitochondrial ribosomal protein
mrps18c: mitochondrial ribosomal protein S18C	+2.1	mitochondrial ribosomal protein
mrps24: mitochondrial ribosomal protein S24	+1.5	mitochondrial ribosomal protein
mrps26: mitochondrial ribosomal protein S26	+1.8	mitochondrial ribosomal protein
mrps31: mitochondrial ribosomal protein S31	+1.5	mitochondrial ribosomal protein
mrps35: mitochondrial ribosomal protein S35	+1.7	mitochondrial ribosomal protein
dap3: death associated protein 3	+1.8	mitochondrial ribosome 28S subunit protein
mrrf: mitochondrial ribosome recycling factor	+1.9	

Supplemental Table 3

Expression of genes functioning in cytoskeleton and extracellular matrix

gene	fold	function
FILAMENTS		
myhz1: myosin, heavy polypeptide 1, skeletal muscle	-2.2	cytoskeleton, skeletal muscle
myhc4: myosin, heavy polypeptide 1 like	-1.9	fast muscle
vmhc: ventricular myosin heavy chain	-1.7	cardiac
mylz3: myosin, light polypeptide 3, skeletal muscle	-1.5	skeletal muscle
myl1: myosin, light chain 1, alkali; skeletal, fast	-1.3	
myl4: myosin, light chain 4, alkali; atrial, embryonic	+1.5	
mylc2pl: myosin light chain 2, precursor lymphocyte-specific	+1.4	
tmod4: tropomodulin 4 (muscle)	-2.0	blocks elongation of actin filament
tpma: alpha-tropomyosin	-1.4	actin filament assembly
tpm4: tropomyosin 4	-1.7	actin filament assembly
add1: adducin 1 (alpha)	-1.4	actin filament assembly
tmsb: thymosin, beta	-2.2	growth/assembly of actin filament
myl9: myosin, light polypeptide 9	+1.5	regulatory
cmlc1: cardiac myosin light chain-1	+1.5	cardiac
gsnb: gelsolin b, similar to Gsn protein	-1.5	actin-binding
capg: capping protein (actin filament), gelsolin-like	+1.3	actin-binding
twf1a: twinfilin, actin-binding protein, homolog 1a	-1.4	actin-binding
coro1b: coronin, actin binding protein, 1B	-1.7	actin-binding
icat: beta-catenin-interacting protein	-1.9	beta-catenin binding
smarcd1: SWI/SNF related, matrix associated, actin dependent regulator of chromatin, family d, member 1	+1.3	actin-dependent
scinla: scinderin like a	-1.8	ac filament-severing, exocytosis
ivns1abpa: influenza virus NS1A binding protein a	-1.7	stabilizer of actin filaments
pdlim1: PDZ and LIM domain 1 (elfin)	+1.8	actin stress fiber formation
emd: emerin (Emery-Dreifuss muscular dystrophy)	+1.7	membrane/cytoskeleton anchorage
tnnt3a: troponin T3a, skeletal, fast	-1.6	thin filament regulatory complex
xirp2: xin actin-binding repeat containing 2	+1.5	
fscn1: fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	-1.4	
actr1b: ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	-1.4	
actn3: actinin, alpha 3	-1.9	
nexn: nexilin (F actin binding protein)	+1.4	F actin binding protein, cell migrat
marcks: myristoylated alanine-rich protein kinase C substr	-1.7	actin filament crosslinking protein
gfap: glial fibrillary acidic protein	-1.4	intermediate filament of astrocytes
evlb: Enah/Vasp-like b	-1.6	actin nucleation polymerization
cd2ap: CD2-associated protein	+1.4	adapter between membrane and the actin cytoskeleton
krt1-19d: keratin, type 1, gene 19d	-1.6	spinous/granular layers of epidermis
krt5: keratin 5	-2.6	basal layer of the epidermis
krt1-19d: keratin, type 1, gene 19d	-3.1	myofibers, expressed in the periderm
krt15: keratin 15	-5.4	basal cell layer
krt12: keratin 12	-2.6	
krt14: keratin 14 (epidermolysis bullosa simplex, Dowling-Meara,	-3.6	
Koebner)keratin, type 2 cytoskeletal 8, BE202093	-20.6	pairs with 18, deficit-pancreatitis
similar to keratin type 2, BE605275	-11.9	proliferation, keratinization
si:dkeyp-113d7.4, cytokeratin	-2.6	
krt18: keratin 18	+2.1	type I intermediate filament chain
krt13: keratin 13	+1.4	
desm: desmin	+2	intermed filaments muscle
scel: sciellin	+1.5	cornified envelope of keratinocytes
MICROTUBULES		
tuba1: tubulin, alpha 1	-1.8	microtubules

tuba8l3: tubulin, alpha 8 like 3	-1.5	microtubules
tuba1: similar to alpha-tubulin isotype M-alpha-2	-1.6	microtubules
tuba2: Tubulin, alpha 2	-2.3	microtubules
tubb5: tubulin, beta 5	-2.2	microtubules
tubb2a: tubulin, beta 2A	-1.4	microtubules
tubb3: tubulin, beta 3	-1.7	microtubules
tubb4: tubulin, beta 4	-2.0	microtubules
tuba4a: tubulin, alpha 4a	-1.4	microtubules
tuba3c: tubulin, alpha 3c	-2.2	microtubules
tuba1c: tubulin, alpha 1c	-1.8	microtubules
eml2: echinoderm microtubule associated protein like 2	-1.8	microtubules
map1lc3a: microtubule-associated protein 1 light chain 3 alpha	-1.6	microtubules
map1lc3b: microtubule-associated protein 1 light chain 3 beta	-1.4	microtubules
dynll2: dynein, light chain, LC8-type 2	+1.3	transport
klc1: kinesin light chain 1	+1.7	may couple cargo to heavy chain
klc4: kinesin light chain 4	+1.7	
kif1b: kinesin family member 1B	-1.8	transport mitochondria synaptic vesicle
kif20a: kinesin family member 20A	-2.5	
bfsp2: beaded filament structural protein 2, phakinin	-3.6	
EXTRACELLULAR MATRIX		
col11a1/col11a2: collagen type XI alpha-2 /alpha 1	-1.8	extracellular matrix
col1a1: collagen, type I, alpha 1	-2.2	extracellular matrix
col9a2: procollagen, type IX, alpha 2	-2.1	extracellular matrix
col9a3: collagen, type IX, alpha 3	-1.9	extracellular matrix
col5a2: collagen, type V, alpha 2	-1.7	extracellular matrix
col1a3/dcxr: collagen, type I, alpha 3/dicarbonyl/L-xylulose reductase	-2.2	extracellular matrix
col2a1a: collagen type II, alpha-1a	-2.2	extracellular matrix
col1a2: collagen, type I, alpha 2	-2.8	extracellular matrix
col10a1: collagen, type X, alpha 1	-35.6	extracellular matrix
spon2b: spondin 2b, extracellular matrix protein	-3.8	extracellular matrix
dcn: decorin	-2.2	binds collagen matrix assembly
tgfbi: transforming growth factor, beta-induced, 68kDa	-1.5	binds I, II, IV collagens,cell adhesion
thbs4b: thrombospondin 4b	-1.9	cell-to-cell/cell-to-matrix bind
thbs1: thrombospondin 1	+2.2	cell to matrix to cell interaction
vcanb: versican b	-2.5	cell to matrix, glia
hapln1a: Hyaluronan and proteoglycan link protein 1a	-1.7	proteoglycan - hyaluronic acid
rtk6: eph-like receptor tyrosine kinase 6	+1.9	activated by collagen, cell/cell
fn1b: fibronectin 1b	+1.8	cell adhesion, motility, shape
p4ha1:procollagen-proline,2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	+3.2	collagen matrix synthesis
optc: Opticin	+9	binds collagen fibrils
mmp9: matrix metalloproteinase 9	+9.8	matrix degradation
mmp13: matrix metalloproteinase 13	+3.3	matrix degradation
pitrm1: pitrilysin metalloproteinase 1	+1.5	matrix degradation
timp2b: tissue inhibitor of metalloproteinase 2b	+8	matrix degradation
sparc: secreted protein, acidic, cysteine-rich (osteonectin)	-1.5	extracellular space
fgg: fibrinogen gamma chain	+1.5	
fgb: fibrinogen beta chain	+1.6	
fga: fibrinogen alpha chain	+1.7	
efemp2: EGF-containing fibulin-like extracellular matrix protein 2	+1.5	
cyr61: cysteine-rich, angiogenic inducer, 61	+2.2	
crtap: cartilage associated protein	+1.3	
aplp1: amyloid beta (A4) precursor-like protein 1	-1.7	
app: amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)	-1.4	
appbp2: amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-1.3	
aamp: angio-associated, migratory cell protein	-1.6	
ctgf: connective tissue growth factor	+1.9	
oc90: otoconin 90	+2.7	

krtcap2: keratinocyte associated protein 2	-1.3	
hs6st2: heparan sulfate 6-O-sulfotransferase 2	+1.5	
muc2: mucin 2	-1.7	insoluble barrier that protects epithel
adam17a: a disintegrin and metalloproteinase domain 17a	+1.5	shedding of TNFalpha
cxadr: coxsackie virus and adenovirus receptor	+2.1	cell adhesion
cdh1: cadherin 1, epithelial	+2.1	cell adhesion
cdh17: cadherin 17, LI cadherin (liver-intestine)	+1.6	cell adhesion
cdh11: cadherin 11, osteoblast	-1.3	cell adhesion
pcdh1g: protocadherin 1 gamma	-1.4	cell adhesion
pcdh2a: protocadherin 2 alpha	-1.8	cell adhesion
pcdh10b: protocadherin 10b	-1.9	cell adhesion
dsg2: desmoglein 2 (cadherin family)	+2	component desmosome junction
lama5: laminin, alpha 5	+1.4	
king1: kininogen 1	+1.4	
myoc: myocilin	-2.3	steroid-responsible meshwork
fryl: furry homolog-like (Drosophila)	+3.6	cell polarity
epb41l5: erythrocyte membrane protein band 4.1 like 5	+2	cell polarity, eye, brain
he1: hatching enzyme 1 /// similar to high choriolytic enzyme	+2.1	Ca /phospholipid-binding
sdc4l: syndecan 4 like - heparan sulfate proteoglycan	+2.1	focal adhesion, actin stress fibers
cldn7: claudin 7	+1.9	tight junctions
f11r: F11 receptor	+1.3	epithelial tight junction formation
elmo1: engulfment and cell motility 1	-1.4	
elmo2: engulfment and cell motility 2	-2.2	
ankra2: ankyrin repeat, family A (RFXANK-like), 2	-1.8	endocytosis by linking megalin to cytoskeleton or endocytic machinery

Supplemental Table 4

Changes in expression of genes involved in synthesis and processing of ribosomal RNA, other non-coding RNAs, mRNA processing, and translation.

gene	fold	function
TRANSCRIPTION of NON-CODING RNAs		
brf1 subunit of RNA pol III transcription initiat factor TFIIIB	+11.4	synthesis of non-coding RNA
polr3e: polymerase (RNA) III (DNA directed) polypeptide E	+2.2	synthesis of non-coding RNA
polr3f: polymerase (RNA) III (DNA directed) polypeptide F	+2.3	synthesis of non-coding RNA
polr3k: polymerase (RNA) III (DNA directed) polypeptide K	+2	synthesis of non-coding RNA
gtf3aa: general transcription factor IIIAa	+3.7	polIII transcrip of non-coding RNA
ssb: Sjogren syndrome antigen B (autoantigen La)	+1.7	polIII termination factor
taf1a: TATA box binding prot, (TBP)-assoc factor, RNA pol I,A	+2.3	synthesis of rRNA TAF for RNA polI.
polr1c: pol (RNA) I polypeptide C	+2.3	synthesis of rRNA
polr1a: polymerase (RNA) I polypeptide A	+2.0	synthesis of rRNA
polr1b: polymerase (RNA) I polypeptide B	+1.9	synthesis of rRNA
polr1e: polymerase (RNA) I polypeptide E, 53kDa	+2.1	synthesis of rRNA
RIBOSOME BIOGENESIS		
imp4: IMP4, U3 small nucleolar ribonucleoprotein	+2.9	rRNA processing
imp3: IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	+1.9	rRNA processing
rnu3ip2: RNA, U3 small nucleolar interacting protein 2	+2.6	rRNA processing
mphosph10: M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	+2.6	rRNA processing
rcl1: rcl1: RNA terminal phosphate cyclase-like 1	+2.0	pre-rRNA at sites A0, A1 and A2, the 18S
dt1p1a10l: hypothetical protein DT1P1A10 (human) - like	+3	may involved in 20S pre-rRNA processing
utp15: U3 small nucleolar ribonucleoprotein, homolog	+1.9	rRNA processing
utp11l: UTP11-like, U3 small nucleolar ribonucleoprotein	+1.9	rRNA processing
utp6: small subunit (SSU) processome component, homolog	+1.8	rRNA processing
utp20: small subunit (SSU) processome component, homolog	+1.7	rRNA processing
utp3: small subunit (SSU) processome component, homolog	+2.2	rRNA processing
rrp1: ribosomal RNA processing 1 homolog (S. cerevisiae)	+2.3	generation of 28S rRNA
dkc1 /// zgc:110395: dyskeratosis congenita 1, dyskerin	+2.3	(members of the H/ACA snoRNPs (small nucleolar ribonucleoproteins) gene family. rRNA processing and modification)
nola1: nucleolar protein family A, member 1	+1.8	
nola2: nucleolar protein family A, member 2	+1.9	
nol1: nucleolar protein 1, 120kDa	+2.0	
nol11: nucleolar protein 11	+2.2	
nol7: nucleolar protein 7, 27kDa	+2.6	
nola2: nucleolar protein family A, member 2,H/ACA small nucl RNPs	+1.9	
nolc1: nucleolar and coiled-body phosphoprotein 1	+2.2	
nusap1: nucleolar and spindle associated protein 1	+1.3	
tsr1: TSR1, 20S rRNA accumulation, homolog (yeast)	+2	40S subunit maturation
tsr2: TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	+3	40S subunit maturation
bop1: block of proliferation 1	+2	spacer processing to 25S and 5.8S rRNAs
bxdc1: brix domain containing 1	+2.4	processing of 27 SB pre-rRNA to 25S
bxdc2: brix domain containing 2	+2	biogenesis of the 60S ribosomal subunit
exosc4: exosome component 2	+1.8	(Components of multisubunit particle called exosome, which mediates mRNA degradation. Mediates 3'-processing of the 7S pre-RNA to the mature 5.8S rRNA)
exosc5: exosome component 4	+2.1	
exosc2: exosome component 5	+1.9	
exosc6: exosome component 6	+1.6	
exosc7: exosome component 7	+1.9	
exosc9: exosome component 9	+1.8	
exosc10: exosome component 10	+1.6	
nip7: nuclear import 7 homolog (S. cerevisiae)	+2.1	27S pre-rRNA processing, 60S assembly
pa2g4a: proliferation-associated 2G4, a	+1.8	rRNA processing, ErbB3 signaling

rrp15: ribosomal RNA processing 15 homolog (S. cerevisiae)	+1.8	rRNA processing
rrp9: ribosomal RNA processing 9, small subunit (SSU) processome component	+2.6	rRNA processing
rrs1: ribosome biogenesis regulator homolog (S. cerevisiae)	+1.5	ribosome biogenesis
fbl: fibrillarin	+1.8	2'-hydroxyl methylation of ribose in rRNA
nol5: nucleolar protein 5	+2	60S ribosomal subunit biogenesis
noc4l: nucleolar complex associated 4 homolog (S. cerevisiae)	+2.1	nuclear export of 40 S pre-ribosomes
gnl2: guanine nucleotide binding protein-like 2	+2	nuclear export of pre-60S subunits
gnl3l: guanine nucleotide binding protein-like 3	+1.9	rRNA processing
nol6: nucleolar protein family 6 (RNA-associated)	+1.7	rRNA processing
nol14: nucleolar protein 14	+1.6	processing of pre-18S rRNA, export
ncl: nucleolin	+1.5	the major nucleolar protein, rRNA
pes: pescadillo	+2.3	60S, cell proliferation, elevated in cancers
esf1: ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	+2.9	pre-rRNA processing
sdad1: SDA1 domain containing 1	+3.7	pre-60S subunits export to the cytoplasm
lsg1: large subunit GTPase 1 homolog (S. cerevisiae)	+2	nuclear export of the 60S ribosomal subunit
gtpbp4: GTP binding protein 4	+1.5	biogenesis of the 60S ribosomal subunit
grwd1: glutamate-rich WD repeat containing 1	+2.3	comp. of 50S/80S preribosomal complexes
fcf1: FCF1 small subunit (SSU) processome component homolog	+2.5	pre-rRNA processing and 40S assembly
cta-126b4.3: CGI-96 protein	+3.2	pre-rRNA processing
bysl: bystin-like	+1.4	pre-rRNA processing and 40S assembly
dnttip2: deoxynucleotidyltransferase, terminal, interacting protein 2	+2.7	regulates the transcriptional activity of DNTT and ESR1, biogenesis 40S subunit
OTHER NUCLEOLAR PROTEINS		
npm1: nucleophosmin 1 (nucleolar phosphoprotein B23, numatrin)	+2.2	RP assembly, transport, centrosome, ARF
mki67ipl: mki67 (FHA domain) interacting	+2.2	binds Ki67, cell-cycle
pwp2h: PWP2 periodic tryptophan protein homolog	+2.3	G1 phase of the cell cycle
nolc1l: nucleolar and coiled-body phosphoprotein 1-like	+2.2	nucleolus maintenance
noc3l: nucleolar complex associated 3 homolog	+1.7	may be required for adipogenesis
mak16: MAK16 homolog (S. cerevisiae)	+2.1	RNA binding
mybbp1a: myb-binding protein 1a	+2.5	c-myb supressor
cirh1a: cirrhosis, autosomal recessive 1A (cirhin)	+2.4	childhood cirrhosis
noc2l: nucleolar complex associated 2 homolog (S. cerevisiae)	+2.3	
mphosp: M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	+2.6	
mki67ip: MKI67 (FHA domain) interacting nucleolar phosphoprotein	+2.2	
rp9: retinitis pigmentosa 9 (autosomal dominant)	+1.8	target protein for the PIM1 kinase
pno1: partner of NOB1 homolog (S. cerevisiae)	+1.5	
lyar: Ly1 antibody reactive homolog (mouse)	+1.9	cell growth-regulating nucleolar protein
wdr3: WD repeat domain 3	+2.6	cell cycle, signal transduction, apoptosis
mki67ip: MKI67 (FHA domain) interacting nucleolar phosphoprotein	+2.2	nucleolar protein interacts with FHA domain of pKI-67
gnl3: guanine nucleotide binding protein-like 3 (nucleolar)	+1.3	G protein shuttle nucleus – nucleolus, proliferation
RNA PROCESSING		
sfrs2ip: splicing factor, arginine/serine-rich 2, interacting protein	+1.5	alternative splicing
sf3a1: splicing factor 3a, subunit 1	+1.4	subunits of SF3A required for 'A'
sf3a3: splicing factor 3a, subunit 3	+1.3	complex assembly
sfrs11: splicing factor, arginine/serine-rich 11	+1.3	may function in pre-mRNA splicing
sf3b5: splicing factor 3b, subunit 5	-1.3	with SF3A and 12SRNA form U2 complex
sfrs3b: splicing factor, arginine/serine-rich 3b	-1.3	splicing related to cellular proliferation
sfrs5: splicing factor, arginine/serine-rich 5	-1.3	alternative splicing,
sfrs7: splicing factor, arginine/serine-rich 7	+1.4	splicing, alternative splicing
ppan: peter pan homolog (Drosophila)	+2.4	second step of mRNA splicing
snupn: snurportin 1	+2.2	U snRNP nuclear import
tnpo3: transportin 3	+2.2	nuclear import splicing factors
sip1: survival of motor neuron protein interacting protein 1	+2.1	spliceosomal snRNP assembly
a2bp1: ataxin 2-binding protein 1	-2.2	alternative splicing

lsm8: LSM8 homolog, U6 small nuclear RNA associated	-1.8	U4/U6 duplex formation
prpf38b: PRP38 pre-mRNA processing factor 38 domain containing B	+1.8	potential role in splicing
prpf38a: PRP38 pre-mRNA processing factor 38 domain containing A	+1.4	
prpf6: PRP6 pre-mRNA processing factor 6 homolog	+1.3	pre-mRNA processing
nhp2l1: NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	+1.7	spliceosome assembly
casc3: cancer susceptibility candidate 3	+1.5	exon junction complex, NMD
clk4: CDC-like kinase 4	-1.7	phosphorylates ser/arg in spliceosome
tnrc4: trinucleotide repeat containing 4	-1.6	pre mRNA alternative splicing
pu60: poly-U binding splicing factor 60KDa	+1.3	splicing
prpf19: PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	+1.3	role in DNA DSB repair, spliceosome assembly, increases resistance to stress
rbm28: RNA binding motif protein 28	+1.9	nucleolar component of the spliceosome
snrpf: small nuclear ribonucleoprotein polypeptide F	+1.3	spliceosome
snrpe: small nuclear ribonucleoprotein polypeptide E	+1.5	spliceosome
snrpb: small nuclear ribonucleoprotein polypeptide B	+1.3	spliceosome
hnrnpa0: heterogeneous nuclear ribonucleoprotein A0	-1.6	component of ribonucleosomes
dcp2: DCP2 decapping enzyme homolog (S. cerevisiae)	-1.3	degradation of mRNAs, cups removal
cugbp2: CUG triplet repeat, RNA binding protein 2	-1.3	pre-mRNA alternative splicing
cstf3: cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	+1.7	polyadenylation and cleavage pre-mRNAs
cpsf3: cleavage and polyadenylation specific factor 3, 73kDa	+1.5	recognizes AAUAAA signal sequence pre-mRNA 3'-end formation
bcas2: breast carcinoma amplified sequence 2	+1.3	spliceosome associated
fip1l1: FIP1 like 1 (S. cerevisiae)	+1.5	subunit of the CPSF complex that polyadenylates mRNA precursors.
ddx27: DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	+2.5	RNA helicase
ddx18: DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	+2.3	RNA helicase
ddx55: DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	+2.2	RNA helicase
ddx49: DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	+2.1	RNA helicase
ddx56: DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	+1.8	RNA helicase
ddx19: DEAD (Asp-Glu-Ala-Asp) box polypeptide 19	+1.4	RNA helicase
ddx21: DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	+1.4	RNA helicase
ddx3y: DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	+2.1	RNA helicase
ddx47: DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	+2.1	RNA helicase
tRNA SYNTHESIS		
rars: arginyl-tRNA synthetase	+3.1	tRNA synthesis
qars: glutaminyl-tRNA synthetase	+2.6	tRNA synthesis
qars: glutaminyl-tRNA synthetase	+2.5	tRNA synthesis
iars: isoleucyl-tRNA synthetase	+2.4	tRNA synthesis
farsa: phenylalanyl-tRNA synthetase, alpha subunit	+2.3	tRNA synthesis
farsb: phenylalanyl-tRNA synthetase, beta subunit	+2.6	tRNA synthesis
kars: lysyl-tRNA synthetase	+2.1	tRNA synthesis
tyw1: tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	+2.1	tRNA synthesis
lars: leucyl-tRNA synthetase	+2.1	tRNA synthesis
hars: histidyl-tRNA synthetase	+1.8	tRNA synthesis
nars: asparaginyl-tRNA synthetase	+1.8	tRNA synthesis
tars: threonyl-tRNA synthetase	+2.0	tRNA synthesis
yars: tyrosyl-tRNA synthetase	+2.8	tRNA synthesis
cars: cysteinyl-tRNA synthetase	+1.6	tRNA synthesis
eprs: glutamyl-prolyl-tRNA synthetase	+1.7	tRNA synthesis
qtrtd1: queuine tRNA-ribosyltransferase domain containing 1	+2	tRNA synthesis
pop7: processing of precursor 7, ribonuclease P family	-1.9	cleaves tRNA 5'-end make mature tRNA
jtv1: JTV1 gene	+1.6	the tRNA synthetase cofactor
trmt1: TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	+2.5	dimethylates G at position 26 of tRNAs
TRANSLATION		
eif6: eukaryotic translation initiation factor 6	+2.7	translation initiation
eif2b1: eukaryotic translation initiation factor 2B, subunit 1 alpha	+2.5	translation initiation
eif2b3: eukaryotic translation initiation factor 2B, subunit 3 gamma	+1.4	translation initiation
eif2b4: eukaryotic translation initiation factor 2B, subunit 4 delta	+2.3	translation initiation

eif4ebp3: eukaryotic translation initiation factor 4E binding protein 3	+2.1	translation regulator
eif2b2: eukaryotic translation initiation factor 2B, subunit 2 beta	+2.0	translation initiation
eif3j: eukaryotic translation initiation factor 3, subunit J	+1.9	translation initiation
eif5b: eukaryotic translation initiation factor 5B	+1.8	translation initiation
eif2a: eukaryotic translation initiation factor 2A	+1.8	translation initiation
eif2s2: eukaryotic translation initiation factor 2, subunit 2 beta	+1.7	translation initiation
eif2s1: eukaryotic translation initiation factor 2, subunit 1 alpha	+1.3	translation initiation
eif3c: eukaryotic translation initiation factor 3, subunit C	+1.7	translation initiation
eif2b5: eukaryotic translation initiation factor 2B, subunit 5 epsilon	+1.6	translation initiation
eif3g: eukaryotic translation initiation factor 3, subunit G	+1.4	translation initiation
eif3d: eukaryotic translation initiation factor 3, subunit D	+1.4	translation initiation
eif5: eukaryotic translation initiation factor 5	+1.4	translation initiation
eif2b3: eukaryotic translation initiation factor 2B, subunit 3 gamma	+1.4	translation initiation
eif3b: eukaryotic translation initiation factor 3, subunit B	+1.3	translation initiation
eif3a: eukaryotic translation initiation factor 3, subunit A	+1.3	translation initiation
eif2s1l: eukaryotic translation initiation factor 2, subunit 1 alpha, like	+1.3	translation initiation
eif3h: eukaryotic translation initiation factor 3, subunit H	+1.3	translation initiation
eif4g2b: eukaryotic translation initiation factor 4, gamma 2b	+1.3	translation initiation
eif2s1: eukaryotic translation initiation factor 2, subunit 1 alpha	+1.3	translation initiation
eif3s10: eukaryotic translation initiation factor 3, subunit 10 (theta)	+1.3	translation initiation
eif4ah: eukaryotic translation initiation factor 4H	+1.3	translation initiation
eif1ay: eukaryotic translation initiation factor 1A, Y-linked	+1.3	translation initiation
eif1ax: eukaryotic translation initiation factor 1A, X-linked	+1.4	translation initiation
eif4a2: eukaryotic translation initiation factor 4A, isoform 2	-1.6	translation initiation
eif4a1b: eukaryotic translation initiation factor 4A, isoform 1B	-!.4	translation initiation
eef1g: eukaryotic translation elongation factor 1 gamma	-1.3	translation regulator
eef2: eukaryotic translation elongation factor 2	-1.5	translation regulator
etf1: eukaryotic translation termination factor 1	+1.5	translation regulator
dohh: deoxyhypusine hydroxylase/monooxygenase	+1.8	post-translational modification of eIF-5A
ngdn: neuroguidin, EIF4E binding protein	+2.9	binds EIF4E and CREB, translation
metap1: methionyl aminopeptidase 1	+2.2	removes Met from peptides
metap2: methionyl aminopeptidase 2	+1.6	removes Met from peptides
mknk2b: MAP kinase-interacting serine/threonine kinase 2b	+2.6	phosphorylates EIF4E
bzw2: basic leucine zipper and W2 domains 2	-1.6	translation regulator
brunol4: bruno-like 4, RNA binding protein (Drosophila)	-1.8	translation regulator
rps6kb1: ribosomal protein S6 kinase, 70kDa, polypeptide 1	+1.6	translation regulator
dohh: deoxyhypusine hydroxylase/monooxygenase	+1.8	forms a.a. hypusine only found in elf5A
denr: density-regulated protein	+1.3	translational initiation
csd1: cold shock domain containing E1, RNA-binding	+1.3	translationally coupled mRNA turnover
mknk2: MAP kinase interacting serine/threonine kinase 2	+2.9	stress, regul translation by phosphorylating EIF4E increasing its binding to mRNA cap
OTHERS		
LOC563247: similar to ribosomal L1 domain containing 1	+2.6	ribosome structural constituent
rpl7l1: ribosomal protein L7-like 1	+1.7	60S subunit, glucose metabolism
rps27l: ribosomal protein S27-like	+4.4	
rrsl1d1: ribosomal L1 domain containing 1	+2.6	
rbp1: ribosome binding protein 1 homolog (dog)	+2.4	interaction between the ribosome and the endoplasmic reticulum

Supplemental Table 5

Expression of genes affecting various aspects of development and functions of tissues and organs

gene	fold	function
NEURAL		
otx2: orthodenticle homolog 2	-2	development of brain and sense organs
ntn1b: netrin 1b	- 5.6	guidance of commissural and motor axons
foxp2: forkhead box P2	-5.4	brain development
atoh2a: atonal homolog 2a	-5.3	brain development
lmo3: LIM domain only 3	-2.7	brain development
otx5: orthodenticle homolog 5	-3.5	pineal and parapineal development
crx: cone-rod homeobox	-11	eye
crygm2c: crystallin, gamma M2c	-12	eye lens
crystallin, gamma B	-7.8	eye lens
crystallin, gamma M2d7	-5.5	eye lens
crystallin, gamma M2d1	-3.9	eye lens
cryba4: crystallin, beta A4	-3.1	eye lens
crybb1: crystallin, beta B1	-2.5	eye lens
crygs1: crystallin, gamma S1	-2	eye lens
six7: sine oculis homeobox homolog 7	-7.9	eye
six3a: sine oculis homeobox homolog 3a	-1.6	eye
vsx1: visual system homeobox 1 homolog, chx10-lik	-6.3	eye
pde6g: phosphodiesterase 6G, cGMP-specific, rod, gamma	-3.9	eye
elavl4:embryonic lethal, abnormal vision 4 (Hu antigen D)	-2.4	eye
elavl1:embryonic lethal, abnormal vision (Drosophila)-like1 (Hu antign R)	-1.3	eye
myoc: myocilin	-2.3	eye trabecular meshwork,intraocular pressure
mab21l1: mab-21-like 1	-2.4	eye and cerebellum development
mab21l2: mab-21-like 2	-2.2	eye and cerebellum development
pax6a: paired box gene 6a	-1.4	eye
olfml3: olfactomedin-like 3	-3.0	olfactory
olfm2: olfactomedin 2	-2.3	olfactory
or103-4:odorant receptor, family C, subfamily 103, mem 4	-2.1	olfactory
pcp4a: Purkinje cell protein 4a	-4.2	nervous system development
snap25b: synaptosome-associated protein 25 b	-3.1	transporter, nervous system
neurod: neurogenic differentiation	-3.9	nervous system development
nxph1: neurexophilin 1	-2.5	nervous system development
cbln1: cerebellin 1 precursor	-2.4	nervous system development
fabp7a: fatty acid binding protein 7, brain, a	-2.4	transporter, nervous system
syt1: Synaptotagmin I	-2.3	nervous system development
gbx2: gastrulation brain homeo box 2	-2.2	nervous system development
slc1a2: solute carrier family 1, 2	-2.2	glial high affinity glutamate transporter
slc32a1: solute carrier family 32 , member 1	-2.2	GABA vesicular transporter
slc6a1: solute carrier family 6, member 1	-3.5	neurotransmitter transporter, GABA
crip2: cysteine-rich protein 2	-4.4	intestinal neurons
pbx3b: pre-B-cell leukemia transcription factor 3b	-3.1	Medulla oblongata neurons, respiration
CH211-69I14.7: novel similar to pannexin 1 (PANX1)	-2.7	CNS gap junctions
sreb2: sreb2 /// similar to sreb2	-2.8	Conserved brain receptor
gpm6ba: glycoprotein M6Ba	-2.8	nervous system development
gpm6ab: glycoprotein M6Ab	-1.9	nervous system development
barhl2 /// LOC100002240: BarH-like 2	-2.6	neural basic helix-loop-helix genes regulator
nell2b: NEL-like 2b	-2.1	growth differentiation, brain
sox4a: SRY (sex determining region Y)-box 4a	-2.1	expressed in brain in zebrafish
meis2.2: myeloid ecotropic viral integration site 2.2	-2.1	brain development
meis2.1: myeloid ecotropic viral integration site 2.1	-1.7	brain, limb, regulates pax6
prph: peripherin	-2.1	neurofilament
gng3: guanine nucleotide binding protein (G protein), gamma 3	-2.0	mostly brain expression, low in others,
lmo1: LIM domain only 1	-2.0	adipose
nrxn1a: neurexin 1a	-2.0	neural, translocation in T cell leukemia
lhx1a: LIM homeobox 1a	-2.0	cell adhesion molecules and receptors

lhx5: LIM homeobox 5	-1.5	differentiation and development of forebrain
dpysl3: dihydropyrimidinase-like 3	-2.0	differentiation of neurons and lymphoid cells
robo1: roundabout, axon guidance receptor, homolog 1 (Drosophila)	-1.3	axon guidance transmembrane receptor
robo2: roundabout homolog 2	-1.9	semaphoring signaling, cytoskeleton rearrange
gad1: glutamate decarboxylase 1	-1.9	axon guidance
ncgb: synuclein, gamma b (breast cancer-specific protein 1)	-1.8	GABA synthesis, deficiency - seizures
tmem59l: transmembrane protein 59-like	-1.8	expressed in CNS
isl1: islet1	-1.9	may play a role in brain
mdkb: midkine-related growth factor b	-1.7	neurons, also regulates insulin promoter
emx2: empty spiracles homeobox 2	-1.7	neurite outgrowth, cell fate, coop with otx2
dpysl5a: dihydropyrimidinase-like 5a	-1.6	brain development, partnerEMX2
dmbx1: diencephalon/mesencephalon homeobox 1	-1.8	brain development
negr1: neuronal growth regulator 1	-1.5	
ncam1: neural cell adhesion molecule 1	-1.3	
snca: synuclein, alpha (non A4 component of amyloid precursor)	-1.8	in brain, inhibit phospholipase D2 selectively
sncb: synuclein, beta	-2.2	in brain, inhibit phospholipase D2 selectively
scg5: secretogranin V (7B2 protein)	-1.8	pituitary hormone secretion
rtn1: reticulon 1	-1.4	neuroendocrine secretion
rgma: RGM domain family, member A	-1.4	guidance of growth cones
mab21l1: mab-21-like 1 (C. elegans)	-2.4	TGFb target, cell fate-determining gene, eye
mab21l2: mab-21-like 2 (C. elegans)	-2.2	cell fate-determining gene, eye
lgi1: leucine-rich, glioma inactivated 1	-1.3	autosomal dominant lateral temporal epilepsy
hmp19: HMP19 protein	-1.9	hypothalamus golgi apparatus expressed
gdi1: GDP dissociation inhibitor 1	-2.1	GDP/GTP exchange, neural cells
gap43: growth associated protein 43	-1.4	In growing and regenerating neural cells
clstn1: calsyntenin 1	-1.5	cargo in axonal anterograde transport
cldn11: claudin 11 (oligodendrocyte transmembrane protein)	-1.7	oligodendrocyte tight junctions
cdr2l: cerebellar degeneration-related protein 2-like	-1.8	
cdk5r2: cyclin-dependent kinase 5, regulatory subunit 2 (p39)	-1.7	neuron-specific activator of CDK5 kinase
atcay: ataxia, cerebellar, Cayman type	-1.4	neuron-spec. bind small lipophilic molecules
armet: arginine-rich, mutated in early stage tumors	-2.2	survival of dopaminergic neurons
anp32e: acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	-1.3	cerebellar development and synaptogenesis
nr2e3: nuclear receptor subfamily 2, group E, member 3	-3.9	retinal nuclear receptor
sox11a: SRY (sex determining region Y)-box 11a	-1.4	function in the developing nervous system
mdkb: midkine-related growth factor b	-1.7	fetal adrenal gland development
bre: brain and reproductive organ-expressed (TNFRSF1A modulator)	-1.5	modulation of E3 ubiquitin ligase activity of the 2-subunit BRCA1/BARD1 complex
drysl3: dihydropyrimidinase-like 3	-2	axon guidance, neur. growth cell migration
drysl5: dihydropyrimidinase-like 5	-1.6	neuronal differentiation and/or axon growth
sept8: septin 8 (septins are GTPases that assemble as filamentous scaffolds)	+1.4	organization of submembranous structures, in neuronal polarity, and vesicle trafficking
ascl1a: achaete-scute complex-like 1a (Drosophila)	+2.5	brain development
lrrn1: leucine rich repeat neuronal 1	+2.2	neurons, olfactory development
neurog1: neurogenin 1	+2	inhibitors of neural development
her9: hairy-related 9	+1.6	
her2: hairy-related 2	+3.5	
her8a: hairy-related 8a	+3.3	
hes5: hairy and enhancer of split 5	+1.9	
ntn1a: netrin 1a	+2	laminin-like axon guidance
dbx1a: developing brain homeobox 1a	+1.8	ventral interneurons
metrn: meteorin, glial cell differentiation regulator	+1.8	promotes astrocyte differentiation
sox19a: SRY-box containing gene 19a	+1.7	
ptprn: protein tyrosine phosphatase, receptor type, N	+1.7	neuroendocrine function
myef2: myelin expression factor 2	+1.3	
sip1: survival of motor neuron protein interacting protein 1	+2.1	
slit homolog 2 (Drosophila)	+1.3	molecular guidance cue in cellular migration
rtc4: reticulon 4	+1.3	neurite growth inhibitor
plp1: proteolipid protein 1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)	+1.3	major myelin protein central nervous system

olig3: oligodendrocyte transcription factor 3	+3.1	promotes class A neurons, spinal cord and suppress specification of class B neurons
ncald: neurocalcin delta	+1.6	Ca-dependent rhodopsin phosphorylation
ifrd1: interferon-related developmental regulator 1	+1.3	NGF response
angptl7: angiopoietin-like 7	+1.5	Cornea
sox3: SRY (sex determining region Y)-box 3	+1.5	X-linked mental retardation with GH deficiency
ascl1: achaete-scute complex homolog 1 (Drosophila)	+2.5	Differentiation of some neural lineages
ptprn: protein tyrosine phosphatase, receptor type, N	+1.7	neuroendocrine secretory processes
reep3: receptor accessory protein 3	+1.5	may enhance cell surface expression of odorant receptors
RETINOL-BINDING	-7.5	retinoic acid transport and metabolism
rlbp1l: retinaldehyde binding protein 1, like	-6.9	retinoic acid transport and metabolism
rbp2a: retinol binding protein 2a	-5.8	retinoic acid transport and metabolism
crabp1a: cellular retinoic acid binding protein	+1.6	transports retinoic acid to the nucleus
crabp2a: cellular retinoic acid binding protein 2, a	-2.4	retinoic acid transport and metabolism
rbp4: retinol binding protein 4, plasma	-1.4	retinoic acid transport and metabolism
rarga: retinoic acid receptor gamma a	+1.7	inhibits 9-cis-retinoic acid-dependent RXRa
tgif1: TGFB-induced factor homeobox 1		
VARIOUS TISSUES	-3.5	various embryonic structures
gsc: goosecoid	–3.2	osteoblast/skeletal differentiation
runx2a: runt-related transcription factor 2a	-2.6	cardiac development
irx4a: iroquois homeobox protein 4a	-1.7	mesoderm, vascular
fli1a / LOC100001509: friend leukemia integration 1a	-3.2	steroidogenesis
pbx1a: pre-B-cell leukemia transcription factor 1a	-2.4	pharyngeal arches
dlx4a: distal-less homeobox gene 4a	-2.1	water-specific channel kidney
aqp3: aquaporin 3	+2.6	mesoderm segmentation
wif1: wnt inhibitory factor 1	+2.4	kidney, urogenital tract, eyes, and the CNS
pax2b: paired box gene 2b	+2.1	antagonize Nodal, axial structures
ncl1: nicalin	+1.5	many tissues
shha : sonic hedgehog a	+1.6	negative regulator in the hh pathway
sufu: suppressor of fused homolog (Drosophila)	+1.9	modulates hedgehog signaling
hhip: hedgehog interacting protein	+2.5	cell fate, differentiation
notch1a: notch homolog 1a	+2.4	cell fate, differentiation
dlb: DeltaB	+2.4	cell fate, differentiation
dld: deltaD	+2.4	
dll1: delta-like 1 (Drosophila)	+2.1	cell fate, differentiation
nrarpb: notch-regulated ankyrin repeat protein b	+2.2	cell fate, differentiation
notch3: Notch homolog 3 (Drosophila)	+1.6	fucos EGF-like repeats of extracellular Notch
lfng: lunatic fringe homolog, fucose glycosyltransferase	+2.4	heart muscle, cardiolipin metabolism
taz: tafazzin	+2.4	vasculogenesis
vegfa: vascular endothelial growth factor A	+2.7	otoconia, vestibular macular organs
oc90: otoconin 90	-1.9	chondrocyte growth, inhibits angiogenesis
lect1: leukocyte cell derived chemotaxin 1	-1.9	circadian clock
csnk1da: casein kinase 1, delta a	-1.7	reduced in cancers
gng7: guanine nucleotide binding protein (G protein), g 7	+2.1	timing of organ development
trim71: tripartite motif-containing 71	+2.1	may antagonize nodal
ncl1: nicalin	+1.9	major connective tissue mitoattractant
ctgf: connective tissue growth factor	+1.9	blue light-dependent regulator feedback loop
cry3: Cryptochrome 3 (circadian clock)	+1.6	adipocytes
klf3: Kruppel-like factor 3 (basic)	+1.3	
klf6: Kruppel-like factor 6	+1.6	germ-cell specific
papolb: poly(A) polymerase beta (testis specific)	+1.6	germ cells adhesion migration
cd9l: CD9 antigen, like	+1.4	transcription regulator
tef: thyrotroph embryonic factor	+1.4	
myod1: myogenic differentiation 1	+1.6	
mynn: myoneurin	-1.9	
lmo4: LIM domain only 4	+1.4	

irx3: iroquois homeobox 3	-1.7	
hey1: hairy/enhancer-of-split related with YRPW motif 1	+2.3	
pes1: pescadillo homolog 1, containing BRCT domain (zebrafish)	+1.3	specification of dorsal limb fate
nps1: RNA binding protein S1, serine-rich domain	+1.7	placenta development
phlda2: pleckstrin homology-like domain, family A, member 2	+2.1	
phlda3: pleckstrin homology-like domain, family A, member 3	+2.0	muscle-specific
murc: muscle-restricted coiled-coil protein	-2.5	deficiency –deafness
lhfpl3: lipoma HMGIC fusion partner-like 3	+1.6	skeletal and cardiac muscle
ifrd2: interferon-related developmental regulator 2	+1.3	basement membranes in kidney
cd151: CD151 molecule (Raph blood group)	+1.6	angiogenesis and cell migration
aamp: angio-associated, migratory cell protein	-1.7	organogenesis and differentiation
rora: RAR-related orphan receptor A	-1.4	differentiation of endothelial cells
s1pr1: sphingosine-1-phosphate receptor 1	+2.8	maintenance of blood pressure and
npr3: natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic		extracellular fluid volume
peptide receptor C)	-1.8	may play a role in chondrogenesis
sox5: SRY (sex determining region Y)-box 5	+1.3	maintain the transcriptionally repressive state
phc2: polyhomeotic homolog 2 (Drosophila)		of genes during development
	+1.5	vascular, hematopoietic and neuronal develop
narg1a: NMDA receptor-regulated gene 1a	+1.8	probable histone methyltransferase
whsc1: Wolf-Hirschhorn syndrome candidate 1		

Supplemental Table 6

Expression of genes affecting function of blood and immune system

gene	fold	function
BLOOD		
klf11a: Kruppel-like factor 11a	-3.5	activates globin genes suppress growth
hbbe2: hemoglobin beta embryonic-2	-2.6	oxygen transporter
hbga: hemoglobin, gamma A	-2.6	oxygen transporter
hbbe3: hemoglobin beta embryonic-3	+1.9	oxygen transporter
hbae1: hemoglobin alpha embryonic-1	-1.4	oxygen transporter, qPCR data
alas2: aminolevulinate, delta-, synthetase 2	-2.4	heme biosynthesis
mb: myoglobin	-1.4	oxygen storage in muscle cells
gpib: glucose phosphate isomerase b	-2.0	platelet adhesion in the arterial circulation
fga: fibrinogen alpha chain	+1.7	blood clots: cleaved by thrombin form fibrin
fgb: fibrinogen, B beta polypeptide	+1.6	blood clots
maea: macrophage erythroblast attacher	+1.5	mediates the attachment of erythroid cell to macrophages This contact inhibits their apoptosis
arl6ip1: ADP-ribosylation factor-like 6 interacting protein 1	-1.3	hematopoietic maturation
IMMUNE		
c6/LOC100003623: complement component 6	+3.2	complement system
clu: clusterin (complement lysis inhibitor, apolipoprotein J)	+2.6	complement system
LOC100003961: similar to complement C3-H1	+1.4	complement system
LOC567902: similar to complement C3-S	+1.4	complement system
cfb: complement factor B	+1.3	complement system
c8b: complement component 8, beta polypeptide	+1.4	complement system
serping1: serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)	+1.7	inhibits activated C1r and C1s of complement
socs3a: suppressor of cytokine signaling 3a	+4.1	INF signaling
socs3b: suppressor of cytokine signaling 3b	+3.2	INF signaling
LOC796252: chemokine CXL-C24a	-4.2	chemokine
LOC795788: similar to CC chemokine SCYA103	-4.7	chemokine
irf7: interferon regulatory factor 7	+5.3	interferon-dependent responses
gtpbp1: GTP binding protein 1	+3	interferon gamma target
ifrd2: interferon-related developmental regulator 2	+1.6	INF signaling
irf2bp2: Interferon regulatory factor 2 binding protein 2	-1.4	INF signaling
ifi30: interferon gamma inducible protein 30	-1.4	interferon inducible
dap1b: death associated protein 1b	-1.5	
prkri: protein-kinase, interferon-inducible dsRNA-dependent inhibitor	-1.7	interferon-gamma-induced cell death
defbl1: LOC100000966 / defensin, beta-like 1	-4.4	antimicrobial peptide
lyz: lysozyme	-!.5	antimicrobial peptide
cebpb: CCAAT/enhancer binding protein (C/EBP), beta	+3.1	activator immune/acute phase, inflammation
abce1:ATP-binding cassette, sub-family E (OABP) mem 1	+1.6	block activity ribonuclease L, antagonize IFN
lyzl2: lysozyme-like 2	-1.5	
prg2: plasticity-related gene 2	-1.3	cytotoxin and helminthotoxin
nktr: natural killer-tumor recognition sequence	-1.5	function of NK cells
lrba: LPS-responsive vesicle trafficking, beach and anchor containing	+1.4	Chediak-Higashi syndrome
il17rd: interleukin 17 receptor D	+1.3	Feedback inhibitor of fibroblast growth factor mediated Ras-MAPK signaling
cd68: CD68 molecule	-1.3	phagocytic activities of tissue macrophages
sqstm1: sequestosome 1	+1.6	binds ubiquitin, regulates activation of NFkB1
ptma: prothymosin, alpha	-2.2	interaction of hist 1 with chromatin, resistance to opportunistic infections
creb3: cAMP responsive element binding protein 3	+1.3	establishment of latency during HSV infection
map7d1: MAP7 domain containing 1	+2.4	histamine receptor activity
tnfrsf1a: tumor necrosis factor receptor superfamily, member 1A	+2.1	activate NF-kB, mediate apoptosis, and function as

scye1: small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	+1.7	a regulator of inflammation

Supplemental Table S7. Primers used in qPCR.

gene	name	Sequence
Actin b	ac	5′-TCTCTTCCAGCCTTCCTTCCT
	acr	5′-CTCATCGTACTCCTGCTTGCT
p53	Dp53e(Delta)	5′-ATATCCTGGCGAACATTTGG
	p53er	5′-ACGTCCACCACCATTTGAAC
	Fp53(TA)	5′-CTCTCCCACCAACATCCACT
	53f	5′-CTGAAGTGGTCCGCAGATG
	53r	5′-CGTTTGGTCCCAGTGGTGG
p63	63f	5′-CCACATCACACTTTTAGGGG
	63r	5′-GAATCCTCCACGTATTGAGCG
p73	p73	5′-TACTCGCAGCCAAACTCAACC
	p73r	5′-AGGAGCCGTCTGACTTTCGT
bax	bx	5′-CGTCGGGTGGAGGCGATACG
	bxr	5′-GAGTCGGCTGAAGATTAGAGTT
puma	zpm	5′-CCTCACATGATGCCTTCAGC
	zpmr	5′-CATTGATGGTGTCCGAGACC
p21	z21	5′-TGAGAACTTACTGGCAGCTTCA
	z21r	5′-AGCTGCATTCGTCTCGTAGC
adenosine deaminase(ADA)	adf	5′-CCATCAAGAGAATAGCGTATG
	adr	5′-GCTTTCTTGTGTCCTGGGTA
myb	mb	5′-AAGACAGGAAAACGCCACC
	mbr	5′-TTGACATCAACAGCATCTCG
gata1	gat	5′-CGACATCTTCAATACTACACTT
	gatr	5′-TAGGGAGAGTTTAGAGAGTGA
cyclin G1	G1f	5′-TCAAGAGAAAGTGGACACAGAAA
	G1r	5′-CATTTGGCTTCTGGCACTTGG
ankirin1	ank1	5′-GATGAGAGACTGCCGAACCA
	ankr1	5′-GCCACTTCTCCTTGTTCTGC
stat3	stat3f	5′-GACACTGAGTTCCCTGACACA
	stat3r	5′-CTTCTCTCATGGGTGACGCAT
triosephosphate isomerase	tri	5′-GTGTGGTCTTGGCGTATGAAC
	trir	5′-GCGTCTGGTTGAGCATCTCTA
pyruvate kinase	pk	5′-CCATATCACCTGAGCGGAAGA
	pkr	5′-CGAGTCCTCATACAAGTGCTG
6-phosphofructokinase	pfk1	5′-CCAGACCAGAGAAGGGCGTTT
	pfkr1	5′-TTGGTGGCTTTGTGCTGTTGT

hemoglobin embryonic be3	hbbe3 hbbe3r	5’-CGCAGCGATTCAGAACATCTT 5’-CTGAGGGCTGACACAACAACA
brf1	brf1 brf1r	5’- CCTTTGTGGAGAGTGGCGGC 5’-GACGAGTGCTGATTCATCTGAA
runx1	runx runxr	5’- CGGATGAAGCAGTAAAGCCAG 5’-GGTTGGGTGAGATTGGTGTTG
caspase 8	cas8 cas8r	5’- GCACTACCTCTCCTACCGACA 5’- CACTTCAGTCTATGGGCAGCA
vegf	vegf vegfr	5’-CTCTCCTCCATCTGTCTGCTG 5’- CGCAGCACCTCCATAGTGAC
goosecoid	gsc gscr	5’- CAAGAGACGACACCGAACCAT 5’-CTCTGACGACGACCTTTTCTG
p27	p27 p27r	5’- GTGTGGATGAAGTGACCCGAA 5’-CTTTATTGTTGAGTGCCAGAAGT
notch1	notch1 notch1r	5’-CAGATTGGAGGATTTCACTGC 5’-CCGTCACGACACACACCATAA
hemoglobin embryonic ae1	hbae1 hbae1r	5’- CGCTGGAAAGGCTGACGACAT 5’- GCCAGAACCACGAGGATGTTG
insulin	ins insr	5’-gctctgttggtcctgttggt 5’- gggcagatttaggaggaagg
cdc25	**cdc25** **cdc25r**	**5’- acctccattaccccgaactc** **5’- ctgccatggctcatgttatg**
catalase	**catz** **catzr**	**5’- aactatttcgcggaggttga** **5’- gcacatgggtccatctctct**
cyclin D1	**d1-1** **d1-1r**	**5’-ggagcaccagttgttttgct** **5’-ggtgggctccacagataaaa**
pinx1	**pinx** **pinxr**	**5’-acaacacggagaaccctacg** **5’-catggtcagagagctggtca**
sox3a	**sox3** **sox3r**	**5’-ggaagacaagagccgagact** **5’-ccttggagctgaaggtcttg**
triosephosphate isomerase, mouse	m-tri m-trir	5’-CGCAGATAATGTGAAAGACTG 5’-GGCATTGATGATGTCCACAAA
ankirin1, mouse	m-ank m-ankr	3’-GAGAGCAGGTGACGGAGGAA 5’-GACAGAGTGTGTGGAGTTCAG
actin, mouse	m-ac m-acr	5’-GGGTATGGAATCCTGTGGCA 5’-CATCTGCTGGAAGGTGGACA